'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 223, 'normalAltCount': 0, 'normalRefCount': 210, 'startPosition': 169369890, 'endPosition': 169369890, 'referenceAllele': 'A', 'proteinChange': 'V346G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DDX60L V346 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001012967.1', 'proteinPosStart': 346, 'proteinPosEnd': 346}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 2180, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 127, 'normalAltCount': 0, 'normalRefCount': 222, 'startPosition': 185686036, 'endPosition': 185686036, 'referenceAllele': 'C', 'proteinChange': 'C468Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ACSL1 C468 missense', 'chr': '4', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001286708.1', 'proteinPosStart': 468, 'proteinPosEnd': 468}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 50805, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 58, 'tumorRefCount': 87, 'normalAltCount': 1, 'normalRefCount': 138, 'startPosition': 1879672, 'endPosition': 1879672, 'referenceAllele': 'C', 'proteinChange': 'E228*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IRX4 truncating', 'chr': '5', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001278634.1', 'proteinPosStart': 228, 'proteinPosEnd': 228}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 134145, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 21, 'normalAltCount': 0, 'normalRefCount': 46, 'startPosition': 10239180, 'endPosition': 10239180, 'referenceAllele': 'A', 'proteinChange': 'I102N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATPSCKMT I102 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_199133.3', 'proteinPosStart': 102, 'proteinPosEnd': 102}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4214, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 113, 'normalAltCount': 0, 'normalRefCount': 222, 'startPosition': 56155597, 'endPosition': 56155597, 'referenceAllele': 'C', 'proteinChange': 'A230V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MAP3K1 A230 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005921.1', 'proteinPosStart': 230, 'proteinPosEnd': 230}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 5924, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 28, 'normalAltCount': 0, 'normalRefCount': 55, 'startPosition': 80409739, 'endPosition': 80409739, 'referenceAllele': 'G', 'proteinChange': 'A824S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RASGRF2 A824 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006909.2', 'proteinPosStart': 824, 'proteinPosEnd': 824}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 56099, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 110, 'normalAltCount': 0, 'normalRefCount': 122, 'startPosition': 140797965, 'endPosition': 140797965, 'referenceAllele': 'T', 'proteinChange': 'L180S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PCDHGB7 L180 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_018927.3', 'proteinPosStart': 180, 'proteinPosEnd': 180}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 2324, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 227, 'normalAltCount': 1, 'normalRefCount': 186, 'startPosition': 180046752, 'endPosition': 180046752, 'referenceAllele': 'C', 'proteinChange': 'G854S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FLT4 G854 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_182925.4', 'proteinPosStart': 854, 'proteinPosEnd': 854}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 134083, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 24, 'normalAltCount': 1, 'normalRefCount': 43, 'startPosition': 180166250, 'endPosition': 180166250, 'referenceAllele': 'C', 'proteinChange': 'G270V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR2Y1 G270 missense', 'chr': '5', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001001657.1', 'proteinPosStart': 270, 'proteinPosEnd': 270}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 81567, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 86, 'startPosition': 7904880, 'endPosition': 7904880, 'referenceAllele': 'C', 'proteinChange': 'V114I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TXNDC5 V114 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_030810.3', 'proteinPosStart': 114, 'proteinPosEnd': 114}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 56658, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 142, 'normalAltCount': 0, 'normalRefCount': 139, 'startPosition': 30297383, 'endPosition': 30297383, 'referenceAllele': 'G', 'proteinChange': 'V97I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIM39 V97 missense', 'chr': '6', 'variantAllele': 'A', 'refseqMrnaId': 'NM_021253.3', 'proteinPosStart': 97, 'proteinPosEnd': 97}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 6499, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 64, 'normalAltCount': 0, 'normalRefCount': 81, 'startPosition': 31927812, 'endPosition': 31927812, 'referenceAllele': 'C', 'proteinChange': 'A51V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SKIC2 A51 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006929.4', 'proteinPosStart': 51,

'proteinPosEnd': 51}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 6499, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 81, 'startPosition': 31927815, 'endPosition': 31927815, 'referenceAllele': 'C', 'proteinChange': 'P52Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SKIC2 P52 missense', 'chr': '6', 'variantAllele': 'A', 'refseqMrnaId': 'NM_006929.4', 'proteinPosStart': 52, 'proteinPosEnd': 52}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4800, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 33, 'tumorRefCount': 200, 'normalAltCount': 0, 'normalRefCount': 178, 'startPosition': 41057410, 'endPosition': 41057410, 'referenceAllele': 'C', 'proteinChange': 'I134M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NFYA I134 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002505.4', 'proteinPosStart': 134, 'proteinPosEnd': 134}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 10695, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 76, 'normalAltCount': 0, 'normalRefCount': 34, 'startPosition': 42897358, 'endPosition': 42897360, 'referenceAllele': 'TGC', 'proteinChange': 'L25del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'CNPY3 25-25 deletion', 'chr': '6', 'variantAllele': '-', 'refseqMrnaId': 'NM_006586.3', 'proteinPosStart': 17, 'proteinPosEnd': 25}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 23113, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 32, 'normalAltCount': 1, 'normalRefCount': 51, 'startPosition': 43181477, 'endPosition': 43181477, 'referenceAllele': 'C', 'proteinChange': 'P1839A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CUL9 P1839 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015089.2', 'proteinPosStart': 1839, 'proteinPosEnd': 1839}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 57515, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 70, 'normalAltCount': 0, 'normalRefCount': 81, 'startPosition': 122772896, 'endPosition': 122772925, 'referenceAllele': 'ATTCCTACAAAAAAAAAAAAAAAAAAAATAT', 'proteinChange': 'X254_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SERINC1 truncating', 'chr': '6', 'variantAllele': '-', 'refseqMrnaId': 'NM_020755.2', 'proteinPosStart': 254, 'proteinPosEnd': 254}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 3908, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 60, 'normalAltCount': 0, 'normalRefCount': 59,

'startPosition': 129465098, 'endPosition': 129465098, 'referenceAllele': 'A', 'proteinChange': 'E231A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LAMA2 E231 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001079823.1', 'proteinPosStart': 231, 'proteinPosEnd': 231}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 9439, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 86, 'tumorRefCount': 102, 'normalAltCount': 0, 'normalRefCount': 209, 'startPosition': 131914268, 'endPosition': 131914268, 'referenceAllele': 'C', 'proteinChange': 'W1092*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MED23 truncating', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_004830.3', 'proteinPosStart': 1092, 'proteinPosEnd': 1092}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 55698, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 42, 'normalAltCount': 0, 'normalRefCount': 8, 'startPosition': 4876135, 'endPosition': 4876135, 'referenceAllele': 'G', 'proteinChange': 'R213C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RADIL R213 missense', 'chr': '7', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018059.4', 'proteinPosStart': 213, 'proteinPosEnd': 213}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 117, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 212, 'normalAltCount': 0, 'normalRefCount': 152, 'startPosition': 31123819, 'endPosition': 31123819, 'referenceAllele': 'T', 'proteinChange': 'F131Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADCYAP1R1 F131 missense', 'chr': '7', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 131, 'proteinPosEnd': 131}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 79974, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 285, 'normalAltCount': 0, 'normalRefCount': 270, 'startPosition': 120768496, 'endPosition': 120768496, 'referenceAllele': 'A', 'proteinChange': 'M455L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CPED1 M455 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024913.4', 'proteinPosStart': 455, 'proteinPosEnd': 455}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 9172, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 126, 'tumorRefCount': 139, 'normalAltCount': 1, 'normalRefCount': 217, 'startPosition': 2040266, 'endPosition': 2040266, 'referenceAllele': 'C', 'proteinChange': 'L641M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYOM2 L641 missense', 'chr': '8', 'variantAllele': 'A', 'refseqMrnaId': 'NM_003970.2', 'proteinPosStart': 641, 'proteinPosEnd': 641}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 286077, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12,

'tumorRefCount': 22, 'normalAltCount': 0, 'normalRefCount': 6, 'startPosition': 144808866, 'endPosition': 144808866, 'referenceAllele': 'C', 'proteinChange': 'R922H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM83H R922 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_198488.3', 'proteinPosStart': 922, 'proteinPosEnd': 922}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 79956, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 667, 'normalAltCount': 0, 'normalRefCount': 142, 'startPosition': 5801292, 'endPosition': 5801292, 'referenceAllele': 'T', 'proteinChange': 'T651Pfs*3', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ERMP1 truncating', 'chr': '9', 'variantAllele': '-', 'refseqMrnaId': 'NM_024896.2', 'proteinPosStart': 651, 'proteinPosEnd': 651}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 115426, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 74, 'normalAltCount': 0, 'normalRefCount': 67, 'startPosition': 6460639, 'endPosition': 6460639, 'referenceAllele': 'G', 'proteinChange': 'L237F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UHRF2 L237 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_152896.2', 'proteinPosStart': 237, 'proteinPosEnd': 237}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 115426, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 98, 'normalAltCount': 0, 'normalRefCount': 87, 'startPosition': 6460721, 'endPosition': 6460721, 'referenceAllele': 'G', 'proteinChange': 'D265H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UHRF2 D265 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_152896.2', 'proteinPosStart': 265, 'proteinPosEnd': 265}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 138474, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 1615, 'normalAltCount': 1, 'normalRefCount': 262, 'startPosition': 32633584, 'endPosition': 32633584, 'referenceAllele': 'T', 'proteinChange': 'K665Rfs*4', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'TAF1L truncating', 'chr': '9', 'variantAllele': '-', 'refseqMrnaId': 'NM_153809.2', 'proteinPosStart': 665, 'proteinPosEnd': 665}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 646962, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 421, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 35906348, 'endPosition': 35906350, 'referenceAllele': 'CTG', 'proteinChange': 'L28del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'HRCT1 28-28 deletion', 'chr': '9', 'variantAllele': '-', 'refseqMrnaId': 'NM_001039792.1', 'proteinPosStart': 22, 'proteinPosEnd': 28}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 389730, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',

'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 75, 'normalAltCount': 0, 'normalRefCount': 106, 'startPosition': 43627272, 'endPosition': 43627272, 'referenceAllele': 'A', 'proteinChange': 'L472P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SPATA31A6 L472 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001145196.1', 'proteinPosStart': 472, 'proteinPosEnd': 472}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 80036, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 117, 'normalAltCount': 0, 'normalRefCount': 83, 'startPosition': 73457979, 'endPosition': 73457979, 'referenceAllele': 'G', 'proteinChange': 'C247W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRPM3 C247 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 247, 'proteinPosEnd': 247}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 10912, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 46, 'normalAltCount': 0, 'normalRefCount': 54, 'startPosition': 92220393, 'endPosition': 92220393, 'referenceAllele': 'C', 'proteinChange': 'Q34*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GADD45G truncating', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006705.3', 'proteinPosStart': 34, 'proteinPosEnd': 34}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 570, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 79, 'tumorRefCount': 115, 'normalAltCount': 1, 'normalRefCount': 172, 'startPosition': 104124861, 'endPosition': 104124861, 'referenceAllele': 'G', 'proteinChange': 'S369Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BAAT S369 missense', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001127610.1', 'proteinPosStart': 369, 'proteinPosEnd': 369}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 138803, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 151, 'normalAltCount': 1, 'normalRefCount': 167, 'startPosition': 107298937, 'endPosition': 107298937, 'referenceAllele': 'A', 'proteinChange': 'I53T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR13C3 I53 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001001961.1', 'proteinPosStart': 53, 'proteinPosEnd': 53}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 25861, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 47, 'tumorRefCount': 140, 'normalAltCount': 0, 'normalRefCount': 166, 'startPosition': 117185706, 'endPosition': 117185706, 'referenceAllele': 'G', 'proteinChange': 'A505V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'WHRN A505 missense', 'chr': '9', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001173425.1', 'proteinPosStart': 505, 'proteinPosEnd': 505}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 22954, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 76, 'normalAltCount': 2, 'normalRefCount': 71, 'startPosition': 119460913, 'endPosition': 119460913, 'referenceAllele': 'C', 'proteinChange': 'P298A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIM32 P298 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_012210.3', 'proteinPosStart': 298, 'proteinPosEnd': 298}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4115, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 41, 'normalAltCount': 0, 'normalRefCount': 63, 'startPosition': 30261199, 'endPosition': 30261199, 'referenceAllele': 'G', 'proteinChange': 'G316E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MAGEB4 G316 missense', 'chr': '23', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002367.3', 'proteinPosStart': 316, 'proteinPosEnd': 316}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 158724, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 94, 'normalAltCount': 3, 'normalRefCount': 98, 'startPosition': 34148844, 'endPosition': 34148844, 'referenceAllele': 'G', 'proteinChange': 'R518G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM47A R518 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_203408.3', 'proteinPosStart': 518, 'proteinPosEnd': 518}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 5303, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 86, 'tumorRefCount': 356, 'normalAltCount': 0, 'normalRefCount': 350, 'startPosition': 71417263, 'endPosition': 71417263, 'referenceAllele': 'C', 'proteinChange': 'Q120E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PIN4 Q120 missense', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_006223.3', 'proteinPosStart': 120, 'proteinPosEnd': 120}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 57692, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 317, 'normalAltCount': 0, 'normalRefCount': 247, 'startPosition': 75648451, 'endPosition': 75648451, 'referenceAllele': 'C', 'proteinChange': 'S43*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MAGEE1 truncating', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_020932.2', 'proteinPosStart': 43, 'proteinPosEnd': 43}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 139067, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 72, 'normalAltCount': 2, 'normalRefCount': 109, 'startPosition': 142605206, 'endPosition': 142605206, 'referenceAllele': 'G', 'proteinChange': 'T5N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SPANXN3 T5 missense', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId':

'NM_001009609.2', 'proteinPosStart': 5, 'proteinPosEnd': 5}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 8021, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 116, 'normalAltCount': 0, 'normalRefCount': 147, 'startPosition': 134073007, 'endPosition': 134073008, 'referenceAllele': '-', 'proteinChange': 'V1379Gfs*60', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'NUP214 truncating', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_005085.3', 'proteinPosStart': 1376, 'proteinPosEnd': 1379}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 400258, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 14, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 105055119, 'endPosition': 105055127, 'referenceAllele': 'GACGGGCAG', 'proteinChange': '*6*', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '14', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 161, 'proteinPosEnd': 6}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 27146, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 6, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 17643848, 'endPosition': 17643848, 'referenceAllele': 'G', 'proteinChange': 'R784W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM184B R784 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_015688.1', 'proteinPosStart': 784, 'proteinPosEnd': 784}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 192134, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 25, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 76751543, 'endPosition': 76751604, 'referenceAllele': 'TGGAGCGCGCCGGCCTGGCGCCCAGCGGCCACGAGGGCATCCTGGCCCTTCGGCGTGCAGCT', 'proteinChange': 'G317Afs*42', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'B3GNT6 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_138706.4', 'proteinPosStart': 316, 'proteinPosEnd': 317}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 157285, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 83, 'normalAltCount': 1, 'normalRefCount': 43, 'startPosition': 8239069, 'endPosition': 8239069, 'referenceAllele': 'C', 'proteinChange': 'R63S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRAG1 R63 missense', 'chr': '8', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 63, 'proteinPosEnd': 63}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 388610, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 27320356, 'endPosition':

27320356, 'referenceAllele': 'T', 'proteinChange': 'W27R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRNP1 W27 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001013642.2', 'proteinPosStart': 27, 'proteinPosEnd': 27}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 23499, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 65, 'tumorRefCount': 101, 'normalAltCount': 2, 'normalRefCount': 170, 'startPosition': 39851188, 'endPosition': 39851188, 'referenceAllele': 'G', 'proteinChange': 'G2582V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MACF1 G2582 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 2582, 'proteinPosEnd': 2582}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 28982, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 99, 'normalAltCount': 0, 'normalRefCount': 113, 'startPosition': 213037122, 'endPosition': 213037122, 'referenceAllele': 'A', 'proteinChange': 'N265S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FLVCR1 N265 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014053.3', 'proteinPosStart': 265, 'proteinPosEnd': 265}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 727897, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 82, 'tumorRefCount': 831, 'normalAltCount': 2, 'normalRefCount': 726, 'startPosition': 1268449, 'endPosition': 1268449, 'referenceAllele': 'G', 'proteinChange': 'V3447M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUC5B V3447 missense', 'chr': '11', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002458.2', 'proteinPosStart': 3447, 'proteinPosEnd': 3447}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 6337, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 151, 'normalAltCount': 0, 'normalRefCount': 178, 'startPosition': 6457898, 'endPosition': 6457898, 'referenceAllele': 'C', 'proteinChange': 'V601I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SCNN1A V601 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001159576.1', 'proteinPosStart': 601, 'proteinPosEnd': 601}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 1053, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 81, 'normalAltCount': 0, 'normalRefCount': 63, 'startPosition': 23588089, 'endPosition': 23588089, 'referenceAllele': 'C', 'proteinChange': 'G71V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CEBPE G71 missense', 'chr': '14', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001805.3', 'proteinPosStart': 71, 'proteinPosEnd': 71}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 8846, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 71, 'normalAltCount': 0, 'normalRefCount': 72,

'startPosition': 78161095, 'endPosition': 78161095, 'referenceAllele': 'G', 'proteinChange': 'S147R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ALKBH1 S147 missense', 'chr': '14', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006020.2', 'proteinPosStart': 147, 'proteinPosEnd': 147}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 388135, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 306, 'normalAltCount': 2, 'normalRefCount': 237, 'startPosition': 74032929, 'endPosition': 74032929, 'referenceAllele': 'C', 'proteinChange': 'D71Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'INSYN1 D71 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 71, 'proteinPosEnd': 71}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 91433, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 24, 'normalAltCount': 0, 'normalRefCount': 4, 'startPosition': 91500017, 'endPosition': 91500017, 'referenceAllele': 'G', 'proteinChange': 'G18V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RCCD1 G18 missense', 'chr': '15', 'variantAllele': 'T', 'refseqMrnaId': 'NM_033544.2', 'proteinPosStart': 18, 'proteinPosEnd': 18}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 1201, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 68, 'normalAltCount': 0, 'normalRefCount': 86, 'startPosition': 28502861, 'endPosition': 28502861, 'referenceAllele': 'G', 'proteinChange': 'P23T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CLN3 P23 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 23, 'proteinPosEnd': 23}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 40, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 99, 'normalAltCount': 0, 'normalRefCount': 85, 'startPosition': 31618452, 'endPosition': 31618452, 'referenceAllele': 'G', 'proteinChange': 'L228V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASIC2 L228 missense', 'chr': '17', 'variantAllele': 'C', 'refseqMrnaId': 'NM_183377.1', 'proteinPosStart': 228, 'proteinPosEnd': 228}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 157, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 8550869, 'endPosition': 8550869, 'referenceAllele': 'C', 'proteinChange': 'P520Lfs*8', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'HNRNPM truncating', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 519, 'proteinPosEnd': 520}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 145, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 8550870, 'endPosition': 8550870, 'referenceAllele': 'C', 'proteinChange': 'P520S',

'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPM P520 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 520, 'proteinPosEnd': 520}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 38, 'tumorRefCount': 129, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 8550874, 'endPosition': 8550874, 'referenceAllele': 'C', 'proteinChange': 'A521G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPM A521 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 521, 'proteinPosEnd': 521}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 146, 'normalAltCount': 0, 'normalRefCount': 40, 'startPosition': 8550876, 'endPosition': 8550876, 'referenceAllele': 'A', 'proteinChange': 'I522V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPM I522 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 522, 'proteinPosEnd': 522}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 129, 'normalAltCount': 0, 'normalRefCount': 40, 'startPosition': 8550878, 'endPosition': 8550878, 'referenceAllele': 'C', 'proteinChange': 'I522M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPM I522 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 522, 'proteinPosEnd': 522}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 83444, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 5, 'startPosition': 74684659, 'endPosition': 74684659, 'referenceAllele': 'G', 'proteinChange': 'A247T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'INO80B A247 missense', 'chr': '2', 'variantAllele': 'A', 'refseqMrnaId': 'NM_031288.3', 'proteinPosStart': 247, 'proteinPosEnd': 247}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 8685, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 124, 'normalAltCount': 2, 'normalRefCount': 112, 'startPosition': 119739941, 'endPosition': 119739941, 'referenceAllele': 'G', 'proteinChange': 'G340W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MARCO G340 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006770.3', 'proteinPosStart': 340, 'proteinPosEnd': 340}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 7273, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 34, 'tumorRefCount': 59,

'normalAltCount': 0, 'normalRefCount': 116, 'startPosition': 179445121, 'endPosition': 179445121, 'referenceAllele': 'C', 'proteinChange': 'A22329S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TTN A22329 missense', 'chr': '2', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001267550.1', 'proteinPosStart': 22329, 'proteinPosEnd': 22329}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4632, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 190, 'normalAltCount': 0, 'normalRefCount': 175, 'startPosition': 211179635, 'endPosition': 211179635, 'referenceAllele': 'C', 'proteinChange': 'K44N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYL1 K44 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NM_079420.2', 'proteinPosStart': 44, 'proteinPosEnd': 44}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 27125, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 76, 'normalAltCount': 0, 'normalRefCount': 120, 'startPosition': 132232343, 'endPosition': 132232343, 'referenceAllele': 'G', 'proteinChange': 'P660H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AFF4 P660 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_014423.3', 'proteinPosStart': 660, 'proteinPosEnd': 660}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 3201, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 27170145, 'endPosition': 27170145, 'referenceAllele': 'T', 'proteinChange': 'T70P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HOXA4 T70 missense', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002141.4', 'proteinPosStart': 70, 'proteinPosEnd': 70}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 8295, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 112, 'normalAltCount': 2, 'normalRefCount': 119, 'startPosition': 98529263, 'endPosition': 98529263, 'referenceAllele': 'C', 'proteinChange': 'T1276M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRRAP T1276 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001244580.1', 'proteinPosStart': 1276, 'proteinPosEnd': 1276}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 9747, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 391, 'normalAltCount': 1, 'normalRefCount': 237, 'startPosition': 143556212, 'endPosition': 143556212, 'referenceAllele': 'G', 'proteinChange': 'S737*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TCAF1 truncating', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_014719.2', 'proteinPosStart': 737, 'proteinPosEnd': 737}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 1757, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 45, 'normalAltCount': 2, 'normalRefCount': 34,

'startPosition': 136577795, 'endPosition': 136577795, 'referenceAllele': 'G', 'proteinChange': 'A425D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SARDH A425 missense', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_007101.3', 'proteinPosStart': 425, 'proteinPosEnd': 425}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 4670, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 157, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 8550873, 'endPosition': 8550874, 'referenceAllele': '-', 'proteinChange': 'A521Dfs*85', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'HNRNPM truncating', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_005968.4', 'proteinPosStart': 521, 'proteinPosEnd': 521}, {'uniqueSampleKey': 'VENHQS1PUi1BNUwyLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUwyOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5L2-01', 'patientId': 'TCGA-OR-A5L2', 'entrezGeneId': 25807, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 279, 'normalAltCount': 0, 'normalRefCount': 177, 'startPosition': 29661518, 'endPosition': 29661519, 'referenceAllele': '-', 'proteinChange': 'A33Gfs*105', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'RHBDD3 truncating', 'chr': '22', 'variantAllele': 'C', 'refseqMrnaId': 'NM_012265.1', 'proteinPosStart': 33, 'proteinPosEnd': 33}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 4985, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 29138975, 'endPosition': 29138975, 'referenceAllele': 'G', 'proteinChange': 'C27F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OPRD1 C27 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000911.3', 'proteinPosStart': 27, 'proteinPosEnd': 27}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 51538, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 70, 'normalAltCount': 0, 'normalRefCount': 105, 'startPosition': 31819587, 'endPosition': 31819587, 'referenceAllele': 'G', 'proteinChange': 'G140C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZCCHC17 G140 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001282570.1', 'proteinPosStart': 140, 'proteinPosEnd': 140}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 22852, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 46, 'tumorRefCount': 17, 'normalAltCount': 0, 'normalRefCount': 109, 'startPosition': 27322227, 'endPosition': 27322227, 'referenceAllele': 'G', 'proteinChange': 'T1245M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD26 T1245 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014915.2', 'proteinPosStart': 1245, 'proteinPosEnd': 1245}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 10004, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4,

'tumorRefCount': 80, 'normalAltCount': 0, 'normalRefCount': 103, 'startPosition': 64813685, 'endPosition': 64813685, 'referenceAllele': 'G', 'proteinChange': 'L611V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NAALADL1 L611 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NM_005468.2', 'proteinPosStart': 611, 'proteinPosEnd': 611}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 55191, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 166, 'normalAltCount': 0, 'normalRefCount': 158, 'startPosition': 71169547, 'endPosition': 71169547, 'referenceAllele': 'G', 'proteinChange': 'V74L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NADSYN1 V74 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NM_018161.4', 'proteinPosStart': 74, 'proteinPosEnd': 74}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 65125, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 64, 'tumorRefCount': 272, 'normalAltCount': 1, 'normalRefCount': 230, 'startPosition': 966392, 'endPosition': 966392, 'referenceAllele': 'C', 'proteinChange': 'C459*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'WNK1 truncating', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018979.3', 'proteinPosStart': 459, 'proteinPosEnd': 459}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 55729, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 41, 'normalAltCount': 0, 'normalRefCount': 57, 'startPosition': 14578126, 'endPosition': 14578126, 'referenceAllele': 'A', 'proteinChange': 'N426S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATF7IP N426 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_018179.3', 'proteinPosStart': 426, 'proteinPosEnd': 426}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 10106, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 73, 'tumorRefCount': 111, 'normalAltCount': 0, 'normalRefCount': 126, 'startPosition': 58217464, 'endPosition': 58217464, 'referenceAllele': 'A', 'proteinChange': 'L246P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CTDSP2 L246 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_005730.3', 'proteinPosStart': 246, 'proteinPosEnd': 246}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 283431, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 175, 'normalAltCount': 0, 'normalRefCount': 126, 'startPosition': 101005850, 'endPosition': 101005850, 'referenceAllele': 'G', 'proteinChange': 'A126P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GAS2L3 A126 missense', 'chr': '12', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 126, 'proteinPosEnd': 126}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 84935, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 31480827, 'endPosition': 31480827, 'referenceAllele': 'A', 'proteinChange': 'R59G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MEDAG R59 missense', 'chr': '13', 'variantAllele': 'G', 'refseqMrnaId': 'NM_032849.3', 'proteinPosStart': 59, 'proteinPosEnd': 59}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 57475, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 78, 'normalAltCount': 0, 'normalRefCount': 101, 'startPosition': 68045912, 'endPosition': 68045912, 'referenceAllele': 'G', 'proteinChange': 'G971R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLEKHH1 G971 missense', 'chr': '14', 'variantAllele': 'A', 'refseqMrnaId': 'NM_020715.2', 'proteinPosStart': 971, 'proteinPosEnd': 971}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 646174, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 47, 'tumorRefCount': 61, 'normalAltCount': 1, 'normalRefCount': 31, 'startPosition': 3544745, 'endPosition': 3544745, 'referenceAllele': 'C', 'proteinChange': 'R60H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'C16ORF90 R60 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001080524.1', 'proteinPosStart': 60, 'proteinPosEnd': 60}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2975, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 193, 'normalAltCount': 0, 'normalRefCount': 156, 'startPosition': 27523174, 'endPosition': 27523190, 'referenceAllele': 'CGTTTAAATTCCTTCAG', 'proteinChange': 'L336Efs*2', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'GTF3C1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_001520.3', 'proteinPosStart': 336, 'proteinPosEnd': 336}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 88599701, 'endPosition': 88599701, 'referenceAllele': 'T', 'proteinChange': 'L446Wfs*352', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 445, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 4763, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 62, 'tumorRefCount': 36, 'normalAltCount': 0, 'normalRefCount': 82, 'startPosition': 29661949, 'endPosition': 29661949, 'referenceAllele': 'A', 'proteinChange': 'R1970Efs*9', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'NF1 truncating', 'chr': '17', 'variantAllele': '-', 'refseqMrnaId': 'NM_001042492.2', 'proteinPosStart': 1969,

'proteinPosEnd': 1970}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 92591, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 42254417, 'endPosition': 42254417, 'referenceAllele': 'A', 'proteinChange': 'N294S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASB16 N294 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_080863.4', 'proteinPosStart': 294, 'proteinPosEnd': 294}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 84634, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 920642, 'endPosition': 920642, 'referenceAllele': 'T', 'proteinChange': 'L364H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KISS1R L364 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_032551.4', 'proteinPosStart': 364, 'proteinPosEnd': 364}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 170961, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 4217919, 'endPosition': 4217919, 'referenceAllele': 'G', 'proteinChange': 'R921Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD24 R921 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_133475.1', 'proteinPosStart': 921, 'proteinPosEnd': 921}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 256949, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 8399635, 'endPosition': 8399635, 'referenceAllele': 'C', 'proteinChange': 'R359H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KANK3 R359 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_198471.2', 'proteinPosStart': 359, 'proteinPosEnd': 359}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 255783, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 47778412, 'endPosition': 47778412, 'referenceAllele': 'G', 'proteinChange': 'R79L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'INAFM1 R79 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_178511.5', 'proteinPosStart': 79, 'proteinPosEnd': 79}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 7288, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 174, 'normalAltCount': 0, 'normalRefCount': 167, 'startPosition': 49400634, 'endPosition': 49400634, 'referenceAllele': 'C', 'proteinChange': 'A18T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TULP2 A18 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_003323.2', 'proteinPosStart': 18, 'proteinPosEnd':

18}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 79784, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 50713713, 'endPosition': 50713713, 'referenceAllele': 'C', 'proteinChange': 'P31T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYH14 P31 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001145809.1', 'proteinPosStart': 31, 'proteinPosEnd': 31}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 554235, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 51015404, 'endPosition': 51015404, 'referenceAllele': 'T', 'proteinChange': 'Q266R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASPDH Q266 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001114598.1', 'proteinPosStart': 266, 'proteinPosEnd': 266}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 5582, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 54393237, 'endPosition': 54393237, 'referenceAllele': 'C', 'proteinChange': 'R166Gfs*10', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'PRKCG truncating', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_002739.3', 'proteinPosStart': 165, 'proteinPosEnd': 166}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 126208, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 1, 'normalAltCount': 4, 'normalRefCount': 0, 'startPosition': 56599438, 'endPosition': 56599440, 'referenceAllele': 'TCG', 'proteinChange': 'D367del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZNF787 367-367 deletion', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_001002836.2', 'proteinPosStart': 367, 'proteinPosEnd': 367}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 7498, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 38, 'normalAltCount': 0, 'normalRefCount': 74, 'startPosition': 31572920, 'endPosition': 31572920, 'referenceAllele': 'G', 'proteinChange': 'T934N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'XDH T934 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000379.3', 'proteinPosStart': 934, 'proteinPosEnd': 934}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 284996, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 6, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 101925026, 'endPosition': 101925026, 'referenceAllele': 'T', 'proteinChange': 'S9G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RNF149 S9 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_173647.3', 'proteinPosStart': 9,

'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2863, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 204, 'normalAltCount': 2, 'normalRefCount': 201, 'startPosition': 133174764, 'endPosition': 133174764, 'referenceAllele': 'C', 'proteinChange': 'A50V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPR39 A50 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001508.2', 'proteinPosStart': 50, 'proteinPosEnd': 50}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 51586, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 149, 'normalAltCount': 0, 'normalRefCount': 180, 'startPosition': 20918916, 'endPosition': 20918918, 'referenceAllele': 'CAG', 'proteinChange': 'Q218del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'MED15 218-218 deletion', 'chr': '22', 'variantAllele': '-', 'refseqMrnaId': 'NM_001003891.1', 'proteinPosStart': 211, 'proteinPosEnd': 218}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 164656, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 174, 'normalAltCount': 2, 'normalRefCount': 362, 'startPosition': 37485724, 'endPosition': 37485724, 'referenceAllele': 'T', 'proteinChange': 'K253E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMPRSS6 K253 missense', 'chr': '22', 'variantAllele': 'C', 'refseqMrnaId': 'NM_153609.2', 'proteinPosStart': 253, 'proteinPosEnd': 253}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 523, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 261, 'normalAltCount': 0, 'normalRefCount': 285, 'startPosition': 113528258, 'endPosition': 113528258, 'referenceAllele': 'G', 'proteinChange': 'R613H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATP6V1A R613 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001690.3', 'proteinPosStart': 613, 'proteinPosEnd': 613}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 285464, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 236, 'normalAltCount': 1, 'normalRefCount': 29, 'startPosition': 1388819, 'endPosition': 1388819, 'referenceAllele': 'T', 'proteinChange': 'C174R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CRIPAK C174 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_175918.3', 'proteinPosStart': 174, 'proteinPosEnd': 174}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 389333, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 13, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 138730037, 'endPosition': 138730037, 'referenceAllele': 'T', 'proteinChange': 'Q245R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PROB1 Q245 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001161546.1', 'proteinPosStart': 245, 'proteinPosEnd':

245}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 8367, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 44, 'normalAltCount': 0, 'normalRefCount': 75, 'startPosition': 26204877, 'endPosition': 26204877, 'referenceAllele': 'C', 'proteinChange': 'S2F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'H4C5 S2 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_003545.3', 'proteinPosStart': 2, 'proteinPosEnd': 2}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 22999, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 34, 'tumorRefCount': 80, 'normalAltCount': 0, 'normalRefCount': 119, 'startPosition': 72945399, 'endPosition': 72945399, 'referenceAllele': 'C', 'proteinChange': 'P609A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RIMS1 P609 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014989.5', 'proteinPosStart': 609, 'proteinPosEnd': 609}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 22999, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 34, 'tumorRefCount': 80, 'normalAltCount': 0, 'normalRefCount': 113, 'startPosition': 72945409, 'endPosition': 72945409, 'referenceAllele': 'C', 'proteinChange': 'S612*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RIMS1 truncating', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014989.5', 'proteinPosStart': 612, 'proteinPosEnd': 612}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 223075, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 235, 'normalAltCount': 0, 'normalRefCount': 162, 'startPosition': 31682453, 'endPosition': 31682453, 'referenceAllele': 'C', 'proteinChange': 'A516V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ITPRID1 A516 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001257968.1', 'proteinPosStart': 516, 'proteinPosEnd': 516}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 5425, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 74, 'normalAltCount': 0, 'normalRefCount': 91, 'startPosition': 44156093, 'endPosition': 44156093, 'referenceAllele': 'T', 'proteinChange': 'K266R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'POLD2 K266 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001256879.1', 'proteinPosStart': 266, 'proteinPosEnd': 266}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 285971, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 3, 'startPosition': 150094851, 'endPosition': 150094851, 'referenceAllele': 'A', 'proteinChange': 'T428A',

'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF775 T428 missense', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_173680.3', 'proteinPosStart': 428, 'proteinPosEnd': 428}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 80139, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 49, 'normalAltCount': 0, 'normalRefCount': 33, 'startPosition': 37554967, 'endPosition': 37554967, 'referenceAllele': 'C', 'proteinChange': 'S183F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF703 S183 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_025069.1', 'proteinPosStart': 183, 'proteinPosEnd': 183}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 114569, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 38, 'tumorRefCount': 3, 'normalAltCount': 4, 'normalRefCount': 0, 'startPosition': 120220776, 'endPosition': 120220776, 'referenceAllele': 'G', 'proteinChange': 'V23Sfs*51', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'MAL2 truncating', 'chr': '8', 'variantAllele': '-', 'refseqMrnaId': 'NM_052886.2', 'proteinPosStart': 22, 'proteinPosEnd': 23}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 340385, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 146033347, 'endPosition': 146033347, 'referenceAllele': 'T', 'proteinChange': 'V349A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF517 V349 missense', 'chr': '8', 'variantAllele': 'C', 'refseqMrnaId': 'NM_213605.2', 'proteinPosStart': 349, 'proteinPosEnd': 349}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 157983, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 214706, 'endPosition': 214706, 'referenceAllele': 'G', 'proteinChange': 'R231G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DOCK8-AS1 R231 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_152569.2', 'proteinPosStart': 231, 'proteinPosEnd': 231}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 89891, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 131418828, 'endPosition': 131418828, 'referenceAllele': 'A', 'proteinChange': 'W60G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DYNC2I2 W60 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_052844.3', 'proteinPosStart': 60, 'proteinPosEnd': 60}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 158586, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 36, 'normalAltCount': 0, 'normalRefCount': 5, 'startPosition': 57618845, 'endPosition': 57618845, 'referenceAllele': 'G', 'proteinChange': 'E122K', 'mutationType': 'Missense_Mutation',

'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZXDB E122 missense', 'chr': '23', 'variantAllele': 'A', 'refseqMrnaId': 'NM_007157.3', 'proteinPosStart': 122, 'proteinPosEnd': 122}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 158586, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 25, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 57618870, 'endPosition': 57618870, 'referenceAllele': 'G', 'proteinChange': 'G130D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZXDB G130 missense', 'chr': '23', 'variantAllele': 'A', 'refseqMrnaId': 'NM_007157.3', 'proteinPosStart': 130, 'proteinPosEnd': 130}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 5303, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 105, 'tumorRefCount': 154, 'normalAltCount': 0, 'normalRefCount': 240, 'startPosition': 71417357, 'endPosition': 71417357, 'referenceAllele': 'T', 'proteinChange': 'M151T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PIN4 M151 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_006223.3', 'proteinPosStart': 151, 'proteinPosEnd': 151}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 50814, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 103, 'tumorRefCount': 180, 'normalAltCount': 2, 'normalRefCount': 176, 'startPosition': 152031231, 'endPosition': 152031231, 'referenceAllele': 'T', 'proteinChange': 'I169T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NSDHL I169 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015922.2', 'proteinPosStart': 169, 'proteinPosEnd': 169}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 84108, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 15, 'normalAltCount': 2, 'normalRefCount': 4, 'startPosition': 105110740, 'endPosition': 105110741, 'referenceAllele': '-', 'proteinChange': 'P27_P28dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '10', 'variantAllele': 'GGAGGC', 'refseqMrnaId': 'NM_001011663.1', 'proteinPosStart': 28, 'proteinPosEnd': 28}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 23098, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 26699367, 'endPosition': 26699368, 'referenceAllele': '-', 'proteinChange': 'A73Gfs*49', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'SARM1 truncating', 'chr': '17', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015077.3', 'proteinPosStart': 72, 'proteinPosEnd': 73}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 4163, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 9, 'startPosition': 112824048, 'endPosition': 112824049, 'referenceAllele': '-', 'proteinChange': 'G21dup', 'mutationType':

'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '5', 'variantAllele': 'GCC', 'refseqMrnaId': 'NM_001085377.1', 'proteinPosStart': 21, 'proteinPosEnd': 21}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2519, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 43, 'tumorRefCount': 21, 'normalAltCount': 0, 'normalRefCount': 6, 'startPosition': 143832707, 'endPosition': 143832708, 'referenceAllele': '-', 'proteinChange': 'L20_L21dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '6', 'variantAllele': 'GCAGCA', 'refseqMrnaId': 'NM_032020.4', 'proteinPosStart': 22, 'proteinPosEnd': 21}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 5420, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 86, 'normalAltCount': 0, 'normalRefCount': 5, 'startPosition': 131241029, 'endPosition': 131241030, 'referenceAllele': '-', 'proteinChange': 'P30_S31dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '7', 'variantAllele': 'GGCGAC', 'refseqMrnaId': 'NA', 'proteinPosStart': 30, 'proteinPosEnd': 31}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 116983, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 158, 'normalAltCount': 2, 'normalRefCount': 225, 'startPosition': 1230833, 'endPosition': 1230833, 'referenceAllele': 'G', 'proteinChange': 'P603T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ACAP3 P603 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_030649.2', 'proteinPosStart': 603, 'proteinPosEnd': 603}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 79707, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6614391, 'endPosition': 6614391, 'referenceAllele': 'A', 'proteinChange': 'S58A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOL9 S58 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024654.4', 'proteinPosStart': 58, 'proteinPosEnd': 58}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 79707, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6614415, 'endPosition': 6614415, 'referenceAllele': 'A', 'proteinChange': 'W50R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOL9 W50 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_024654.4', 'proteinPosStart': 50, 'proteinPosEnd': 50}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 3953, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 66087142, 'endPosition': 66087142, 'referenceAllele': 'G', 'proteinChange': 'X866_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LEPR truncating', 'chr': '1',

'variantAllele': 'T', 'refseqMrnaId': 'NM_002303.5', 'proteinPosStart': 866, 'proteinPosEnd': 866}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2328, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 85, 'normalAltCount': 0, 'normalRefCount': 106, 'startPosition': 171083226, 'endPosition': 171083226, 'referenceAllele': 'G', 'proteinChange': 'V303L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FMO3 V303 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001002294.2', 'proteinPosStart': 303, 'proteinPosEnd': 303}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 112464, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6341397, 'endPosition': 6341397, 'referenceAllele': 'C', 'proteinChange': 'A104T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CAVIN3 A104 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_145040.2', 'proteinPosStart': 104, 'proteinPosEnd': 104}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 91433, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 36, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 91499986, 'endPosition': 91499986, 'referenceAllele': 'G', 'proteinChange': 'A8S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RCCD1 A8 missense', 'chr': '15', 'variantAllele': 'T', 'refseqMrnaId': 'NM_033544.2', 'proteinPosStart': 8, 'proteinPosEnd': 8}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 29108, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 131, 'normalAltCount': 0, 'normalRefCount': 38, 'startPosition': 31213958, 'endPosition': 31213958, 'referenceAllele': 'C', 'proteinChange': 'L62F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PYCARD L62 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 62, 'proteinPosEnd': 62}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 79191, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 54318528, 'endPosition': 54318528, 'referenceAllele': 'A', 'proteinChange': 'L422P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IRX3 L422 missense', 'chr': '16', 'variantAllele': 'G', 'refseqMrnaId': 'NM_024336.2', 'proteinPosStart': 422, 'proteinPosEnd': 422}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 88599696, 'endPosition': 88599697, 'referenceAllele': 'GA', 'proteinChange': 'E444Afs*227', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-',

'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 444}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 27, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 88599697, 'endPosition': 88599705, 'referenceAllele': 'AGCCTCTGG', 'proteinChange': 'E444_L446del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599703, 'endPosition': 88599705, 'referenceAllele': 'TGG', 'proteinChange': 'L446_A447delinsP', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 446, 'proteinPosEnd': 447}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 9611, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 76, 'normalAltCount': 0, 'normalRefCount': 86, 'startPosition': 16097787, 'endPosition': 16097787, 'referenceAllele': 'G', 'proteinChange': 'R33S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NCOR1 R33 missense', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006311.3', 'proteinPosStart': 33, 'proteinPosEnd': 33}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 124989, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 101, 'normalAltCount': 0, 'normalRefCount': 129, 'startPosition': 45452257, 'endPosition': 45452257, 'referenceAllele': 'A', 'proteinChange': 'K433*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'EFCAB13 truncating', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_152347.4', 'proteinPosStart': 433, 'proteinPosEnd': 433}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 9150, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 77440128, 'endPosition': 77440128, 'referenceAllele': 'T', 'proteinChange': 'S61A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CTDP1 S61 missense', 'chr': '18', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001202504.1', 'proteinPosStart': 61, 'proteinPosEnd': 61}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 643905, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 347, 'normalAltCount': 6, 'normalRefCount': 374, 'startPosition': 240982228, 'endPosition': 240982228, 'referenceAllele': 'C', 'proteinChange': 'G58S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRR21 G58 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001080835.1', 'proteinPosStart': 58, 'proteinPosEnd':

58}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 132720, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 113066831, 'endPosition':
113066831, 'referenceAllele': 'G', 'proteinChange': 'G32E', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM241A G32 missense', 'chr': '4',
'variantAllele': 'A', 'refseqMrnaId': 'NM_152400.2', 'proteinPosStart': 32, 'proteinPosEnd': 32},
{'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2559, 'studyId': 'acc_tcga',
'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6,
'tumorRefCount': 222, 'normalAltCount': 1, 'normalRefCount': 168, 'startPosition': 161128694,
'endPosition': 161128694, 'referenceAllele': 'C', 'proteinChange': 'P426R', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GABRA6 P426 missense',
'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 426, 'proteinPosEnd': 426},
{'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 3107, 'studyId': 'acc_tcga',
'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8,
'tumorRefCount': 245, 'normalAltCount': 2, 'normalRefCount': 164, 'startPosition': 31239449,
'endPosition': 31239449, 'referenceAllele': 'C', 'proteinChange': 'K90N', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HLA-C K90 missense',
'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002117.5', 'proteinPosStart': 90, 'proteinPosEnd': 90},
{'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 441168, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 116783390, 'endPosition':
116783390, 'referenceAllele': 'A', 'proteinChange': 'T100A', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CALHM6 T100 missense', 'chr': '6',
'variantAllele': 'G', 'refseqMrnaId': 'NM_001010919.2', 'proteinPosStart': 100, 'proteinPosEnd': 100},
{'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 353091, 'studyId': 'acc_tcga',
'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13,
'tumorRefCount': 557, 'normalAltCount': 4, 'normalRefCount': 595, 'startPosition': 150240829,
'endPosition': 150240829, 'referenceAllele': 'G', 'proteinChange': 'T70R', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RAET1G T70 missense',
'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001001788.2', 'proteinPosStart': 70, 'proteinPosEnd':
70}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 8427, 'studyId': 'acc_tcga',
'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7,
'tumorRefCount': 117, 'normalAltCount': 0, 'normalRefCount': 41, 'startPosition': 148892715,
'endPosition': 148892715, 'referenceAllele': 'C', 'proteinChange': 'Q12K', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF282 Q12 missense',
'chr': '7', 'variantAllele': 'A', 'refseqMrnaId': 'NM_003575.2', 'proteinPosStart': 12, 'proteinPosEnd': 12},
{'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 2356, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 130565267, 'endPosition': 130565267, 'referenceAllele': 'A', 'proteinChange': 'I22V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FPGS I22 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_004957.4', 'proteinPosStart': 22, 'proteinPosEnd': 22}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 57680, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 41, 'normalAltCount': 0, 'normalRefCount': 69, 'startPosition': 21863156, 'endPosition': 21863157, 'referenceAllele': '-', 'proteinChange': 'A1769Rfs*19', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'CHD8 truncating', 'chr': '14', 'variantAllele': 'CTCTATCTTCATTTGTTCT', 'refseqMrnaId': 'NM_001170629.1', 'proteinPosStart': 1768, 'proteinPosEnd': 1769}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 23080, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 274, 'normalAltCount': 0, 'normalRefCount': 79, 'startPosition': 32535342, 'endPosition': 32535343, 'referenceAllele': '-', 'proteinChange': 'D9Gfs*25', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'AVL9 truncating', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015060.1', 'proteinPosStart': 7, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 139804, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 219, 'normalAltCount': 0, 'normalRefCount': 49, 'startPosition': 114425192, 'endPosition': 114425193, 'referenceAllele': '-', 'proteinChange': 'P397_D398insNAHSGGRSP', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '23', 'variantAllele': 'CCCAACGCCCACAGCGGAGGCCGCTCG', 'refseqMrnaId': 'NM_001145346.1', 'proteinPosStart': 396, 'proteinPosEnd': 398}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxGLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxGOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LF-01', 'patientId': 'TCGA-OR-A5LF', 'entrezGeneId': 7405, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 75526481, 'endPosition': 75526482, 'referenceAllele': 'CC', 'proteinChange': 'P10Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'UVRAG P10 missense', 'chr': '11', 'variantAllele': 'AG', 'refseqMrnaId': 'NM_003369.3', 'proteinPosStart': 10, 'proteinPosEnd': 10}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4985, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 29138975, 'endPosition': 29138975, 'referenceAllele': 'G', 'proteinChange': 'C27F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OPRD1 C27 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000911.3', 'proteinPosStart': 27, 'proteinPosEnd': 27}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh',

'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599701, 'endPosition': 88599701, 'referenceAllele': 'T', 'proteinChange': 'L446Wfs*352', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 445, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 92591, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 10, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 42254417, 'endPosition': 42254417, 'referenceAllele': 'A', 'proteinChange': 'N294S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASB16 N294 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_080863.4', 'proteinPosStart': 294, 'proteinPosEnd': 294}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 554235, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 51015404, 'endPosition': 51015404, 'referenceAllele': 'T', 'proteinChange': 'Q266R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASPDH Q266 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001114598.1', 'proteinPosStart': 266, 'proteinPosEnd': 266}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 126208, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 0, 'normalAltCount': 2, 'normalRefCount': 0, 'startPosition': 56599438, 'endPosition': 56599440, 'referenceAllele': 'TCG', 'proteinChange': 'D367del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZNF787 367-367 deletion', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_001002836.2', 'proteinPosStart': 367, 'proteinPosEnd': 367}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 114569, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 0, 'normalAltCount': 2, 'normalRefCount': 0, 'startPosition': 120220776, 'endPosition': 120220776, 'referenceAllele': 'G', 'proteinChange': 'V23Sfs*51', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'MAL2 truncating', 'chr': '8', 'variantAllele': '-', 'refseqMrnaId': 'NM_052886.2', 'proteinPosStart': 22, 'proteinPosEnd': 23}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 340385, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 146033347, 'endPosition': 146033347, 'referenceAllele': 'T', 'proteinChange': 'V349A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF517 V349 missense', 'chr': '8', 'variantAllele': 'C', 'refseqMrnaId': 'NM_213605.2', 'proteinPosStart': 349, 'proteinPosEnd': 349}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 23098, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 26699367, 'endPosition': 26699368, 'referenceAllele': '-', 'proteinChange': 'A73Gfs*49', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'SARM1 truncating', 'chr': '17', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015077.3', 'proteinPosStart': 72, 'proteinPosEnd': 73}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9721, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 155, 'normalAltCount': 0, 'normalRefCount': 109, 'startPosition': 46999601, 'endPosition': 46999601, 'referenceAllele': 'G', 'proteinChange': 'V241M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPRIN2 V241 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 241, 'proteinPosEnd': 241}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 144193, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 9, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 96337183, 'endPosition': 96337183, 'referenceAllele': 'A', 'proteinChange': 'S3G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AMDHD1 S3 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_152435.2', 'proteinPosStart': 3, 'proteinPosEnd': 3}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 92922, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 57562804, 'endPosition': 57562804, 'referenceAllele': 'G', 'proteinChange': 'R96W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CCDC102A R96 missense', 'chr': '16', 'variantAllele': 'A', 'refseqMrnaId': 'NM_033212.3', 'proteinPosStart': 96, 'proteinPosEnd': 96}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 89887, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 16, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 55993260, 'endPosition': 55993260, 'referenceAllele': 'A', 'proteinChange': 'T234A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF628 T234 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_033113.2', 'proteinPosStart': 234, 'proteinPosEnd': 234}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 221833, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 33, 'tumorRefCount': 27, 'normalAltCount': 0, 'normalRefCount': 11, 'startPosition': 20824941, 'endPosition': 20824943, 'referenceAllele': 'GCC', 'proteinChange': 'G165del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SP8 165-165 deletion', 'chr': '7', 'variantAllele': '-', 'refseqMrnaId': 'NM_182700.4', 'proteinPosStart': 165, 'proteinPosEnd': 165}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 79946, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 10, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 104210735, 'endPosition': 104210735, 'referenceAllele': 'C', 'proteinChange': 'A85S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'C10ORF95 A85 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_024886.1', 'proteinPosStart': 85, 'proteinPosEnd': 85}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 137075, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 20, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 8560536, 'endPosition': 8560536, 'referenceAllele': 'G', 'proteinChange': 'V210M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CLDN23 V210 missense', 'chr': '8', 'variantAllele': 'A', 'refseqMrnaId': 'NM_194284.2', 'proteinPosStart': 210, 'proteinPosEnd': 210}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 285464, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 57, 'normalAltCount': 0, 'normalRefCount': 21, 'startPosition': 1388726, 'endPosition': 1388726, 'referenceAllele': 'T', 'proteinChange': 'C143R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CRIPAK C143 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_175918.3', 'proteinPosStart': 143, 'proteinPosEnd': 143}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 728318, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 241, 'normalAltCount': 0, 'normalRefCount': 109, 'startPosition': 39346616, 'endPosition': 39346617, 'referenceAllele': '-', 'proteinChange': 'P161_C162insSCGSSCCQP', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '17', 'variantAllele': 'AGCCTAGCTGTGGGTCCAGCTGCTGCC', 'refseqMrnaId': 'NM_001190460.1', 'proteinPosStart': 160, 'proteinPosEnd': 162}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4853, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 4, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 120611964, 'endPosition': 120611964, 'referenceAllele': 'G', 'proteinChange': 'C19W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOTCH2 C19 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024408.3', 'proteinPosStart': 19, 'proteinPosEnd': 19}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 51320, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 18, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 48723146, 'endPosition': 48723154, 'referenceAllele': 'GCCGCCGCG', 'proteinChange': 'A182_A184del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '18', 'variantAllele': '-', 'refseqMrnaId': 'NM_016626.4', 'proteinPosStart': 179, 'proteinPosEnd': 184}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 133060, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 8, 'startPosition': 4228274, 'endPosition': 4228282, 'referenceAllele': 'CCACAGCAG', 'proteinChange': 'L104_W106del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '4', 'variantAllele': '-', 'refseqMrnaId': 'NM_177998.1', 'proteinPosStart': 104, 'proteinPosEnd': 106}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84132, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 17, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 6193521, 'endPosition': 6193521, 'referenceAllele': 'G', 'proteinChange': 'R779P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'USP42 R779 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032172.2', 'proteinPosStart': 779, 'proteinPosEnd': 779}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 26873, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 145106939, 'endPosition': 145106940, 'referenceAllele': 'CC', 'proteinChange': 'G1167Lfs*21', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'OPLAH truncating', 'chr': '8', 'variantAllele': '-', 'refseqMrnaId': 'NM_017570.3', 'proteinPosStart': 1167, 'proteinPosEnd': 1167}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 6707, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 105, 'normalAltCount': 0, 'normalRefCount': 160, 'startPosition': 152975659, 'endPosition': 152975682, 'referenceAllele': 'GAGCCAGGCTGTACCAAGGTCCCT', 'proteinChange': 'C98_G105del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '1', 'variantAllele': '-', 'refseqMrnaId': 'NM_005416.2', 'proteinPosStart': 55, 'proteinPosEnd': 105}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 8525, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 3, 'startPosition': 46387868, 'endPosition': 46387868, 'referenceAllele': 'A', 'proteinChange': 'Q21R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DGKZ Q21 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001105540.1', 'proteinPosStart': 21, 'proteinPosEnd': 21}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 161931, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 11, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 84224967, 'endPosition': 84224967, 'referenceAllele': 'G', 'proteinChange': 'G44E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADAD2 G44 missense', 'chr': '16', 'variantAllele': 'A', 'refseqMrnaId': 'NM_139174.3', 'proteinPosStart': 44, 'proteinPosEnd': 44}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 388323, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 4693342, 'endPosition': 4693342, 'referenceAllele': 'C', 'proteinChange': 'D209E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GLTPD2 D209 missense', 'chr': '17', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001014985.2', 'proteinPosStart': 209, 'proteinPosEnd': 209}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84913, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 85981761, 'endPosition': 85981761, 'referenceAllele': 'T', 'proteinChange': 'L150P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATOH8 L150 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032827.6', 'proteinPosStart': 150, 'proteinPosEnd': 150}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 80025, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 3870124, 'endPosition': 3870124, 'referenceAllele': 'G', 'proteinChange': 'G126A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PANK2 G126 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_153638.2', 'proteinPosStart': 126, 'proteinPosEnd': 126}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 6239, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 7230680, 'endPosition': 7230680, 'referenceAllele': 'G', 'proteinChange': 'G783V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RREB1 G783 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001003700.1', 'proteinPosStart': 783, 'proteinPosEnd': 783}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 1490, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 132271952, 'endPosition': 132271952, 'referenceAllele': 'G', 'proteinChange': 'H83D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CCN2 H83 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001901.2', 'proteinPosStart': 83, 'proteinPosEnd': 83}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 388531, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 33167455, 'endPosition': 33167455, 'referenceAllele': 'G', 'proteinChange': 'A96S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RGS9BP A96 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_207391.2', 'proteinPosStart': 96, 'proteinPosEnd': 96}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 51676, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 50,

'tumorRefCount': 163, 'normalAltCount': 11, 'normalRefCount': 37, 'startPosition': 94405527, 'endPosition': 94405527, 'referenceAllele': 'T', 'proteinChange': 'H515P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASB2 H515 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001202429.1', 'proteinPosStart': 515, 'proteinPosEnd': 515}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 85364, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 0, 'normalAltCount': 3, 'normalRefCount': 0, 'startPosition': 278688, 'endPosition': 278690, 'referenceAllele': 'CGG', 'proteinChange': 'A159del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZCCHC3 159-159 deletion', 'chr': '20', 'variantAllele': '-', 'refseqMrnaId': 'NM_033089.6', 'proteinPosStart': 154, 'proteinPosEnd': 159}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 51222, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 28, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 21560753, 'endPosition': 21560758, 'referenceAllele': 'GAGGCT', 'proteinChange': 'Q233_P234del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '14', 'variantAllele': '-', 'refseqMrnaId': 'NM_016423.2', 'proteinPosStart': 233, 'proteinPosEnd': 234}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 29123, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 15, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 89346883, 'endPosition': 89346883, 'referenceAllele': 'C', 'proteinChange': 'A2023P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD11 A2023 missense', 'chr': '16', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001256183.1', 'proteinPosStart': 2023, 'proteinPosEnd': 2023}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 2837, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 21, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 80332223, 'endPosition': 80332223, 'referenceAllele': 'C', 'proteinChange': 'P8R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UTS2R P8 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_018949.1', 'proteinPosStart': 8, 'proteinPosEnd': 8}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 158135, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 28, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 124855330, 'endPosition': 124855331, 'referenceAllele': '-', 'proteinChange': 'A122_T123insKA', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '9', 'variantAllele': 'TGGCCT', 'refseqMrnaId': 'NM_001139442.1', 'proteinPosStart': 123, 'proteinPosEnd': 123}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 750, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 250, 'normalAltCount': 3, 'normalRefCount': 142, 'startPosition': 90095558,

'endPosition': 90095558, 'referenceAllele': 'C', 'proteinChange': 'G65S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GAS8-AS1 G65 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001214.3', 'proteinPosStart': 65, 'proteinPosEnd': 65}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 100131211, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 191399378, 'endPosition': 191399378, 'referenceAllele': 'C', 'proteinChange': 'G2R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NEMP2 G2 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001142645.1', 'proteinPosStart': 2, 'proteinPosEnd': 2}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 57479, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 50104897, 'endPosition': 50104897, 'referenceAllele': 'C', 'proteinChange': 'P1499S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRR12 P1499 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_020719.1', 'proteinPosStart': 1499, 'proteinPosEnd': 1499}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4583, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 117, 'normalAltCount': 2, 'normalRefCount': 99, 'startPosition': 1093292, 'endPosition': 1093292, 'referenceAllele': 'C', 'proteinChange': 'T1704I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUC2 T1704 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_002457.2', 'proteinPosStart': 1704, 'proteinPosEnd': 1704}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 163782, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 233, 'normalAltCount': 0, 'normalRefCount': 255, 'startPosition': 62732421, 'endPosition': 62732421, 'referenceAllele': 'T', 'proteinChange': 'T768A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KANK4 T768 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_181712.4', 'proteinPosStart': 768, 'proteinPosEnd': 768}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 55243, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 150, 'normalAltCount': 0, 'normalRefCount': 170, 'startPosition': 158058203, 'endPosition': 158058203, 'referenceAllele': 'C', 'proteinChange': 'P335S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KIRREL1 P335 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 335, 'proteinPosEnd': 335}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 6401, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 92, 'normalAltCount': 0, 'normalRefCount': 83,

'startPosition': 169697005, 'endPosition': 169697005, 'referenceAllele': 'A', 'proteinChange': 'I448T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SELE I448 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_000450.2', 'proteinPosStart': 448, 'proteinPosEnd': 448}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4548, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 81, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 237060314, 'endPosition': 237060314, 'referenceAllele': 'T', 'proteinChange': 'L1203I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MTR L1203 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_000254.2', 'proteinPosStart': 1203, 'proteinPosEnd': 1203}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4360, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 69, 'tumorRefCount': 158, 'normalAltCount': 0, 'normalRefCount': 202, 'startPosition': 18122634, 'endPosition': 18122634, 'referenceAllele': 'G', 'proteinChange': 'G215D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MRC1 G215 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002438.3', 'proteinPosStart': 215, 'proteinPosEnd': 215}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9044, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 31, 'tumorRefCount': 72, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 93711281, 'endPosition': 93711281, 'referenceAllele': 'G', 'proteinChange': 'L174F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BTAF1 L174 missense', 'chr': '10', 'variantAllele': 'C', 'refseqMrnaId': 'NM_003972.2', 'proteinPosStart': 174, 'proteinPosEnd': 174}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 2805, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 280, 'normalAltCount': 0, 'normalRefCount': 168, 'startPosition': 101157345, 'endPosition': 101157345, 'referenceAllele': 'C', 'proteinChange': 'V401M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GOT1 V401 missense', 'chr': '10', 'variantAllele': 'T', 'refseqMrnaId': 'NM_002079.2', 'proteinPosStart': 401, 'proteinPosEnd': 401}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 57715, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 70, 'tumorRefCount': 283, 'normalAltCount': 0, 'normalRefCount': 170, 'startPosition': 102740027, 'endPosition': 102740027, 'referenceAllele': 'G', 'proteinChange': 'R426H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SEMA4G R426 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 426, 'proteinPosEnd': 426}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 27288, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 7110751, 'endPosition': 7110751, 'referenceAllele': 'A', 'proteinChange': 'T134A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RBMXL2 T134 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014469.4', 'proteinPosStart': 134, 'proteinPosEnd': 134}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84767, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 27, 'startPosition': 55658957, 'endPosition': 55658957, 'referenceAllele': 'C', 'proteinChange': 'P403R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIM51 P403 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_032681.3', 'proteinPosStart': 403, 'proteinPosEnd': 403}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 85456, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 86, 'normalAltCount': 0, 'normalRefCount': 82, 'startPosition': 57076797, 'endPosition': 57076797, 'referenceAllele': 'C', 'proteinChange': 'D1130N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TNKS1BP1 D1130 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 1130, 'proteinPosEnd': 1130}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 8499, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 45, 'tumorRefCount': 87, 'normalAltCount': 0, 'normalRefCount': 114, 'startPosition': 81769579, 'endPosition': 81769579, 'referenceAllele': 'C', 'proteinChange': 'R376Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PPFIA2 R376 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NM_003625.3', 'proteinPosStart': 376, 'proteinPosEnd': 376}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 5781, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 77, 'tumorRefCount': 302, 'normalAltCount': 1, 'normalRefCount': 331, 'startPosition': 112893833, 'endPosition': 112893833, 'referenceAllele': 'A', 'proteinChange': 'D241G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PTPN11 D241 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002834.3', 'proteinPosStart': 241, 'proteinPosEnd': 241}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 57666, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 133067343, 'endPosition': 133067343, 'referenceAllele': 'A', 'proteinChange': 'T63A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FBRSL1 T63 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001142641.1', 'proteinPosStart': 63, 'proteinPosEnd': 63}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 8881, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 118, 'normalAltCount': 0, 'normalRefCount': 143, 'startPosition': 115027384, 'endPosition': 115027384, 'referenceAllele': 'C', 'proteinChange': 'P446R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CDC16 P446 missense', 'chr': '13', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001078645.1', 'proteinPosStart': 446, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 80821, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 74, 'tumorRefCount': 282, 'normalAltCount': 2, 'normalRefCount': 115, 'startPosition': 53619554, 'endPosition': 53619554, 'referenceAllele': 'T', 'proteinChange': 'N88T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DDHD1 N88 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001160148.1', 'proteinPosStart': 88, 'proteinPosEnd': 88}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 3306, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 44, 'normalAltCount': 1, 'normalRefCount': 78, 'startPosition': 65009483, 'endPosition': 65009483, 'referenceAllele': 'A', 'proteinChange': 'D639G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HSPA2 D639 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_021979.3', 'proteinPosStart': 639, 'proteinPosEnd': 639}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9493, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 33, 'tumorRefCount': 106, 'normalAltCount': 0, 'normalRefCount': 120, 'startPosition': 69721517, 'endPosition': 69721517, 'referenceAllele': 'G', 'proteinChange': 'R346Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KIF23 R346 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_138555.3', 'proteinPosStart': 346, 'proteinPosEnd': 346}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9513, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 58, 'startPosition': 7495630, 'endPosition': 7495630, 'referenceAllele': 'C', 'proteinChange': 'R623H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FXR2 R623 missense', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_004860.3', 'proteinPosStart': 623, 'proteinPosEnd': 623}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 91133, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 27, 'normalAltCount': 0, 'normalRefCount': 32, 'startPosition': 6093437, 'endPosition': 6093437, 'referenceAllele': 'T', 'proteinChange': 'E430Dfs*15', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'L3MBTL4 truncating', 'chr': '18', 'variantAllele': '-', 'refseqMrnaId': 'NM_173464.3', 'proteinPosStart': 430, 'proteinPosEnd': 430}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 284217, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 140, 'normalAltCount': 0, 'normalRefCount': 114, 'startPosition': 7023307, 'endPosition': 7023307, 'referenceAllele': 'C', 'proteinChange': 'G853S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LAMA1 G853 missense', 'chr': '18', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005559.3', 'proteinPosStart': 853, 'proteinPosEnd': 853}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 1824, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 54, 'tumorRefCount': 180, 'normalAltCount': 0, 'normalRefCount': 163, 'startPosition': 28651720, 'endPosition': 28651720, 'referenceAllele': 'G', 'proteinChange': 'S659Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DSC2 S659 missense', 'chr': '18', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024422.3', 'proteinPosStart': 659, 'proteinPosEnd': 659}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 162699, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 814, 'normalAltCount': 2, 'normalRefCount': 494, 'startPosition': 44555127, 'endPosition': 44555127, 'referenceAllele': 'G', 'proteinChange': 'L363F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ELOA3P L363 missense', 'chr': '18', 'variantAllele': 'A', 'refseqMrnaId': 'NM_145653.3', 'proteinPosStart': 363, 'proteinPosEnd': 363}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 22904, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 77, 'normalAltCount': 0, 'normalRefCount': 69, 'startPosition': 1127619, 'endPosition': 1127619, 'referenceAllele': 'G', 'proteinChange': 'P142L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SBNO2 P142 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014963.2', 'proteinPosStart': 142, 'proteinPosEnd': 142}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 645191, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 2290499, 'endPosition': 2290499, 'referenceAllele': 'C', 'proteinChange': 'R426H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LINGO3 R426 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 426, 'proteinPosEnd': 426}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 163183, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 167, 'normalAltCount': 0, 'normalRefCount': 139, 'startPosition': 36494356, 'endPosition': 36494364, 'referenceAllele': 'GAGGAGGAA', 'proteinChange': 'F364_L366del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '19',

'variantAllele': '-', 'refseqMrnaId': 'NM_001039876.1', 'proteinPosStart': 364, 'proteinPosEnd': 366}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 79042, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 140, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 54695770, 'endPosition': 54695770, 'referenceAllele': 'G', 'proteinChange': 'D148N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TSEN34 D148 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 148, 'proteinPosEnd': 148}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 388, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 55, 'tumorRefCount': 172, 'normalAltCount': 1, 'normalRefCount': 127, 'startPosition': 20647308, 'endPosition': 20647308, 'referenceAllele': 'G', 'proteinChange': 'D28H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RHOB D28 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004040.2', 'proteinPosStart': 28, 'proteinPosEnd': 28}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 388963, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 71, 'normalAltCount': 5, 'normalRefCount': 47, 'startPosition': 74643337, 'endPosition': 74643337, 'referenceAllele': 'A', 'proteinChange': 'V20G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'C2ORF81 V20 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001145054.1', 'proteinPosStart': 20, 'proteinPosEnd': 20}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 376940, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 33, 'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 114, 'startPosition': 113079374, 'endPosition': 113079374, 'referenceAllele': 'T', 'proteinChange': 'Y340H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZC3H6 Y340 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_198581.2', 'proteinPosStart': 340, 'proteinPosEnd': 340}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 8647, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 61, 'normalAltCount': 0, 'normalRefCount': 91, 'startPosition': 169853195, 'endPosition': 169853195, 'referenceAllele': 'T', 'proteinChange': 'S143G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ABCB11 S143 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_003742.2', 'proteinPosStart': 143, 'proteinPosEnd': 143}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 2335, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 116, 'normalAltCount': 0, 'normalRefCount': 75,

'startPosition': 216299458, 'endPosition': 216299458, 'referenceAllele': 'C', 'proteinChange': 'G80R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FN1 G80 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 80, 'proteinPosEnd': 80}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 80309, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 115, 'normalAltCount': 1, 'normalRefCount': 108, 'startPosition': 228883336, 'endPosition': 228883336, 'referenceAllele': 'C', 'proteinChange': 'R745K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SPHKAP R745 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001142644.1', 'proteinPosStart': 745, 'proteinPosEnd': 745}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 22918, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 104, 'normalAltCount': 1, 'normalRefCount': 58, 'startPosition': 23065458, 'endPosition': 23065458, 'referenceAllele': 'A', 'proteinChange': 'W458G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CD93 W458 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_012072.3', 'proteinPosStart': 458, 'proteinPosEnd': 458}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4987, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 29, 'tumorRefCount': 134, 'normalAltCount': 0, 'normalRefCount': 107, 'startPosition': 62724242, 'endPosition': 62724242, 'referenceAllele': 'C', 'proteinChange': 'L57F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OPRL1 L57 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001200019.1', 'proteinPosStart': 57, 'proteinPosEnd': 57}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9980, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 49, 'normalAltCount': 0, 'normalRefCount': 52, 'startPosition': 37635944, 'endPosition': 37635944, 'referenceAllele': 'C', 'proteinChange': 'L1806F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DOP1B L1806 missense', 'chr': '21', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005128.2', 'proteinPosStart': 1806, 'proteinPosEnd': 1806}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 1417, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 53, 'normalAltCount': 0, 'normalRefCount': 134, 'startPosition': 25601196, 'endPosition': 25601196, 'referenceAllele': 'C', 'proteinChange': 'H113D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CRYBB3 H113 missense', 'chr': '22', 'variantAllele': 'G', 'refseqMrnaId': 'NM_004076.4', 'proteinPosStart': 113, 'proteinPosEnd': 113}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 25817, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',

'validationStatus': 'Untested', 'tumorAltCount': 72, 'tumorRefCount': 139, 'normalAltCount': 0, 'normalRefCount': 52, 'startPosition': 49042499, 'endPosition': 49042499, 'referenceAllele': 'G', 'proteinChange': 'C68Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TAFA5 C68 missense', 'chr': '22', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001082967.1', 'proteinPosStart': 68, 'proteinPosEnd': 68}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 54986, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 120, 'normalAltCount': 0, 'normalRefCount': 98, 'startPosition': 41756965, 'endPosition': 41756965, 'referenceAllele': 'C', 'proteinChange': 'V851I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ULK4 V851 missense', 'chr': '3', 'variantAllele': 'T', 'refseqMrnaId': 'NM_017886.2', 'proteinPosStart': 851, 'proteinPosEnd': 851}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 5361, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 41, 'tumorRefCount': 85, 'normalAltCount': 0, 'normalRefCount': 119, 'startPosition': 126739102, 'endPosition': 126739102, 'referenceAllele': 'G', 'proteinChange': 'G1318D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLXNA1 G1318 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_032242.3', 'proteinPosStart': 1318, 'proteinPosEnd': 1318}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 344658, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 70, 'normalAltCount': 1, 'normalRefCount': 129, 'startPosition': 169654233, 'endPosition': 169654233, 'referenceAllele': 'C', 'proteinChange': 'S383*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SAMD7 truncating', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_182610.2', 'proteinPosStart': 383, 'proteinPosEnd': 383}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 1181, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 129, 'tumorRefCount': 344, 'normalAltCount': 1, 'normalRefCount': 477, 'startPosition': 184072697, 'endPosition': 184072697, 'referenceAllele': 'A', 'proteinChange': 'V464G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CLCN2 V464 missense', 'chr': '3', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004366.5', 'proteinPosStart': 464, 'proteinPosEnd': 464}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 285550, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 107, 'normalAltCount': 0, 'normalRefCount': 156, 'startPosition': 15689928, 'endPosition': 15689928, 'referenceAllele': 'G', 'proteinChange': 'S443N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM200B S443 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001145191.1', 'proteinPosStart': 443, 'proteinPosEnd': 443}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 174, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 29, 'tumorRefCount': 80, 'normalAltCount': 0, 'normalRefCount': 132, 'startPosition': 74313330, 'endPosition': 74313330, 'referenceAllele': 'G', 'proteinChange': 'R332K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AFP R332 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001134.1', 'proteinPosStart': 332, 'proteinPosEnd': 332}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4283, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 25, 'normalAltCount': 0, 'normalRefCount': 60, 'startPosition': 76926002, 'endPosition': 76926002, 'referenceAllele': 'G', 'proteinChange': 'S79*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CXCL9 truncating', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_002416.1', 'proteinPosStart': 79, 'proteinPosEnd': 79}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 1834, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 63, 'tumorRefCount': 122, 'normalAltCount': 1, 'normalRefCount': 77, 'startPosition': 88537151, 'endPosition': 88537151, 'referenceAllele': 'G', 'proteinChange': 'D1113N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DSPP D1113 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014208.3', 'proteinPosStart': 1113, 'proteinPosEnd': 1113}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84162, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 70, 'normalAltCount': 0, 'normalRefCount': 92, 'startPosition': 123201033, 'endPosition': 123201033, 'referenceAllele': 'A', 'proteinChange': 'I2899V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BLTP1 I2899 missense', 'chr': '4', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 2899, 'proteinPosEnd': 2899}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 25819, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 51, 'tumorRefCount': 125, 'normalAltCount': 0, 'normalRefCount': 167, 'startPosition': 139966424, 'endPosition': 139966424, 'referenceAllele': 'G', 'proteinChange': 'W364*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOCT truncating', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_012118.3', 'proteinPosStart': 364, 'proteinPosEnd': 364}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 8467, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 54, 'normalAltCount': 0, 'normalRefCount': 91, 'startPosition': 144469148, 'endPosition': 144469148, 'referenceAllele': 'A', 'proteinChange': 'Y947C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SMARCA5 Y947 missense', 'chr': '4', 'variantAllele': 'G', 'refseqMrnaId': 'NM_003601.3',

'proteinPosStart': 947, 'proteinPosEnd': 947}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 23022, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 61, 'normalAltCount': 0, 'normalRefCount': 66, 'startPosition': 169606648, 'endPosition': 169606648, 'referenceAllele': 'A', 'proteinChange': 'T425S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PALLD T425 missense', 'chr': '4', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 425, 'proteinPosEnd': 425}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 56172, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 73, 'normalAltCount': 0, 'normalRefCount': 91, 'startPosition': 14758635, 'endPosition': 14758635, 'referenceAllele': 'C', 'proteinChange': 'R129K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKH R129 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_054027.4', 'proteinPosStart': 129, 'proteinPosEnd': 129}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 55814, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 101, 'normalAltCount': 0, 'normalRefCount': 157, 'startPosition': 70819810, 'endPosition': 70819810, 'referenceAllele': 'T', 'proteinChange': 'L1811R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BDP1 L1811 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_018429.2', 'proteinPosStart': 1811, 'proteinPosEnd': 1811}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 340120, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 46, 'normalAltCount': 0, 'normalRefCount': 57, 'startPosition': 79855316, 'endPosition': 79855316, 'referenceAllele': 'C', 'proteinChange': 'D175H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD34B D175 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001004441.2', 'proteinPosStart': 175, 'proteinPosEnd': 175}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 285596, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 129, 'tumorRefCount': 1286, 'normalAltCount': 0, 'normalRefCount': 1295, 'startPosition': 177171892, 'endPosition': 177171892, 'referenceAllele': 'C', 'proteinChange': 'M35I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM153A M35 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_173663.3', 'proteinPosStart': 35, 'proteinPosEnd': 35}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 135656, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 68, 'tumorRefCount': 184,

'normalAltCount': 0, 'normalRefCount': 231, 'startPosition': 30917535, 'endPosition': 30917535, 'referenceAllele': 'G', 'proteinChange': 'E432K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUCL3 E432 missense', 'chr': '6', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 432, 'proteinPosEnd': 432}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 2783, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 103, 'normalAltCount': 0, 'normalRefCount': 97, 'startPosition': 100274423, 'endPosition': 100274424, 'referenceAllele': 'GT', 'proteinChange': 'X68_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'GNB2 truncating', 'chr': '7', 'variantAllele': '-', 'refseqMrnaId': 'NM_005273.3', 'proteinPosStart': 68, 'proteinPosEnd': 68}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 94137, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 231, 'normalAltCount': 1, 'normalRefCount': 136, 'startPosition': 10469233, 'endPosition': 10469233, 'referenceAllele': 'A', 'proteinChange': 'L792P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RP1L1 L792 missense', 'chr': '8', 'variantAllele': 'G', 'refseqMrnaId': 'NM_178857.5', 'proteinPosStart': 792, 'proteinPosEnd': 792}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 157574, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 131, 'startPosition': 28309857, 'endPosition': 28309857, 'referenceAllele': 'G', 'proteinChange': 'A215V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FBXO16 A215 missense', 'chr': '8', 'variantAllele': 'A', 'refseqMrnaId': 'NM_172366.3', 'proteinPosStart': 215, 'proteinPosEnd': 215}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9919, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 143, 'normalAltCount': 0, 'normalRefCount': 100, 'startPosition': 139360883, 'endPosition': 139360883, 'referenceAllele': 'C', 'proteinChange': 'D1321N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SEC16A D1321 missense', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_014866.1', 'proteinPosStart': 1321, 'proteinPosEnd': 1321}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 395, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 48, 'normalAltCount': 0, 'normalRefCount': 123, 'startPosition': 11204435, 'endPosition': 11204435, 'referenceAllele': 'A', 'proteinChange': 'D398E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ARHGAP6 D398 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_013427.2', 'proteinPosStart': 398, 'proteinPosEnd': 398}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 139378, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 67, 'tumorRefCount': 73, 'normalAltCount': 2, 'normalRefCount': 185, 'startPosition': 135432457, 'endPosition': 135432457, 'referenceAllele': 'A', 'proteinChange': 'T2198A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADGRG4 T2198 missense', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_153834.3', 'proteinPosStart': 2198, 'proteinPosEnd': 2198}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9612, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 90, 'normalAltCount': 0, 'normalRefCount': 7, 'startPosition': 124824739, 'endPosition': 124824740, 'referenceAllele': '-', 'proteinChange': 'S1834Rfs*194', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'NCOR2 truncating', 'chr': '12', 'variantAllele': 'GCCG', 'refseqMrnaId': 'NA', 'proteinPosStart': 1833, 'proteinPosEnd': 1834}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 9625, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 72, 'normalAltCount': 0, 'normalRefCount': 12, 'startPosition': 79093270, 'endPosition': 79093271, 'referenceAllele': '-', 'proteinChange': 'T1330_P1331dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '17', 'variantAllele': 'GGGCGT', 'refseqMrnaId': 'NM_001080395.2', 'proteinPosStart': 1331, 'proteinPosEnd': 1331}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 79191, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 54318528, 'endPosition': 54318528, 'referenceAllele': 'A', 'proteinChange': 'L422P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IRX3 L422 missense', 'chr': '16', 'variantAllele': 'G', 'refseqMrnaId': 'NM_024336.2', 'proteinPosStart': 422, 'proteinPosEnd': 422}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599696, 'endPosition': 88599697, 'referenceAllele': 'GA', 'proteinChange': 'E444Afs*227', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 444}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 24, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599697, 'endPosition': 88599705, 'referenceAllele': 'AGCCTCTGG', 'proteinChange': 'E444_L446del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599703, 'endPosition': 88599705, 'referenceAllele': 'TGG', 'proteinChange': 'L446_A447delinsP', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 446, 'proteinPosEnd': 447}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 132720, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 113066831, 'endPosition': 113066831, 'referenceAllele': 'G', 'proteinChange': 'G32E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM241A G32 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_152400.2', 'proteinPosStart': 32, 'proteinPosEnd': 32}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 126432, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 48, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 39360720, 'endPosition': 39360720, 'referenceAllele': 'G', 'proteinChange': 'P402L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RINL P402 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 402, 'proteinPosEnd': 402}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 85441, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 25, 'normalAltCount': 0, 'normalRefCount': 3, 'startPosition': 62194713, 'endPosition': 62194713, 'referenceAllele': 'A', 'proteinChange': 'L1821R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HELZ2 L1821 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001037335.2', 'proteinPosStart': 1821, 'proteinPosEnd': 1821}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 6877, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 14, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 105128134, 'endPosition': 105128134, 'referenceAllele': 'T', 'proteinChange': 'S130A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TAF5 S130 missense', 'chr': '10', 'variantAllele': 'G', 'refseqMrnaId': 'NM_006951.3', 'proteinPosStart': 130, 'proteinPosEnd': 130}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 144717, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 28, 'normalAltCount': 0, 'normalRefCount': 6, 'startPosition': 111800827, 'endPosition': 111800835, 'referenceAllele': 'GCCACCCCC', 'proteinChange': 'G146_G148del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '12', 'variantAllele': '-', 'refseqMrnaId': 'NM_001177996.1', 'proteinPosStart': 146, 'proteinPosEnd': 148}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 11078, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 35, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 38122462, 'endPosition': 38122462, 'referenceAllele': 'A', 'proteinChange': 'H1300R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIOBP H1300 missense', 'chr': '22', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001039141.2', 'proteinPosStart': 1300, 'proteinPosEnd': 1300}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 192134, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 45, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 76751585, 'endPosition': 76751604, 'referenceAllele': 'TGGCCCTTCGGCGTGCAGCT', 'proteinChange': 'G331Afs*42', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'B3GNT6 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_138706.4', 'proteinPosStart': 330, 'proteinPosEnd': 331}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 57104, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 824789, 'endPosition': 824789, 'referenceAllele': 'T', 'proteinChange': 'L481P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PNPLA2 L481 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NM_020376.3', 'proteinPosStart': 481, 'proteinPosEnd': 481}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 192134, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 76751543, 'endPosition': 76751604, 'referenceAllele': 'TGGAGCGCGCCGGCCTGGCGCCCAGCGGCCACGAGGGCATCCTGGCCCTTCGGCGTGCAGCT', 'proteinChange': 'G317Afs*42', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'B3GNT6 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_138706.4', 'proteinPosStart': 316, 'proteinPosEnd': 317}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 80233, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 192, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 79517591, 'endPosition': 79517591, 'referenceAllele': 'T', 'proteinChange': 'D310Afs*90', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'FAAP100 truncating', 'chr': '17', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 310, 'proteinPosEnd': 310}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 645369, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 15, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 5890571, 'endPosition': 5890571, 'referenceAllele': 'T', 'proteinChange': 'S498G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMEM200C S498 missense', 'chr': '18', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 498, 'proteinPosEnd': 498}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 3755, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 143, 'normalAltCount': 0, 'normalRefCount': 40, 'startPosition': 49626376, 'endPosition': 49626376, 'referenceAllele': 'C', 'proteinChange': 'R167L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KCNG1 R167 missense', 'chr': '20', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002237.3', 'proteinPosStart': 167, 'proteinPosEnd': 167}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 85442, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 21, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 135012315, 'endPosition': 135012315, 'referenceAllele': 'A', 'proteinChange': 'N768S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KNDC1 N768 missense', 'chr': '10', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 768, 'proteinPosEnd': 768}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4666, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 57, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 57107325, 'endPosition': 57107325, 'referenceAllele': 'G', 'proteinChange': 'A836D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NACA A836 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 836, 'proteinPosEnd': 836}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 29080, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 126, 'normalAltCount': 0, 'normalRefCount': 116, 'startPosition': 82752037, 'endPosition': 82752037, 'referenceAllele': 'T', 'proteinChange': 'N40T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CCDC59 N40 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014167.4', 'proteinPosStart': 40, 'proteinPosEnd': 40}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 283638, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 104, 'normalAltCount': 1, 'normalRefCount': 15, 'startPosition': 105352650, 'endPosition': 105352650, 'referenceAllele': 'T', 'proteinChange': 'S692A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CEP170B S692 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001112726.2', 'proteinPosStart': 692, 'proteinPosEnd': 692}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 390664, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 151, 'normalAltCount': 0, 'normalRefCount': 30, 'startPosition': 1143513, 'endPosition': 1143529, 'referenceAllele': 'GGCCGGCTTGACCAGGT', 'proteinChange': 'H244Rfs*125', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'C1QTNF8 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_207419.3', 'proteinPosStart': 244, 'proteinPosEnd': 244}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 826, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 307, 'normalAltCount': 0, 'normalRefCount': 173, 'startPosition': 36633865, 'endPosition': 36633865, 'referenceAllele': 'C', 'proteinChange': 'R130*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CAPNS1 truncating', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001749.2', 'proteinPosStart': 130, 'proteinPosEnd': 130}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 284325, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 239, 'normalAltCount': 0, 'normalRefCount': 119, 'startPosition': 41248646, 'endPosition': 41248647, 'referenceAllele': 'TG', 'proteinChange': 'L251Rfs*4', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ACTMAP truncating', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_198476.3', 'proteinPosStart': 249, 'proteinPosEnd': 251}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 5794, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 66, 'normalAltCount': 0, 'normalRefCount': 50, 'startPosition': 55715359, 'endPosition': 55715359, 'referenceAllele': 'A', 'proteinChange': 'L226P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PTPRH L226 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002842.3', 'proteinPosStart': 226, 'proteinPosEnd': 226}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 151393, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 30, 'normalAltCount': 0, 'normalRefCount': 38, 'startPosition': 38216713, 'endPosition': 38216713, 'referenceAllele': 'A', 'proteinChange': 'E452V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RMDN2 E452 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_144713.3', 'proteinPosStart': 452, 'proteinPosEnd': 452}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 27429, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 74757554, 'endPosition': 74757554, 'referenceAllele': 'G', 'proteinChange': 'A141S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HTRA2 A141 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_013247.4', 'proteinPosStart': 141, 'proteinPosEnd': 141}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 150483, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 355, 'normalAltCount': 1, 'normalRefCount': 108, 'startPosition': 95537377, 'endPosition': 95537377, 'referenceAllele': 'C', 'proteinChange': 'A18D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TEKT4 A18 missense', 'chr': '2', 'variantAllele': 'A', 'refseqMrnaId': 'NM_144705.2', 'proteinPosStart': 18, 'proteinPosEnd': 18}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId':

64699, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 157, 'normalAltCount': 1, 'normalRefCount': 122, 'startPosition': 43808632, 'endPosition': 43808632, 'referenceAllele': 'C', 'proteinChange': 'R109Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMPRSS3 R109 missense', 'chr': '21', 'variantAllele': 'T', 'refseqMrnaId': 'NM_032404.2', 'proteinPosStart': 109, 'proteinPosEnd': 109}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 55267, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 6, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 46449891, 'endPosition': 46449891, 'referenceAllele': 'G', 'proteinChange': 'P28R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRR34 P28 missense', 'chr': '22', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 28, 'proteinPosEnd': 28}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 79722, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 45, 'normalAltCount': 0, 'normalRefCount': 49, 'startPosition': 55407592, 'endPosition': 55407592, 'referenceAllele': 'G', 'proteinChange': 'P328H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD55 P328 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024669.2', 'proteinPosStart': 328, 'proteinPosEnd': 328}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 114825, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 159546158, 'endPosition': 159546158, 'referenceAllele': 'G', 'proteinChange': 'R80C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PWWP2A R80 missense', 'chr': '5', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001130864.1', 'proteinPosStart': 80, 'proteinPosEnd': 80}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 3106, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 223, 'normalAltCount': 0, 'normalRefCount': 150, 'startPosition': 31324602, 'endPosition': 31324604, 'referenceAllele': 'TCT', 'proteinChange': 'E70del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'HLA-B 70-70 deletion', 'chr': '6', 'variantAllele': '-', 'refseqMrnaId': 'NM_005514.6', 'proteinPosStart': 68, 'proteinPosEnd': 70}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 6446, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 87, 'normalAltCount': 0, 'normalRefCount': 70, 'startPosition': 134494667, 'endPosition': 134494669, 'referenceAllele': 'GAC', 'proteinChange': 'S184del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SGK1 184-184 deletion', 'chr': '6', 'variantAllele': '-', 'refseqMrnaId': 'NM_001143676.1', 'proteinPosStart': 183, 'proteinPosEnd': 184}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 4010, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 159, 'normalAltCount': 0, 'normalRefCount': 61, 'startPosition': 129376780, 'endPosition': 129376780, 'referenceAllele': 'C', 'proteinChange': 'Q18K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LMX1B Q18 missense', 'chr': '9', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001174146.1', 'proteinPosStart': 18, 'proteinPosEnd': 18}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 10159, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 71, 'startPosition': 40458870, 'endPosition': 40458870, 'referenceAllele': 'G', 'proteinChange': 'K205N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATP6AP2 K205 missense', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005765.2', 'proteinPosStart': 205, 'proteinPosEnd': 205}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 23133, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 104, 'normalAltCount': 0, 'normalRefCount': 153, 'startPosition': 54014243, 'endPosition': 54014243, 'referenceAllele': 'T', 'proteinChange': 'D658G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PHF8 D658 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001184896.1', 'proteinPosStart': 658, 'proteinPosEnd': 658}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84465, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 139, 'normalAltCount': 0, 'normalRefCount': 67, 'startPosition': 66209208, 'endPosition': 66209209, 'referenceAllele': '-', 'proteinChange': 'C725Lfs*38', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'MEGF11 truncating', 'chr': '15', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 724, 'proteinPosEnd': 725}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 2201, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 109, 'normalAltCount': 0, 'normalRefCount': 134, 'startPosition': 127685053, 'endPosition': 127685054, 'referenceAllele': '-', 'proteinChange': 'G992Vfs*22', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'FBN2 truncating', 'chr': '5', 'variantAllele': 'CAGTCCCATCCAA', 'refseqMrnaId': 'NA', 'proteinPosStart': 992, 'proteinPosEnd': 992}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 84342, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 252, 'normalAltCount': 0, 'normalRefCount': 184, 'startPosition': 69368962, 'endPosition': 69368963, 'referenceAllele': 'AT', 'proteinChange': 'I292D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'COG8 I292 missense', 'chr': '16', 'variantAllele': 'TC', 'refseqMrnaId': 'NM_032382.4', 'proteinPosStart': 292, 'proteinPosEnd': 292}, {'uniqueSampleKey': 'VENHQS1PUi1BNUxJLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1PUi1BNUxJOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-OR-A5LI-01', 'patientId': 'TCGA-OR-A5LI', 'entrezGeneId': 131578, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 97, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 194080017, 'endPosition': 194080213, 'referenceAllele': 'GCCTGCCTCTTTAACACTCATTGGGTGCCTTCATCTGCATCAGGACAGCTTGGCTCCTCTTC TTGCAGCAGCAACAGCCGACGCAGGCAGCCAGGGAGCAGGCCAGGGCGACAATGCCAATT ACAATGGCGGCAATGGCCAGCCCGCTCTGGGCCTGGGTCATGCCCCAAACGCTGCGGTCAT CAGTGACCTGAATG', 'proteinChange': '*526*', 'mutationType': 'Nonstop_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'LRRC15 truncating', 'chr': '3', 'variantAllele': '-', 'refseqMrnaId': 'NM_001135057.2', 'proteinPosStart': 526, 'proteinPosEnd': 526}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4985, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 29138975, 'endPosition': 29138975, 'referenceAllele': 'G', 'proteinChange': 'C27F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OPRD1 C27 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000911.3', 'proteinPosStart': 27, 'proteinPosEnd': 27}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599701, 'endPosition': 88599701, 'referenceAllele': 'T', 'proteinChange': 'L446Wfs*352', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 445, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 126208, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 56599438, 'endPosition': 56599440, 'referenceAllele': 'TCG', 'proteinChange': 'D367del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZNF787 367-367 deletion', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_001002836.2', 'proteinPosStart': 367, 'proteinPosEnd': 367}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 340385, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 146033347, 'endPosition': 146033347, 'referenceAllele': 'T', 'proteinChange': 'V349A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF517 V349 missense', 'chr': '8', 'variantAllele': 'C', 'refseqMrnaId': 'NM_213605.2', 'proteinPosStart': 349, 'proteinPosEnd': 349}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9721, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 117, 'normalAltCount': 0, 'normalRefCount': 95, 'startPosition': 46999601, 'endPosition': 46999601, 'referenceAllele': 'G', 'proteinChange': 'V241M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPRIN2 V241 missense',

'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 241, 'proteinPosEnd': 241},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9721, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10,
'tumorRefCount': 25, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 47000217, 'endPosition':
47000217, 'referenceAllele': 'G', 'proteinChange': 'R446H', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPRIN2 R446 missense', 'chr': '10',
'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 446, 'proteinPosEnd': 446},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 144193, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 96337183, 'endPosition':
96337183, 'referenceAllele': 'A', 'proteinChange': 'S3G', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AMDHD1 S3 missense', 'chr': '12',
'variantAllele': 'G', 'refseqMrnaId': 'NM_152435.2', 'proteinPosStart': 3, 'proteinPosEnd': 3},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 89887, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 55993260, 'endPosition':
55993260, 'referenceAllele': 'A', 'proteinChange': 'T234A', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF628 T234 missense', 'chr': '19',
'variantAllele': 'G', 'refseqMrnaId': 'NM_033113.2', 'proteinPosStart': 234, 'proteinPosEnd': 234},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2617, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 30634661, 'endPosition':
30634661, 'referenceAllele': 'C', 'proteinChange': 'P42A', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GARS1 P42 missense', 'chr': '7', 'variantAllele':
'G', 'refseqMrnaId': 'NM_002047.2', 'proteinPosStart': 42, 'proteinPosEnd': 42}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10811, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4,
'tumorRefCount': 10, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 140317999,
'endPosition': 140317999, 'referenceAllele': 'C', 'proteinChange': 'D6E', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOXA1 D6 missense',
'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001256067.1', 'proteinPosStart': 6, 'proteinPosEnd':
6}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 343069, 'studyId': 'acc_tcga',
'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount':
10, 'tumorRefCount': 49, 'normalAltCount': 0, 'normalRefCount': 88, 'startPosition': 12907358,
'endPosition': 12907358, 'referenceAllele': 'T', 'proteinChange': 'Q262R', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPCL1 Q262
missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001013631.1', 'proteinPosStart': 262,

'proteinPosEnd': 262}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 26018, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 66550762, 'endPosition': 66550762, 'referenceAllele': 'G', 'proteinChange': 'L24V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LRIG1 L24 missense', 'chr': '3', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015541.2', 'proteinPosStart': 24, 'proteinPosEnd': 24}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3856, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 101, 'normalAltCount': 0, 'normalRefCount': 40, 'startPosition': 53298675, 'endPosition': 53298675, 'referenceAllele': 'A', 'proteinChange': 'S59A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KRT8 S59 missense', 'chr': '12', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001256282.1', 'proteinPosStart': 59, 'proteinPosEnd': 59}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 285704, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 98109838, 'endPosition': 98109838, 'referenceAllele': 'A', 'proteinChange': 'S63R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RGMB S63 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001012761.2', 'proteinPosStart': 63, 'proteinPosEnd': 63}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84132, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6193521, 'endPosition': 6193521, 'referenceAllele': 'G', 'proteinChange': 'R779P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'USP42 R779 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032172.2', 'proteinPosStart': 779, 'proteinPosEnd': 779}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1952, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 1, 'normalAltCount': 2, 'normalRefCount': 1, 'startPosition': 109792735, 'endPosition': 109792736, 'referenceAllele': '-', 'proteinChange': 'P16dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '1', 'variantAllele': 'CGC', 'refseqMrnaId': 'NM_001408.2', 'proteinPosStart': 12, 'proteinPosEnd': 16}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 51278, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 181058313, 'endPosition': 181058313, 'referenceAllele': 'G', 'proteinChange': 'R92H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IER5 R92 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_016545.4', 'proteinPosStart': 92, 'proteinPosEnd': 92}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 8525, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 46387868, 'endPosition': 46387868, 'referenceAllele': 'A', 'proteinChange': 'Q21R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DGKZ Q21 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001105540.1', 'proteinPosStart': 21, 'proteinPosEnd': 21}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9819, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 15, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 150128392, 'endPosition': 150128392, 'referenceAllele': 'G', 'proteinChange': 'A419T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TSC22D2 A419 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014779.2', 'proteinPosStart': 419, 'proteinPosEnd': 419}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2737, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 42005678, 'endPosition': 42005678, 'referenceAllele': 'G', 'proteinChange': 'P998L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GLI3 P998 missense', 'chr': '7', 'variantAllele': 'A', 'refseqMrnaId': 'NM_000168.5', 'proteinPosStart': 998, 'proteinPosEnd': 998}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 51133, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 43, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 215741053, 'endPosition': 215741053, 'referenceAllele': 'T', 'proteinChange': 'F9V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KCTD3 F9 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_016121.3', 'proteinPosStart': 9, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 80025, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 3870124, 'endPosition': 3870124, 'referenceAllele': 'G', 'proteinChange': 'G126A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PANK2 G126 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_153638.2', 'proteinPosStart': 126, 'proteinPosEnd': 126}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 11054, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 61444633, 'endPosition': 61444633, 'referenceAllele': 'G', 'proteinChange': 'E556K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OGFR E556 missense', 'chr': '20', 'variantAllele': 'A', 'refseqMrnaId': 'NM_007346.2', 'proteinPosStart': 556, 'proteinPosEnd': 556}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 11054, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 38, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 61444637, 'endPosition': 61444637, 'referenceAllele': 'G', 'proteinChange': 'S557T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OGFR S557 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_007346.2', 'proteinPosStart': 557, 'proteinPosEnd': 557}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 56126, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 78, 'normalAltCount': 0, 'normalRefCount': 9, 'startPosition': 140574170, 'endPosition': 140574175, 'referenceAllele': 'AGGCCG', 'proteinChange': 'E684_A685del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '5', 'variantAllele': '-', 'refseqMrnaId': 'NM_018930.3', 'proteinPosStart': 682, 'proteinPosEnd': 685}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5339, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 24, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 145001588, 'endPosition': 145001588, 'referenceAllele': 'C', 'proteinChange': 'R1386Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLEC R1386 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_201380.2', 'proteinPosStart': 1386, 'proteinPosEnd': 1386}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 220081, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 34, 'normalAltCount': 0, 'normalRefCount': 80, 'startPosition': 46170726, 'endPosition': 46170726, 'referenceAllele': 'A', 'proteinChange': 'Y139H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ERICH6B Y139 missense', 'chr': '13', 'variantAllele': 'G', 'refseqMrnaId': 'NM_182542.2', 'proteinPosStart': 139, 'proteinPosEnd': 139}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 220081, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 34, 'normalAltCount': 0, 'normalRefCount': 79, 'startPosition': 46170735, 'endPosition': 46170735,
 'referenceAllele': 'C', 'proteinChange': 'E136K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ERICH6B E136 missense', 'chr': '13', 'variantAllele': 'T', 'refseqMrnaId': 'NM_182542.2', 'proteinPosStart': 136, 'proteinPosEnd': 136}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 220081, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 35, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 46170737, 'endPosition': 46170737, 'referenceAllele': 'T', 'proteinChange': 'E135G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ERICH6B E135 missense', 'chr': '13', 'variantAllele': 'C', 'refseqMrnaId': 'NM_182542.2', 'proteinPosStart': 135, 'proteinPosEnd': 135}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57666, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 133159733, 'endPosition': 133159733, 'referenceAllele': 'C', 'proteinChange': 'A836V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FBRSL1 A836 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001142641.1', 'proteinPosStart': 836, 'proteinPosEnd': 836}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10544, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 56, 'normalAltCount': 2, 'normalRefCount': 18, 'startPosition': 33762727, 'endPosition': 33762727, 'referenceAllele': 'G', 'proteinChange': 'R98L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PROCR R98 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006404.4', 'proteinPosStart': 98, 'proteinPosEnd': 98}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4524, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 251, 'normalAltCount': 3, 'normalRefCount': 196, 'startPosition': 11850927, 'endPosition': 11850927, 'referenceAllele': 'C', 'proteinChange': 'R594Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MTHFR R594 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 594, 'proteinPosEnd': 594}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 79814, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 74, 'startPosition': 15909850, 'endPosition': 15909850, 'referenceAllele': 'C', 'proteinChange': 'G105R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AGMAT G105 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_024758.4', 'proteinPosStart': 105, 'proteinPosEnd': 105}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10163, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 80, 'normalAltCount': 1, 'normalRefCount': 67, 'startPosition': 27736665, 'endPosition': 27736665, 'referenceAllele': 'G', 'proteinChange': 'A287V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'WASF2 A287 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_006990.3', 'proteinPosStart': 287, 'proteinPosEnd': 287}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84970, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 173, 'normalAltCount': 0, 'normalRefCount': 143, 'startPosition': 34666398, 'endPosition': 34666398, 'referenceAllele': 'A', 'proteinChange': 'K347Rfs*33', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'C1ORF94 truncating', 'chr': '1', 'variantAllele': '-', 'refseqMrnaId': 'NM_001134734.1', 'proteinPosStart': 345, 'proteinPosEnd': 347}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 54507, 'studyId': 'acc_tcga',

'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 178, 'normalAltCount': 0, 'normalRefCount': 123, 'startPosition': 150526044, 'endPosition': 150526044, 'referenceAllele': 'G', 'proteinChange': 'A193P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADAMTSL4 A193 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_019032.4', 'proteinPosStart': 193, 'proteinPosEnd': 193}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2312, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 232, 'normalAltCount': 2, 'normalRefCount': 217, 'startPosition': 152280782, 'endPosition': 152280782, 'referenceAllele': 'A', 'proteinChange': 'Y2194H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FLG Y2194 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002016.1', 'proteinPosStart': 2194, 'proteinPosEnd': 2194}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57459, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 34, 'normalAltCount': 0, 'normalRefCount': 25, 'startPosition': 153800736, 'endPosition': 153800736, 'referenceAllele': 'T', 'proteinChange': 'K30*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GATAD2B truncating', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_020699.2', 'proteinPosStart': 30, 'proteinPosEnd': 30}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57863, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 114, 'tumorRefCount': 278, 'normalAltCount': 0, 'normalRefCount': 343, 'startPosition': 159170626, 'endPosition': 159170626, 'referenceAllele': 'G', 'proteinChange': 'D405N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CADM3 D405 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_021189.3', 'proteinPosStart': 405, 'proteinPosEnd': 405}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 92235, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 449, 'normalAltCount': 0, 'normalRefCount': 397, 'startPosition': 167095939, 'endPosition': 167095939, 'referenceAllele': 'G', 'proteinChange': 'G524A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'STYXL2 G524 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 524, 'proteinPosEnd': 524}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 7143, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 109, 'normalAltCount': 0, 'normalRefCount': 100, 'startPosition': 175375841, 'endPosition': 175375841, 'referenceAllele': 'C', 'proteinChange': 'D4H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TNR D4 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 4, 'proteinPosEnd': 4}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 353299, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',
'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 100, 'normalAltCount': 0,
'normalRefCount': 145, 'startPosition': 182525184, 'endPosition': 182525184, 'referenceAllele': 'G',
'proteinChange': 'E1075Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':
'SNP', 'keyword': 'RGSL1 E1075 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId':
'NM_001137669.1', 'proteinPosStart': 1075, 'proteinPosEnd': 1075}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 115019, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',
'validationStatus': 'Untested', 'tumorAltCount': 26, 'tumorRefCount': 59, 'normalAltCount': 0,
'normalRefCount': 62, 'startPosition': 205890762, 'endPosition': 205890762, 'referenceAllele': 'G',
'proteinChange': 'H663N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':
'SNP', 'keyword': 'SLC26A9 H663 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId':
'NM_134325.2', 'proteinPosStart': 663, 'proteinPosEnd': 663}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3930, 'studyId': 'acc_tcga',
'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested',
'tumorAltCount': 53, 'tumorRefCount': 236, 'normalAltCount': 1, 'normalRefCount': 279, 'startPosition':
225600179, 'endPosition': 225600179, 'referenceAllele': 'T', 'proteinChange': 'N354S', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LBR N354 missense',
'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_194442.2', 'proteinPosStart': 354, 'proteinPosEnd':
354}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 170392, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus':
'Untested', 'tumorAltCount': 40, 'tumorRefCount': 174, 'normalAltCount': 0, 'normalRefCount': 152,
'startPosition': 74684374, 'endPosition': 74684374, 'referenceAllele': 'G', 'proteinChange': 'V447I',
'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OIT3
V447 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_152635.1', 'proteinPosStart': 447,
'proteinPosEnd': 447}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh',
'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId':
'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId':
83938, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus':
'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 93, 'normalAltCount': 0,
'normalRefCount': 102, 'startPosition': 77542776, 'endPosition': 77542776, 'referenceAllele': 'A',
'proteinChange': 'K15*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':
'SNP', 'keyword': 'LRMDA truncating', 'chr': '10', 'variantAllele': 'T', 'refseqMrnaId': 'NM_032024.3',
'proteinPosStart': 15, 'proteinPosEnd': 15}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84445, 'studyId': 'acc_tcga',
'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',
'validationStatus': 'Untested', 'tumorAltCount': 44, 'tumorRefCount': 203, 'normalAltCount': 1,
'normalRefCount': 83, 'startPosition': 102766836, 'endPosition': 102766836, 'referenceAllele': 'G',
'proteinChange': 'E641K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':
'SNP', 'keyword': 'LZTS2 E641 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA',

'proteinPosStart': 641, 'proteinPosEnd': 641}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 53841, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 38, 'tumorRefCount': 302, 'normalAltCount': 0, 'normalRefCount': 121, 'startPosition': 624261, 'endPosition': 624263, 'referenceAllele': 'CTC', 'proteinChange': 'E88del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'CDHR5 88-88 deletion', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 88, 'proteinPosEnd': 88}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 390066, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 96, 'normalAltCount': 0, 'normalRefCount': 122, 'startPosition': 5510738, 'endPosition': 5510738, 'referenceAllele': 'G', 'proteinChange': 'G268R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR52D1 G268 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001005163.2', 'proteinPosStart': 268, 'proteinPosEnd': 268}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 144132, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 45, 'tumorRefCount': 197, 'normalAltCount': 1, 'normalRefCount': 143, 'startPosition': 6579406, 'endPosition': 6579406, 'referenceAllele': 'G', 'proteinChange': 'A2961T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DNHD1 A2961 missense', 'chr': '11', 'variantAllele': 'A', 'refseqMrnaId': 'NM_144666.2', 'proteinPosStart': 2961, 'proteinPosEnd': 2961}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2188, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 86, 'normalAltCount': 0, 'normalRefCount': 93, 'startPosition': 22646416, 'endPosition': 22646416, 'referenceAllele': 'A', 'proteinChange': 'L314P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FANCF L314 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_022725.3', 'proteinPosStart': 314, 'proteinPosEnd': 314}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 8525, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 46387906, 'endPosition': 46387906, 'referenceAllele': 'C', 'proteinChange': 'R34W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DGKZ R34 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001105540.1', 'proteinPosStart': 34, 'proteinPosEnd': 34}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1643, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 211, 'normalAltCount': 0, 'normalRefCount': 107, 'startPosition': 47256376, 'endPosition': 47256376, 'referenceAllele': 'C', 'proteinChange': 'L258Wfs*6',

'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'DDB2 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_000107.2', 'proteinPosStart': 257, 'proteinPosEnd': 258}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 390168, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 74, 'tumorRefCount': 288, 'normalAltCount': 0, 'normalRefCount': 350, 'startPosition': 56380625, 'endPosition': 56380625, 'referenceAllele': 'C', 'proteinChange': 'M118I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR5M1 M118 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001004740.1', 'proteinPosStart': 118, 'proteinPosEnd': 118}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 219960, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 265, 'normalAltCount': 0, 'normalRefCount': 276, 'startPosition': 57995729, 'endPosition': 57995729, 'referenceAllele': 'C', 'proteinChange': 'V207M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR10Q1 V207 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001004471.2', 'proteinPosStart': 207, 'proteinPosEnd': 207}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 6712, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 10, 'normalAltCount': 0, 'normalRefCount': 11, 'startPosition': 66461607, 'endPosition': 66461608, 'referenceAllele': 'CA', 'proteinChange': 'X1501_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SPTBN2 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 1501, 'proteinPosEnd': 1501}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 26011, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 103, 'normalAltCount': 0, 'normalRefCount': 114, 'startPosition': 78369696, 'endPosition': 78369696, 'referenceAllele': 'C', 'proteinChange': 'A2573S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TENM4 A2573 missense', 'chr': '11', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001098816.2', 'proteinPosStart': 2573, 'proteinPosEnd': 2573}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 65084, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 93, 'normalAltCount': 1, 'normalRefCount': 97, 'startPosition': 86749164, 'endPosition': 86749164, 'referenceAllele': 'C', 'proteinChange': 'S26F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMEM135 S26 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_022918.3', 'proteinPosStart': 26, 'proteinPosEnd': 26}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 120114, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 105, 'normalAltCount': 2, 'normalRefCount': 148, 'startPosition':

92624186, 'endPosition': 92624186, 'referenceAllele': 'A', 'proteinChange': 'E4559D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAT3 E4559 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 4559, 'proteinPosEnd': 4559}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2288, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 47, 'normalAltCount': 0, 'normalRefCount': 36, 'startPosition': 2912330, 'endPosition': 2912330, 'referenceAllele': 'C', 'proteinChange': 'A429G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FKBP4 A429 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002014.3', 'proteinPosStart': 429, 'proteinPosEnd': 429}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 716, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 77, 'normalAltCount': 0, 'normalRefCount': 84, 'startPosition': 7177252, 'endPosition': 7177252, 'referenceAllele': 'T', 'proteinChange': 'F455Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'C1S F455 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 455, 'proteinPosEnd': 455}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10526, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 66, 'normalAltCount': 0, 'normalRefCount': 116, 'startPosition': 30783824, 'endPosition': 30783824, 'referenceAllele': 'A', 'proteinChange': 'F1028L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IPO8 F1028 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006390.3', 'proteinPosStart': 1028, 'proteinPosEnd': 1028}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4035, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 136, 'normalAltCount': 0, 'normalRefCount': 82, 'startPosition': 57594933, 'endPosition': 57594933, 'referenceAllele': 'T', 'proteinChange': 'C3448S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LRP1 C3448 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002332.2', 'proteinPosStart': 3448, 'proteinPosEnd': 3448}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 55832, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 82, 'normalAltCount': 0, 'normalRefCount': 112, 'startPosition': 67691276, 'endPosition': 67691276, 'referenceAllele': 'G', 'proteinChange': 'R194T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CAND1 R194 missense', 'chr': '12', 'variantAllele': 'C', 'refseqMrnaId': 'NM_018448.3', 'proteinPosStart': 194, 'proteinPosEnd': 194}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 196477, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 107, 'normalAltCount': 0, 'normalRefCount': 132, 'startPosition': 91347423, 'endPosition': 91347423, 'referenceAllele': 'G', 'proteinChange': 'S366L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CCER1 S366 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NM_152638.2', 'proteinPosStart': 366, 'proteinPosEnd': 366}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 144717, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 13, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 111800570, 'endPosition': 111800570, 'referenceAllele': 'A', 'proteinChange': 'M234T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PHETA1 M234 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001177996.1', 'proteinPosStart': 234, 'proteinPosEnd': 234}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5985, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 43, 'tumorRefCount': 133, 'normalAltCount': 1, 'normalRefCount': 102, 'startPosition': 118454660, 'endPosition': 118454660, 'referenceAllele': 'G', 'proteinChange': 'E10K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RFC5 E10 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NM_007370.5', 'proteinPosStart': 10, 'proteinPosEnd': 10}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23281, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 137, 'startPosition': 29599410, 'endPosition': 29599410, 'referenceAllele': 'C', 'proteinChange': 'P202L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MTUS2 P202 missense', 'chr': '13', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001033602.2', 'proteinPosStart': 202, 'proteinPosEnd': 202}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 643677, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 18, 'normalAltCount': 0, 'normalRefCount': 35, 'startPosition': 103389045, 'endPosition': 103389045, 'referenceAllele': 'C', 'proteinChange': 'E39K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CCDC168 E39 missense', 'chr': '13', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001146197.1', 'proteinPosStart': 39, 'proteinPosEnd': 39}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1284, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 156, 'normalAltCount': 1, 'normalRefCount': 167, 'startPosition': 111111235, 'endPosition': 111111235, 'referenceAllele': 'G', 'proteinChange': 'R517K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'COL4A2 R517 missense', 'chr': '13', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001846.2', 'proteinPosStart': 517, 'proteinPosEnd': 517}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 114088, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 127, 'normalAltCount': 0, 'normalRefCount': 71, 'startPosition': 51561207, 'endPosition': 51561207, 'referenceAllele': 'G', 'proteinChange': 'L151M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIM9 L151 missense', 'chr': '14', 'variantAllele': 'T', 'refseqMrnaId': 'NM_015163.5', 'proteinPosStart': 151, 'proteinPosEnd': 151}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3958, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 102, 'normalAltCount': 0, 'normalRefCount': 113, 'startPosition': 55611906, 'endPosition': 55611906, 'referenceAllele': 'C', 'proteinChange': 'R224W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LGALS3 R224 missense', 'chr': '14', 'variantAllele': 'T', 'refseqMrnaId': 'NM_002306.3', 'proteinPosStart': 224, 'proteinPosEnd': 224}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 145508, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 65, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 81259439, 'endPosition': 81259439, 'referenceAllele': 'G', 'proteinChange': 'L409V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CEP128 L409 missense', 'chr': '14', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 409, 'proteinPosEnd': 409}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 78990, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 194, 'normalAltCount': 0, 'normalRefCount': 220, 'startPosition': 94510351, 'endPosition': 94510353, 'referenceAllele': 'CTT', 'proteinChange': 'L86del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'OTUB2 86-86 deletion', 'chr': '14', 'variantAllele': '-', 'refseqMrnaId': 'NM_023112.3', 'proteinPosStart': 85, 'proteinPosEnd': 86}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23742, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 28, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 24921967, 'endPosition': 24921967, 'referenceAllele': 'C', 'proteinChange': 'P318H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NPAP1 P318 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018958.2', 'proteinPosStart': 318, 'proteinPosEnd': 318}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 440279, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 47, 'tumorRefCount': 143, 'normalAltCount': 0, 'normalRefCount': 261, 'startPosition': 54542551, 'endPosition': 54542551, 'referenceAllele': 'G', 'proteinChange': 'W1119C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':

'SNP', 'keyword': 'UNC13C W1119 missense', 'chr': '15', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001080534.1', 'proteinPosStart': 1119, 'proteinPosEnd': 1119}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3671, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 27, 'normalAltCount': 0, 'normalRefCount': 39, 'startPosition': 74467204, 'endPosition': 74467204, 'referenceAllele': 'A', 'proteinChange': 'Q2R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ISLR Q2 missense', 'chr': '15', 'variantAllele': 'G', 'refseqMrnaId': 'NM_005545.3', 'proteinPosStart': 2, 'proteinPosEnd': 2}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5780, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 29, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 103, 'startPosition': 75809664, 'endPosition': 75809665, 'referenceAllele': 'AT', 'proteinChange': 'M155Vfs*4', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'PTPN9 truncating', 'chr': '15', 'variantAllele': '-', 'refseqMrnaId': 'NM_002833.2', 'proteinPosStart': 155, 'proteinPosEnd': 155}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 145873, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 4, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 90319773, 'endPosition': 90319773, 'referenceAllele': 'G', 'proteinChange': 'R62Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MESP2 R62 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001039958.1', 'proteinPosStart': 62, 'proteinPosEnd': 62}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 64718, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 108, 'normalAltCount': 0, 'normalRefCount': 15, 'startPosition': 1417283, 'endPosition': 1417283, 'referenceAllele': 'C', 'proteinChange': 'R616Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UNKL R616 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001193388.3', 'proteinPosStart': 616, 'proteinPosEnd': 616}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1773, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 50, 'tumorRefCount': 154, 'normalAltCount': 0, 'normalRefCount': 126, 'startPosition': 3705910, 'endPosition': 3705910, 'referenceAllele': 'G', 'proteinChange': 'V70L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DNASE1 V70 missense', 'chr': '16', 'variantAllele': 'C', 'refseqMrnaId': 'NM_005223.3', 'proteinPosStart': 70, 'proteinPosEnd': 70}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 113, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',

'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 33, 'startPosition': 50326734, 'endPosition': 50326734, 'referenceAllele': 'C', 'proteinChange': 'Q229*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADCY7 truncating', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 229, 'proteinPosEnd': 229}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 999, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 122, 'normalAltCount': 0, 'normalRefCount': 85, 'startPosition': 68867311, 'endPosition': 68867314, 'referenceAllele': 'CAGA', 'proteinChange': 'D854Kfs*8', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'CDH1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_004360.3', 'proteinPosStart': 853, 'proteinPosEnd': 854}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4620, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 40, 'normalAltCount': 0, 'normalRefCount': 78, 'startPosition': 10428659, 'endPosition': 10428659, 'referenceAllele': 'A', 'proteinChange': 'I1515N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYH2 I1515 missense', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_017534.5', 'proteinPosStart': 1515, 'proteinPosEnd': 1515}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9955, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 406, 'normalAltCount': 1, 'normalRefCount': 271, 'startPosition': 13400090, 'endPosition': 13400090, 'referenceAllele': 'C', 'proteinChange': 'K215N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HS3ST3A1 K215 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_006042.1', 'proteinPosStart': 215, 'proteinPosEnd': 215}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 7314, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 83, 'tumorRefCount': 354, 'normalAltCount': 0, 'normalRefCount': 214, 'startPosition': 16285604, 'endPosition': 16285604, 'referenceAllele': 'A', 'proteinChange': 'D128G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UBB D128 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001281720.1', 'proteinPosStart': 128, 'proteinPosEnd': 128}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 83897, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 187, 'normalAltCount': 3, 'normalRefCount': 312, 'startPosition': 39156027, 'endPosition': 39156027, 'referenceAllele': 'G', 'proteinChange': 'R27C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KRTAP3-2 R27 missense', 'chr': '17', 'variantAllele': 'A', 'refseqMrnaId': 'NM_031959.2', 'proteinPosStart': 27, 'proteinPosEnd': 27}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 60681, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 45, 'tumorRefCount': 97, 'normalAltCount': 0, 'normalRefCount': 149, 'startPosition': 39974745, 'endPosition': 39974745, 'referenceAllele': 'C', 'proteinChange': 'I231M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FKBP10 I231 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_021939.3', 'proteinPosStart': 231, 'proteinPosEnd': 231}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 8678, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 70, 'normalAltCount': 0, 'normalRefCount': 85, 'startPosition': 40963676, 'endPosition': 40963676, 'referenceAllele': 'T', 'proteinChange': 'Y394C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BECN1 Y394 missense', 'chr': '17', 'variantAllele': 'C', 'refseqMrnaId': 'NM_003766.3', 'proteinPosStart': 394, 'proteinPosEnd': 394}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2896, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 150, 'normalAltCount': 0, 'normalRefCount': 99, 'startPosition': 42427607, 'endPosition': 42427607, 'referenceAllele': 'G', 'proteinChange': 'V121M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GRN V121 missense', 'chr': '17', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002087.2', 'proteinPosStart': 121, 'proteinPosEnd': 121}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 162333, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 59, 'startPosition': 60779069, 'endPosition': 60779069, 'referenceAllele': 'C', 'proteinChange': 'V808I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MARCHF10 V808 missense', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_152598.2', 'proteinPosStart': 808, 'proteinPosEnd': 808}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 8632, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 43, 'tumorRefCount': 111, 'normalAltCount': 0, 'normalRefCount': 88, 'startPosition': 76424635, 'endPosition': 76424635, 'referenceAllele': 'C', 'proteinChange': 'A4181Qfs*14', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'DNAH17 truncating', 'chr': '17', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 4181, 'proteinPosEnd': 4181}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 374860, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 44, 'normalAltCount': 0, 'normalRefCount': 46, 'startPosition': 14763720, 'endPosition': 14763720, 'referenceAllele': 'C', 'proteinChange': 'P286T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD30B P286 missense', 'chr': '18', 'variantAllele': 'A', 'refseqMrnaId':

'NM_001145029.1', 'proteinPosStart': 286, 'proteinPosEnd': 286}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 80816, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 22, 'normalAltCount': 0, 'normalRefCount': 51, 'startPosition': 31323513, 'endPosition': 31323513, 'referenceAllele': 'A', 'proteinChange': 'N1234I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASXL3 N1234 missense', 'chr': '18', 'variantAllele': 'T', 'refseqMrnaId': 'NM_030632.1', 'proteinPosStart': 1234, 'proteinPosEnd': 1234}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 26040, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 125, 'normalAltCount': 0, 'normalRefCount': 158, 'startPosition': 42531586, 'endPosition': 42531586, 'referenceAllele': 'G', 'proteinChange': 'V761M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SETBP1 V761 missense', 'chr': '18', 'variantAllele': 'A', 'refseqMrnaId': 'NM_015559.2', 'proteinPosStart': 761, 'proteinPosEnd': 761}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1005, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 52, 'normalAltCount': 0, 'normalRefCount': 50, 'startPosition': 63547655, 'endPosition': 63547655, 'referenceAllele': 'T', 'proteinChange': 'V628A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CDH7 V628 missense', 'chr': '18', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004361.2', 'proteinPosStart': 628, 'proteinPosEnd': 628}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 116444, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 1009551, 'endPosition': 1009577, 'referenceAllele': 'GCCCCGCGGAGGCCCCACCACACTCT', 'proteinChange': 'A1028_S1036del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '19', 'variantAllele': '-', 'refseqMrnaId': 'NM_138690.1', 'proteinPosStart': 1028, 'proteinPosEnd': 1036}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84699, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 41, 'normalAltCount': 2, 'normalRefCount': 44, 'startPosition': 4168347, 'endPosition': 4168347, 'referenceAllele': 'G', 'proteinChange': 'X239_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CREB3L3 truncating', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_032607.2', 'proteinPosStart': 239, 'proteinPosEnd': 239}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9817, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 237, 'normalAltCount': 0, 'normalRefCount': 60, 'startPosition': 10600462, 'endPosition': 10600462, 'referenceAllele': 'C', 'proteinChange': 'V465M',

'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KEAP1 V465 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_203500.1', 'proteinPosStart': 465, 'proteinPosEnd': 465}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4854, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 92, 'normalAltCount': 1, 'normalRefCount': 20, 'startPosition': 15284881, 'endPosition': 15284881, 'referenceAllele': 'G', 'proteinChange': 'I1578=', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_000435.2', 'proteinPosStart': 1578, 'proteinPosEnd': -1}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57616, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 34, 'normalAltCount': 0, 'normalRefCount': 26, 'startPosition': 31770605, 'endPosition': 31770605, 'referenceAllele': 'G', 'proteinChange': 'P32S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TSHZ3 P32 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_020856.2', 'proteinPosStart': 32, 'proteinPosEnd': 32}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2116, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 144, 'normalAltCount': 1, 'normalRefCount': 47, 'startPosition': 36135558, 'endPosition': 36135558, 'referenceAllele': 'C', 'proteinChange': 'A278D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ETV2 A278 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014209.2', 'proteinPosStart': 278, 'proteinPosEnd': 278}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1555, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 46, 'tumorRefCount': 309, 'normalAltCount': 0, 'normalRefCount': 180, 'startPosition': 41509976, 'endPosition': 41509976, 'referenceAllele': 'T', 'proteinChange': 'V81A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CYP2B6 V81 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_000767.4', 'proteinPosStart': 81, 'proteinPosEnd': 81}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4680, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 160, 'normalAltCount': 0, 'normalRefCount': 92, 'startPosition': 42270108, 'endPosition': 42270108, 'referenceAllele': 'T', 'proteinChange': 'S326P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CEACAM6 S326 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_002483.4', 'proteinPosStart': 326, 'proteinPosEnd': 326}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 63946, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 107, 'normalAltCount': 0, 'normalRefCount': 92, 'startPosition': 42354402, 'endPosition': 42354402, 'referenceAllele': 'C', 'proteinChange': 'P260A',

'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DMRTC2 P260 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001040283.1', 'proteinPosStart': 260, 'proteinPosEnd': 260}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23152, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 117, 'normalAltCount': 0, 'normalRefCount': 43, 'startPosition': 42795782, 'endPosition': 42795782, 'referenceAllele': 'T', 'proteinChange': 'V924E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CIC V924 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_015125.3', 'proteinPosStart': 924, 'proteinPosEnd': 924}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 58506, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 159, 'normalAltCount': 0, 'normalRefCount': 97, 'startPosition': 50157674, 'endPosition': 50157674, 'referenceAllele': 'C', 'proteinChange': 'Q1129E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SCAF1 Q1129 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_021228.2', 'proteinPosStart': 1129, 'proteinPosEnd': 1129}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 147808, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 9, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 56133551, 'endPosition': 56133551, 'referenceAllele': 'C', 'proteinChange': 'E180K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF784 E180 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_203374.1', 'proteinPosStart': 180, 'proteinPosEnd': 180}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5178, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 60, 'tumorRefCount': 158, 'normalAltCount': 0, 'normalRefCount': 225, 'startPosition': 57335765, 'endPosition': 57335765, 'referenceAllele': 'C', 'proteinChange': 'E87Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PEG3 E87 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_006210.2', 'proteinPosStart': 87, 'proteinPosEnd': 87}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 730051, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 42, 'startPosition': 58385790, 'endPosition': 58385790, 'referenceAllele': 'G', 'proteinChange': 'P323H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF814 P323 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 323, 'proteinPosEnd': 323}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 730051, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus':

'Untested', 'tumorAltCount': 15, 'tumorRefCount': 89, 'normalAltCount': 0, 'normalRefCount': 42, 'startPosition': 58385793, 'endPosition': 58385793, 'referenceAllele': 'C', 'proteinChange': 'R322K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF814 R322 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 322, 'proteinPosEnd': 322}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10887, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 118, 'normalAltCount': 0, 'normalRefCount': 100, 'startPosition': 68873425, 'endPosition': 68873425, 'referenceAllele': 'A', 'proteinChange': 'I158V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PROKR1 I158 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 158, 'proteinPosEnd': 158}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3099, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 236, 'normalAltCount': 0, 'normalRefCount': 188, 'startPosition': 75115104, 'endPosition': 75115104, 'referenceAllele': 'G', 'proteinChange': 'G765V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HK2 G765 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000189.4', 'proteinPosStart': 765, 'proteinPosEnd': 765}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 10618, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 42, 'tumorRefCount': 250, 'normalAltCount': 0, 'normalRefCount': 168, 'startPosition': 85553698, 'endPosition': 85553700, 'referenceAllele': 'AAG', 'proteinChange': 'F386del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'TGOLN2 386-386 deletion', 'chr': '2', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 385, 'proteinPosEnd': 386}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3899, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 26, 'tumorRefCount': 64, 'normalAltCount': 0, 'normalRefCount': 49, 'startPosition': 100167958, 'endPosition': 100167958, 'referenceAllele': 'C', 'proteinChange': 'R1245Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AFF3 R1245 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001025108.1', 'proteinPosStart': 1245, 'proteinPosEnd': 1245}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 100131211, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 191399378, 'endPosition': 191399378, 'referenceAllele': 'C', 'proteinChange': 'G2R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NEMP2 G2 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001142645.1', 'proteinPosStart': 2, 'proteinPosEnd': 2}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId':

23549, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 203, 'normalAltCount': 0, 'normalRefCount': 130, 'startPosition': 220250725, 'endPosition': 220250725, 'referenceAllele': 'G', 'proteinChange': 'I185M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DNPEP I185 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_012100.2', 'proteinPosStart': 185, 'proteinPosEnd': 185}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 7150, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 47, 'tumorRefCount': 304, 'normalAltCount': 0, 'normalRefCount': 230, 'startPosition': 39746844, 'endPosition': 39746844, 'referenceAllele': 'A', 'proteinChange': 'N620Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TOP1 N620 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_003286.2', 'proteinPosStart': 620, 'proteinPosEnd': 620}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5335, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 44, 'tumorRefCount': 174, 'normalAltCount': 4, 'normalRefCount': 148, 'startPosition': 39794128, 'endPosition': 39794128, 'referenceAllele': 'G', 'proteinChange': 'K516N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLCG1 K516 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_002660.2', 'proteinPosStart': 516, 'proteinPosEnd': 516}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 11317, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 372, 'normalAltCount': 0, 'normalRefCount': 193, 'startPosition': 43945172, 'endPosition': 43945172, 'referenceAllele': 'C', 'proteinChange': 'A411V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RBPJL A411 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001281449.1', 'proteinPosStart': 411, 'proteinPosEnd': 411}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 140831, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 154, 'normalAltCount': 0, 'normalRefCount': 117, 'startPosition': 44505469, 'endPosition': 44505472, 'referenceAllele': 'TATT', 'proteinChange': 'F92Sfs*4', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZSWIM3 truncating', 'chr': '20', 'variantAllele': '-', 'refseqMrnaId': 'NM_080752.3', 'proteinPosStart': 91, 'proteinPosEnd': 92}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 54033, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 188, 'normalAltCount': 0, 'normalRefCount': 208, 'startPosition': 15592023, 'endPosition': 15592023, 'referenceAllele': 'C', 'proteinChange': 'P79Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RBM11 P79 missense', 'chr': '21', 'variantAllele': 'A', 'refseqMrnaId': 'NM_144770.3', 'proteinPosStart': 79, 'proteinPosEnd': 79}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 5297, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 64, 'tumorRefCount': 165, 'normalAltCount': 0, 'normalRefCount': 192, 'startPosition': 21150535, 'endPosition': 21150535, 'referenceAllele': 'C', 'proteinChange': 'V726L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PI4KA V726 missense', 'chr': '22', 'variantAllele': 'G', 'refseqMrnaId': 'NM_058004.3', 'proteinPosStart': 726, 'proteinPosEnd': 726}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 11252, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 159, 'normalAltCount': 0, 'normalRefCount': 132, 'startPosition': 43289603, 'endPosition': 43289603, 'referenceAllele': 'C', 'proteinChange': 'R26Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PACSIN2 R26 missense', 'chr': '22', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001184970.1', 'proteinPosStart': 26, 'proteinPosEnd': 26}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 22908, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 84, 'normalAltCount': 0, 'normalRefCount': 109, 'startPosition': 45776839, 'endPosition': 45776839, 'referenceAllele': 'C', 'proteinChange': 'R405C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SACM1L R405 missense', 'chr': '3', 'variantAllele': 'T', 'refseqMrnaId': 'NM_014016.3', 'proteinPosStart': 405, 'proteinPosEnd': 405}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 22937, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 137, 'normalAltCount': 0, 'normalRefCount': 103, 'startPosition': 47455478, 'endPosition': 47455481, 'referenceAllele': 'CTGT', 'proteinChange': 'T1235Sfs*?', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SCAP truncating', 'chr': '3', 'variantAllele': '-', 'refseqMrnaId': 'NM_012235.2', 'proteinPosStart': 1235, 'proteinPosEnd': 1235}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 28990, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 105, 'normalAltCount': 0, 'normalRefCount': 160, 'startPosition': 130737507, 'endPosition': 130737507, 'referenceAllele': 'C', 'proteinChange': 'Q452H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASTE1 Q452 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014065.2', 'proteinPosStart': 452, 'proteinPosEnd': 452}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 79782, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 193, 'normalAltCount': 0, 'normalRefCount': 137, 'startPosition': 169558017, 'endPosition': 169558017, 'referenceAllele': 'G',

'proteinChange': 'T471I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LRRC31 T471 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_024727.3', 'proteinPosStart': 471, 'proteinPosEnd': 471}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 200909, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 75, 'tumorRefCount': 413, 'normalAltCount': 1, 'normalRefCount': 279, 'startPosition': 183756600, 'endPosition': 183756600, 'referenceAllele': 'G', 'proteinChange': 'G401D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HTR3D G401 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001163646.1', 'proteinPosStart': 401, 'proteinPosEnd': 401}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 152789, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 58, 'normalAltCount': 0, 'normalRefCount': 60, 'startPosition': 6114570, 'endPosition': 6114570, 'referenceAllele': 'T', 'proteinChange': 'K3R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'JAKMIP1 K3 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001099433.1', 'proteinPosStart': 3, 'proteinPosEnd': 3}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 80216, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 99, 'normalAltCount': 1, 'normalRefCount': 123, 'startPosition': 113352657, 'endPosition': 113352657, 'referenceAllele': 'G', 'proteinChange': 'E652K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ALPK1 E652 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001102406.1', 'proteinPosStart': 652, 'proteinPosEnd': 652}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 27152, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 110, 'normalAltCount': 0, 'normalRefCount': 151, 'startPosition': 128628123, 'endPosition': 128628123, 'referenceAllele': 'A', 'proteinChange': 'K757M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'INTU K757 missense', 'chr': '4', 'variantAllele': 'T', 'refseqMrnaId': 'NM_015693.3', 'proteinPosStart': 757, 'proteinPosEnd': 757}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 83894, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 57, 'startPosition': 147830303, 'endPosition': 147830303, 'referenceAllele': 'T', 'proteinChange': 'D92A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TTC29 D92 missense', 'chr': '4', 'variantAllele': 'G', 'refseqMrnaId': 'NM_031956.2', 'proteinPosStart': 92, 'proteinPosEnd': 92}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 133584, 'studyId': 'acc_tcga',

'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 170, 'normalAltCount': 2, 'normalRefCount': 150, 'startPosition': 38418285, 'endPosition': 38418285, 'referenceAllele': 'C', 'proteinChange': 'L538F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'EGFLAM L538 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001205301.1', 'proteinPosStart': 538, 'proteinPosEnd': 538}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3156, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 38, 'tumorRefCount': 257, 'normalAltCount': 0, 'normalRefCount': 278, 'startPosition': 74639696, 'endPosition': 74639698, 'referenceAllele': 'ATT', 'proteinChange': 'I64del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'HMGCR 64-64 deletion', 'chr': '5', 'variantAllele': '-', 'refseqMrnaId': 'NM_000859.2', 'proteinPosStart': 62, 'proteinPosEnd': 64}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84059, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 100, 'normalAltCount': 0, 'normalRefCount': 90, 'startPosition': 90055402, 'endPosition': 90055402, 'referenceAllele': 'G', 'proteinChange': 'K4039N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ADGRV1 K4039 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032119.3', 'proteinPosStart': 4039, 'proteinPosEnd': 4039}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 133923, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 72, 'normalAltCount': 0, 'normalRefCount': 94, 'startPosition': 121487769, 'endPosition': 121487769, 'referenceAllele': 'C', 'proteinChange': 'N28K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF474 N28 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_207317.1', 'proteinPosStart': 28, 'proteinPosEnd': 28}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 337876, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 237, 'normalAltCount': 0, 'normalRefCount': 148, 'startPosition': 129241282, 'endPosition': 129241282, 'referenceAllele': 'T', 'proteinChange': 'Y254H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CHSY3 Y254 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_175856.4', 'proteinPosStart': 254, 'proteinPosEnd': 254}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 56140, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 66, 'tumorRefCount': 410, 'normalAltCount': 0, 'normalRefCount': 435, 'startPosition': 140221852, 'endPosition': 140221852, 'referenceAllele': 'T', 'proteinChange': 'Y316Tfs*22', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'PCDHA8 truncating', 'chr': '5', 'variantAllele': '-', 'refseqMrnaId': 'NM_018911.2', 'proteinPosStart': 316, 'proteinPosEnd': 316}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh',

'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57528, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 110, 'normalAltCount': 0, 'normalRefCount': 133, 'startPosition': 143853595, 'endPosition': 143853595, 'referenceAllele': 'T', 'proteinChange': 'F402S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KCTD16 F402 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_020768.3', 'proteinPosStart': 402, 'proteinPosEnd': 402}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 90249, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 320, 'normalAltCount': 0, 'normalRefCount': 201, 'startPosition': 176305481, 'endPosition': 176305481, 'referenceAllele': 'C', 'proteinChange': 'I675M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UNC5A I675 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_133369.2', 'proteinPosStart': 675, 'proteinPosEnd': 675}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 94234, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 1313117, 'endPosition': 1313117, 'referenceAllele': 'A', 'proteinChange': 'T60P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FOXQ1 T60 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_033260.3', 'proteinPosStart': 60, 'proteinPosEnd': 60}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 94234, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 1313121, 'endPosition': 1313121, 'referenceAllele': 'A', 'proteinChange': 'Q61P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FOXQ1 Q61 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_033260.3', 'proteinPosStart': 61, 'proteinPosEnd': 61}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 8859, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 30, 'normalAltCount': 0, 'normalRefCount': 44, 'startPosition': 31940267, 'endPosition': 31940267, 'referenceAllele': 'G', 'proteinChange': 'D137H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'STK19 D137 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004197.1', 'proteinPosStart': 137, 'proteinPosEnd': 137}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3710, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 64, 'tumorRefCount': 162, 'normalAltCount': 1, 'normalRefCount': 131, 'startPosition': 33651116, 'endPosition': 33651116, 'referenceAllele': 'C', 'proteinChange': 'P1577R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ITPR3 P1577 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NA',

'proteinPosStart': 1577, 'proteinPosEnd': 1577}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 55166, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 31, 'tumorRefCount': 145, 'normalAltCount': 0, 'normalRefCount': 228, 'startPosition': 49456158, 'endPosition': 49456158, 'referenceAllele': 'G', 'proteinChange': 'E191*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CENPQ truncating', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_018132.3', 'proteinPosStart': 191, 'proteinPosEnd': 191}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 54443, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 78, 'normalAltCount': 0, 'normalRefCount': 142, 'startPosition': 36436004, 'endPosition': 36436006, 'referenceAllele': 'CAG', 'proteinChange': 'Q51del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ANLN 51-51 deletion', 'chr': '7', 'variantAllele': '-', 'refseqMrnaId': 'NM_018685.2', 'proteinPosStart': 50, 'proteinPosEnd': 51}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2737, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 296, 'normalAltCount': 0, 'normalRefCount': 215, 'startPosition': 42005406, 'endPosition': 42005406, 'referenceAllele': 'C', 'proteinChange': 'E1089K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GLI3 E1089 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000168.5', 'proteinPosStart': 1089, 'proteinPosEnd': 1089}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 114049, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 76, 'normalAltCount': 0, 'normalRefCount': 61, 'startPosition': 73101340, 'endPosition': 73101340, 'referenceAllele': 'G', 'proteinChange': 'D93H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BUD23 D93 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001202560.2', 'proteinPosStart': 93, 'proteinPosEnd': 93}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1174, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 26, 'normalAltCount': 0, 'normalRefCount': 25, 'startPosition': 100800053, 'endPosition': 100800053, 'referenceAllele': 'G', 'proteinChange': 'R61T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AP1S1 R61 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001283.3', 'proteinPosStart': 61, 'proteinPosEnd': 61}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 54329, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 95, 'normalAltCount': 0, 'normalRefCount': 99, 'startPosition': 112724050, 'endPosition': 112724050, 'referenceAllele': 'A',

'proteinChange': 'W243R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPR85 W243 missense', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001146266.1', 'proteinPosStart': 243, 'proteinPosEnd': 243}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 3751, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 27, 'tumorRefCount': 95, 'normalAltCount': 0, 'normalRefCount': 141, 'startPosition': 119915231, 'endPosition': 119915231, 'referenceAllele': 'C', 'proteinChange': 'T182M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KCND2 T182 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_012281.2', 'proteinPosStart': 182, 'proteinPosEnd': 182}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 89882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 70, 'normalAltCount': 0, 'normalRefCount': 83, 'startPosition': 6328653, 'endPosition': 6328653, 'referenceAllele': 'G', 'proteinChange': 'E20Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TPD52L3 E20 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_033516.5', 'proteinPosStart': 20, 'proteinPosEnd': 20}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23230, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 105, 'normalAltCount': 0, 'normalRefCount': 149, 'startPosition': 79933239, 'endPosition': 79933241, 'referenceAllele': 'CTA', 'proteinChange': 'T1683del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'VPS13A 1683-1683 deletion', 'chr': '9', 'variantAllele': '-', 'refseqMrnaId': 'NM_033305.2', 'proteinPosStart': 1682, 'proteinPosEnd': 1683}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 80010, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 45, 'normalAltCount': 0, 'normalRefCount': 57, 'startPosition': 86616405, 'endPosition': 86616405, 'referenceAllele': 'G', 'proteinChange': 'L168F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RMI1 L168 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024945.2', 'proteinPosStart': 168, 'proteinPosEnd': 168}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23196, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 66, 'normalAltCount': 1, 'normalRefCount': 61, 'startPosition': 96318860, 'endPosition': 96318860, 'referenceAllele': 'T', 'proteinChange': 'L824P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM120A L824 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_014612.3', 'proteinPosStart': 824, 'proteinPosEnd': 824}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2356, 'studyId': 'acc_tcga',

'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 218, 'normalAltCount': 1, 'normalRefCount': 113, 'startPosition': 130572350, 'endPosition': 130572350, 'referenceAllele': 'G', 'proteinChange': 'D418N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FPGS D418 missense', 'chr': '9', 'variantAllele': 'A', 'refseqMrnaId': 'NM_004957.4', 'proteinPosStart': 418, 'proteinPosEnd': 418}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 139599, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 42, 'normalAltCount': 0, 'normalRefCount': 79, 'startPosition': 75003782, 'endPosition': 75003782, 'referenceAllele': 'T', 'proteinChange': 'I369L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MAGEE2 I369 missense', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_138703.4', 'proteinPosStart': 369, 'proteinPosEnd': 369}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 158800, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 36, 'normalAltCount': 0, 'normalRefCount': 36, 'startPosition': 119249707, 'endPosition': 119249707, 'referenceAllele': 'G', 'proteinChange': 'S22R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RHOXF1 S22 missense', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId': 'NM_139282.2', 'proteinPosStart': 22, 'proteinPosEnd': 22}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 139170, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 169, 'normalAltCount': 0, 'normalRefCount': 223, 'startPosition': 125685583, 'endPosition': 125685583, 'referenceAllele': 'C', 'proteinChange': 'D337N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DCAF12L1 D337 missense', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId': 'NM_178470.4', 'proteinPosStart': 337, 'proteinPosEnd': 337}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 139170, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 250, 'normalAltCount': 0, 'normalRefCount': 285, 'startPosition': 125685622, 'endPosition': 125685622, 'referenceAllele': 'C', 'proteinChange': 'G324S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DCAF12L1 G324 missense', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId': 'NM_178470.4', 'proteinPosStart': 324, 'proteinPosEnd': 324}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 55558, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 227, 'normalAltCount': 0, 'normalRefCount': 85, 'startPosition': 153689643, 'endPosition': 153689643, 'referenceAllele': 'G', 'proteinChange': 'A267T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLXNA3 A267 missense', 'chr': '23', 'variantAllele': 'A', 'refseqMrnaId': 'NM_017514.3', 'proteinPosStart': 267, 'proteinPosEnd': 267}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 284348, 'studyId': 'acc_tcga',
'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11,
'tumorRefCount': 84, 'normalAltCount': 0, 'normalRefCount': 45, 'startPosition': 44302693,
'endPosition': 44302694, 'referenceAllele': '-', 'proteinChange': 'D144Gfs*28', 'mutationType':
'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'LYPD5 truncating', 'chr': '19',
'variantAllele': 'CC', 'refseqMrnaId': 'NM_001031749.2', 'proteinPosStart': 144, 'proteinPosEnd': 144},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 730051, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7,
'tumorRefCount': 93, 'normalAltCount': 0, 'normalRefCount': 35, 'startPosition': 58385798,
'endPosition': 58385799, 'referenceAllele': 'CC', 'proteinChange': 'G320E', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'ZNF814 G320 missense',
'chr': '19', 'variantAllele': 'TT', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 320,
'proteinPosEnd': 320}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh',
'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId':
'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId':
161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus':
'Untested', 'tumorAltCount': 10, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 0,
'startPosition': 88599696, 'endPosition': 88599697, 'referenceAllele': 'GA', 'proteinChange':
'E444Afs*227', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL',
'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2',
'proteinPosStart': 444, 'proteinPosEnd': 444}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 161882, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10,
'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599703, 'endPosition':
88599705, 'referenceAllele': 'TGG', 'proteinChange': 'L446_A447delinsP', 'mutationType':
'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-',
'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 446, 'proteinPosEnd': 447}, {'uniqueSampleKey':
'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 353091, 'studyId': 'acc_tcga',
'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16,
'tumorRefCount': 588, 'normalAltCount': 7, 'normalRefCount': 586, 'startPosition': 150240829,
'endPosition': 150240829, 'referenceAllele': 'G', 'proteinChange': 'T70R', 'mutationType':
'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RAET1G T70 missense',
'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001001788.2', 'proteinPosStart': 70, 'proteinPosEnd':
70}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':
'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 27164, 'studyId': 'acc_tcga',
'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6,
'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 76753768, 'endPosition':
76753768, 'referenceAllele': 'C', 'proteinChange': 'L593V', 'mutationType': 'Missense_Mutation',
'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SALL3 L593 missense', 'chr': '18',
'variantAllele': 'G', 'refseqMrnaId': 'NM_171999.3', 'proteinPosStart': 593, 'proteinPosEnd': 593},
{'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':
'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 90850, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 2059674, 'endPosition': 2059674, 'referenceAllele': 'T', 'proteinChange': 'E25G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF598 E25 missense', 'chr': '16', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 25, 'proteinPosEnd': 25}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 326340, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 48492434, 'endPosition': 48492434, 'referenceAllele': 'G', 'proteinChange': 'Q42H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZAR1 Q42 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_175619.2', 'proteinPosStart': 42, 'proteinPosEnd': 42}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 220107, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 51417535, 'endPosition': 51417535, 'referenceAllele': 'G', 'proteinChange': 'A83V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DLEU7 A83 missense', 'chr': '13', 'variantAllele': 'A', 'refseqMrnaId': 'NM_198989.2', 'proteinPosStart': 83, 'proteinPosEnd': 83}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 192134, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 32, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 76751585, 'endPosition': 76751604, 'referenceAllele': 'TGGCCCTTCGGCGTGCAGCT', 'proteinChange': 'G331Afs*42', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'B3GNT6 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_138706.4', 'proteinPosStart': 330, 'proteinPosEnd': 331}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 199720, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 38876464, 'endPosition': 38876464, 'referenceAllele': 'C', 'proteinChange': 'A480P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GGN A480 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_152657.3', 'proteinPosStart': 480, 'proteinPosEnd': 480}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 79155, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 2757800, 'endPosition': 2757800, 'referenceAllele': 'G', 'proteinChange': 'R73G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TNIP2 R73 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024309.3', 'proteinPosStart': 73, 'proteinPosEnd': 73}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId':

2306, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 47904909, 'endPosition': 47904909, 'referenceAllele': 'G', 'proteinChange': 'A368P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FOXD2 A368 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004474.3', 'proteinPosStart': 368, 'proteinPosEnd': 368}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 387522, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 48770159, 'endPosition': 48770159, 'referenceAllele': 'T', 'proteinChange': 'N6D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PEDS1-UBE2V1 N6 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001257399.1', 'proteinPosStart': 6, 'proteinPosEnd': 6}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4583, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 181, 'normalAltCount': 1, 'normalRefCount': 113, 'startPosition': 1092947, 'endPosition': 1092947, 'referenceAllele': 'C', 'proteinChange': 'T1589N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUC2 T1589 missense', 'chr': '11', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002457.2', 'proteinPosStart': 1589, 'proteinPosEnd': 1589}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 54700, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 85, 'normalAltCount': 3, 'normalRefCount': 78, 'startPosition': 15168670, 'endPosition': 15168670, 'referenceAllele': 'G', 'proteinChange': 'L303I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RRN3 L303 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_018427.3', 'proteinPosStart': 303, 'proteinPosEnd': 303}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 27237, 'studyId': 'acc_tcga', 'center': 'ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 57, 'normalAltCount': 0, 'normalRefCount': 72, 'startPosition': 3395174, 'endPosition': 3395174, 'referenceAllele': 'C', 'proteinChange': 'S604=', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014448.3', 'proteinPosStart': 604, 'proteinPosEnd': -1}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23499, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 107, 'normalAltCount': 0, 'normalRefCount': 110, 'startPosition': 39920766, 'endPosition': 39920766, 'referenceAllele': 'T', 'proteinChange': 'H4965Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MACF1 H4965 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 4965, 'proteinPosEnd': 4965}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId':

91181, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 52, 'normalAltCount': 0, 'normalRefCount': 36, 'startPosition': 154067601, 'endPosition': 154067601, 'referenceAllele': 'G', 'proteinChange': 'T666K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NUP210L T666 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_207308.2', 'proteinPosStart': 666, 'proteinPosEnd': 666}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 58504, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 20, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 49659006, 'endPosition': 49659006, 'referenceAllele': 'G', 'proteinChange': 'P405L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ARHGAP22 P405 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 405, 'proteinPosEnd': 405}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 65217, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 32, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 55582342, 'endPosition': 55582342, 'referenceAllele': 'C', 'proteinChange': 'R1717I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PCDH15 R1717 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001142768.1', 'proteinPosStart': 1717, 'proteinPosEnd': 1717}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 9066, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 261, 'normalAltCount': 0, 'normalRefCount': 169, 'startPosition': 61291923, 'endPosition': 61291923, 'referenceAllele': 'A', 'proteinChange': 'I310T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SYT7 I310 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001252065.1', 'proteinPosStart': 310, 'proteinPosEnd': 310}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 79849, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 153, 'normalAltCount': 0, 'normalRefCount': 130, 'startPosition': 119057343, 'endPosition': 119057343, 'referenceAllele': 'G', 'proteinChange': 'G92*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NHERF4 truncating', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001168468.1', 'proteinPosStart': 92, 'proteinPosEnd': 92}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1272, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 66, 'normalAltCount': 1, 'normalRefCount': 109, 'startPosition': 41419057, 'endPosition': 41419057, 'referenceAllele': 'T', 'proteinChange': 'Y877D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CNTN1 Y877 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001843.3', 'proteinPosStart': 877, 'proteinPosEnd': 877}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 25875, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 95, 'normalAltCount': 0, 'normalRefCount': 73, 'startPosition': 51451824, 'endPosition': 51451824, 'referenceAllele': 'C', 'proteinChange': 'L322V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LETMD1 L322 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001243689.1', 'proteinPosStart': 322, 'proteinPosEnd': 322}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 84189, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 64, 'normalAltCount': 0, 'normalRefCount': 126, 'startPosition': 86369481, 'endPosition': 86369481, 'referenceAllele': 'G', 'proteinChange': 'T388N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SLITRK6 T388 missense', 'chr': '13', 'variantAllele': 'T', 'refseqMrnaId': 'NM_032229.2', 'proteinPosStart': 388, 'proteinPosEnd': 388}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57578, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 242, 'normalAltCount': 0, 'normalRefCount': 312, 'startPosition': 93962775, 'endPosition': 93962775, 'referenceAllele': 'T', 'proteinChange': 'L67Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UNC79 L67 missense', 'chr': '14', 'variantAllele': 'A', 'refseqMrnaId': 'NM_020818.3', 'proteinPosStart': 67, 'proteinPosEnd': 67}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2009, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 34, 'tumorRefCount': 139, 'normalAltCount': 1, 'normalRefCount': 124, 'startPosition': 100404174, 'endPosition': 100404174, 'referenceAllele': 'C', 'proteinChange': 'Q725*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'EML1 truncating', 'chr': '14', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001008707.1', 'proteinPosStart': 725, 'proteinPosEnd': 725}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23742, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 24921115, 'endPosition': 24921115, 'referenceAllele': 'C', 'proteinChange': 'P34Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NPAP1 P34 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018958.2', 'proteinPosStart': 34, 'proteinPosEnd': 34}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 53905, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 148, 'normalAltCount': 0, 'normalRefCount': 147, 'startPosition': 45453135, 'endPosition': 45453135, 'referenceAllele': 'T', 'proteinChange': 'L1268Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DUOX1 L1268 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_017434.3', 'proteinPosStart': 1268, 'proteinPosEnd': 1268}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4210, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 3304463, 'endPosition': 3304463, 'referenceAllele': 'C', 'proteinChange': 'R202Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MEFV R202 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000243.2', 'proteinPosStart': 202, 'proteinPosEnd': 202}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 140775, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 180, 'normalAltCount': 0, 'normalRefCount': 133, 'startPosition': 18221001, 'endPosition': 18221001, 'referenceAllele': 'A', 'proteinChange': 'N634Mfs*45', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'SMCR8 truncating', 'chr': '17', 'variantAllele': '-', 'refseqMrnaId': 'NM_144775.2', 'proteinPosStart': 633, 'proteinPosEnd': 634}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2232, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 102, 'tumorRefCount': 299, 'normalAltCount': 1, 'normalRefCount': 183, 'startPosition': 72862635, 'endPosition': 72862635, 'referenceAllele': 'C', 'proteinChange': 'G152A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FDXR G152 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001258012.1', 'proteinPosStart': 152, 'proteinPosEnd': 152}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 57597, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 97, 'normalAltCount': 0, 'normalRefCount': 30, 'startPosition': 79410879, 'endPosition': 79410881, 'referenceAllele': 'GAG', 'proteinChange': 'E756del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'BAHCC1 756-756 deletion', 'chr': '17', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 754, 'proteinPosEnd': 756}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1463, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 102, 'normalAltCount': 0, 'normalRefCount': 58, 'startPosition': 19339014, 'endPosition': 19339014, 'referenceAllele': 'A', 'proteinChange': 'Q862P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NCAN Q862 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004386.2', 'proteinPosStart': 862, 'proteinPosEnd': 862}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23094, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 38573068, 'endPosition': 38573068, 'referenceAllele': 'C', 'proteinChange': 'A288V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SIPA1L3 A288 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_015073.1', 'proteinPosStart': 288, 'proteinPosEnd': 288}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 147965, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 38894307, 'endPosition': 38894307, 'referenceAllele': 'G', 'proteinChange': 'E108K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FAM98C E108 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_174905.3', 'proteinPosStart': 108, 'proteinPosEnd': 108}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 11027, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 230, 'normalAltCount': 0, 'normalRefCount': 142, 'startPosition': 55098715, 'endPosition': 55098715, 'referenceAllele': 'C', 'proteinChange': 'R452C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LILRA2 R452 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 452, 'proteinPosEnd': 452}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 130271, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 307, 'normalAltCount': 0, 'normalRefCount': 230, 'startPosition': 43953487, 'endPosition': 43953487, 'referenceAllele': 'A', 'proteinChange': 'Y873S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLEKHH2 Y873 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_172069.3', 'proteinPosStart': 873, 'proteinPosEnd': 873}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 50487, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 73, 'normalAltCount': 0, 'normalRefCount': 71, 'startPosition': 31535872, 'endPosition': 31535872, 'referenceAllele': 'G', 'proteinChange': 'L157V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PLA2G3 L157 missense', 'chr': '22', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015715.3', 'proteinPosStart': 157, 'proteinPosEnd': 157}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4671, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 198, 'normalAltCount': 0, 'normalRefCount': 120, 'startPosition': 70308258, 'endPosition': 70308258, 'referenceAllele': 'C', 'proteinChange': 'R162T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NAIP R162 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_004536.2', 'proteinPosStart': 162, 'proteinPosEnd': 162}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 7903, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 82, 'normalAltCount': 0, 'normalRefCount': 51, 'startPosition': 100147798, 'endPosition': 100147798, 'referenceAllele': 'G', 'proteinChange': 'P278H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ST8SIA4 P278 missense', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005668.5', 'proteinPosStart': 278, 'proteinPosEnd': 278}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 81545, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 115, 'normalAltCount': 0, 'normalRefCount': 131, 'startPosition': 147820759, 'endPosition': 147820759, 'referenceAllele': 'C', 'proteinChange': 'P1041R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FBXO38 P1041 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 1041, 'proteinPosEnd': 1041}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1627, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 135, 'tumorRefCount': 553, 'normalAltCount': 3, 'normalRefCount': 289, 'startPosition': 176885468, 'endPosition': 176885468, 'referenceAllele': 'T', 'proteinChange': 'D458A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DBN1 D458 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_080881.2', 'proteinPosStart': 458, 'proteinPosEnd': 458}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 1627, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 87, 'normalAltCount': 0, 'normalRefCount': 34, 'startPosition': 176894041, 'endPosition': 176894041, 'referenceAllele': 'T', 'proteinChange': 'E195A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DBN1 E195 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_080881.2', 'proteinPosStart': 195, 'proteinPosEnd': 195}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 7918, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 178, 'normalAltCount': 0, 'normalRefCount': 92, 'startPosition': 31630170, 'endPosition': 31630170, 'referenceAllele': 'C', 'proteinChange': 'R315Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPANK1 R315 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001199237.1', 'proteinPosStart': 315, 'proteinPosEnd': 315}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23469, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 23, 'normalAltCount': 0, 'normalRefCount': 43, 'startPosition': 64422984, 'endPosition': 64422984, 'referenceAllele': 'C', 'proteinChange': 'H1834Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PHF3 H1834 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 1834, 'proteinPosEnd': 1834}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 94120, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 114, 'normalAltCount': 0, 'normalRefCount': 105, 'startPosition': 159178345, 'endPosition': 159178345, 'referenceAllele': 'C', 'proteinChange': 'P414S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SYTL3 P414 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 414, 'proteinPosEnd': 414}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 96764, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 51, 'normalAltCount': 0, 'normalRefCount': 60, 'startPosition': 56705325, 'endPosition': 56705325, 'referenceAllele': 'A', 'proteinChange': 'K450M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TGS1 K450 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024831.6', 'proteinPosStart': 450, 'proteinPosEnd': 450}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 29979, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 126, 'normalAltCount': 1, 'normalRefCount': 152, 'startPosition': 86294747, 'endPosition': 86294747, 'referenceAllele': 'C', 'proteinChange': 'L218F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UBQLN1 L218 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_053067.2', 'proteinPosStart': 218, 'proteinPosEnd': 218}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 26609, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 140, 'normalAltCount': 0, 'normalRefCount': 200, 'startPosition': 7811812, 'endPosition': 7811812, 'referenceAllele': 'C', 'proteinChange': 'Q126E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'VCX Q126 missense', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_013452.2', 'proteinPosStart': 126, 'proteinPosEnd': 126}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 340547, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 76, 'normalAltCount': 0, 'normalRefCount': 176, 'startPosition': 107320488, 'endPosition': 107320488, 'referenceAllele': 'G', 'proteinChange': 'E383D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'VSIG1 E383 missense', 'chr': '23', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001170553.1', 'proteinPosStart': 383, 'proteinPosEnd': 383}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 2719, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 62, 'tumorRefCount': 207, 'normalAltCount': 1, 'normalRefCount': 395, 'startPosition': 132730533, 'endPosition': 132730535, 'referenceAllele': 'TCT', 'proteinChange': 'E525del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'GPC3 525-525 deletion', 'chr': '23', 'variantAllele': '-', 'refseqMrnaId': 'NM_001164617.1', 'proteinPosStart': 525, 'proteinPosEnd': 525}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23373, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 341, 'normalAltCount': 0, 'normalRefCount': 66, 'startPosition': 18856713, 'endPosition': 18856714, 'referenceAllele': '-', 'proteinChange': 'R126Pfs*43', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'CRTC1 truncating', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001098482.1', 'proteinPosStart': 124, 'proteinPosEnd': 126}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh',

'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 646643, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 39, 'normalAltCount': 2, 'normalRefCount': 6, 'startPosition': 56041209, 'endPosition': 56041210, 'referenceAllele': '-', 'proteinChange': 'R313Pfs*?', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'SBK2 truncating', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001101401.2', 'proteinPosStart': 313, 'proteinPosEnd': 313}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 4774, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 143, 'normalAltCount': 0, 'normalRefCount': 198, 'startPosition': 61554105, 'endPosition': 61554106, 'referenceAllele': 'TC', 'proteinChange': 'L150F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'NFIA L150 missense', 'chr': '1', 'variantAllele': 'AT', 'refseqMrnaId': 'NM_001145512.1', 'proteinPosStart': 149, 'proteinPosEnd': 150}, {'uniqueSampleKey': 'VENHQS1QNi1BNU9ILTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QNi1BNU9IOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-P6-A5OH-01', 'patientId': 'TCGA-P6-A5OH', 'entrezGeneId': 23145, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 313, 'normalAltCount': 0, 'normalRefCount': 180, 'startPosition': 149476671, 'endPosition': 149476672, 'referenceAllele': 'TG', 'proteinChange': 'X374_splice', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'chr': '7', 'variantAllele': 'CT', 'refseqMrnaId': 'NA', 'proteinPosStart': 374, 'proteinPosEnd': 374}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 4, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599701, 'endPosition': 88599701, 'referenceAllele': 'T', 'proteinChange': 'L446Wfs*352', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 445, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 92591, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 42254417, 'endPosition': 42254417, 'referenceAllele': 'A', 'proteinChange': 'N294S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASB16 N294 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_080863.4', 'proteinPosStart': 294, 'proteinPosEnd': 294}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 389333, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 138730037, 'endPosition': 138730037, 'referenceAllele': 'T', 'proteinChange': 'Q245R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PROB1 Q245 missense', 'chr': '5', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001161546.1', 'proteinPosStart': 245, 'proteinPosEnd': 245}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 144193, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 96337183, 'endPosition': 96337183, 'referenceAllele': 'A', 'proteinChange': 'S3G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AMDHD1 S3 missense', 'chr': '12', 'variantAllele': 'G', 'refseqMrnaId': 'NM_152435.2', 'proteinPosStart': 3, 'proteinPosEnd': 3}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 114294, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 63414083, 'endPosition': 63414083, 'referenceAllele': 'A', 'proteinChange': 'M5L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LACTB M5 missense', 'chr': '15', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032857.3', 'proteinPosStart': 5, 'proteinPosEnd': 5}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 56005, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 7, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 4670313, 'endPosition': 4670313, 'referenceAllele': 'C', 'proteinChange': 'G12R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYDGF G12 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_019107.3', 'proteinPosStart': 12, 'proteinPosEnd': 12}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 388946, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 41, 'tumorRefCount': 264, 'normalAltCount': 5, 'normalRefCount': 114, 'startPosition': 46707808, 'endPosition': 46707808, 'referenceAllele': 'C', 'proteinChange': 'Q128E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMEM247 Q128 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001145051.2', 'proteinPosStart': 128, 'proteinPosEnd': 128}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 90019, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 1858572, 'endPosition': 1858572, 'referenceAllele': 'C', 'proteinChange': 'R373W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SYT8 R373 missense', 'chr': '11', 'variantAllele': 'T', 'refseqMrnaId': 'NM_138567.3', 'proteinPosStart': 373, 'proteinPosEnd': 373}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2617, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 14, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 30634661, 'endPosition': 30634661, 'referenceAllele': 'C', 'proteinChange': 'P42A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GARS1 P42 missense', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002047.2', 'proteinPosStart': 42, 'proteinPosEnd': 42}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId':

'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 8321, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 25, 'normalAltCount': 2, 'normalRefCount': 0, 'startPosition': 90894459, 'endPosition': 90894460, 'referenceAllele': '-', 'proteinChange': 'P93dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '7', 'variantAllele': 'CCG', 'refseqMrnaId': 'NM_003505.1', 'proteinPosStart': 88, 'proteinPosEnd': 93}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 750, 'studyId': 'acc_tcga', 'center': 'ucsc.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 224, 'normalAltCount': 0, 'normalRefCount': 58, 'startPosition': 90095596, 'endPosition': 90095597, 'referenceAllele': 'AT', 'proteinChange': 'I52A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'GAS8-AS1 I52 missense', 'chr': '16', 'variantAllele': 'GC', 'refseqMrnaId': 'NM_001214.3', 'proteinPosStart': 52, 'proteinPosEnd': 52}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84918, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 150184882, 'endPosition': 150184882, 'referenceAllele': 'G', 'proteinChange': 'P92R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LRP11 P92 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032832.5', 'proteinPosStart': 92, 'proteinPosEnd': 92}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 3654, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 334, 'normalAltCount': 3, 'normalRefCount': 342, 'startPosition': 153284192, 'endPosition': 153284192, 'referenceAllele': 'A', 'proteinChange': 'F196S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IRAK1 F196 missense', 'chr': '23', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001569.3', 'proteinPosStart': 196, 'proteinPosEnd': 196}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79258, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 301, 'normalAltCount': 0, 'normalRefCount': 6, 'startPosition': 2560819, 'endPosition': 2560821, 'referenceAllele': 'CAG', 'proteinChange': 'L35del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'MMEL1 35-35 deletion', 'chr': '1', 'variantAllele': '-', 'refseqMrnaId': 'NA', 'proteinPosStart': 35, 'proteinPosEnd': 35}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4853, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 4, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 120611964, 'endPosition': 120611964, 'referenceAllele': 'G', 'proteinChange': 'C19W', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOTCH2 C19 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024408.3', 'proteinPosStart': 19, 'proteinPosEnd': 19}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 117145, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 151881885, 'endPosition': 151881885, 'referenceAllele': 'A', 'proteinChange': 'L17R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'THEM4 L17 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_053055.4', 'proteinPosStart': 17, 'proteinPosEnd': 17}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84439, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 100141689, 'endPosition': 100141689, 'referenceAllele': 'T', 'proteinChange': 'V692A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HHIPL1 V692 missense', 'chr': '14', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001127258.1', 'proteinPosStart': 692, 'proteinPosEnd': 692}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1952, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 23, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 109792735, 'endPosition': 109792736, 'referenceAllele': '-', 'proteinChange': 'P16dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '1', 'variantAllele': 'CGC', 'refseqMrnaId': 'NM_001408.2', 'proteinPosStart': 12, 'proteinPosEnd': 16}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51133, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 49, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 215741053, 'endPosition': 215741053, 'referenceAllele': 'T', 'proteinChange': 'F9V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KCTD3 F9 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_016121.3', 'proteinPosStart': 9, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 6929, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 9, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 1619350, 'endPosition': 1619350, 'referenceAllele': 'C', 'proteinChange': 'G431S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TCF3 G431 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001136139.2', 'proteinPosStart': 431, 'proteinPosEnd': 431}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 54102, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 4, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 36042579, 'endPosition': 36042579, 'referenceAllele': 'C', 'proteinChange': 'Q298E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CLIC6 Q298 missense', 'chr': '21', 'variantAllele': 'G', 'refseqMrnaId': 'NM_053277.1', 'proteinPosStart': 298, 'proteinPosEnd': 298}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1761, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6,

'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 841971, 'endPosition': 841971, 'referenceAllele': 'T', 'proteinChange': 'S45T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DMRT1 S45 missense', 'chr': '9', 'variantAllele': 'A', 'refseqMrnaId': 'NM_021951.2', 'proteinPosStart': 45, 'proteinPosEnd': 45}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 7133, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 176, 'normalAltCount': 1, 'normalRefCount': 36, 'startPosition': 12262126, 'endPosition': 12262126, 'referenceAllele': 'G', 'proteinChange': 'A335S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TNFRSF1B A335 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001066.2', 'proteinPosStart': 335, 'proteinPosEnd': 335}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 126402, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 15133926, 'endPosition': 15133926, 'referenceAllele': 'C', 'proteinChange': 'P499T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TEKTL1 P499 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_173482.2', 'proteinPosStart': 499, 'proteinPosEnd': 499}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 340152, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 48, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 149772190, 'endPosition': 149772190, 'referenceAllele': 'G', 'proteinChange': 'P405S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZC3H12D P405 missense', 'chr': '6', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 405, 'proteinPosEnd': 405}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2177, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 124, 'normalAltCount': 0, 'normalRefCount': 88, 'startPosition': 10108913, 'endPosition': 10108913, 'referenceAllele': 'G', 'proteinChange': 'Q802H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FANCD2 Q802 missense', 'chr': '3', 'variantAllele': 'T', 'refseqMrnaId': 'NM_033084.3', 'proteinPosStart': 802, 'proteinPosEnd': 802}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84132, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 20, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 6193464, 'endPosition': 6193464, 'referenceAllele': 'T', 'proteinChange': 'L760R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'USP42 L760 missense', 'chr': '7', 'variantAllele': 'G', 'refseqMrnaId': 'NM_032172.2', 'proteinPosStart': 760, 'proteinPosEnd': 760}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1834, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 813, 'normalAltCount': 12, 'normalRefCount': 591, 'startPosition': 88537027,

'endPosition': 88537027, 'referenceAllele': 'C', 'proteinChange': 'D1071E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DSPP D1071 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014208.3', 'proteinPosStart': 1071, 'proteinPosEnd': 1071}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2815, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 118, 'normalAltCount': 1, 'normalRefCount': 22, 'startPosition': 128780901, 'endPosition': 128780901, 'referenceAllele': 'G', 'proteinChange': 'A107S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GP9 A107 missense', 'chr': '3', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000174.3', 'proteinPosStart': 107, 'proteinPosEnd': 107}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 23062, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 23521643, 'endPosition': 23521643, 'referenceAllele': 'G', 'proteinChange': 'L30=', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '16', 'variantAllele': 'C', 'refseqMrnaId': 'NM_015044.4', 'proteinPosStart': 30, 'proteinPosEnd': -1}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51168, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 18024266, 'endPosition': 18024266, 'referenceAllele': 'T', 'proteinChange': 'W718G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYO15A W718 missense', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_016239.3', 'proteinPosStart': 718, 'proteinPosEnd': 718}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2876, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 18, 'tumorRefCount': 38, 'normalAltCount': 0, 'normalRefCount': 4, 'startPosition': 49395674, 'endPosition': 49395679, 'referenceAllele': 'GCCGCC', 'proteinChange': 'A12_A13del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '3', 'variantAllele': '-', 'refseqMrnaId': 'NM_000581.2', 'proteinPosStart': 11, 'proteinPosEnd': 13}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 439915, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 125, 'normalAltCount': 0, 'normalRefCount': 10, 'startPosition': 1651159, 'endPosition': 1651169, 'referenceAllele': 'GCTGTGGCTCT', 'proteinChange': 'C31Lfs*146', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'KRTAP5-5 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_001001480.2', 'proteinPosStart': 30, 'proteinPosEnd': 31}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1822, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 282, 'normalAltCount': 0, 'normalRefCount': 88, 'startPosition': 7045924, 'endPosition': 7045924, 'referenceAllele': 'G', 'proteinChange': 'Q498H',

'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATN1 Q498 missense', 'chr': '12', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001007026.1', 'proteinPosStart': 498, 'proteinPosEnd': 498}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 730051, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 74, 'normalAltCount': 0, 'normalRefCount': 87, 'startPosition': 58385790, 'endPosition': 58385790, 'referenceAllele': 'G', 'proteinChange': 'P323H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF814 P323 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 323, 'proteinPosEnd': 323}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 730051, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 71, 'normalAltCount': 0, 'normalRefCount': 84, 'startPosition': 58385793, 'endPosition': 58385793, 'referenceAllele': 'C', 'proteinChange': 'R322K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF814 R322 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 322, 'proteinPosEnd': 322}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 100131211, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 2, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 191399378, 'endPosition': 191399378, 'referenceAllele': 'C', 'proteinChange': 'G2R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NEMP2 G2 missense', 'chr': '2', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001142645.1', 'proteinPosStart': 2, 'proteinPosEnd': 2}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 730051, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 71, 'normalAltCount': 0, 'normalRefCount': 77, 'startPosition': 58385798, 'endPosition': 58385799, 'referenceAllele': 'CC', 'proteinChange': 'G320E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'DNP', 'keyword': 'ZNF814 G320 missense', 'chr': '19', 'variantAllele': 'TT', 'refseqMrnaId': 'NM_001144989.1', 'proteinPosStart': 320, 'proteinPosEnd': 320}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 200205, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 141, 'normalAltCount': 1, 'normalRefCount': 28, 'startPosition': 228362441, 'endPosition': 228362441, 'referenceAllele': 'C', 'proteinChange': 'S130R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IBA57 S130 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001010867.2', 'proteinPosStart': 130, 'proteinPosEnd': 130}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 773, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 13409696, 'endPosition': 13409696, 'referenceAllele': 'C', 'proteinChange': 'E917D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword':

'CACNA1A E917 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001127222.1', 'proteinPosStart': 917, 'proteinPosEnd': 917}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 115572, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 27339103, 'endPosition': 27339103, 'referenceAllele': 'G', 'proteinChange': 'T20K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TENT5B T20 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_052943.3', 'proteinPosStart': 20, 'proteinPosEnd': 20}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 10695, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 171, 'normalAltCount': 0, 'normalRefCount': 13, 'startPosition': 42897358, 'endPosition': 42897360, 'referenceAllele': 'TGC', 'proteinChange': 'L25del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'CNPY3 25-25 deletion', 'chr': '6', 'variantAllele': '-', 'refseqMrnaId': 'NM_006586.3', 'proteinPosStart': 17, 'proteinPosEnd': 25}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 6754, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 87, 'normalAltCount': 2, 'normalRefCount': 125, 'startPosition': 23016970, 'endPosition': 23016970, 'referenceAllele': 'T', 'proteinChange': 'F284V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SSTR4 F284 missense', 'chr': '20', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001052.2', 'proteinPosStart': 284, 'proteinPosEnd': 284}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 10555, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 31, 'normalAltCount': 0, 'normalRefCount': 4, 'startPosition': 139581758, 'endPosition': 139581759, 'referenceAllele': '-', 'proteinChange': 'L17dup', 'mutationType': 'In_Frame_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'chr': '9', 'variantAllele': 'CAG', 'refseqMrnaId': 'NM_006412.3', 'proteinPosStart': 17, 'proteinPosEnd': 17}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 284297, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 1, 'tumorRefCount': 119, 'normalAltCount': 0, 'normalRefCount': 72, 'startPosition': 56029616, 'endPosition': 56029616, 'referenceAllele': 'C', 'proteinChange': 'P1325T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SSC5D P1325 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001144950.1', 'proteinPosStart': 1325, 'proteinPosEnd': 1325}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 54700, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 386, 'normalAltCount': 0, 'normalRefCount': 108, 'startPosition': 15188060, 'endPosition': 15188060, 'referenceAllele': 'G', 'proteinChange': 'P11S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RRN3

P11 missense', 'chr': '16', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018427.3', 'proteinPosStart': 11, 'proteinPosEnd': 11}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 54700, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 378, 'normalAltCount': 0, 'normalRefCount': 104, 'startPosition': 15188066, 'endPosition': 15188066, 'referenceAllele': 'G', 'proteinChange': 'R9C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RRN3 R9 missense', 'chr': '16', 'variantAllele': 'A', 'refseqMrnaId': 'NM_018427.3', 'proteinPosStart': 9, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84196, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 112, 'normalAltCount': 0, 'normalRefCount': 100, 'startPosition': 22055060, 'endPosition': 22055060, 'referenceAllele': 'G', 'proteinChange': 'X484_splice', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_032236.5', 'proteinPosStart': 484, 'proteinPosEnd': 484}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2517, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 197, 'normalAltCount': 1, 'normalRefCount': 143, 'startPosition': 24180962, 'endPosition': 24180962, 'referenceAllele': 'T', 'proteinChange': 'Q286R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FUCA1 Q286 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_000147.4', 'proteinPosStart': 286, 'proteinPosEnd': 286}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51118, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 51, 'normalAltCount': 0, 'normalRefCount': 41, 'startPosition': 38482069, 'endPosition': 38482069, 'referenceAllele': 'G', 'proteinChange': 'K34N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'UTP11 K34 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_016037.3', 'proteinPosStart': 34, 'proteinPosEnd': 34}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 58155, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 80, 'normalAltCount': 0, 'normalRefCount': 96, 'startPosition': 97272469, 'endPosition': 97272469, 'referenceAllele': 'G', 'proteinChange': 'D376N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PTBP2 D376 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_021190.2', 'proteinPosStart': 376, 'proteinPosEnd': 376}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 913, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 73, 'normalAltCount': 0,

'normalRefCount': 89, 'startPosition': 158324185, 'endPosition': 158324185, 'referenceAllele': 'C', 'proteinChange': 'S26Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CD1E S26 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_030893.3', 'proteinPosStart': 26, 'proteinPosEnd': 26}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 128371, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 92, 'tumorRefCount': 311, 'normalAltCount': 0, 'normalRefCount': 278, 'startPosition': 158725430, 'endPosition': 158725430, 'referenceAllele': 'C', 'proteinChange': 'F275L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR6K6 F275 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001005184.1', 'proteinPosStart': 275, 'proteinPosEnd': 275}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 25782, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 62, 'normalAltCount': 0, 'normalRefCount': 94, 'startPosition': 220369717, 'endPosition': 220369717, 'referenceAllele': 'C', 'proteinChange': 'D279H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RAB3GAP2 D279 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_012414.3', 'proteinPosStart': 279, 'proteinPosEnd': 279}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 55127, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 263, 'normalAltCount': 1, 'normalRefCount': 193, 'startPosition': 236758887, 'endPosition': 236758887, 'referenceAllele': 'T', 'proteinChange': 'H348R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HEATR1 H348 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_018072.5', 'proteinPosStart': 348, 'proteinPosEnd': 348}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 88, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 63, 'tumorRefCount': 168, 'normalAltCount': 0, 'normalRefCount': 107, 'startPosition': 236902810, 'endPosition': 236902810, 'referenceAllele': 'C', 'proteinChange': 'P362L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ACTN2 P362 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001278344.1', 'proteinPosStart': 362, 'proteinPosEnd': 362}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 391211, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 49, 'tumorRefCount': 161, 'normalAltCount': 1, 'normalRefCount': 182, 'startPosition': 248685138, 'endPosition': 248685138, 'referenceAllele': 'G', 'proteinChange': 'S64I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR2G6 S64 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001013355.1', 'proteinPosStart': 64, 'proteinPosEnd': 64}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 55526, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 147, 'normalAltCount': 1, 'normalRefCount': 136, 'startPosition': 12143105, 'endPosition': 12143105, 'referenceAllele': 'C', 'proteinChange': 'I607M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DHTKD1 I607 missense', 'chr': '10', 'variantAllele': 'G', 'refseqMrnaId': 'NM_018706.6', 'proteinPosStart': 607, 'proteinPosEnd': 607}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 9721, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 15, 'normalAltCount': 0, 'normalRefCount': 3, 'startPosition': 47000193, 'endPosition': 47000193, 'referenceAllele': 'G', 'proteinChange': 'R438Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPRIN2 R438 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 438, 'proteinPosEnd': 438}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 142940, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 134, 'normalAltCount': 0, 'normalRefCount': 129, 'startPosition': 116719543, 'endPosition': 116719543, 'referenceAllele': 'G', 'proteinChange': 'R167K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRUB1 R167 missense', 'chr': '10', 'variantAllele': 'A', 'refseqMrnaId': 'NM_139169.4', 'proteinPosStart': 167, 'proteinPosEnd': 167}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 119695, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 128, 'normalAltCount': 0, 'normalRefCount': 116, 'startPosition': 4825225, 'endPosition': 4825225, 'referenceAllele': 'A', 'proteinChange': 'I129T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR52R1 I129 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001005177.3', 'proteinPosStart': 129, 'proteinPosEnd': 129}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 338323, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 141, 'normalAltCount': 2, 'normalRefCount': 188, 'startPosition': 7079038, 'endPosition': 7079038, 'referenceAllele': 'G', 'proteinChange': 'E808K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NLRP14 E808 missense', 'chr': '11', 'variantAllele': 'A', 'refseqMrnaId': 'NM_176822.3', 'proteinPosStart': 808, 'proteinPosEnd': 808}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 219493, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 49, 'tumorRefCount': 93, 'normalAltCount': 1, 'normalRefCount': 120, 'startPosition': 56431814, 'endPosition': 56431814, 'referenceAllele': 'A', 'proteinChange': 'Y218C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'OR5AR1 Y218 missense', 'chr': '11', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001004730.1', 'proteinPosStart': 218, 'proteinPosEnd': 218}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4297, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 23, 'tumorRefCount': 33, 'normalAltCount': 0, 'normalRefCount': 82, 'startPosition': 118374844, 'endPosition': 118374844, 'referenceAllele': 'G', 'proteinChange': 'R2746T', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'KMT2A R2746 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NM_005933.3', 'proteinPosStart': 2746, 'proteinPosEnd': 2746}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 57460, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 127, 'normalAltCount': 0, 'normalRefCount': 103, 'startPosition': 63131354, 'endPosition': 63131354, 'referenceAllele': 'G', 'proteinChange': 'I294M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PPM1H I294 missense', 'chr': '12', 'variantAllele': 'C', 'refseqMrnaId': 'NM_020700.1', 'proteinPosStart': 294, 'proteinPosEnd': 294}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 22985, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 161, 'normalAltCount': 1, 'normalRefCount': 125, 'startPosition': 23549319, 'endPosition': 23549319, 'referenceAllele': 'A', 'proteinChange': 'S467P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ACIN1 S467 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001164814.1', 'proteinPosStart': 467, 'proteinPosEnd': 467}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 64806, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 441, 'normalAltCount': 0, 'normalRefCount': 222, 'startPosition': 23845057, 'endPosition': 23845058, 'referenceAllele': 'TG', 'proteinChange': 'V171Afs*41', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'IL25 truncating', 'chr': '14', 'variantAllele': '-', 'refseqMrnaId': 'NM_022789.3', 'proteinPosStart': 168, 'proteinPosEnd': 171}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 80017, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 56, 'normalAltCount': 0, 'normalRefCount': 57, 'startPosition': 91647656, 'endPosition': 91647656, 'referenceAllele': 'C', 'proteinChange': 'P286H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DGLUCY P286 missense', 'chr': '14', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001286470.1', 'proteinPosStart': 286, 'proteinPosEnd': 286}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 113146, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 60, 'tumorRefCount': 112, 'normalAltCount': 0, 'normalRefCount': 129, 'startPosition': 105414374, 'endPosition': 105414374, 'referenceAllele': 'C',

'proteinChange': 'A2472P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'AHNAK2 A2472 missense', 'chr': '14', 'variantAllele': 'G', 'refseqMrnaId': 'NM_138420.2', 'proteinPosStart': 2472, 'proteinPosEnd': 2472}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 400410, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 200, 'normalAltCount': 1, 'normalRefCount': 255, 'startPosition': 80191343, 'endPosition': 80191343, 'referenceAllele': 'G', 'proteinChange': 'P57L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ST20 P57 missense', 'chr': '15', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001100879.1', 'proteinPosStart': 57, 'proteinPosEnd': 57}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 7249, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 242, 'normalAltCount': 0, 'normalRefCount': 69, 'startPosition': 2136869, 'endPosition': 2136869, 'referenceAllele': 'C', 'proteinChange': 'I1662M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TSC2 I1662 missense', 'chr': '16', 'variantAllele': 'G', 'refseqMrnaId': 'NM_000548.3', 'proteinPosStart': 1662, 'proteinPosEnd': 1662}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79838, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 37, 'tumorRefCount': 97, 'normalAltCount': 0, 'normalRefCount': 73, 'startPosition': 19451450, 'endPosition': 19451450, 'referenceAllele': 'G', 'proteinChange': 'L30F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMC5 L30 missense', 'chr': '16', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001105248.1', 'proteinPosStart': 30, 'proteinPosEnd': 30}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79838, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 50, 'tumorRefCount': 161, 'normalAltCount': 0, 'normalRefCount': 152, 'startPosition': 19488768, 'endPosition': 19488768, 'referenceAllele': 'C', 'proteinChange': 'I699M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TMC5 I699 missense', 'chr': '16', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001105248.1', 'proteinPosStart': 699, 'proteinPosEnd': 699}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1003, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 286, 'normalAltCount': 1, 'normalRefCount': 233, 'startPosition': 66420931, 'endPosition': 66420931, 'referenceAllele': 'G', 'proteinChange': 'V144M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CDH5 V144 missense', 'chr': '16', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001795.3', 'proteinPosStart': 144, 'proteinPosEnd': 144}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 643664, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic',

'validationStatus': 'Untested', 'tumorAltCount': 43, 'tumorRefCount': 177, 'normalAltCount': 0, 'normalRefCount': 93, 'startPosition': 7385476, 'endPosition': 7385476, 'referenceAllele': 'C', 'proteinChange': 'S58F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SLC35G6 S58 missense', 'chr': '17', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001102614.1', 'proteinPosStart': 58, 'proteinPosEnd': 58}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 5598, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 88, 'normalAltCount': 0, 'normalRefCount': 11, 'startPosition': 19285118, 'endPosition': 19285118, 'referenceAllele': 'C', 'proteinChange': 'A501D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MAPK7 A501 missense', 'chr': '17', 'variantAllele': 'A', 'refseqMrnaId': 'NM_139033.2', 'proteinPosStart': 501, 'proteinPosEnd': 501}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 246176, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 57, 'tumorRefCount': 63, 'normalAltCount': 0, 'normalRefCount': 88, 'startPosition': 34073260, 'endPosition': 34073260, 'referenceAllele': 'G', 'proteinChange': 'S419C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GAS2L2 S419 missense', 'chr': '17', 'variantAllele': 'C', 'refseqMrnaId': 'NM_139285.3', 'proteinPosStart': 419, 'proteinPosEnd': 419}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 9063, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 108, 'normalAltCount': 0, 'normalRefCount': 106, 'startPosition': 44435530, 'endPosition': 44435530, 'referenceAllele': 'C', 'proteinChange': 'L211F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PIAS2 L211 missense', 'chr': '18', 'variantAllele': 'A', 'refseqMrnaId': 'NM_004671.3', 'proteinPosStart': 211, 'proteinPosEnd': 211}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 94025, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 240, 'normalAltCount': 0, 'normalRefCount': 139, 'startPosition': 9056461, 'endPosition': 9056461, 'referenceAllele': 'G', 'proteinChange': 'P10329S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUC16 P10329 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_024690.2', 'proteinPosStart': 10329, 'proteinPosEnd': 10329}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 94025, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 40, 'tumorRefCount': 122, 'normalAltCount': 0, 'normalRefCount': 116, 'startPosition': 9090327, 'endPosition': 9090327, 'referenceAllele': 'G', 'proteinChange': 'S496R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUC16 S496 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024690.2', 'proteinPosStart': 496, 'proteinPosEnd': 496}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 374918, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 39, 'tumorRefCount': 71, 'normalAltCount': 0, 'normalRefCount': 71, 'startPosition': 46733364, 'endPosition': 46733364, 'referenceAllele': 'G', 'proteinChange': 'X9_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IGFL1 truncating', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_198541.1', 'proteinPosStart': 9, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 8541, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 134, 'tumorRefCount': 341, 'normalAltCount': 0, 'normalRefCount': 159, 'startPosition': 49637077, 'endPosition': 49637077, 'referenceAllele': 'G', 'proteinChange': 'E396K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PPFIA3 E396 missense', 'chr': '19', 'variantAllele': 'A', 'refseqMrnaId': 'NM_003660.3', 'proteinPosStart': 396, 'proteinPosEnd': 396}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 89858, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 58, 'tumorRefCount': 195, 'normalAltCount': 0, 'normalRefCount': 188, 'startPosition': 52003536, 'endPosition': 52003536, 'referenceAllele': 'G', 'proteinChange': 'S149*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SIGLEC12 truncating', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_053003.2', 'proteinPosStart': 149, 'proteinPosEnd': 149}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 11006, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 215, 'normalAltCount': 1, 'normalRefCount': 190, 'startPosition': 55175009, 'endPosition': 55175009, 'referenceAllele': 'G', 'proteinChange': 'R18S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'LILRB4 R18 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001278430.2', 'proteinPosStart': 18, 'proteinPosEnd': 18}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 352909, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 29, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 55672055, 'endPosition': 55672055, 'referenceAllele': 'A', 'proteinChange': 'L402P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DNAAF3 L402 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001256714.1', 'proteinPosStart': 402, 'proteinPosEnd': 402}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 284297, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 44, 'normalAltCount': 0, 'normalRefCount': 33, 'startPosition': 56030009, 'endPosition': 56030009, 'referenceAllele': 'C', 'proteinChange': 'P1456S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SSC5D P1456 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001144950.1', 'proteinPosStart': 1456, 'proteinPosEnd': 1456}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh',

'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 388566, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 78, 'normalAltCount': 0, 'normalRefCount': 68, 'startPosition': 57088558, 'endPosition': 57088558, 'referenceAllele': 'A', 'proteinChange': 'K254R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF470 K254 missense', 'chr': '19', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001001668.3', 'proteinPosStart': 254, 'proteinPosEnd': 254}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 65982, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 1, 'startPosition': 58596077, 'endPosition': 58596077, 'referenceAllele': 'G', 'proteinChange': 'P559R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZSCAN18 P559 missense', 'chr': '19', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001145542.1', 'proteinPosStart': 559, 'proteinPosEnd': 559}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 440854, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 96, 'tumorRefCount': 183, 'normalAltCount': 0, 'normalRefCount': 245, 'startPosition': 31428282, 'endPosition': 31428282, 'referenceAllele': 'C', 'proteinChange': 'W11L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CAPN14 W11 missense', 'chr': '2', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001145122.1', 'proteinPosStart': 11, 'proteinPosEnd': 11}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 129852, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 157, 'normalAltCount': 2, 'normalRefCount': 219, 'startPosition': 54562012, 'endPosition': 54562012, 'referenceAllele': 'C', 'proteinChange': 'H29N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'C2ORF73 H29 missense', 'chr': '2', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001100396.1', 'proteinPosStart': 29, 'proteinPosEnd': 29}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 23020, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 87, 'tumorRefCount': 190, 'normalAltCount': 1, 'normalRefCount': 168, 'startPosition': 96962720, 'endPosition': 96962720, 'referenceAllele': 'T', 'proteinChange': 'Y489C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SNRNP200 Y489 missense', 'chr': '2', 'variantAllele': 'C', 'refseqMrnaId': 'NM_014014.4', 'proteinPosStart': 489, 'proteinPosEnd': 489}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 56261, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 171, 'normalAltCount': 1, 'normalRefCount': 270, 'startPosition': 5556512, 'endPosition': 5556512, 'referenceAllele': 'G', 'proteinChange': 'T273I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GPCPD1 T273 missense', 'chr': '20', 'variantAllele': 'A', 'refseqMrnaId': 'NM_019593.3', 'proteinPosStart': 273, 'proteinPosEnd':

273}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 375337, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 80, 'tumorRefCount': 273, 'normalAltCount': 0, 'normalRefCount': 174, 'startPosition': 44283769, 'endPosition': 44283769, 'referenceAllele': 'G', 'proteinChange': 'G75A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TOPAZ1 G75 missense', 'chr': '3', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001145030.1', 'proteinPosStart': 75, 'proteinPosEnd': 75}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 8618, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 53, 'tumorRefCount': 164, 'normalAltCount': 0, 'normalRefCount': 150, 'startPosition': 62631437, 'endPosition': 62631437, 'referenceAllele': 'C', 'proteinChange': 'E429Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CADPS E429 missense', 'chr': '3', 'variantAllele': 'G', 'refseqMrnaId': 'NM_003716.3', 'proteinPosStart': 429, 'proteinPosEnd': 429}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4638, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 26, 'tumorRefCount': 66, 'normalAltCount': 0, 'normalRefCount': 60, 'startPosition': 123385189, 'endPosition': 123385189, 'referenceAllele': 'C', 'proteinChange': 'M1236I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MYLK M1236 missense', 'chr': '3', 'variantAllele': 'T', 'refseqMrnaId': 'NM_053025.3', 'proteinPosStart': 1236, 'proteinPosEnd': 1236}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 23101, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 113, 'normalAltCount': 0, 'normalRefCount': 100, 'startPosition': 183027542, 'endPosition': 183027542, 'referenceAllele': 'T', 'proteinChange': 'I359L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MCF2L2 I359 missense', 'chr': '3', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015078.2', 'proteinPosStart': 359, 'proteinPosEnd': 359}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 344905, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 54, 'normalAltCount': 0, 'normalRefCount': 111, 'startPosition': 193039524, 'endPosition': 193039524, 'referenceAllele': 'C', 'proteinChange': 'V621F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ATP13A5 V621 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_198505.2', 'proteinPosStart': 621, 'proteinPosEnd': 621}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 26057, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 174, 'normalAltCount': 1,

'normalRefCount': 106, 'startPosition': 74012588, 'endPosition': 74012588, 'referenceAllele': 'C', 'proteinChange': 'A588S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ANKRD17 A588 missense', 'chr': '4', 'variantAllele': 'A', 'refseqMrnaId': 'NM_032217.3', 'proteinPosStart': 588, 'proteinPosEnd': 588}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 55601, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 287, 'normalAltCount': 3, 'normalRefCount': 323, 'startPosition': 169188780, 'endPosition': 169188780, 'referenceAllele': 'T', 'proteinChange': 'I998V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DDX60 I998 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_017631.5', 'proteinPosStart': 998, 'proteinPosEnd': 998}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 57688, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 60628774, 'endPosition': 60628774, 'referenceAllele': 'C', 'proteinChange': 'V225=', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_020928.1', 'proteinPosStart': 225, 'proteinPosEnd': -1}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 64283, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 64, 'tumorRefCount': 166, 'normalAltCount': 0, 'normalRefCount': 185, 'startPosition': 73169041, 'endPosition': 73169041, 'referenceAllele': 'C', 'proteinChange': 'I928M', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ARHGEF28 I928 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001080479.2', 'proteinPosStart': 928, 'proteinPosEnd': 928}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4437, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 79950781, 'endPosition': 79950781, 'referenceAllele': 'A', 'proteinChange': 'I79V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MSH3 I79 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_002439.4', 'proteinPosStart': 79, 'proteinPosEnd': 79}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 26167, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 63, 'tumorRefCount': 86, 'normalAltCount': 0, 'normalRefCount': 125, 'startPosition': 140515063, 'endPosition': 140515063, 'referenceAllele': 'T', 'proteinChange': 'F16C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PCDHB5 F16 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015669.2', 'proteinPosStart': 16, 'proteinPosEnd': 16}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 6949, 'studyId': 'acc_tcga',

'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 87, 'tumorRefCount': 271, 'normalAltCount': 1, 'normalRefCount': 194, 'startPosition': 149758877, 'endPosition': 149758877, 'referenceAllele': 'C', 'proteinChange': 'A855G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TCOF1 A855 missense', 'chr': '5', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 855, 'proteinPosEnd': 855}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 7738, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 119, 'normalAltCount': 0, 'normalRefCount': 109, 'startPosition': 27419101, 'endPosition': 27419101, 'referenceAllele': 'C', 'proteinChange': 'R746K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF184 R746 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_007149.2', 'proteinPosStart': 746, 'proteinPosEnd': 746}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 135656, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 13, 'tumorRefCount': 229, 'normalAltCount': 4, 'normalRefCount': 183, 'startPosition': 30917365, 'endPosition': 30917365, 'referenceAllele': 'C', 'proteinChange': 'P375L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUCL3 P375 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 375, 'proteinPosEnd': 375}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 27242, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 163, 'normalAltCount': 0, 'normalRefCount': 92, 'startPosition': 47200618, 'endPosition': 47200618, 'referenceAllele': 'C', 'proteinChange': 'E617D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TNFRSF21 E617 missense', 'chr': '6', 'variantAllele': 'A', 'refseqMrnaId': 'NM_014452.4', 'proteinPosStart': 617, 'proteinPosEnd': 617}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4594, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 132, 'normalAltCount': 0, 'normalRefCount': 108, 'startPosition': 49416590, 'endPosition': 49416590, 'referenceAllele': 'C', 'proteinChange': 'E461D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MMUT E461 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_000255.3', 'proteinPosStart': 461, 'proteinPosEnd': 461}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 22858, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 32, 'tumorRefCount': 100, 'normalAltCount': 0, 'normalRefCount': 81, 'startPosition': 52871155, 'endPosition': 52871155, 'referenceAllele': 'T', 'proteinChange': 'M568V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CILK1 M568 missense', 'chr': '6', 'variantAllele': 'C', 'refseqMrnaId': 'NM_016513.4', 'proteinPosStart': 568, 'proteinPosEnd': 568}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey':

'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1310, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 33, 'tumorRefCount': 185, 'normalAltCount': 0, 'normalRefCount': 143, 'startPosition': 70890358, 'endPosition': 70890358, 'referenceAllele': 'G', 'proteinChange': 'E906D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'COL19A1 E906 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001858.4', 'proteinPosStart': 906, 'proteinPosEnd': 906}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 10973, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 83, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 101246658, 'endPosition': 101246658, 'referenceAllele': 'C', 'proteinChange': 'R442S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ASCC3 R442 missense', 'chr': '6', 'variantAllele': 'G', 'refseqMrnaId': 'NM_006828.2', 'proteinPosStart': 442, 'proteinPosEnd': 442}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 26053, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 121, 'normalAltCount': 0, 'normalRefCount': 14, 'startPosition': 70255577, 'endPosition': 70255579, 'referenceAllele': 'CCA', 'proteinChange': 'H1133del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'AUTS2 1133-1133 deletion', 'chr': '7', 'variantAllele': '-', 'refseqMrnaId': 'NM_015570.2', 'proteinPosStart': 1125, 'proteinPosEnd': 1133}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 6522, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 137, 'normalAltCount': 1, 'normalRefCount': 127, 'startPosition': 150761314, 'endPosition': 150761314, 'referenceAllele': 'G', 'proteinChange': 'G26E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SLC4A2 G26 missense', 'chr': '7', 'variantAllele': 'A', 'refseqMrnaId': 'NM_001199692.1', 'proteinPosStart': 26, 'proteinPosEnd': 26}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51422, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 21, 'tumorRefCount': 15, 'normalAltCount': 0, 'normalRefCount': 40, 'startPosition': 151478345, 'endPosition': 151478345, 'referenceAllele': 'C', 'proteinChange': 'R120H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRKAG2 R120 missense', 'chr': '7', 'variantAllele': 'T', 'refseqMrnaId': 'NM_016203.3', 'proteinPosStart': 120, 'proteinPosEnd': 120}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 83648, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 43, 'tumorRefCount': 60, 'normalAltCount': 0, 'normalRefCount': 90, 'startPosition': 11282142, 'endPosition': 11282142, 'referenceAllele': 'C', 'proteinChange': 'E129K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType':

'SNP', 'keyword': 'FAM167A E129 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_053279.2', 'proteinPosStart': 129, 'proteinPosEnd': 129}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 54714, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 14, 'tumorRefCount': 38, 'normalAltCount': 0, 'normalRefCount': 80, 'startPosition': 87683246, 'endPosition': 87683246, 'referenceAllele': 'C', 'proteinChange': 'R140H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CNGB3 R140 missense', 'chr': '8', 'variantAllele': 'T', 'refseqMrnaId': 'NM_019098.4', 'proteinPosStart': 140, 'proteinPosEnd': 140}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 138199, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 8, 'tumorRefCount': 105, 'normalAltCount': 0, 'normalRefCount': 89, 'startPosition': 77631307, 'endPosition': 77631307, 'referenceAllele': 'T', 'proteinChange': 'D156G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CARNMT1 D156 missense', 'chr': '9', 'variantAllele': 'C', 'refseqMrnaId': 'NM_152420.1', 'proteinPosStart': 156, 'proteinPosEnd': 156}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 158471, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 48, 'tumorRefCount': 148, 'normalAltCount': 0, 'normalRefCount': 139, 'startPosition': 79438595, 'endPosition': 79438595, 'referenceAllele': 'C', 'proteinChange': 'D237H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PRUNE2 D237 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015225.2', 'proteinPosStart': 237, 'proteinPosEnd': 237}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 5069, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 148, 'normalAltCount': 1, 'normalRefCount': 173, 'startPosition': 118974097, 'endPosition': 118974097, 'referenceAllele': 'G', 'proteinChange': 'D602Y', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PAPPA D602 missense', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_002581.3', 'proteinPosStart': 602, 'proteinPosEnd': 602}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 169436, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 11, 'tumorRefCount': 269, 'normalAltCount': 1, 'normalRefCount': 147, 'startPosition': 136268084, 'endPosition': 136268084, 'referenceAllele': 'A', 'proteinChange': 'K473E', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'STKLD1 K473 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_153710.4', 'proteinPosStart': 473, 'proteinPosEnd': 473}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 8228, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 101, 'normalAltCount': 0, 'normalRefCount': 154,

'startPosition': 7890140, 'endPosition': 7890140, 'referenceAllele': 'C', 'proteinChange': 'X61_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PNPLA4 truncating', 'chr': '23', 'variantAllele': 'T', 'refseqMrnaId': 'NM_004650.2', 'proteinPosStart': 61, 'proteinPosEnd': 61}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 94121, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 44, 'tumorRefCount': 26, 'normalAltCount': 0, 'normalRefCount': 133, 'startPosition': 99955985, 'endPosition': 99955985, 'referenceAllele': 'T', 'proteinChange': 'R149S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SYTL4 R149 missense', 'chr': '23', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 149, 'proteinPosEnd': 149}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 7157, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 47, 'tumorRefCount': 17, 'normalAltCount': 0, 'normalRefCount': 53, 'startPosition': 7579470, 'endPosition': 7579471, 'referenceAllele': '-', 'proteinChange': 'V73Rfs*76', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'TP53 truncating', 'chr': '17', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001126112.2', 'proteinPosStart': 72, 'proteinPosEnd': 73}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 96459, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 26, 'tumorRefCount': 59, 'normalAltCount': 0, 'normalRefCount': 102, 'startPosition': 131007363, 'endPosition': 131007364, 'referenceAllele': '-', 'proteinChange': 'I925Nfs*6', 'mutationType': 'Frame_Shift_Ins', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'FNIP1 truncating', 'chr': '5', 'variantAllele': 'T', 'refseqMrnaId': 'NM_133372.2', 'proteinPosStart': 925, 'proteinPosEnd': 925}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 776, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 734, 'normalAltCount': 0, 'normalRefCount': 231, 'startPosition': 53529193, 'endPosition': 53529195, 'referenceAllele': 'GAT', 'proteinChange': 'M7del', 'mutationType': 'Translation_Start_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'CACNA1D truncating', 'chr': '3', 'variantAllele': '-', 'refseqMrnaId': 'NM_000720.3', 'proteinPosStart': 7, 'proteinPosEnd': 7}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79707, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6614391, 'endPosition': 6614391, 'referenceAllele': 'A', 'proteinChange': 'S58A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NOL9 S58 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_024654.4', 'proteinPosStart': 58, 'proteinPosEnd': 58}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus':

'Untested', 'tumorAltCount': 18, 'tumorRefCount': 5, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 88599696, 'endPosition': 88599697, 'referenceAllele': 'GA', 'proteinChange': 'E444Afs*227', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'ZFPM1 truncating', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 444}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 0, 'tumorRefCount': 23, 'normalAltCount': 0, 'normalRefCount': 2, 'startPosition': 88599697, 'endPosition': 88599705, 'referenceAllele': 'AGCCTCTGG', 'proteinChange': 'E444_L446del', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 444, 'proteinPosEnd': 446}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 161882, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 15, 'tumorRefCount': 6, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 88599703, 'endPosition': 88599705, 'referenceAllele': 'TGG', 'proteinChange': 'L446_A447delinsP', 'mutationType': 'In_Frame_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'chr': '16', 'variantAllele': '-', 'refseqMrnaId': 'NM_153813.2', 'proteinPosStart': 446, 'proteinPosEnd': 447}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2356, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 12, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 130565267, 'endPosition': 130565267, 'referenceAllele': 'A', 'proteinChange': 'I22V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FPGS I22 missense', 'chr': '9', 'variantAllele': 'G', 'refseqMrnaId': 'NM_004957.4', 'proteinPosStart': 22, 'proteinPosEnd': 22}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 90850, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 1, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 2059674, 'endPosition': 2059674, 'referenceAllele': 'T', 'proteinChange': 'E25G', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF598 E25 missense', 'chr': '16', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 25, 'proteinPosEnd': 25}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 11078, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 19, 'tumorRefCount': 16, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 38122462, 'endPosition': 38122462, 'referenceAllele': 'A', 'proteinChange': 'H1300R', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIOBP H1300 missense', 'chr': '22', 'variantAllele': 'G', 'refseqMrnaId': 'NM_001039141.2', 'proteinPosStart': 1300, 'proteinPosEnd': 1300}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 387522, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 48770159, 'endPosition': 48770159, 'referenceAllele': 'T', 'proteinChange': 'N6D', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PEDS1-UBE2V1 N6 missense', 'chr': '20', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001257399.1', 'proteinPosStart': 6, 'proteinPosEnd': 6}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 439915, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 10, 'tumorRefCount': 127, 'normalAltCount': 0, 'normalRefCount': 11, 'startPosition': 1651157, 'endPosition': 1651157, 'referenceAllele': 'A', 'proteinChange': 'G30Afs*221', 'mutationType': 'Frame_Shift_Del', 'ncbiBuild': 'GRCh37', 'variantType': 'DEL', 'keyword': 'KRTAP5-5 truncating', 'chr': '11', 'variantAllele': '-', 'refseqMrnaId': 'NM_001001480.2', 'proteinPosStart': 29, 'proteinPosEnd': 30}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51232, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 54, 'tumorRefCount': 12, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 36583461, 'endPosition': 36583461, 'referenceAllele': 'G', 'proteinChange': 'G9V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CRIM1 G9 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NM_016441.2', 'proteinPosStart': 9, 'proteinPosEnd': 9}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 11186, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 3, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 50378176, 'endPosition': 50378176, 'referenceAllele': 'T', 'proteinChange': 'K21Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RASSF1 K21 missense', 'chr': '3', 'variantAllele': 'G', 'refseqMrnaId': 'NA', 'proteinPosStart': 21, 'proteinPosEnd': 21}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 390992, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 16, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 6305201, 'endPosition': 6305201, 'referenceAllele': 'A', 'proteinChange': 'Q65H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HES3 Q65 missense', 'chr': '1', 'variantAllele': 'C', 'refseqMrnaId': 'NM_001024598.3', 'proteinPosStart': 65, 'proteinPosEnd': 65}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51592, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 8, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 115053471, 'endPosition': 115053471, 'referenceAllele': 'T', 'proteinChange': 'Q76P', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'TRIM33 Q76 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_015906.3', 'proteinPosStart': 76, 'proteinPosEnd': 76}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 9909, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested',

'tumorAltCount': 9, 'tumorRefCount': 120, 'normalAltCount': 0, 'normalRefCount': 46, 'startPosition': 153907278, 'endPosition': 153907278, 'referenceAllele': 'C', 'proteinChange': 'E911Q', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'DENND4B E911 missense', 'chr': '1', 'variantAllele': 'G', 'refseqMrnaId': 'NM_014856.2', 'proteinPosStart': 911, 'proteinPosEnd': 911}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 3428, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 35, 'tumorRefCount': 112, 'normalAltCount': 0, 'normalRefCount': 126, 'startPosition': 159021731, 'endPosition': 159021731, 'referenceAllele': 'A', 'proteinChange': 'E587V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IFI16 E587 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_005531.2', 'proteinPosStart': 587, 'proteinPosEnd': 587}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2205, 'studyId': 'acc_tcga', 'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 50, 'normalAltCount': 0, 'normalRefCount': 58, 'startPosition': 159277689, 'endPosition': 159277689, 'referenceAllele': 'C', 'proteinChange': 'N247K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FCER1A N247 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NM_002001.3', 'proteinPosStart': 247, 'proteinPosEnd': 247}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 1314, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 158, 'normalAltCount': 1, 'normalRefCount': 92, 'startPosition': 160277011, 'endPosition': 160277011, 'referenceAllele': 'C', 'proteinChange': 'G415V', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'COPA G415 missense', 'chr': '1', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 415, 'proteinPosEnd': 415}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 91156, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 38, 'tumorRefCount': 125, 'normalAltCount': 0, 'normalRefCount': 137, 'startPosition': 201182038, 'endPosition': 201182038, 'referenceAllele': 'G', 'proteinChange': 'G2673C', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IGFN1 G2673 missense', 'chr': '1', 'variantAllele': 'T', 'refseqMrnaId': 'NM_001164586.1', 'proteinPosStart': 2673, 'proteinPosEnd': 2673}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84858, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 28, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 19, 'startPosition': 77158945, 'endPosition': 77158945, 'referenceAllele': 'G', 'proteinChange': 'Y501*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ZNF503 truncating', 'chr': '10', 'variantAllele': 'T', 'refseqMrnaId': 'NM_032772.4', 'proteinPosStart': 501, 'proteinPosEnd': 501}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 57661, 'studyId': 'acc_tcga',

'center': 'hgsc.bcm.edu;broad.mit.edu;ucsc.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 62, 'tumorRefCount': 128, 'normalAltCount': 0, 'normalRefCount': 66, 'startPosition': 608465, 'endPosition': 608465, 'referenceAllele': 'G', 'proteinChange': 'K1002N', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'PHRF1 K1002 missense', 'chr': '11', 'variantAllele': 'C', 'refseqMrnaId': 'NA', 'proteinPosStart': 1002, 'proteinPosEnd': 1002}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79611, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 25, 'tumorRefCount': 14, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 81472014, 'endPosition': 81472014, 'referenceAllele': 'G', 'proteinChange': 'V39I', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'ACSS3 V39 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NA', 'proteinPosStart': 39, 'proteinPosEnd': 39}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 115811, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 161, 'normalAltCount': 0, 'normalRefCount': 111, 'startPosition': 113633505, 'endPosition': 113633505, 'referenceAllele': 'C', 'proteinChange': 'A307S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'IQCD A307 missense', 'chr': '12', 'variantAllele': 'A', 'refseqMrnaId': 'NM_138451.1', 'proteinPosStart': 307, 'proteinPosEnd': 307}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 4902, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 20, 'tumorRefCount': 16, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 5828125, 'endPosition': 5828125, 'referenceAllele': 'G', 'proteinChange': 'A179S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'NRTN A179 missense', 'chr': '19', 'variantAllele': 'T', 'refseqMrnaId': 'NM_004558.3', 'proteinPosStart': 179, 'proteinPosEnd': 179}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 92906, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu;broad.mit.edu;bcgsc.ca;mdanderson.org', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 36, 'tumorRefCount': 81, 'normalAltCount': 0, 'normalRefCount': 113, 'startPosition': 38800509, 'endPosition': 38800509, 'referenceAllele': 'G', 'proteinChange': 'P307H', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'HNRNPLL P307 missense', 'chr': '2', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 307, 'proteinPosEnd': 307}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 6431, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 7, 'tumorRefCount': 162, 'normalAltCount': 1, 'normalRefCount': 56, 'startPosition': 42086696, 'endPosition': 42086696, 'referenceAllele': 'G', 'proteinChange': 'R8L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'SRSF6 R8 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NM_006275.5', 'proteinPosStart': 8, 'proteinPosEnd': 8}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId':

'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 51750, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 3, 'tumorRefCount': 36, 'normalAltCount': 0, 'normalRefCount': 58, 'startPosition': 62321687, 'endPosition': 62321687, 'referenceAllele': 'G', 'proteinChange': 'R793L', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'RTEL1 R793 missense', 'chr': '20', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 793, 'proteinPosEnd': 793}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 54584, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 34, 'tumorRefCount': 150, 'normalAltCount': 1, 'normalRefCount': 51, 'startPosition': 19794180, 'endPosition': 19794180, 'referenceAllele': 'A', 'proteinChange': 'X172_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GNB1L truncating', 'chr': '22', 'variantAllele': 'C', 'refseqMrnaId': 'NM_053004.2', 'proteinPosStart': 172, 'proteinPosEnd': 172}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 10491, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 9, 'tumorRefCount': 59, 'normalAltCount': 0, 'normalRefCount': 5, 'startPosition': 33155738, 'endPosition': 33155738, 'referenceAllele': 'G', 'proteinChange': 'G57S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'CRTAP G57 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_006371.4', 'proteinPosStart': 57, 'proteinPosEnd': 57}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 25827, 'studyId': 'acc_tcga', 'center': 'broad.mit.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 4, 'tumorRefCount': 60, 'normalAltCount': 1, 'normalRefCount': 95, 'startPosition': 33339167, 'endPosition': 33339167, 'referenceAllele': 'C', 'proteinChange': 'N5K', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'FBXL2 N5 missense', 'chr': '3', 'variantAllele': 'A', 'refseqMrnaId': 'NM_012157.3', 'proteinPosStart': 5, 'proteinPosEnd': 5}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 683, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 6, 'tumorRefCount': 0, 'normalAltCount': 0, 'normalRefCount': 0, 'startPosition': 15704874, 'endPosition': 15704874, 'referenceAllele': 'G', 'proteinChange': 'G36A', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'BST1 G36 missense', 'chr': '4', 'variantAllele': 'C', 'refseqMrnaId': 'NM_004334.2', 'proteinPosStart': 36, 'proteinPosEnd': 36}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 2891, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 5, 'tumorRefCount': 84, 'normalAltCount': 0, 'normalRefCount': 120, 'startPosition': 158256822, 'endPosition': 158256822, 'referenceAllele': 'G', 'proteinChange': 'X423_splice', 'mutationType': 'Splice_Site', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'GRIA2 truncating', 'chr': '4', 'variantAllele': 'T', 'refseqMrnaId': 'NM_000826.3', 'proteinPosStart': 423, 'proteinPosEnd': 423}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 135656, 'studyId': 'acc_tcga',

'center': 'bcgsc.ca', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 24, 'tumorRefCount': 219, 'normalAltCount': 3, 'normalRefCount': 177, 'startPosition': 30917368, 'endPosition': 30917368, 'referenceAllele': 'C', 'proteinChange': 'S376F', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'MUCL3 S376 missense', 'chr': '6', 'variantAllele': 'T', 'refseqMrnaId': 'NA', 'proteinPosStart': 376, 'proteinPosEnd': 376}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 5447, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 17, 'tumorRefCount': 333, 'normalAltCount': 0, 'normalRefCount': 65, 'startPosition': 75615364, 'endPosition': 75615364, 'referenceAllele': 'T', 'proteinChange': 'F598S', 'mutationType': 'Missense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'keyword': 'POR F598 missense', 'chr': '7', 'variantAllele': 'C', 'refseqMrnaId': 'NM_000941.2', 'proteinPosStart': 598, 'proteinPosEnd': 598}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 79813, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 22, 'tumorRefCount': 39, 'normalAltCount': 0, 'normalRefCount': 3, 'startPosition': 140728974, 'endPosition': 140728974, 'referenceAllele': 'C', 'proteinChange': 'L1238=', 'mutationType': 'Splice_Region', 'ncbiBuild': 'GRCh37', 'variantType': 'SNP', 'chr': '9', 'variantAllele': 'T', 'refseqMrnaId': 'NM_024757.4', 'proteinPosStart': 1238, 'proteinPosEnd': -1}, {'uniqueSampleKey': 'VENHQS1QSy1BNUhDLTAxOmFjY190Y2dh', 'uniquePatientKey': 'VENHQS1QSy1BNUhDOmFjY190Y2dh', 'molecularProfileId': 'acc_tcga_mutations', 'sampleId': 'TCGA-PK-A5HC-01', 'patientId': 'TCGA-PK-A5HC', 'entrezGeneId': 84858, 'studyId': 'acc_tcga', 'center': 'hgsc.bcm.edu', 'mutationStatus': 'Somatic', 'validationStatus': 'Untested', 'tumorAltCount': 30, 'tumorRefCount': 53, 'normalAltCount': 0, 'normalRefCount': 22, 'startPosition': 77158939, 'endPosition': 77158940, 'referenceAllele': '-', 'proteinChange': 'Y503*', 'mutationType': 'Nonsense_Mutation', 'ncbiBuild': 'GRCh37', 'variantType': 'INS', 'keyword': 'ZNF503 truncating', 'chr': '10', 'variantAllele': 'T', 'refseqMrnaId': 'NM_032772.4', 'proteinPosStart': 503, 'proteinPosEnd': 503}]

(cbio_ml_pl_env) D:\000_AI_Helper\000_Do_Informatics\Final_info_controller\ InfoProj_CG_PTTD_CTS\pipeline_interface\cbio_ml_pl\cbioportal_api_project>python list_studies.py
[{'name': 'Adenoid Cystic Carcinoma (MSK, Nat Genet 2013)', 'description': 'Whole-exome or whole-genome sequencing analysis of 60 ACC tumor/normal pairs', 'publicStudy': True, 'pmid': '23685749', 'citation': 'Ho et al. Nat Genet 2013', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2023-12-06 19:10:40', 'allSampleCount': 60, 'readPermission': True, 'studyId': 'acyc_mskcc_2013', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma (FMI, Am J Surg Pathl. 2014)', 'description': 'Targeted Sequencing of 28 metastatic Adenoid Cystic Carcinoma samples.', 'publicStudy': True, 'pmid': '24418857', 'citation': 'Ross et al. Am J Surg Pathl 2014', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2023-12-06 19:11:06', 'allSampleCount': 28, 'readPermission': True, 'studyId': 'acyc_fmi_2014', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma (JHU, Cancer Prev Res 2016)', 'description': 'Whole-genome or whole-exome sequencing of 25 adenoid cystic carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '26862087', 'citation': 'Rettig et al, Cancer Prev Res 2016', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2023-12-06 19:11:07', 'allSampleCount': 25, 'readPermission': True, 'studyId': 'acyc_jhu_2016', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma (MDA, Clin Cancer Res 2015)', 'description': 'WGS of 21 salivary ACCs and targeted molecular analyses of a validation set (81 patients).', 'publicStudy': True, 'pmid': '26631609', 'citation': 'Mitani et al. Clin Cancer Res 2015',

'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2023-12-06 19:11:08', 'allSampleCount': 102, 'readPermission': True, 'studyId': 'acyc_mda_2015', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma (MGH, Nat Gen 2016)', 'description': 'Whole-genome/exome sequencing of 10 ACC PDX models.', 'publicStudy': True, 'pmid': '26829750', 'citation': 'Drier et al. Nature Genetics 2016', 'groups': 'ACYC', 'status': 0, 'importDate': '2023-12-06 19:11:09', 'allSampleCount': 10, 'readPermission': True, 'studyId': 'acyc_mgh_2016', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma (Sanger/MDA, JCI 2013)', 'description': 'Whole exome sequencing of 24 ACCs.', 'publicStudy': True, 'pmid': '23778141', 'citation': 'Stephens et al. JCI 2013', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2023-12-06 19:11:10', 'allSampleCount': 24, 'readPermission': True, 'studyId': 'acyc_sanger_2013', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}, {'name': 'Basal Cell Carcinoma (UNIGE, Nat Genet 2016)', 'description': 'Whole-exome sequencing of 126 basal cell carcinoma tumor/normal pairs; targeted sequencing of 163 sporadic samples (40 tumor/normal pairs) and 4 Gorlin symdrome basal cell carcinomas.', 'publicStudy': True, 'pmid': '26950094', 'citation': 'Bonilla et al. Nat Genet 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:48:55', 'allSampleCount': 293, 'readPermission': True, 'studyId': 'bcc_unige_2016', 'cancerTypeId': 'bcc', 'referenceGenome': 'hg19'}, {'name': 'Acute Lymphoblastic Leukemia (St Jude, Nat Genet 2015)', 'description': 'Comprehensive profiling of infant MLL-rearranged acute lymphoblastic leukemia (MLL-R ALL)', 'publicStudy': True, 'pmid': '25730765', 'citation': 'Andersson et al. Nat Genet 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:49:48', 'allSampleCount': 93, 'readPermission': True, 'studyId': 'all_stjude_2015', 'cancerTypeId': 'bll', 'referenceGenome': 'hg19'}, {'name': 'Ampullary Carcinoma (Baylor College of Medicine, Cell Reports 2016)', 'description': 'Exome sequencing analysis of 160 cancers arising in the periampullary region, 62 of these clearly arising from either the bile duct (n = 44) or the duodenum (n = 18) and 98 for which the epithelium of origin could not be clearly defined morphologically (AMPCA).', 'publicStudy': True, 'pmid': '26804919', 'citation': 'Gingras et al. Cell Rep 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:49:56', 'allSampleCount': 160, 'readPermission': True, 'studyId': 'ampca_bcm_2016', 'cancerTypeId': 'ampca', 'referenceGenome': 'hg19'}, {'name': 'Hypodiploid Acute Lymphoid Leukemia (St Jude, Nat Genet 2013)', 'description': 'Whole genome or exome sequencing of 44 (20 whole genome, 20 exome) ALL tumor/normal pairs.', 'publicStudy': True, 'pmid': '23334668', 'citation': 'Holmfeldt et al. Nat Genet 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-07 09:50:20', 'allSampleCount': 44, 'readPermission': True, 'studyId': 'all_stjude_2013', 'cancerTypeId': 'myeloid', 'referenceGenome': 'hg19'}, {'name': 'Acute Lymphoblastic Leukemia (St Jude, Nat Genet 2016)', 'description': 'Whole-genome and/or whole-exome sequencing of ERG-altered B-ALL tumor/normal pairs.', 'publicStudy': True, 'pmid': '27776115', 'citation': 'Zhang et al. Nat Genet 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:50:27', 'allSampleCount': 73, 'readPermission': True, 'studyId': 'all_stjude_2016', 'cancerTypeId': 'bll', 'referenceGenome': 'hg19'}, {'name': 'The Angiosarcoma Project - Count Me In (Nature Medicine, 2020)', 'description': 'The Angiosarcoma Project is an ongoing patient-driven initiative. This archived Angiosarcoma Project dataset was analyzed in the linked Nature Medicine 2020 manuscript, and is derived from 48 samples from 36 angiosarcoma patients. Angiosarcoma tumor specimens (FFPE) were subjected to whole-exome sequencing (along with matched germline whole-exome sequencing). In addition to genomic data, this study includes patient-reported data (pre-pended as PRD), medical record data (MedR), and pathology report data (PATH). All annotations have been de-identified. Questions about these data can be directed to data@ascproject.org.', 'publicStudy': True, 'pmid': '32042194', 'citation': 'Painter et al. Nat Med 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-07 09:50:36', 'allSampleCount': 48, 'readPermission': True, 'studyId': 'angs_project_painter_2018', 'cancerTypeId': 'angs', 'referenceGenome': 'hg19'}, {'name': 'Breast Fibroepithelial Tumors (Duke-NUS, Nat Genet 2015)', 'description': 'Whole exome sequencing of 22 phyllodes tumors', 'publicStudy': True, 'pmid': '26437033', 'citation': 'Tan et al. Nat Genet 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-

07 09:55:28', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'bfn_duke_nus_2015', 'cancerTypeId': 'bfn', 'referenceGenome': 'hg19'}, {'name': 'Acute Myeloid Leukemia (OHSU, Nature 2018)', 'description': 'Whole-exome sequencing of 672 acute myeloid leukemia samples (with 454 matched normals) from the Beat AML program.', 'publicStudy': True, 'pmid': '30333627', 'citation': 'Tyner et al. Nature 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:57:07', 'allSampleCount': 672, 'readPermission': True, 'studyId': 'aml_ohsu_2018', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Appendiceal Cancer (MSK, J Clin Oncol 2022)', 'description': 'Targeted sequencing of 273 appendiceal tumor/normal pairs via MSK-IMPACT platform.', 'publicStudy': True, 'pmid': '36493333', 'citation': 'Michael B et al. J Clin Oncol 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 09:58:28', 'allSampleCount': 273, 'readPermission': True, 'studyId': 'appendiceal_msk_2022', 'cancerTypeId': 'apad', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Biliary Tract Cancers (SUMMIT - Neratinib Basket Trial, 2022)', 'description': 'Targeted sequencing of 25 advanced biliary tract cancers and their matched normals.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-07 09:58:32', 'allSampleCount': 36, 'readPermission': True, 'studyId': 'biliary_tract_summit_2022', 'cancerTypeId': 'biliary_tract', 'referenceGenome': 'hg19'}, {'name': 'Bladder Urothelial Carcinoma (DFCI/MSK, Cancer Discov 2014)', 'description': 'Whole exome sequencing of tumor/normal samples from 50 patients treated with cisplatin-based chemotherapy for muscle invasive urothelial carcinoma.', 'publicStudy': True, 'pmid': '25096233', 'citation': 'Van Allen et al. Cancer Discov 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:15:02', 'allSampleCount': 50, 'readPermission': True, 'studyId': 'blca_dfarber_mskcc_2014', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK, J Clin Onco 2013)', 'description': 'Comprehensive profiling of 97 high-grade bladder tumors, including targeted sequencing of 15 cancer genes', 'publicStudy': True, 'pmid': '23897969', 'citation': 'Iyer et al. J Clin Oncol 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:15:10', 'allSampleCount': 97, 'readPermission': True, 'studyId': 'blca_mskcc_solit_2012', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Bladder Urothelial Carcinoma (BGI, Nat Genet 2013)', 'description': 'Whole-exome and whole-genome sequencing of 99 bladder cancer tumor/normal pairs. Generated by BGI.', 'publicStudy': True, 'pmid': '24121792', 'citation': 'Guo et al. Nat Genet 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:15:22', 'allSampleCount': 99, 'readPermission': True, 'studyId': 'blca_bgi', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK, Eur Urol 2014)', 'description': 'Genomic Predictors of Survival in Patients with High-grade Urothelial Carcinoma of the Bladder. Targeted sequencing of 109 tumor samples (MSKCC, European Urology 2014).', 'publicStudy': True, 'pmid': '25092538', 'citation': 'Kim et al. Eur Urol 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:15:28', 'allSampleCount': 109, 'readPermission': True, 'studyId': 'blca_mskcc_solit_2014', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Nonmuscle Invasive Bladder Cancer (MSK Eur Urol 2017)', 'description': 'IMPACT sequencing of 105 High Risk Nonmuscle Invasive Bladder Cancer samples.', 'publicStudy': True, 'pmid': '28583311', 'citation': 'Pietzak et al. Eur Urol 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:15:31', 'allSampleCount': 105, 'readPermission': True, 'studyId': 'blca_nmibc_2017', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK, Nat Genet 2016)', 'description': 'Whole exome and targeted sequencing of 34 plasmacytoid-variant (signet ring cell) tumors of the bladder', 'publicStudy': True, 'pmid': '26901067', 'citation': 'Al-Ahmadie et al. Nat Genet 2016', 'groups': '', 'status': 0, 'importDate': '2023-12-07 10:28:53', 'allSampleCount': 34, 'readPermission': True, 'studyId': 'blca_plasmacytoid_mskcc_2016', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (Broad, Nature 2012)', 'description': 'Whole-exome sequencing of 103 breast cancer tumor/normal sample pairs. Generated by the Broad Institute.', 'publicStudy': True, 'pmid': '22722202', 'citation': 'Banerji et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:29:04', 'allSampleCount': 103, 'readPermission': True, 'studyId': 'brca_broad', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Bladder Urothelial Carcinoma (TCGA, Nature 2014)',

'description': 'Whole-exome sequencing of 131 high-grade muscle-invasive urothelial bladder carcinomas', 'publicStudy': True, 'pmid': '24476821', 'citation': 'TCGA, Nature 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:29:08', 'allSampleCount': 131, 'readPermission': True, 'studyId': 'blca_tcga_pub', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Brain Cancer (CPTAC/CHOP, Cell 2020)', 'description': 'Integrated proteogenomic characterization across major histological types of pediatric brain cancer . We report a comprehensive proteogenomics analysis, including whole-genome sequencing, RNA sequencing, and proteomics and phosphoproteomics profiling, of 218 tumors across 7 histological types of childhood brain cancer: low-grade glioma (n = 93), ependymoma (32), high-grade glioma (25), medulloblastoma (22), ganglio-glioma (18), craniopharyngioma (16), and atypical teratoid rhabdoid tumor (12). Proteomics data identify common biological themes that span histological boundaries, suggesting that treatments used for one histological type may be applied effectively to other tumors sharing similar proteomics features. Immune landscape characterization reveals diverse tumor microenvironments across and within diagnoses. Proteomics data further reveal functional effects of somatic mutations and copy number variations (CNVs) not evident in transcriptomics data.', 'publicStudy': True, 'pmid': '33242424', 'citation': 'CPTAC, Cell 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 10:36:21', 'allSampleCount': 218, 'readPermission': True, 'studyId': 'brain_cptac_2020', 'cancerTypeId': 'brain', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Breast Cancer (INSERM, PLoS Med 2016)', 'description': 'Whole exome sequencing of 216 tumor/normal (blood) pairs from metastatic breast cancer patients who underwent a biopsy in the context of the SAFIR01/SAFIR02 (Unicancer, France), SHIVA (Institut Curie, France) or MOSCATO (Gustave Roussy, France) prospective trials.', 'publicStudy': True, 'pmid': '28027327', 'citation': 'Lefebvre et al. PLoS Med 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 11:08:13', 'allSampleCount': 216, 'readPermission': True, 'studyId': 'brca_igr_2015', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (MSK, NPJ Breast Cancer 2019)', 'description': 'Targeted Sequencing of buparlisib + letrozole and alpelisib + letrozole-treated metastatic ER+ unmatched breast tumors.', 'publicStudy': True, 'pmid': '31552290', 'citation': 'Nixon et al. NPJ Breast Cancer 2019', 'groups': 'SOLITD;COMPONC;PUBLIC', 'status': 0, 'importDate': '2023-12-07 11:14:51', 'allSampleCount': 70, 'readPermission': True, 'studyId': 'brca_mskcc_2019', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Juvenile Papillomatosis and Breast Cancer (MSK,J Pathol. 2015)', 'description': 'Whole-exome sequencing analysis of juvenile papillomatosis and coexisting breast carcinoma.', 'publicStudy': True, 'pmid': '33263939', 'citation': 'Timothy M et al. J Pathol 2021', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 11:14:55', 'allSampleCount': 5, 'readPermission': True, 'studyId': 'brca_jup_msk_2020', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'MAPK on resistance to anti-HER2 therapy for breast cancer (MSK, Nat Commun. 2022)', 'description': 'MSK-IMPACT targeted sequencing of 145 breast tumors with matched normal samples.', 'publicStudy': True, 'pmid': '34795269', 'citation': 'Alison E et al. Nat Commun 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-07 11:14:58', 'allSampleCount': 145, 'readPermission': True, 'studyId': 'brca_mapk_hp_msk_2021', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (MSK, Clinical Cancer Res 2020)', 'description': 'Whole-exome and MSK-IMPACT sequencing of 60 tumor/normal matched samples.', 'publicStudy': True, 'pmid': '32220886', 'citation': 'Fresia et al. Clinical Cancer Res 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 11:15:04', 'allSampleCount': 60, 'readPermission': True, 'studyId': 'brca_pareja_msk_2020', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Proteogenomic landscape of breast cancer (CPTAC, Cell 2020)', 'description': 'Proteogenomic landscape of breast cancer tumorigenesis and targeted therapy. Whole exome sequencing 122 samples. Generated by CPTAC.', 'publicStudy': True, 'pmid': '33212010', 'citation': 'Krug et al. Cell 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 11:15:08', 'allSampleCount': 122, 'readPermission': True, 'studyId': 'brca_cptac_2020', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (HTAN, 2022)', 'description': 'Sequencing data from breast cancer patient from

HTAN', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-07 11:47:30', 'allSampleCount': 5, 'readPermission': True, 'studyId': 'brca_hta9_htan_2022', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (Sanger, Nature 2012)', 'description': 'Whole exome sequencing from 100 breast cancer tumor/normal sample pairs. Generated by the Sanger Institute.', 'publicStudy': True, 'pmid': '22722201', 'citation': 'Stephens et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:07:15', 'allSampleCount': 100, 'readPermission': True, 'studyId': 'brca_sanger', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (TCGA, Nature 2012)', 'description': 'Whole-exome sequencing (510 samples with matched normals), genomic DNA copy number arrays, DNA methylation, messenger RNA arrays, microRNA sequencing and reverse-phase protein arrays analysis on 825 primary breast cancer samples. The Cancer Genome Atlas (TCGA) Breast Invasive Carcinoma project. 825 cases.
<i>Nature 2012.</i> Raw data via the TCGA Data Portal.', 'publicStudy': True, 'pmid': '23000897', 'citation': 'TCGA, Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:18:04', 'allSampleCount': 825, 'readPermission': True, 'studyId': 'brca_tcga_pub', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Cancer Cell Line Encyclopedia (Novartis/Broad, Nature 2012)', 'description': 'Targeted sequencing of 1020 samples from Cancer Cell Line Encyclopedia from the Broad Institute and Novartis.', 'publicStudy': True, 'pmid': '22460905', 'citation': 'Barretina et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:23:47', 'allSampleCount': 1020, 'readPermission': True, 'studyId': 'cellline_ccle_broad', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Clear Cell Carcinoma (IRC, Nat Genet 2014)', 'description': 'Multi region exome sequencing of 10 clear cell renal cell carcinomas (ccRCCs)', 'publicStudy': True, 'pmid': '24487277', 'citation': 'Gerlinger et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:41:48', 'allSampleCount': 79, 'readPermission': True, 'studyId': 'ccrcc_irc_2014', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Renal Clear Cell Carcinoma (UTokyo, Nat Genet 2013)', 'description': 'Whole exome and/or whole genome sequencing of 106 clear cell renal cell carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '23797736', 'citation': 'Sato et al. Nat Genet 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:41:53', 'allSampleCount': 106, 'readPermission': True, 'studyId': 'ccrcc_utokyo_2013', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'NCI-60 Cell Lines (NCI, Cancer Res 2012)', 'description': 'Whole-exome sequencing of 67 samples by NCI-60 cell line project; raw data at <A HREF="http://discover.nci.nih.gov/cellminer/loadDownload.do">CellMiner</A>.', 'publicStudy': True, 'pmid': '22802077', 'citation': 'Reinhold et al. Cancer Res 2012', 'groups': '', 'status': 0, 'importDate': '2023-12-07 12:42:03', 'allSampleCount': 67, 'readPermission': True, 'studyId': 'cellline_nci60', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (MSK, Cancer Cell 2018)', 'description': 'Targeted Sequencing of tumor/normal sample pairs from 1918 Breast cancers.', 'publicStudy': True, 'pmid': '30205045', 'citation': 'Razavi et al. Cancer Cell 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-07 12:43:05', 'allSampleCount': 1918, 'readPermission': True, 'studyId': 'breast_msk_2018', 'cancerTypeId': 'breast', 'referenceGenome': 'hg19'}, {'name': 'Cancer Cell Line Encyclopedia (Broad, 2019)', 'description': 'Cancer Cell Line Encyclopedia from the Broad Institute and Novartis, updated 2019. Data downloaded from the Broad CCLE Portal. For more info about the proteomics data, see the README.', 'publicStudy': True, 'pmid': '31068700,31978347', 'citation': 'Stransky et al. Nature. 2015, Nusinow et al. Cell. 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 12:43:33', 'allSampleCount': 1739, 'readPermission': True, 'studyId': 'ccle_broad_2019', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (MSK, Nature Cancer 2020)', 'description': 'Targeted sequencing of pre- and post-treatment tumor/cfDNA samples from 51 Breast Cancer patients

to understand the mechanisms of resistance to Alepelisib.', 'publicStudy': True, 'pmid': '32864625', 'citation': 'Razavi et al. Nature Cancer 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 13:21:06', 'allSampleCount': 141, 'readPermission': True, 'studyId': 'breast_alpelisib_2020', 'cancerTypeId': 'breast', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (SMC 2018)', 'description': 'Whole-exome sequencing of 187 primary tumors from a Korean breast cancer cohort (SMC).', 'publicStudy': True, 'pmid': '29713003', 'citation': 'Kan et al. Nature Communications 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-07 13:21:17', 'allSampleCount': 187, 'readPermission': True, 'studyId': 'brca_smc_2018', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Clear Cell Renal Cell Carcinoma (DFCI, Science 2019)', 'description': 'Whole-exome sequencing of metastatic clear cell renal carcinoma (ccRCC) from 35 tumor/normal pairs.', 'publicStudy': True, 'pmid': '29301960', 'citation': 'Miao et al. Science 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 13:21:38', 'allSampleCount': 35, 'readPermission': True, 'studyId': 'ccrcc_dfci_2019', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Breast Cancer (MSK, Cancer Discovery 2022)', 'description': 'Targeted Sequencing of 1365 metastatic Breast Cancer tumor/normal pairs via MSK-IMPACT to understand the role of INK4 on CDK4/6 resistance.', 'publicStudy': True, 'pmid': '34544752', 'citation': 'Qing et al. Cancer Discovery 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-07 13:21:52', 'allSampleCount': 1365, 'readPermission': True, 'studyId': 'breast_ink4_msk_2021', 'cancerTypeId': 'breast', 'referenceGenome': 'hg19'}, {'name': 'Intrahepatic Cholangiocarcinoma (JHU, Nat Genet 2013)', 'description': 'Exome sequencing of tumor/normal pairs from 32 intrahepatic cholangiocarcinoma cases and 8 gall bladder carcinoma cases.', 'publicStudy': True, 'pmid': '24185509', 'citation': 'Jiao et al. Nat Genet 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:43:30', 'allSampleCount': 40, 'readPermission': True, 'studyId': 'chol_jhu_2013', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (National Cancer Centre of Singapore, Nat Genet 2013)', 'description': 'Exome sequencing of 15 cholangiocarcinoma cases.', 'publicStudy': True, 'pmid': '24185513', 'citation': 'Chan-on et al. Nat Genet 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:44:25', 'allSampleCount': 15, 'readPermission': True, 'studyId': 'chol_nccs_2013', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (National University of Singapore, Nat Genet 2012)', 'description': 'Exome Sequencing for Opisthorchis viverrini-related cholangiocarcinoma in 8 O.viverrini-related tumors and matched normal tissue.', 'publicStudy': True, 'pmid': '22561520', 'citation': 'Ong et al. Nat Genet 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:45:19', 'allSampleCount': 8, 'readPermission': True, 'studyId': 'chol_nus_2012', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Chronic Lymphocytic Leukemia (IUOPA, Nature 2015)', 'description': 'Mutation data from whole-genome or whole-exome sequencing of 428 CLL, 54 MBL, and 24 SLL tumor/normal pairs.', 'publicStudy': True, 'pmid': '26200345', 'citation': 'Puente et al. Nature 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-07 15:46:13', 'allSampleCount': 506, 'readPermission': True, 'studyId': 'cll_iuopa_2015', 'cancerTypeId': 'cllsll', 'referenceGenome': 'hg19'}, {'name': 'Chronic Lymphocytic Leukemia (Broad, Nature 2015)', 'description': 'Whole exome sequencing of 537 chronic lymphocytic leukemia tumor/normal pairs.', 'publicStudy': True, 'pmid': '26466571', 'citation': 'Landau et al. Nature 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:47:14', 'allSampleCount': 537, 'readPermission': True, 'studyId': 'cll_broad_2015', 'cancerTypeId': 'cllsll', 'referenceGenome': 'hg19'}, {'name': 'Chronic lymphocytic leukemia (ICGC, Nature Genetics 2011)', 'description': 'Whole-exome sequencing of 105 Chronic Lymphocytic Leukemia samples.', 'publicStudy': True, 'pmid': '22158541', 'citation': 'Quesada et al. Nature Genetics 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:48:21', 'allSampleCount': 105, 'readPermission': True, 'studyId': 'cllsll_icgc_2011', 'cancerTypeId': 'cllsll', 'referenceGenome': 'hg19'}, {'name': 'Colon Adenocarcinoma (CaseCCC, PNAS 2015)', 'description': 'Whole-exome sequencing of tumor/normal pairs from 29 African American Colon Cancers.', 'publicStudy': True, 'pmid': '25583493', 'citation': 'Guda et al. PNAS 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:49:16', 'allSampleCount': 29, 'readPermission': True, 'studyId':

'coad_caseccc_2015', 'cancerTypeId': 'coad', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (MSK, Clin Cancer Res 2018)', 'description': 'Targeted sequencing (MSK-IMPACT) of 195 tumor samples (194 with matched normals) from 192 cholangiocarcinoma patients.', 'publicStudy': True, 'pmid': '29848569', 'citation': 'Lowery et al. Clin Cancer Res 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-07 15:50:14', 'allSampleCount': 195, 'readPermission': True, 'studyId': 'chol_msk_2018', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (ICGC, Cancer Discov 2017)', 'description': 'Whole-exome sequencing and Targeted/Exome sequencing of 489 Cholangiocarcinoma samples from 10 countries.', 'publicStudy': True, 'pmid': '28667006', 'citation': 'Jusakul et al. Cancer Discov 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 15:51:10', 'allSampleCount': 489, 'readPermission': True, 'studyId': 'chol_icgc_2017', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Colorectal Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/COADREAD/ 20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 16:32:06', 'allSampleCount': 640, 'readPermission': True, 'studyId': 'coadread_tcga', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (Genentech, Nature 2012)', 'description': 'Whole-genome sequencing of 74 paired colon tumor-normal samples.', 'publicStudy': True, 'pmid': '22895193', 'citation': 'Seshagiri et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 16:37:33', 'allSampleCount': 74, 'readPermission': True, 'studyId': 'coadread_genentech', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma Triplets (MSK, Genome Biol 2014)', 'description': 'Targeted sequencing of primary, metastatic, and normal tissues from 69 colorectal adenocarcinoma patients.', 'publicStudy': True, 'pmid': '25164765', 'citation': 'Brannon et al. Genome Biol 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 16:37:59', 'allSampleCount': 138, 'readPermission': True, 'studyId': 'coadread_mskcc', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Cutaneous Squamous Cell Carcinoma (DFCI, Clin Cancer Res 2015)', 'description': 'Targeted sequencing of 29 metastatic cutaneous squamous cell carcinoma samples.', 'publicStudy': True, 'pmid': '25589618', 'citation': 'Li et al. Clin Cancer Res 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 16:40:33', 'allSampleCount': 29, 'readPermission': True, 'studyId': 'cscc_dfarber_2015', 'cancerTypeId': 'cscc', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (DFCI, Cell Reports 2016)', 'description': 'Whole-exome sequencing of 619 colorectal cancers with clinicopathologic annotations.', 'publicStudy': True, 'pmid': '27149842', 'citation': 'Giannakis et al. Cell Reports 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 16:40:45', 'allSampleCount': 619, 'readPermission': True, 'studyId': 'coadread_dfci_2016', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Cutaneous Squamous Cell Carcinoma (MD Anderson, Clin Cancer Res 2014)', 'description': 'Whole-exome sequencing of tumor/normal pairs from 39 aggressive cutaneous squamous cell carcinoma cases.', 'publicStudy': True, 'pmid': '25303977', 'citation': 'Pickering et al. Clin Cancer Res 2014', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:42:11', 'allSampleCount': 39, 'readPermission': True, 'studyId': 'cscc_hgsc_bcm_2014', 'cancerTypeId': 'cscc', 'referenceGenome': 'hg19'}, {'name': 'Colon Cancer (CPTAC-2 Prospective, Cell 2019)', 'description': 'Proteogenomic analysis of prospectively collected 110 human colon adenocarcinoma tumor normal pairs. Data generated by CPTAC.', 'publicStudy': True, 'pmid': '31031003', 'citation': 'Vasaikar et al. Cell 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:43:15', 'allSampleCount': 110, 'readPermission': True, 'studyId': 'coad_cptac_2019', 'cancerTypeId': 'coad', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Cancer (MSK, JNCI 2021)', 'description': 'Targeted sequencing of 1,516 samples from 818 patients with early onset and 698 patients with average onset colorectal cancer and their matched normals.', 'publicStudy': True, 'pmid': '34405229', 'citation': 'Cercek et al. JNCI 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:46:19', 'allSampleCount': 1516, 'readPermission': True, 'studyId': 'crc_eo_2020', 'cancerTypeId': 'bowel',

'referenceGenome': 'hg19'}, {'name': 'Colorectal Cancer (MSK, Gastroenterology 2020)', 'description': 'Targeted sequencing of 471 unresectable colorectal tumor/normal pairs via MSK-IMPACT.', 'publicStudy': True, 'pmid': '32730818', 'citation': 'Mondaca et al. Gastroenterology 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:46:51', 'allSampleCount': 471, 'readPermission': True, 'studyId': 'crc_apc_impact_2020', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Disparities in metastatic colorectal cancer between Africans and Americans (MSK, 2020)', 'description': 'Targeted sequencing of 64 colorectal tumor/normal pairs via MSK-IMPACT to determine the epigenetic differences seen in Nigerian patients.', 'publicStudy': True, 'pmid': '34819518', 'citation': 'Alatise et al. Nat Commun 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:47:09', 'allSampleCount': 64, 'readPermission': True, 'studyId': 'crc_nigerian_2020', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Cancer (MSK, JCO Precis Oncol 2022)', 'description': 'Molecular characterization of 47 BRAF inhibitor-naive colorectal cancer patients with dual RAS hotspot/BRAF V600E mutations.', 'publicStudy': True, 'pmid': '35235413', 'citation': 'Gularte-Merida et al. JCO Precis Oncol 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:47:22', 'allSampleCount': 47, 'readPermission': True, 'studyId': 'crc_dd_2022', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Cancer (MSK, Cancer Discovery 2022)', 'description': 'Targeted sequencing of patient-derived xenografts, cell lines, tumors and their matched normals from 22 colorectal samples via MSK-IMPACT.', 'publicStudy': True, 'pmid': '36355783', 'citation': 'Yaeger et al. Cancer Discovery 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-07 16:47:35', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'coadread_mskresistance_2022', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Desmoplastic Melanoma (Broad Institute, Nat Genet 2015)', 'description': 'Exome/Whole Genome sequencing of 20 desmoplastic melanoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '26343386', 'citation': 'Shain et al. Nat Genet 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 17:56:54', 'allSampleCount': 20, 'readPermission': True, 'studyId': 'desm_broad_2015', 'cancerTypeId': 'desm', 'referenceGenome': 'hg19'}, {'name': 'Gastric Adenocarcinoma (TMUCIH, PNAS 2015)', 'description': 'Whole-exome sequencing of 78 Gastric Adenocarcinomas and their matched normal samples.', 'publicStudy': True, 'pmid': '25583476', 'citation': 'Chen et al. PNAS 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 17:57:14', 'allSampleCount': 78, 'readPermission': True, 'studyId': 'egc_tmucih_2015', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Cutaneous T Cell Lymphoma (Columbia U, Nat Genet 2015)', 'description': 'Whole-Exome Sequencing (WXS) of tumor-normal sample pairs from 25 patients with Sezary Syndrome and 17 patients with other Cutaneous T Cell Lymphoma (CTCLs).', 'publicStudy': True, 'pmid': '26551667', 'citation': 'Da Silva Almeida et al. Nat Genet 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-07 17:57:31', 'allSampleCount': 43, 'readPermission': True, 'studyId': 'ctcl_columbia_2015', 'cancerTypeId': 'nhl', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Large B-Cell Lymphoma (Broad, PNAS 2012)', 'description': 'Whole exome sequencing of 58 primary DLBCL samples and their matched normals.', 'publicStudy': True, 'pmid': '22343534', 'citation': 'Lohr et al. PNAS 2012', 'groups': '', 'status': 0, 'importDate': '2023-12-07 17:57:45', 'allSampleCount': 58, 'readPermission': True, 'studyId': 'dlbc_broad_2012', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Esophagogastric Cancer (MSK, Cancer Discovery 2017)', 'description': 'Targeted sequencing of 341 samples from 305 metastatic esophagogastric cancer patients', 'publicStudy': True, 'pmid': '29122777', 'citation': 'Janjigian et al. Cancer Discov 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 17:58:02', 'allSampleCount': 341, 'readPermission': True, 'studyId': 'egc_msk_2017', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Large B-Cell Lymphoma (Duke, Cell 2017)', 'description': 'Whole-exome sequencing of 1,001 Diffuse Large B Cell Lymphoma (DLBCL) tumors (N = 1001) and paired-normal tissue (N = 400).', 'publicStudy': True, 'pmid': '28985567', 'citation': 'Reddy et al. Cell 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 17:58:17', 'allSampleCount': 1001, 'readPermission': True, 'studyId': 'dlbcl_duke_2017', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Large B

cell Lymphoma (DFCI, Nat Med 2018)', 'description': 'Whole-exome sequencing of tumor/matching normal sample pairs from 135 DLBCL patients.', 'publicStudy': True, 'pmid': '29713087', 'citation': 'Chapuy et al. Nat Med 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 17:58:31', 'allSampleCount': 135, 'readPermission': True, 'studyId': 'dlbcl_dfci_2018', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg19'}, {'name': 'Cutaneous Squamous Cell Carcinoma (UCSF, NPJ Genom Med 2021)', 'description': 'Catalogue of driver genes in cutaneous squamous cell carcinoma. Meta-analysis of 105 normal/tumor pairs.', 'publicStudy': True, 'pmid': '34272401', 'citation': 'Chang et al. NPJ Genom Med 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:01:02', 'allSampleCount': 83, 'readPermission': True, 'studyId': 'cscc_ucsf_2021', 'cancerTypeId': 'cscc', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Squamous Cell Carcinoma (UCLA, Nat Genet 2014)', 'description': 'Whole exome sequencing (WXS) or targeted deep sequencing (TDS) of 139 paired esophageal squamous cell carcinoma patients.', 'publicStudy': True, 'pmid': '24686850', 'citation': 'Lin et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:20:47', 'allSampleCount': 139, 'readPermission': True, 'studyId': 'escc_ucla_2014', 'cancerTypeId': 'escc', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Adenocarcinoma (DFCI, Nat Genet 2013)', 'description': 'Whole-exome sequencing of 149 tumor/normal pairs and whole-genome sequencing of 16 pairs from 149 esophageal adenocarcinoma patients.', 'publicStudy': True, 'pmid': '23525077', 'citation': 'Dulak et al. Nat Genet 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:21:04', 'allSampleCount': 151, 'readPermission': True, 'studyId': 'esca_broad', 'cancerTypeId': 'esca', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Squamous Cell Carcinoma (ICGC, Nature 2014)', 'description': 'Whole-genome or whole-exome sequencing of 88 esophageal squamous cell carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '24670651', 'citation': 'Song et al. Nature 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:21:27', 'allSampleCount': 88, 'readPermission': True, 'studyId': 'escc_icgc', 'cancerTypeId': 'escc', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Ewing Sarcoma (DFCI, Cancer Discov 2014)', 'description': 'Whole exome sequencing of 96 pediatric Ewing Sarcoma tumors and 11 cell lines.', 'publicStudy': True, 'pmid': '25186949', 'citation': 'Crompton et al. Cancer Discov 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:21:46', 'allSampleCount': 107, 'readPermission': True, 'studyId': 'es_dfarber_broad_2014', 'cancerTypeId': 'es', 'referenceGenome': 'hg19'}, {'name': 'Ewing Sarcoma (Institut Curie, Cancer Discov 2014)', 'description': 'Whole-genome sequencing of 112 Ewing sarcoma samples and matched germ line DNA.', 'publicStudy': True, 'pmid': '25223734', 'citation': 'Tirode et al. Cancer Discov 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:22:05', 'allSampleCount': 115, 'readPermission': True, 'studyId': 'es_iocurie_2014', 'cancerTypeId': 'es', 'referenceGenome': 'hg19'}, {'name': 'Gallbladder Carcinoma (Shanghai, Nat Genet 2014)', 'description': 'Whole exome sequencing of 32 gallbladder carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '24997986', 'citation': 'Maolan Li et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:22:20', 'allSampleCount': 32, 'readPermission': True, 'studyId': 'gbc_shanghai_2014', 'cancerTypeId': 'gbc', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma (TCGA, Nature 2008)', 'description': 'Targeted sequencing in 91 of the 206 primary glioblastoma tumors (143 with matched normals) from the Cancer Genome Atlas (TCGA) Glioblastoma Project.', 'publicStudy': True, 'pmid': '18772890', 'citation': 'TCGA, Nature 2008', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:22:35', 'allSampleCount': 206, 'readPermission': True, 'studyId': 'gbm_tcga_pub', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma (TCGA, Cell 2013)', 'description': 'Whole-exome and/or whole-genome sequencing of 291 of the 577 glioblastoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) Glioblastoma Project.', 'publicStudy': True, 'pmid': '24120142', 'citation': 'TCGA, Cell 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:23:22', 'allSampleCount': 577, 'readPermission': True, 'studyId': 'gbm_tcga_pub2013', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Germ Cell Tumors (MSK, J Clin Oncol 2016)', 'description': 'Whole-exome and Targeted sequencing of 19 samples and Targeted sequencing of 161 samples from 180 Germ Cell Tumor patients.', 'publicStudy': True, 'pmid': '27646943', 'citation':

'Bagrodia et al. J Clin Oncol 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:25:42', 'allSampleCount': 180, 'readPermission': True, 'studyId': 'gct_msk_2016', 'cancerTypeId': 'testis', 'referenceGenome': 'hg19'}, {'name': 'Gallbladder Cancer (MSK, Cancer 2018)', 'description': 'Targeted Sequencing of 103 samples with matched normals from 101 Gallbladder cancer patients.', 'publicStudy': True, 'pmid': '30427539', 'citation': 'Raja et al, Cancer 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:25:57', 'allSampleCount': 103, 'readPermission': True, 'studyId': 'gbc_msk_2018', 'cancerTypeId': 'gbc', 'referenceGenome': 'hg19'}, {'name': 'Brain Tumor PDXs (Mayo Clinic, Clin Cancer Res 2020)', 'description': 'WES on a total of 106 PDXs and 80 PDXs have the matched germline (blood) samples sequenced. A total of 66 PDXs have RNASeq available', 'publicStudy': True, 'pmid': '31852831', 'citation': 'Vaubel et al. Clin Cancer Res 2020', 'groups': 'SHULANTIANMAYO;PUBLIC;DECKERPAULMAYO', 'status': 0, 'importDate': '2023-12-07 18:26:12', 'allSampleCount': 106, 'readPermission': True, 'studyId': 'gbm_mayo_pdx_sarkaria_2019', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Cancer-TRAP Project (MSK, Lancet Oncol 2020)', 'description': 'Targeted and WES recapture sequencing of tumor/normal samples from 37 Esophageal Cancer patients.', 'publicStudy': True, 'pmid': '32437664', 'citation': 'Janjigian et al. Lancet Oncol 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:27:12', 'allSampleCount': 68, 'readPermission': True, 'studyId': 'egc_trap_msk_2020', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma (Columbia, Nat Med. 2019)', 'description': 'Whole-exome sequencing of 32 out of 42 glioblastomas patients with matched normals.', 'publicStudy': True, 'pmid': '30742119', 'citation': 'Zhao et al. Nat Med 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:27:52', 'allSampleCount': 42, 'readPermission': True, 'studyId': 'gbm_columbia_2019', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma (CPTAC, Cell 2021)', 'description': 'Proteogenomic and metabolomic characterization of human glioblastoma. Whole genome or whole exome sequencing of 99 samples. Generated by CPTAC.', 'publicStudy': True, 'pmid': '33577785', 'citation': 'Wang et al. Cell 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:28:07', 'allSampleCount': 99, 'readPermission': True, 'studyId': 'gbm_cptac_2021', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Recurrent and Metastatic Head & Neck Cancer (MSK, JAMA Oncol 2016)', 'description': 'Targeted sequencing of 151 patients with advanced, treatment resistant head and neck tumors', 'publicStudy': True, 'pmid': '27442865', 'citation': 'Morris et al. JAMA Oncol 2016', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:39:56', 'allSampleCount': 151, 'readPermission': True, 'studyId': 'hnc_mskcc_2016', 'cancerTypeId': 'head_neck', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinomas (INSERM, Nat Genet 2015)', 'description': 'Whole-exome sequencing of 243 liver tumors and matched normals.', 'publicStudy': True, 'pmid': '25822088', 'citation': 'Schulze et al. Nat Genet 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:40:12', 'allSampleCount': 243, 'readPermission': True, 'studyId': 'hcc_inserm_fr_2015', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinoma (MSK, Clin Cancer Res 2018)', 'description': 'MSK-IMPACT sequencing of 127 Hepatocellular Carcinoma tumor samples with matched normals.', 'publicStudy': True, 'pmid': '30373752', 'citation': 'Harding et al. Clin Cancer Res 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:40:37', 'allSampleCount': 127, 'readPermission': True, 'studyId': 'hcc_mskimpact_2018', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Liver Hepatocellular Adenoma and Carcinomas (MSK, PLOS One 2018)', 'description': 'Targeted sequencing of tumor/normal pairs of 9 LIAD and 10 HCC patients via MSK-IMPACT platform.', 'publicStudy': True, 'pmid': '30052636', 'citation': 'Zheng et al. PLOS One 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:40:52', 'allSampleCount': 19, 'readPermission': True, 'studyId': 'hcc_msk_venturaa_2018', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Glioma (MSK, Clin Cancer Res 2019)', 'description': 'Targeted sequencing on MSK-IMPACT and FMI Panels of 1004 samples (837 with matched normals) from 923 glioma patients.', 'publicStudy': True, 'pmid': '31263031', 'citation': 'Jonsson et al. Clin Cancer Res 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:41:06', 'allSampleCount': 1004, 'readPermission':

True, 'studyId': 'glioma_mskcc_2019', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Glioma (MSK, Nature 2019)', 'description': 'Targeted Sequencing of CSF samples (91 samples with 86 matched normals) from 42 glioma patients.', 'publicStudy': True, 'pmid': '30675060', 'citation': 'Miller et al. Nature 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-07 18:41:29', 'allSampleCount': 91, 'readPermission': True, 'studyId': 'glioma_msk_2018', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Histiocytosis Cobimetinib (MSK, Nature 2019)', 'description': 'Targeted and whole exome sequencing of 52 histiocytosis tumor/normal pairs.', 'publicStudy': True, 'pmid': '30867592', 'citation': 'Eli et al. Nature 2019', 'groups': 'DIAMONDHISTCOBI;PUBLIC;HYMANHISTCOBI;OMARHISTCOBI', 'status': 0, 'importDate': '2023-12-07 18:41:56', 'allSampleCount': 52, 'readPermission': True, 'studyId': 'histiocytosis_cobi_msk_2019', 'cancerTypeId': 'hdcn', 'referenceGenome': 'hg19'}, {'name': 'Germ Cell Tumors and Shared Leukemias (MSK, J Clin Invest 2020)', 'description': 'Targeted and WES sequencing of germ cell tumor and shared leukemia samples.', 'publicStudy': True, 'pmid': '32897884', 'citation': 'Taylor et al. J Clin Invest 2020', 'groups': 'JTMED11;DONOGHUM;PUBLIC;ABDELWAO2', 'status': 0, 'importDate': '2023-12-07 18:42:11', 'allSampleCount': 21, 'readPermission': True, 'studyId': 'gct_msk_2020', 'cancerTypeId': 'testis', 'referenceGenome': 'hg19'}, {'name': 'Combined Hepatocellular and Intrahepatic Cholangiocarcinoma (Peking University, Cancer Cell 2019)', 'description': 'Whole-exome sequencing of 121 combined hepatocellular and intrahepatic cholangiocarcinoma (cHCC-ICC) patients with matched normal pairs (whole-genome sequenced samples are not included here).', 'publicStudy': True, 'pmid': '31130341', 'citation': 'Xue et al. Cancer Cell 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:42:24', 'allSampleCount': 173, 'readPermission': True, 'studyId': 'hccihch_pku_2019', 'cancerTypeId': 'hccihch', 'referenceGenome': 'hg19'}, {'name': 'High-Grade Serous Ovarian Cancer (MSK, NPJ Genome Med 2021)', 'description': 'Targeted Sequencing of 45 Serous Ovarian Cancer tumor/normal pairs from 45 patients.', 'publicStudy': True, 'pmid': '34819508', 'citation': 'Elkin et al. NPJ Genome Med 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:42:45', 'allSampleCount': 45, 'readPermission': True, 'studyId': 'hgsoc_msk_2021', 'cancerTypeId': 'hgsoc', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinoma (MERiC/Basel, Nat Commun. 2022)', 'description': 'Whole-exome sequencing of 122 Hepatocellular carcinomas and their matched normals. Dataset was generated in 2021 by MERiC and Charlotte Ng (hg19 original; Basel/Bern research pipeline).', 'publicStudy': True, 'pmid': '35508466', 'citation': 'Charlotte Ng et al. Nat Commun. 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:42:59', 'allSampleCount': 122, 'readPermission': True, 'studyId': 'hcc_meric_2021', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'MSK-IMPACT Heme Tumors (MSK, 2022)', 'description': 'Targeted sequencing of 2383 myeloid and lymphoid neoplasms and their matched normals via MSK-IMPACT Heme panel.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:43:22', 'allSampleCount': 2383, 'readPermission': True, 'studyId': 'heme_msk_impact_2022', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Gastrointestinal Stromal Tumor (MSK, NPJ Precis Oncol 2023)', 'description': 'Paired analysis of 499 Gastrointestinal stromal tumor/normal pairs via MSK-IMPACT platform.', 'publicStudy': True, 'pmid': '36593350', 'citation': 'Diana et al. NPJ Precis Oncol 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-07 18:43:53', 'allSampleCount': 499, 'readPermission': True, 'studyId': 'gist_msk_2022', 'cancerTypeId': 'gist', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Clear Cell Carcinoma (BGI, Nat Genet 2012)', 'description': 'Whole-exome sequencing of 10 ccRCC tumor/normal pairs and targeted sequencing of 88 clear cell carcinoma tumor/normal pairs. Generated by BGI-Shenzhen.', 'publicStudy': True, 'pmid': '22138691', 'citation': 'Guo et al. Nat Genet 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:52:13', 'allSampleCount': 98, 'readPermission': True, 'studyId': 'kirc_bgi', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Clear Cell Carcinoma (TCGA, Nature 2013)', 'description': 'Whole-exome sequencing in 417 of 446 clear cell renal cell carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '23792563', 'citation': 'TCGA,

Nature 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:52:29', 'allSampleCount': 446, 'readPermission': True, 'studyId': 'kirc_tcga_pub', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Chromophobe (TCGA, Cancer Cell 2014)', 'description': 'Whole-exome sequencing of 66 chromophobe renal cell carcinoma (ChRCCs) tumor/normal pairs.', 'publicStudy': True, 'pmid': '25155756', 'citation': 'TCGA, Cancer Cell 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:54:00', 'allSampleCount': 66, 'readPermission': True, 'studyId': 'kich_tcga_pub', 'cancerTypeId': 'chrcc', 'referenceGenome': 'hg19'}, {'name': 'Head and Neck Squamous Cell Carcinoma (Broad, Science 2011)', 'description': 'Whole-exome sequencing of 74 head and neck squamous cell carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '21798893', 'citation': 'Stransky et al. Science 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:54:27', 'allSampleCount': 74, 'readPermission': True, 'studyId': 'hnsc_broad', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Head and Neck Squamous Cell Carcinoma (Johns Hopkins, Science 2011)', 'description': 'Exome sequencing of 32 head and neck squamous cell carcinoma tumor/normal sample pairs.', 'publicStudy': True, 'pmid': '21798897', 'citation': 'Agrawal et al. Science 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:54:47', 'allSampleCount': 32, 'readPermission': True, 'studyId': 'hnsc_jhu', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Head and Neck Squamous Cell Carcinoma (TCGA, Nature 2015)', 'description': 'Whole-exome sequencing and/or whole-genome sequencing of 279 head and neck squamous cell carcinoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) head and neck squamous cell carcinoma Project.', 'publicStudy': True, 'pmid': '25631445', 'citation': 'TCGA, Nature 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:55:04', 'allSampleCount': 279, 'readPermission': True, 'studyId': 'hnsc_tcga_pub', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Oral Squamous Cell Carcinoma (MD Anderson, Cancer Discov 2013)', 'description': 'Whole-exome sequencing of 40 oral squamous cell carcinoma tumor/normal sample pairs.', 'publicStudy': True, 'pmid': '23619168', 'citation': 'Pickering et al. Cancer Discov 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 10:58:15', 'allSampleCount': 40, 'readPermission': True, 'studyId': 'hnsc_mdanderson_2013', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Chronic Lymphocytic Leukemia (Broad, Cell 2013)', 'description': 'Whole-exome sequencing of 160 CLL tumor/normal pairs.', 'publicStudy': True, 'pmid': '23415222', 'citation': 'Landau et al. Cell 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 10:58:31', 'allSampleCount': 160, 'readPermission': True, 'studyId': 'lcll_broad_2013', 'cancerTypeId': 'cllsll', 'referenceGenome': 'hg19'}, {'name': 'Intrahepatic Cholangiocarcinoma (Shanghai, Nat Commun 2014)', 'description': 'Whole exome sequencing of 103 tumor/normal sample pairs in 103 intrahepatic cholangiocarcinoma patients.', 'publicStudy': True, 'pmid': '25526346', 'citation': 'Shanshan et al. Nat Commun 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:58:48', 'allSampleCount': 103, 'readPermission': True, 'studyId': 'ihch_smmu_2014', 'cancerTypeId': 'ihch', 'referenceGenome': 'hg19'}, {'name': 'Intrahepatic Cholangiocarcinoma (MSK, Clin Cancer Res 2021)', 'description': 'Targeted sequencing of IMPACT and CMO samples', 'publicStudy': True, 'pmid': '33963001', 'citation': 'Jolissaint et al. Clin Cancer Res 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-08 10:59:07', 'allSampleCount': 219, 'readPermission': True, 'studyId': 'ihch_mskcc_2020', 'cancerTypeId': 'ihch', 'referenceGenome': 'hg19'}, {'name': 'Intrahepatic Cholangiocarcinoma (Mount Sinai 2015)', 'description': 'Whole-exome sequencing of 8 tumor-normal paired iCCA samples by Liver Cancer Program at the Icahn School of Medicine at Mount Sinai, in collaboration with Barcelona-ClÃ\xadnic Liver Cancer Group.', 'publicStudy': True, 'pmid': '25608663', 'citation': 'Sia et al. Nature Commun 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-08 10:59:23', 'allSampleCount': 8, 'readPermission': True, 'studyId': 'ihch_ismms_2015', 'cancerTypeId': 'ihch', 'referenceGenome': 'hg19'}, {'name': 'Intrahepatic Cholangiocarcinoma (MSK, Hepatology 2021)', 'description': 'Targeted sequencing of 412 intrahepatic cholangiocarcinoma tumor/normal sample pairs.', 'publicStudy': True, 'pmid': '33765338', 'citation': 'Boerner et al. Hepatology 2021', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 10:59:39', 'allSampleCount': 412, 'readPermission': True, 'studyId':

'ihch_msk_2021', 'cancerTypeId': 'ihch', 'referenceGenome': 'hg19'}, {'name': 'Low-Grade Gliomas (UCSF, Science 2014)', 'description': 'Whole exome sequencing of 23 grade II glioma tumor/normal pairs.', 'publicStudy': True, 'pmid': '24336570', 'citation': 'Johnson et al. Science 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:06:19', 'allSampleCount': 61, 'readPermission': True, 'studyId': 'lgg_ucsf_2014', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Merged Cohort of LGG and GBM (TCGA, Cell 2016)', 'description': 'Whole exome sequencing of 1,122 LGG and GBM tumor/normal pairs.', 'publicStudy': True, 'pmid': '26824661', 'citation': 'TCGA, Cell 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:06:41', 'allSampleCount': 1122, 'readPermission': True, 'studyId': 'lgggbm_tcga_pub', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Liver Hepatocellular Carcinoma (AMC, Hepatology 2014)', 'description': 'Whole exome sequencing of 231 hepatocellular carcinomas and matched normal tissue pairs.', 'publicStudy': True, 'pmid': '24798001', 'citation': 'Ahn et al. Hepatology 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:10:51', 'allSampleCount': 231, 'readPermission': True, 'studyId': 'lihc_amc_prv', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Liver Hepatocellular Carcinoma (RIKEN, Nat Genet 2012)', 'description': 'Whole-genome sequencing of 27 hepatocellular carcinoma tumor/norma pairs from RIKEN.', 'publicStudy': True, 'pmid': '22634756', 'citation': 'Fujimoto et al. Nat Genet 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:11:28', 'allSampleCount': 27, 'readPermission': True, 'studyId': 'lihc_riken', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (MSK, Science 2015)', 'description': 'Whole-exome sequencing of 34 non small cell lung cancer tumor/normal pairs.', 'publicStudy': True, 'pmid': '25765070', 'citation': 'Rizvi et al. Science 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:11:45', 'allSampleCount': 35, 'readPermission': True, 'studyId': 'luad_mskcc_2015', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (Broad, Cell 2012)', 'description': 'Whole-exome and/or whole-genome sequencing of 183 lung adenocarcinomas and matched normal tissue pairs.', 'publicStudy': True, 'pmid': '22980975', 'citation': 'Imielinksi et al. Cell 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:12:09', 'allSampleCount': 183, 'readPermission': True, 'studyId': 'luad_broad', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (TCGA, Nature 2014)', 'description': 'Whole exome sequencing of 230 lung adenocarcinoma tumor/normal pairs. Raw data via the TCGA Data Portal.', 'publicStudy': True, 'pmid': '25079552', 'citation': 'TCGA, Nature 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:13:57', 'allSampleCount': 230, 'readPermission': True, 'studyId': 'luad_tcga_pub', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (TSP, Nature 2008)', 'description': 'Targeted sequencing of 163 lung adenocarcinoma tumor/normal pairs. Generated by WashU/Broad.', 'publicStudy': True, 'pmid': '18948947', 'citation': 'Ding et al. Nature 2008', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:17:44', 'allSampleCount': 163, 'readPermission': True, 'studyId': 'luad_tsp', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Adenoma (INSERM, Cancer Cell 2014)', 'description': 'Whole-exome sequencing of 46 liver tumor/normal pairs.', 'publicStudy': True, 'pmid': '24735922', 'citation': 'Pilati et al. Cancer Cell 2014', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:18:01', 'allSampleCount': 46, 'readPermission': True, 'studyId': 'liad_inserm_fr_2014', 'cancerTypeId': 'liad', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Cancer (MSK, Cancer Discov 2017)', 'description': 'Targeted sequencing of 860 patients with metastatic lung adenocarcinoma', 'publicStudy': True, 'pmid': '28336552', 'citation': 'Jordan et al. Cancer Discov 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:18:18', 'allSampleCount': 915, 'readPermission': True, 'studyId': 'lung_msk_2017', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (MSK, J Thorac Oncol 2020)', 'description': 'Targeted sequencing of 604 lung adenocarcinoma tumor/normal pairs via MSK-IMPACT.', 'publicStudy': True, 'pmid': '32791233', 'citation': 'Caso et al. J Thorac Oncol 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:18:42', 'allSampleCount': 604, 'readPermission': True, 'studyId': 'luad_mskcc_2020', 'cancerTypeId':

'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma Met Organotropism (MSK, Cancer Cell 2023)', 'description': 'Targeted and whole-exome sequencing of 2653 lung adenocarcinoma tumor/normal sample pairs.', 'publicStudy': True, 'pmid': '37084736', 'citation': 'Lengel, Harry B et al. Cancer Cell 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:19:03', 'allSampleCount': 2653, 'readPermission': True, 'studyId': 'luad_mskcc_2023_met_organotropism', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (MSK, NPJ Precision Oncology 2021)', 'description': 'Targeted sequencing of 426 matched normal samples from 426 lung adenocarcinoma patients.', 'publicStudy': True, 'pmid': '34290393', 'citation': 'Caso et al. NPJ Precis Oncol 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:23:29', 'allSampleCount': 426, 'readPermission': True, 'studyId': 'luad_msk_npjpo_2021', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (MSK, 2021)', 'description': 'Targeted sequencing of 186 matched normal samples from 186 lung adenocarcinoma patient via MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:23:49', 'allSampleCount': 186, 'readPermission': True, 'studyId': 'luad_mskimpact_2021', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (CPTAC, Cell 2020)', 'description': 'Whole genome (WGS) or whole exome sequencing (WES) of 110 tumors and 101 matched normal adjacent tissues in lung adenocarcinoma. Proteogenomic characterization generated by CPTAC.', 'publicStudy': True, 'pmid': '32649874', 'citation': 'M.A. Gillette et al. Cell 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:24:08', 'allSampleCount': 110, 'readPermission': True, 'studyId': 'luad_cptac_2020', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Low-Grade Serous Ovarian Cancer (MSK, Clin Cancer Res 2022)', 'description': 'Characterization of the somatic mutational landscape of MAPK pathway in 119 low-grade serous ovarian carcinomas and their matched normals.', 'publicStudy': True, 'pmid': '35443055', 'citation': 'Manning-Geist et al. Clin Cancer Res. 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:25:07', 'allSampleCount': 119, 'readPermission': True, 'studyId': 'lgsoc_mapk_msk_2022', 'cancerTypeId': 'lgsoc', 'referenceGenome': 'hg19'}, {'name': 'Lung Squamous Cell Carcinoma (TCGA, Nature 2012)', 'description': 'Whole exome sequencing of 178 lung squamous cell carcinoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) Lung Squamous Cell Carcinoma project.', 'publicStudy': True, 'pmid': '22960745', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:36:53', 'allSampleCount': 178, 'readPermission': True, 'studyId': 'lusc_tcga_pub', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg19'}, {'name': 'Medulloblastoma (Broad, Nature 2012)', 'description': 'Whole exome sequencing of 92 primary medulloblastoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '22820256', 'citation': 'Pugh et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:39:10', 'allSampleCount': 92, 'readPermission': True, 'studyId': 'mbl_broad_2012', 'cancerTypeId': 'mbl', 'referenceGenome': 'hg19'}, {'name': 'Medulloblastoma (ICGC, Nature 2012)', 'description': 'Comprehensive profiling of 125 matched tumor and germline medulloblastoma samples', 'publicStudy': True, 'pmid': '22832583', 'citation': 'Jones et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:39:29', 'allSampleCount': 125, 'readPermission': True, 'studyId': 'mbl_icgc', 'cancerTypeId': 'mbl', 'referenceGenome': 'hg19'}, {'name': 'Medulloblastoma (PCGP, Nature 2012)', 'description': "Whole genome sequencing of 37 medulloblastoma tumors and their matched normals from the Pediatric Cancer Genome Project (PCGP), a joint project by St. Jude Children's Research Hospital and Washington University.", 'publicStudy': True, 'pmid': '22722829', 'citation': 'Robinson et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:39:47', 'allSampleCount': 37, 'readPermission': True, 'studyId': 'mbl_pcgp', 'cancerTypeId': 'mbl', 'referenceGenome': 'hg19'}, {'name': 'Mantle Cell Lymphoma (IDIBIPS, PNAS 2013)', 'description': 'Whole exome sequencing of 29 primary mantle cell lymphomas and their matched normals.', 'publicStudy': True, 'pmid': '24145436', 'citation': 'BeÃ\xa0 et al. PNAS 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:40:05', 'allSampleCount': 29, 'readPermission': True, 'studyId': 'mcl_idibips_2013', 'cancerTypeId': 'mcl', 'referenceGenome': 'hg19'}, {'name': 'Myelodysplasia

(UTokyo, Nature 2011)', 'description': 'Whole exome sequencing of 29 myelodysplasia tumor/normal pairs.', 'publicStudy': True, 'pmid': '21909114', 'citation': 'Yoshida et al. Nature 2011', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:40:23', 'allSampleCount': 29, 'readPermission': True, 'studyId': 'mds_tokyo_2011', 'cancerTypeId': 'mds', 'referenceGenome': 'hg19'}, {'name': 'Medulloblastoma (Sickkids, Nature 2016)', 'description': 'Whole-genome sequencing of 46 recurrent medulloblastoma samples.', 'publicStudy': True, 'pmid': '26760213', 'citation': 'Morrissy et al. Nature 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:40:41', 'allSampleCount': 46, 'readPermission': True, 'studyId': 'mbl_sickkids_2016', 'cancerTypeId': 'mbl', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Melanoma (UCLA, Cell 2016)', 'description': 'Whole-exome sequencing of 38 pretreated (pembrolizumab, nivolumab) melanoma tumor-normal pairs.', 'publicStudy': True, 'pmid': '26997480', 'citation': 'Hugo et al. Cell 2016', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:41:37', 'allSampleCount': 38, 'readPermission': True, 'studyId': 'mel_ucla_2016', 'cancerTypeId': 'mel', 'referenceGenome': 'hg19'}, {'name': 'Thoracic PDX (MSK, Provisional)', 'description': 'Targeted sequencing of thoracic PDX lines to characterize genetic alterations in 318 tumor/normal pairs via MSK-IMPACT. This cohort is a PDX tracker of all lung cancer PDX generated at MSK that have been through IMPACT sequencing. This is a live datafeed, increasing over time, not published as a cohort.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:43:37', 'allSampleCount': 318, 'readPermission': True, 'studyId': 'lung_msk_pdx', 'cancerTypeId': 'lung', 'referenceGenome': 'hg19'}, {'name': 'Lymphoma Cell Lines (MSK, Blood 2020)', 'description': 'Targeted sequencing of 34 lymphoma cell lines using HemePACT_v3', 'publicStudy': True, 'pmid': '33067607', 'citation': 'Neeta et al. Blood 2021', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:44:43', 'allSampleCount': 34, 'readPermission': True, 'studyId': 'lymphoma_cellline_msk_2020', 'cancerTypeId': 'lymph', 'referenceGenome': 'hg19'}, {'name': 'Myelodysplastic (MSK, 2020)', 'description': 'Single-cell genomics reveals the genetic and molecular bases for escape from mutational epistasis in myeloid neoplasms', 'publicStudy': True, 'pmid': '27276561,30333627,24030381', 'citation': 'Papaemmanuil et al. NEJM 2016; Tyner et al. Nature 2018; Papaemmanuil et al. Blood 2013', 'groups': 'PENSONA;OMARHISTCOBI', 'status': 0, 'importDate': '2023-12-08 12:45:01', 'allSampleCount': 4231, 'readPermission': True, 'studyId': 'mds_mskcc_2020', 'cancerTypeId': 'mds', 'referenceGenome': 'hg19'}, {'name': 'Lung Cancer (SMC, Cancer Research 2016)', 'description': 'Whole exome and whole transcriptome sequencing of primary and multiple metastatic lymph node samples from 6 lung cancer patients with their matched normals.', 'publicStudy': True, 'pmid': '27634761', 'citation': 'Sang-Won et al. Cancer Research 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:47:26', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'lung_smc_2016', 'cancerTypeId': 'lung', 'referenceGenome': 'hg19'}, {'name': 'Metaplastic Breast Cancer (MSK,NPJ Breast Cancer 2021)', 'description': 'Targeted or whole-exome sequencing of 19 Metaplastic Breast Cancer tumor/normal pairs.', 'publicStudy': True, 'pmid': '33863915', 'citation': 'Edaise M et al. NPJ Breast Cancer 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:47:46', 'allSampleCount': 19, 'readPermission': True, 'studyId': 'mbc_msk_2021', 'cancerTypeId': 'mbc', 'referenceGenome': 'hg19'}, {'name': 'Melanoma (MSK, Clin Cancer Res 2021)', 'description': 'Targeted sequencing (MSK-IMPACT) of 696 melanoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '33509808', 'citation': 'Alexander N et al. Clin Cancer Res 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:48:05', 'allSampleCount': 696, 'readPermission': True, 'studyId': 'mel_mskimpact_2020', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Thoracic Cancer (MSK, Nat Commun 2021)', 'description': 'Targeted sequencing of tumor and PDX thoracic samples.', 'publicStudy': True, 'pmid': '35440124', 'citation': 'Rebecca et al. Nat Commun. 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:48:34', 'allSampleCount': 69, 'readPermission': True, 'studyId': 'lung_pdx_msk_2021', 'cancerTypeId': 'lung', 'referenceGenome': 'hg19'}, {'name': 'Medulloblastoma (DKFZ, Nature 2017)', 'description': 'Whole genome or whole exome sequencing of 491 previously untreated Medulloblastoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '28726821', 'citation': 'Northcott et al. Nature 2017', 'groups': 'PUBLIC', 'status': 0,

'importDate': '2023-12-08 12:48:55', 'allSampleCount': 491, 'readPermission': True, 'studyId': 'mbl_dkfz_2017', 'cancerTypeId': 'mbl', 'referenceGenome': 'hg19'}, {'name': 'Lung Squamous Cell Carcinoma (CPTAC, Cell 2021)', 'description': 'Whole genome / whole exome sequencing and proteogenomic portrait of 108 prospectively collected, treatment-naive, primary LSCC tumors and 99 paired normal adjacent tissues. Generated by CPTAC.', 'publicStudy': True, 'pmid': '34358469', 'citation': 'Shankha Satpathy et al. 2021 Cell.', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:49:33', 'allSampleCount': 80, 'readPermission': True, 'studyId': 'lusc_cptac_2021', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg19'}, {'name': 'Lung Cancer in Never Smokers (NCI, Nature Genetics 2021)', 'description': 'Whole-genome sequencing of 232 treatment-naive never smoker patients with Lung cancer and their matched normals.', 'publicStudy': True, 'pmid': '34493867', 'citation': 'Zhang et al. Nature Genetics 2021', 'groups': '', 'status': 0, 'importDate': '2023-12-08 12:50:18', 'allSampleCount': 232, 'readPermission': True, 'studyId': 'lung_nci_2022', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Myelodysplastic Syndromes (MDS IWG, IPSSM, NEJM Evidence 2022)', 'description': 'International Working Group for the prognosis of Myelodysplastic Syndromes. Derivation of the Molecular International Prognosis Scoring System for MDS. Comprehensive profiling of 3,323 treatment-naive MDS samples. Data generated by the Papaemmanuil Lab 2022.', 'publicStudy': True, 'citation': 'Bernard et al. NEJM Evidence 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 12:50:43', 'allSampleCount': 3323, 'readPermission': True, 'studyId': 'mds_iwg_2022', 'cancerTypeId': 'mds', 'referenceGenome': 'hg19'}, {'name': 'Multiple Myeloma (Broad, Cancer Cell 2014)', 'description': 'Whole-exome or whole-genome sequencing of 203 multiple myeloma paired tumor/normal sample pairs.', 'publicStudy': True, 'pmid': '24434212', 'citation': 'Lohr et al. Cancer Cell 2014', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:16:59', 'allSampleCount': 211, 'readPermission': True, 'studyId': 'mm_broad', 'cancerTypeId': 'pcm', 'referenceGenome': 'hg19'}, {'name': 'Malignant Peripheral Nerve Sheath Tumor (MSK, Nat Genet 2014)', 'description': 'Whole exome sequencing of 15 malignant peripheral nerve sheath tumor/normal pairs.', 'publicStudy': True, 'pmid': '25240281', 'citation': 'Lee et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:17:26', 'allSampleCount': 15, 'readPermission': True, 'studyId': 'mpnst_mskcc', 'cancerTypeId': 'mpnst', 'referenceGenome': 'hg19'}, {'name': 'Neuroblastoma (AMC Amsterdam, Nature 2012)', 'description': 'Whole genome sequencing of 87 primary neuroblastoma tumors and their matched normals.', 'publicStudy': True, 'pmid': '22367537', 'citation': 'Molenaar et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:17:57', 'allSampleCount': 87, 'readPermission': True, 'studyId': 'nbl_amc_2012', 'cancerTypeId': 'nbl', 'referenceGenome': 'hg19'}, {'name': 'Rhabdoid Cancer (BCGSC, Cancer Cell 2016)', 'description': 'Whole-genome sequencing of tumor-normal sample pairs from 40 patients with Malignant Rhabdoid Cancer.', 'publicStudy': True, 'pmid': '26977886', 'citation': 'E. Chun et al. Cancer Cell 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:18:16', 'allSampleCount': 40, 'readPermission': True, 'studyId': 'mrt_bcgsc_2016', 'cancerTypeId': 'mrt', 'referenceGenome': 'hg19'}, {'name': 'MSK-IMPACT Clinical Sequencing Cohort (MSK, Nat Med 2017)', 'description': 'Targeted sequencing of 10,000 clinical cases using the MSK-IMPACT assay', 'publicStudy': True, 'pmid': '28481359', 'citation': 'Zehir et al. Nat Med 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:18:35', 'allSampleCount': 10945, 'readPermission': True, 'studyId': 'msk_impact_2017', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Pan-cancer (Columbia U, Genome Med 2016)', 'description': 'Whole exome sequencing of 103 samples (88 with matched normals) from 88 high-risk pediatric cancer patients.', 'publicStudy': True, 'pmid': '28007021', 'citation': 'Oberg et al. Genome Med 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:20:28', 'allSampleCount': 103, 'readPermission': True, 'studyId': 'mixed_pipseq_2017', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'MSS Mixed Solid Tumors (Broad/Dana-Farber, Nat Genet 2018)', 'description': 'Whole exome sequencing of tumor/normal pairs and corresponding clinical outcomes from patients treated with immune checkpoint inhibitors across multiple cancer types including melanoma, non-small cell lung cancer, head and neck

cancer, and bladder cancer.', 'publicStudy': True, 'pmid': '30150660', 'citation': 'Miao et al. Nat Genet 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:20:58', 'allSampleCount': 249, 'readPermission': True, 'studyId': 'mixed_allen_2018', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Myeloproliferative Neoplasms (CIMR, NEJM 2013)', 'description': 'Whole exome sequencing of paired tumor/normal pairs from 151 cases of Myeloproliferative Neoplasms.', 'publicStudy': True, 'pmid': '24325359', 'citation': 'Nangalia et al. NEJM 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:22:02', 'allSampleCount': 151, 'readPermission': True, 'studyId': 'mpn_cimr_2013', 'cancerTypeId': 'mpn', 'referenceGenome': 'hg19'}, {'name': 'Acute myeloid leukemia or myelodysplastic syndromes (WashU, 2016)', 'description': "Enhanced exome or targeted sequencing of 116 acute myeloid leukemia (AML) or myelodysplastic syndromes (MDS) patients' tumor/normal pairs .", 'publicStudy': True, 'pmid': '27959731', 'citation': 'Welch et al. N Engl J Med. 2016', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:22:23', 'allSampleCount': 136, 'readPermission': True, 'studyId': 'mnm_washu_2016', 'cancerTypeId': 'mnm', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Solid Cancers (UMich, Nature 2017)', 'description': 'Whole-exome and -transcriptome sequencing of 500 adult patients with metastatic solid tumor/primary normal pairs of diverse lineage and biopsy site.', 'publicStudy': True, 'pmid': '28783718', 'citation': 'Robinson et al. Nature 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:22:43', 'allSampleCount': 500, 'readPermission': True, 'studyId': 'metastatic_solid_tumors_mich_2017', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Mixed Tumors Selpercatinib RET Trial (MSK, Nat Commun. 2022)', 'description': 'Targeted sequencing of Selpercatinib treated RET-driven solid cancers.', 'publicStudy': True, 'pmid': '35304457', 'citation': 'Ezra Y et al. Nat Commun 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:23:36', 'allSampleCount': 188, 'readPermission': True, 'studyId': 'mixed_selpercatinib_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Mixed cfDNA (MSK, Genome Med 2021)', 'description': 'IMPACT sequencing of 229 cell-free DNA (cfDNA) and associated tumor samples with matched normal', 'publicStudy': True, 'pmid': '34059130', 'citation': 'Tsui et al. Genome Med 2021', 'groups': 'TSUIW;DANALHE3', 'status': 0, 'importDate': '2023-12-08 13:23:57', 'allSampleCount': 229, 'readPermission': True, 'studyId': 'mixed_cfdna_msk_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Cancer Therapy and Clonal Hematopoiesis (MSK, Nat Genet 2020)', 'description': 'Clonal hematopoiesis mutations identified in blood samples from 24,146 patients whose tumor-blood pairs were analyzed using MSK-IMPACT.', 'publicStudy': True, 'pmid': '33106634', 'citation': 'Kelly et al. Nat Genet 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:24:19', 'allSampleCount': 24146, 'readPermission': True, 'studyId': 'msk_ch_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'MSK MetTropism (MSK, Cell 2021)', 'description': 'MSK-MET (Memorial Sloan Kettering - Metastatic Events and Tropisms) is an integrated pan-cancer cohort of tumor genomic and clinical outcome data from 25,000 patients. We analyzed this dataset to identify associations between tumor genomic alterations and patterns of metastatic dissemination across 50 tumor types. We found that chromosomal instability is strongly correlated with metastatic burden in some tumor types, including prostate adenocarcinoma, lung adenocarcinoma and HR+/HER2+ breast ductal carcinoma, but not in others, such as colorectal MSS, pancreatic adenocarcinoma and high-grade serous ovarian cancer. We also identified specific somatic alterations associated with increased metastatic burden and specific routes of metastatic spread. Our data offer a unique resource for the investigation of the biologic basis for metastatic spread and highlight the crucial role of chromosomal instability in cancer progression', 'publicStudy': True, 'pmid': '35120664', 'citation': 'Nguyen et al. Cell 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:25:01', 'allSampleCount': 25775, 'readPermission': True, 'studyId': 'msk_met_2021', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'MSK-IMPACT and MSK-ACCESS Mixed Cohort (MSK, Nat Commun 2021)', 'description': 'Targeted sequencing of 1446 Tumor and cfDNA samples (1440 with matched normals) from MSK-IMPACT and MSK-ACCESS.', 'publicStudy': True, 'pmid': '34145282', 'citation': 'Brannon et al. Nat Commun 2021', 'groups': 'IMPACT_ACCESS;PUBLIC', 'status': 0, 'importDate': '2023-12-08

13:29:31', 'allSampleCount': 1446, 'readPermission': True, 'studyId': 'msk_access_2021', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'The Metastatic Prostate Cancer Project (Provisional, June 2021)', 'description': 'The Metastatic Prostate Cancer Project is a patient-driven initiative. This study includes genomic data, cfDNA tumor fractions, patient-reported data (pre-pended as PRD), medical record data (MedR), and pathology report data (PATH). As these data were generated in a research, not a clinical, laboratory, they are for research purposes only and cannot be used to inform clinical decision-making. All annotations have been de-identified. More information is available at www.mpcproject.org. For questions about these data, including how to cite, please visit www.mpcproject.org/data-release or direct questions to data@mpcproject.org.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:32:58', 'allSampleCount': 123, 'readPermission': True, 'studyId': 'mpcproject_broad_2021', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Cancer Therapy and Clonal Hematopoiesis (MSK, Clin Cancer Res 2022)', 'description': 'Clonal hematopoiesis mutations identified in blood samples from patients whose tumor-blood pairs were analyzed using MSK-IMPACT.', 'publicStudy': True, 'pmid': '35078859', 'citation': 'Barbara et al. Clin Cancer Res 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:34:52', 'allSampleCount': 657, 'readPermission': True, 'studyId': 'msk_ch_ped_2021', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Pancan Tumors (MSK,Nat Commun. 2022)', 'description': 'Targeted NGS of mixed pediatric tumors from MSK-IMPACT testing.', 'publicStudy': True, 'pmid': '35585047', 'citation': 'Shukla,N et al. Nat Commun 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 13:35:14', 'allSampleCount': 135, 'readPermission': True, 'studyId': 'mixed_kunga_msk_2022', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pan-Cancer MSK-IMPACT MET Validation Cohort (MSK 2022)', 'description': 'Targeted sequencing of clinical cases via MSK-IMPACT.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 13:35:38', 'allSampleCount': 69, 'readPermission': True, 'studyId': 'mixed_impact_subset_2022', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Renal Non-Clear Cell Carcinoma (Genentech, Nat Genet 2014)', 'description': 'Exome sequencing of 139 samples with matched normals and RNA-sequencing of 7 samples (5 samples with matched normals) from 145 Renal Non-Clear Cell Carcinoma (nccRCC) patients.', 'publicStudy': True, 'pmid': '25401301', 'citation': 'Durinck et al. Nat Genet 2014', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:05:20', 'allSampleCount': 146, 'readPermission': True, 'studyId': 'nccrcc_genentech_2014', 'cancerTypeId': 'nccrcc', 'referenceGenome': 'hg19'}, {'name': 'Nasopharyngeal Carcinoma (Singapore, Nat Genet 2014)', 'description': 'Whole exome sequencing of 56 NPC tumor/normal pairs.', 'publicStudy': True, 'pmid': '24952746', 'citation': 'Lin et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:05:48', 'allSampleCount': 56, 'readPermission': True, 'studyId': 'npc_nusingapore', 'cancerTypeId': 'npc', 'referenceGenome': 'hg19'}, {'name': 'Neuroendocrine Prostate Cancer (Multi-Institute, Nat Med 2016)', 'description': 'Whole exome sequencing of 114 metastatic tumor/normal pairs to understand genomic overlap between castration resistant adenocarcinoma (CRPC-Adeno) and neuroendocrine histologies (CRPC-NE).', 'publicStudy': True, 'pmid': '26855148', 'citation': 'Beltran et al. Nat Med 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:06:12', 'allSampleCount': 114, 'readPermission': True, 'studyId': 'nepc_wcm_2016', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Neuroblastoma (Broad, Nature 2015)', 'description': 'Whole-genome sequencing of 56 neuroblastoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '26466568', 'citation': 'Peifer et al. Nature 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:06:45', 'allSampleCount': 56, 'readPermission': True, 'studyId': 'nbl_ucologne_2015', 'cancerTypeId': 'nbl', 'referenceGenome': 'hg19'}, {'name': 'Pan-Lung Cancer (TCGA, Nat Genet 2016)', 'description': 'Whole-exome sequencing of 660 lung ADC and 484 lung SqCC tumor/normal pairs.', 'publicStudy': True, 'pmid': '27158780', 'citation': 'TCGA, Nat Genet 2016', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:07:10', 'allSampleCount': 1144, 'readPermission': True, 'studyId': 'nsclc_tcga_broad_2016', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Neuroblastoma (Broad, Nat Genet 2013)', 'description': 'Whole Genome and Whole Exome sequencing

of 240 high-risk neuroblastoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '23334666', 'citation': 'Pugh et al. Nat Genet 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:20:17', 'allSampleCount': 240, 'readPermission': True, 'studyId': 'nbl_broad_2013', 'cancerTypeId': 'nbl', 'referenceGenome': 'hg19'}, {'name': 'Non-Hodgkin Lymphoma (BCGSC, Nature 2011)', 'description': 'Whole genome or whole exome sequencing of 14 NHL tumors and their matched normals.', 'publicStudy': True, 'pmid': '21796119', 'citation': 'Morin et al. Nature 2011', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:20:46', 'allSampleCount': 14, 'readPermission': True, 'studyId': 'nhl_bcgsc_2011', 'cancerTypeId': 'nhl', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Large B-cell Lymphoma (BCGSC, Blood 2013)', 'description': 'Whole genome sequencing of 40 DLBCL tumor/normal pairs and 13 cell lines.', 'publicStudy': True, 'pmid': '23699601', 'citation': 'Morin et al. Blood 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:21:12', 'allSampleCount': 53, 'readPermission': True, 'studyId': 'nhl_bcgsc_2013', 'cancerTypeId': 'nhl', 'referenceGenome': 'hg19'}, {'name': 'Anaplastic Oligodendroglioma and Anaplastic Oligoastrocytoma (MSK, Neuro Oncol 2017)', 'description': 'IMPACT sequencing of 22 Anaplastic Oligodendroglioma and Anaplastic Oligoastrocytomas.', 'publicStudy': True, 'pmid': '28472509', 'citation': 'Thomas et al. Neuro Oncol 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:21:44', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'odg_msk_2017', 'cancerTypeId': 'odg', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer (University of Turin, Lung Cancer 2017)', 'description': 'Targeted next-generation sequencing of 41 NSCLC samples.', 'publicStudy': True, 'pmid': '27346245', 'citation': 'VavalÃ\xa0 et al. Lung Cancer 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:22:10', 'allSampleCount': 41, 'readPermission': True, 'studyId': 'nsclc_unito_2016', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer (TRACERx, NEJM & Nature 2017)', 'description': 'Whole-exome sequencing of 327 primary tumors with matched germline samples, and phylogenetic ctDNA sequencing of 96 pre- and 24 postoperative samples from 100 NSCLC TRACERx patients.', 'publicStudy': True, 'pmid': '28445112,28445469', 'citation': 'Hanjani et al. NEJM 2017, Abbosh et al. Nature 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:22:36', 'allSampleCount': 447, 'readPermission': True, 'studyId': 'nsclc_tracerx_2017', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Neuroblastoma (TARGET, 2018)', 'description': 'Whole genome or whole exome sequencing on 1089 NBL samples. Comprehensive profiling of 1089 NBL samples. <p>TARGET data is intended exclusively for biomedical research using pediatric data (i.e., the research objectives cannot be accomplished using data from adults) that focus on the development of more effective treatments, diagnostic tests, or prognostic markers for childhood cancers. Moreover, TARGET data can be used for research relevant to the biology, causes, treatment and late complications of treatment of pediatric cancers, but is not intended for the sole purposes of methods and/or tool development (please see Using TARGET Data section of the OCG website). If you are interested in using TARGET data for publication or other research purposes, you must follow the TARGET Publication Guidelines.</p>', 'publicStudy': True, 'groups': 'NCI-TARGET;PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:23:30', 'allSampleCount': 1089, 'readPermission': True, 'studyId': 'nbl_target_2018_pub', 'cancerTypeId': 'nbl', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer (MSK, J Clin Oncol 2018)', 'description': 'IMPACT sequencing of 240 NSCLC tumor/normal pairs treated at MSKCC with anti-PD-(L)1 based therapy.', 'publicStudy': True, 'pmid': '29337640', 'citation': 'Rizvi et al. J Clin Oncol 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:24:36', 'allSampleCount': 240, 'readPermission': True, 'studyId': 'nsclc_pd1_msk_2018', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer (MSK, Science 2015)', 'description': 'Whole-exome sequencing of tumor-normal tissue pairs from 16 non-small cell lung cancer samples.', 'publicStudy': True, 'pmid': '25765070', 'citation': 'Rivzi et al. Science 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:25:05',

'allSampleCount': 16, 'readPermission': True, 'studyId': 'nsclc_mskcc_2015', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer (MSK, Cancer Cell 2018)', 'description': 'Whole-exome sequencing of 75 tumor/normal NSCLC pairs treated with PD-1 plus CTLA-4 blockade..', 'publicStudy': True, 'pmid': '29657128', 'citation': 'Hellmann et al. Cancer Cell 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:25:33', 'allSampleCount': 75, 'readPermission': True, 'studyId': 'nsclc_mskcc_2018', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Non-Small Cell Lung Cancer (MSK, Nature Medicine 2022)', 'description': 'Targeted sequencing of ctDNA samples drawn from patients with metastatic NSCLC using the Resolution ctDx Lung platform. For more information contact jeej@mskcc.org or lib1@mskcc.org', 'publicStudy': True, 'pmid': '36357680', 'citation': 'Jee et al. Nature Medicine 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:26:13', 'allSampleCount': 2621, 'readPermission': True, 'studyId': 'nsclc_ctdx_msk_2022', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Neuroblastoma (MSK, Nat Genet 2023)', 'description': 'Targeted sequencing of 223 pediatric neuroblastoma tumor/normal pairs via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37169874', 'citation': 'Gunes et al. Nat Genet 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-08 14:26:51', 'allSampleCount': 223, 'readPermission': True, 'studyId': 'nbl_msk_2023', 'cancerTypeId': 'nbl', 'referenceGenome': 'hg19'}, {'name': 'Ovarian Serous Cystadenocarcinoma (TCGA, Nature 2011)', 'description': 'Whole exome sequencing of 489 high-grade serous ovarian adenocarcinoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) Serous Ovarian Cancer project. 489 cases.
Raw data via the TCGA Data Portal.', 'publicStudy': True, 'pmid': '21720365', 'citation': 'TCGA, Nature 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 14:55:27', 'allSampleCount': 489, 'readPermission': True, 'studyId': 'ov_tcga_pub', 'cancerTypeId': 'hgsoc', 'referenceGenome': 'hg19'}, {'name': 'Acinar Cell Carcinoma of the Pancreas (JHU, J Pathol 2014)', 'description': 'Whole exome sequencing of 23 surgically resected pancreatic carcinomas with acinar differentiation and their matched normals.', 'publicStudy': True, 'pmid': '24293293', 'citation': 'Jial et al. J Pathol 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:02:08', 'allSampleCount': 23, 'readPermission': True, 'studyId': 'paac_jhu_2014', 'cancerTypeId': 'paac', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Adenocarcinoma (ICGC, Nature 2012)', 'description': 'Whole-exome sequencing of 99 pancreatic samples and their matched normals.', 'publicStudy': True, 'pmid': '23103869', 'citation': 'Biankin et al. Nature 2012', 'groups': '', 'status': 0, 'importDate': '2023-12-08 15:02:37', 'allSampleCount': 99, 'readPermission': True, 'studyId': 'paad_icgc', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Cancer (UTSW, Nat Commun 2015)', 'description': 'Whole exome sequencing of 109 micro-dissected pancreatic cancer cases and normal control tissue.', 'publicStudy': True, 'pmid': '25855536', 'citation': 'Witkiewicz et al. Nat Commun 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:03:10', 'allSampleCount': 109, 'readPermission': True, 'studyId': 'paad_utsw_2015', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Neuroendocrine Tumors (Johns Hopkins University, Science 2011)', 'description': 'Whole exome sequencing of 10 pancreatic neuroendocrine tumor patients.', 'publicStudy': True, 'pmid': '21252315', 'citation': 'Jiao et al. Science 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:08:06', 'allSampleCount': 10, 'readPermission': True, 'studyId': 'panet_jhu_2011', 'cancerTypeId': 'panet', 'referenceGenome': 'hg19'}, {'name': 'Primary Central Nervous System Lymphoma (Mayo Clinic, Clin Cancer Res 2015)', 'description': 'Exome sequencing of 19 immunocompetent primary central nervous system lymphoma (PCNSL) samples.', 'publicStudy': True, 'pmid': '25991819', 'citation': 'Braggio et al. Clin Cancer Res 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-08 15:08:31', 'allSampleCount': 19, 'readPermission': True, 'studyId': 'pcnsl_mayo_2015', 'cancerTypeId': 'pcnsl', 'referenceGenome': 'hg19'}, {'name': 'Insulinoma (Shanghai, Nat Commun 2013)', 'description': 'Whole exome sequencing of 10 benign insulinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '24326773', 'citation': 'Cao et

al. Nat Commun 2013', 'groups': '', 'status': 0, 'importDate': '2023-12-08 15:08:59', 'allSampleCount': 10, 'readPermission': True, 'studyId': 'panet_shanghai_2013', 'cancerTypeId': 'panet', 'referenceGenome': 'hg19'}, {'name': 'Pleural Mesothelioma (NYU, Cancer Res 2015)', 'description': 'Whole-exome sequencing of 22 malignant pleural mesotheliomas (PLMESO) tumor/normal pairs.', 'publicStudy': True, 'pmid': '25488749', 'citation': 'Guo et al. Cancer Res 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-08 15:09:25', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'plmeso_nyu_2015', 'cancerTypeId': 'plmeso', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Adenocarcinoma (QCMG, Nature 2016)', 'description': 'Whole-genome and deep-exome sequencing analysis of 456 pancreatic ductal adenocarcinomas', 'publicStudy': True, 'pmid': '26909576', 'citation': 'Bailey et al. Nature 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:09:51', 'allSampleCount': 456, 'readPermission': True, 'studyId': 'paad_qcmg_uq_2016', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Cystic Tumor of the Pancreas (Johns Hopkins, PNAS 2011)', 'description': 'Whole-exome sequencing of major neoplastic cyst types of the pancreas: 8 serous cystadenomas (SCAs), 8 intraductal papillary mucinous neoplasms (IPMNs), 8 mucinous cystic neoplasms (MCNs), and 8 solid pseudopapillary neoplasms (SPNs).', 'publicStudy': True, 'pmid': '22158988', 'citation': 'Wu et al. PNAS 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:10:32', 'allSampleCount': 32, 'readPermission': True, 'studyId': 'pact_jhu_2011', 'cancerTypeId': 'pact', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Neuroendocrine Tumors (Multi-Institute, Nature 2017)', 'description': 'Whole-genome sequencing of 98 pancreatic neuroendocrine tumours (PanNETs) and matched normal DNA pairs.', 'publicStudy': True, 'pmid': '28199314', 'citation': 'Scarpa et al. Nature 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:10:58', 'allSampleCount': 98, 'readPermission': True, 'studyId': 'panet_arcnet_2017', 'cancerTypeId': 'panet', 'referenceGenome': 'hg19'}, {'name': 'Pilocytic Astrocytoma (ICGC, Nature Genetics 2013)', 'description': 'Whole-genome sequencing of 96 pilocytic astrocytoma tumor/normal pairs. Conducted by the International Cancer Genome Consortium (ICGC) PedBrain Tumor Project.', 'publicStudy': True, 'pmid': '23817572', 'citation': 'Jones et al. Nature Genetics 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:11:26', 'allSampleCount': 96, 'readPermission': True, 'studyId': 'past_dkfz_heidelberg_2013', 'cancerTypeId': 'past', 'referenceGenome': 'hg19'}, {'name': 'Pheochromocytoma and Paraganglioma (TCGA, Cell 2017)', 'description': 'Whole-exome sequencing of 178 Pheochromocytoma or Paraganglioma tumor/normal pairs.', 'publicStudy': True, 'pmid': '28162975', 'citation': 'Fishbein et al. Cancer Cell 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:11:51', 'allSampleCount': 178, 'readPermission': True, 'studyId': 'pcpg_tcga_pub', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Pan-Cancer (DKFZ, Nature 2017)', 'description': 'Whole-genome/exome sequencing of 961 Pediatric Cancer samples. Data generated from Pfister Lab & DKFZ/German Cancer Consortium.', 'publicStudy': True, 'pmid': '29489754', 'citation': 'Grobner et al. Nature 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:12:32', 'allSampleCount': 961, 'readPermission': True, 'studyId': 'pediatric_dkfz_2017', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Tumors with TRK fusions (MSK, Clin Cancer Res 2020)', 'description': 'Tumors with TRK fusions based on MSK-IMPACT targeted sequencing.', 'publicStudy': True, 'pmid': '31871300', 'citation': 'Rosen et al. Clin Cancer Res 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-08 15:14:29', 'allSampleCount': 106, 'readPermission': True, 'studyId': 'ntrk_msk_2019', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'China Pan-cancer (OrigiMed, Nature 2022)', 'description': 'Landscape of genomic alterations in 10,194 solid tumors from the Chinese population', 'publicStudy': True, 'pmid': '35871175', 'citation': 'Wu, Liqun et al. Nature 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 15:14:55', 'allSampleCount': 10194, 'readPermission': True, 'studyId': 'pan_origimed_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Ductal Adenocarcinoma (CPTAC, Cell 2021)', 'description': 'Whole-genome sequencing (WGS) and whole-exome sequencing (WES) of 140 pancreatic cancers with 67 normal adjacent tissues. Proteogenomic characterization generated by CPTAC.', 'publicStudy': True, 'pmid': '34534465', 'citation': 'Liwei Cao et al. Cell 2021', 'groups': '',

'status': 0, 'importDate': '2023-12-08 16:10:23', 'allSampleCount': 140, 'readPermission': True, 'studyId': 'paad_cptac_2021', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK, Cell Reports 2022)', 'description': 'Targeted sequencing of 1659 Bladder Cancer tumor/normal samples via MSK-IMPACT.', 'publicStudy': True, 'pmid': '36543146', 'citation': 'Clinton et al. Cell Reports 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 16:20:21', 'allSampleCount': 1659, 'readPermission': True, 'studyId': 'paired_bladder_2022', 'cancerTypeId': 'bladder', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Acinar Cell Carcinoma (MSK, JCO 2023)', 'description': 'Targeted sequencing of pancreatic acinar cell carcinoma tumor and normal samples via MSK-IMPACT.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 16:21:16', 'allSampleCount': 47, 'readPermission': True, 'studyId': 'paac_msk_jco_2023', 'cancerTypeId': 'paac', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (Fred Hutchinson CRC, Nat Med 2016)', 'description': 'Whole-exome sequencing, array comparative genomic hybridization (CGH) and RNA transcript profiling of 176 tumors from 63 patients with disseminated prostate cancer with matched normals.', 'publicStudy': True, 'pmid': '26928463', 'citation': 'Kumar et al. Nat Med 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 16:51:36', 'allSampleCount': 176, 'readPermission': True, 'studyId': 'prad_fhcrc', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (Broad/Cornell, Nat Genet 2012)', 'description': "Whole-exome sequencing of 112 prostate adenocarcinomas and matched normal samples. Generated by Levi Garraway's lab at the Broad Institute and Mark Rubin's lab at Cornell.", 'publicStudy': True, 'pmid': '22610119', 'citation': 'Barbieri et al. Nat Genet 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 16:57:01', 'allSampleCount': 123, 'readPermission': True, 'studyId': 'prad_broad', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (Broad/Cornell, Cell 2013)', 'description': 'Whole genome sequencing of 57 prostate tumor and matches normal tissues.', 'publicStudy': True, 'pmid': '23622249', 'citation': 'Baca et al. Cell 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 16:57:49', 'allSampleCount': 82, 'readPermission': True, 'studyId': 'prad_broad_2013', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Prostate Adenocarcinoma (MCTP, Nature 2012)', 'description': "Exome sequencing of 61 prostate cancer tumor/normal pairs (50 metastatic CRPCs and 11 high-grade localized prostate cancers). Generated by Arul Chinnaiyan's and Scott Tomlins' labs at the University of Michigan.", 'publicStudy': True, 'pmid': '22722839', 'citation': 'Grasso et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 16:59:09', 'allSampleCount': 121, 'readPermission': True, 'studyId': 'prad_mich', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (MSK, Cancer Cell 2010)', 'description': 'Comprehensive profiling of 218 prostate tumors (181 primaries, 37 metastases) and 14 prostate cancer cell lines and xenografts. MSKCC Prostate Oncogenome Project.
Normalized flat data files. Raw data via GEO (GSE21032).', 'publicStudy': True, 'pmid': '20579941', 'citation': 'Taylor et al. Cancer Cell 2010', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:01:58', 'allSampleCount': 240, 'readPermission': True, 'studyId': 'prad_mskcc', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (MSK, PNAS 2014)', 'description': 'Genome-wide copy number profiling in 104 primary prostate cancer tumor/normal pairs. Raw data via GEO (GSE54691).', 'publicStudy': True, 'pmid': '25024180', 'citation': 'Hieronymus et al. PNAS 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:03:58', 'allSampleCount': 104, 'readPermission': True, 'studyId': 'prad_mskcc_2014', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Prostate Cancer (SU2C/PCF Dream Team, Cell 2015)', 'description': 'Whole-exome sequencing of 150 metastatic prostate cancer tumor/normal pairs by the SU2C/PCF Dream Team.', 'publicStudy': True, 'pmid': '26000489', 'citation': 'Robinson et al. Cell 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:04:09', 'allSampleCount': 150, 'readPermission': True, 'studyId':

'prad_su2c_2015', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (TCGA, Cell 2015)', 'description': 'Whole exome and/or whole genome sequencing of 333 primary prostate adenocarcinoma tumor/normal pairs; raw data at the <A HREF="https://tcga-data.nci.nih.gov/docs/publications/prad_2015/">NCI</A>.', 'publicStudy': True, 'pmid': '26544944', 'citation': 'TCGA, Cell 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:08:01', 'allSampleCount': 333, 'readPermission': True, 'studyId': 'prad_tcga_pub', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (CPC-GENE, Nature 2017)', 'description': 'Whole-genome/exome sequencing of 477 prostate samples from CPC-GENE and public data sets, including TCGA-PRAD.', 'publicStudy': True, 'pmid': '28068672', 'citation': 'Fraser et al. Nature 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-08 17:15:35', 'allSampleCount': 477, 'readPermission': True, 'studyId': 'prad_cpcg_2017', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma Organoids (MSK, Cell 2014)', 'description': 'Exome sequencing of 12 advanced prostate cancer samples and matched organoids', 'publicStudy': True, 'pmid': '25201530', 'citation': 'Gao et al. Cell 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:18:04', 'allSampleCount': 12, 'readPermission': True, 'studyId': 'prad_mskcc_cheny1_organoids_2014', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Metastatic castration-sensitive prostate cancer (MSK, Clin Cancer Res 2020)', 'description': 'MSK-IMPACT sequencing of 424 matched tumor-normal samples from patients with metastatic castration-sensitive prostate cancer. Germline alterations are not shown here.', 'publicStudy': True, 'pmid': '32220891', 'citation': 'Stopsack et al. Clin Cancer Res 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-08 17:18:37', 'allSampleCount': 424, 'readPermission': True, 'studyId': 'prad_mcspc_mskcc_2020', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Retinoblastoma cfDNA (MSK, Cancer Med 2020)', 'description': 'Cell-free DNA profiling in 14 retinoblastoma patients with advanced intraocular disease: An MSKCC experience', 'publicStudy': True, 'pmid': '32633890', 'citation': 'Kothari et al. Cancer Med 2020', 'groups': 'TSUIW', 'status': 0, 'importDate': '2023-12-08 17:19:14', 'allSampleCount': 14, 'readPermission': True, 'studyId': 'rbl_cfdna_msk_2020', 'cancerTypeId': 'rbl', 'referenceGenome': 'hg19'}, {'name': 'Race Differences in Prostate Cancer (MSK, 2021)', 'description': 'Targeted sequencing of 2,069 prostate cancers from different races via MSK-IMPACT.', 'publicStudy': True, 'pmid': '34667026', 'citation': 'Stopsack et al. Clin Cancer Res 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 17:19:48', 'allSampleCount': 2069, 'readPermission': True, 'studyId': 'prad_msk_stopsack_2021', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (MSK, Clin Cancer Res. 2022)', 'description': 'Targeted sequencing of 1417 Prostate Adenocarcinoma tumor/normal sample pairs via MSK-IMPACT to analyze the significance of PIK3R1 alterations.', 'publicStudy': True, 'pmid': '35670774', 'citation': 'Chakraborty et al. Clin Cancer Research 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 17:20:35', 'allSampleCount': 1417, 'readPermission': True, 'studyId': 'prad_pik3r1_msk_2021', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer Brain Metastases (Bern, Nat Commun. 2022)', 'description': 'Prostate Cancer Brain Metastases, Switzerland. Dataset was generated in 2019 by Antonio Rodriguez, John Gallon, Salvatore Piscuoglio and Mark Rubin.', 'publicStudy': True, 'pmid': '35504881', 'citation': 'Rodriguez-Calero et al. Nat Commun. 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-08 17:21:51', 'allSampleCount': 168, 'readPermission': True, 'studyId': 'prostate_pcbm_swiss_2019', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Skin Cutaneous Melanoma (TCGA, Firehose Legacy)', 'description': 'TCGA Skin Cutaneous Melanoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/SKCM/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:46:07', 'allSampleCount': 480, 'readPermission': True, 'studyId': 'skcm_tcga', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Small Cell Lung Cancer (CLCGP, Nat Genet 2012)', 'description': 'Comprehensive whole exam profiling of 29 small cell lung cancer samples. Generated by the Clinical Lung Cancer Genome Project. Data from Peifer et al., Nat

Genet 2012 (German group). Paper states data available at http://www.uni-koeln.edu/sclc/SCLC_data.tgz .', 'publicStudy': True, 'pmid': '22941188', 'citation': 'Peifer et al. Nat Genet 2012', 'groups': 'SCLCPORTAL;PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:56:51', 'allSampleCount': 29, 'readPermission': True, 'studyId': 'sclc_clcgp', 'cancerTypeId': 'sclc', 'referenceGenome': 'hg19'}, {'name': 'Small Cell Lung Cancer (Johns Hopkins, Nat Genet 2012)', 'description': 'Whole exome-sequencing of 80 human SCLCs, including 36 primary SCLC human tumor and adjacent normal sample pairs and 17 paired SCLC cell lines and their patient-matched lymphoblastoid lines, as well as 4 primary SCLC tumors and 23 SCLC cell lines without matched normal controls. Data from Rudin et al., Nat Gene 2012. Sequencing data are publicly available in EGA (EGAS0000100334)', 'publicStudy': True, 'pmid': '22941189', 'citation': 'Rudin et al. Nat Genet 2012', 'groups': 'SCLCPORTAL;PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:57:26', 'allSampleCount': 80, 'readPermission': True, 'studyId': 'sclc_jhu', 'cancerTypeId': 'sclc', 'referenceGenome': 'hg19'}, {'name': 'Skin Cutaneous Melanoma (Broad, Cell 2012)', 'description': 'Whole-exome sequencing of 121 melanoma samples with matched normals.', 'publicStudy': True, 'pmid': '22817889', 'citation': 'Hodis et al. Cell 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:58:02', 'allSampleCount': 121, 'readPermission': True, 'studyId': 'skcm_broad', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Melanoma (Broad/Dana Farber, Nature 2012)', 'description': 'Whole Genome Sequencing of 25 metastatic melanoma samples with matched normals', 'publicStudy': True, 'pmid': '22622578', 'citation': 'Berger et al. Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:59:10', 'allSampleCount': 26, 'readPermission': True, 'studyId': 'skcm_broad_dfarber', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Small Cell Carcinoma of the Ovary (MSK, Nat Genet 2014)', 'description': 'Targeted sequencing of 12 SCCO paired tumor and normal samples.', 'publicStudy': True, 'pmid': '24658004', 'citation': 'Jelinic et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-10 23:59:44', 'allSampleCount': 12, 'readPermission': True, 'studyId': 'scco_mskcc', 'cancerTypeId': 'scco', 'referenceGenome': 'hg19'}, {'name': 'Rhabdomyosarcoma (NIH, Cancer Discov 2014)', 'description': 'Whole-genome or whole-exome sequencing of 43 rhabdomyosarcoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '24436047', 'citation': 'Shern et al. Cancer Discov 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 00:00:13', 'allSampleCount': 43, 'readPermission': True, 'studyId': 'rms_nih_2014', 'cancerTypeId': 'rms', 'referenceGenome': 'hg19'}, {'name': 'Sarcoma (MSKCC/Broad, Nat Genet 2010)', 'description': 'Sanger-sequenced 226 protein-coding genes (3,849 exons and adjacent intronic) on 207 samples (with 205 matched normals) encompassing 7 major sarcoma subtypes.', 'publicStudy': True, 'pmid': '20601955', 'citation': 'Barretina et al. Nat Genet 2010', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:00:43', 'allSampleCount': 207, 'readPermission': True, 'studyId': 'sarc_mskcc', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Skin Cutaneous Melanoma(Broad, Cancer Discov 2014)', 'description': 'Exome Sequencing of tumors (with matched normals) from 45 patients with BRAFV600-mutant metastatic melanoma who received vemurafenib or dabrafenib monotherapy.', 'publicStudy': True, 'pmid': '24265153', 'citation': 'Van Allen et al. Cancer Discov. 2012', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:03:32', 'allSampleCount': 78, 'readPermission': True, 'studyId': 'skcm_broad_brafresist_2012', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Adult Soft Tissue Sarcomas (TCGA, Cell 2017)', 'description': 'Whole-exome sequencing of 206 Adult Soft Tissue Sarcoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '29100075', 'citation': 'TCGA, Cell 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 00:04:24', 'allSampleCount': 206, 'readPermission': True, 'studyId': 'sarc_tcga_pub', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Melanoma (MSK, NEJM 2014)', 'description': 'Whole-exome sequencing of 64 pretreated (ipilimumab or tremelimumab) melanoma tumor-normal pairs.', 'publicStudy': True, 'pmid': '25409260', 'citation': 'Snyder et al. NEJM 2014', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:07:25', 'allSampleCount': 64, 'readPermission': True, 'studyId': 'skcm_mskcc_2014', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Small-Cell Lung Cancer (Multi-Institute, Cancer Cell

2017)', 'description': 'Whole Exome Sequencing of 10 paired chemosensitive and chemoresistant SCLC PDX. Data from Gardner et al., Cancer Cell 2017. Data available in dbGaP (PHS001249.v1.p1).', 'publicStudy': True, 'pmid': '28196596', 'citation': 'Gardner et al. Cancer Cell 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:11:21', 'allSampleCount': 20, 'readPermission': True, 'studyId': 'sclc_cancercell_gardner_2017', 'cancerTypeId': 'sclc', 'referenceGenome': 'hg19'}, {'name': 'Melanomas (TCGA, Cell 2015)', 'description': 'Whole-exome sequencing of 333 primary and/or metastatic melanomas.', 'publicStudy': True, 'pmid': '26091043', 'citation': 'TCGA, Cell 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 00:12:41', 'allSampleCount': 359, 'readPermission': True, 'studyId': 'skcm_tcga_pub_2015', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Melanoma (DFCI, Science 2015)', 'description': 'Whole-exome sequencing of 110 metastatic melanoma tumor-normal pairs.', 'publicStudy': True, 'pmid': '26359337', 'citation': 'Van Allen et al. Science 2015', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:14:59', 'allSampleCount': 110, 'readPermission': True, 'studyId': 'skcm_dfci_2015', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Small Cell Lung Cancer (U Cologne, Nature 2015)', 'description': 'Whole-genome sequencing of 120 small cell lung cancer(SCLC) tumour samples and matched normal material. Data from George et al., Nature 2015 (German group). Paper states data available in GEO (GSE69091).', 'publicStudy': True, 'pmid': '26168399', 'citation': 'George et al. Nature 2015', 'groups': 'SCLCPORTAL;PUBLIC', 'status': 0, 'importDate': '2023-12-11 00:17:32', 'allSampleCount': 120, 'readPermission': True, 'studyId': 'sclc_ucologne_2015', 'cancerTypeId': 'sclc', 'referenceGenome': 'hg19'}, {'name': 'Sarcoma (MSK, Nat Commun. 2022)', 'description': 'Targeted Sequencing of 2138 Sarcoma samples and matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '35705560', 'citation': 'Nacev et al. Nat Commun. 2022', 'groups': '', 'status': 0, 'importDate': '2023-12-11 00:18:20', 'allSampleCount': 2138, 'readPermission': True, 'studyId': 'sarcoma_mskcc_2022', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Retinoblastoma (MSK, Cancers 2021)', 'description': 'Targeted sequencing of 83 Retinoblastoma tumor-normal pairs via MSK-IMPACT. Genomic data provided is limited to somatic alterations.', 'publicStudy': True, 'pmid': '33466343', 'citation': 'Francis et al. Cancers 2021', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 00:19:12', 'allSampleCount': 83, 'readPermission': True, 'studyId': 'rbl_mskcc_2020', 'cancerTypeId': 'rbl', 'referenceGenome': 'hg19'}, {'name': 'Skin Cutaneous Melanoma (Yale, Nat Genet 2012)', 'description': 'Exome sequencing of 147 melanoma samples with 99 matched normals.', 'publicStudy': True, 'pmid': '22842228', 'citation': 'Krauthammer et al. Nat Genet 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:06:47', 'allSampleCount': 147, 'readPermission': True, 'studyId': 'skcm_yale', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (Pfizer and UHK, Nat Genet 2014)', 'description': 'Whole genome sequencing of 100 gastric cancer tumor-normal pairs from the University of Hong Kong and Pfizer.', 'publicStudy': True, 'pmid': '24816253', 'citation': 'Wang et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:07:30', 'allSampleCount': 100, 'readPermission': True, 'studyId': 'stad_pfizer_uhongkong', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (TCGA, Nature 2014)', 'description': 'Whole-exome sequencing of 295 primary gastric adenocarcinomas tumors with matched normals. TCGA Stomach Adenocarcinoma Project; raw data at the <A HREF="https://tcga-data.nci.nih.gov/docs/publications/stad_2014/">NCI</A>.', 'publicStudy': True, 'pmid': '25079317', 'citation': 'TCGA, Nature 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:08:11', 'allSampleCount': 295, 'readPermission': True, 'studyId': 'stad_tcga_pub', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (UHK, Nat Genet 2011)', 'description': 'Exome sequencing of 22 gastric cancer samples with matched normals.', 'publicStudy': True, 'pmid': '22037554', 'citation': 'Wang et al. Nat Genet 2011', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:12:43', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'stad_uhongkong', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (U Tokyo, Nat Genet 2014)', 'description': 'Whole exome sequencing of 30 diffuse-

type gastric adenocarcinoma samples (with matched normals) from the University of Tokyo.', 'publicStudy': True, 'pmid': '24816255', 'citation': 'Kakiuchi et al. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:13:18', 'allSampleCount': 30, 'readPermission': True, 'studyId': 'stad_utokyo', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Thymic Epithelial Tumors (NCI, Nat Genet 2014)', 'description': 'Whole exome sequencing of 28 thymic epithelial tumors (TETs) with matched normals', 'publicStudy': True, 'pmid': '24974848', 'citation': 'Petrini at el. Nat Genet 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:13:49', 'allSampleCount': 32, 'readPermission': True, 'studyId': 'tet_nci_2014', 'cancerTypeId': 'tet', 'referenceGenome': 'hg19'}, {'name': 'Poorly-Differentiated and Anaplastic Thyroid Cancers (MSK, JCI 2016)', 'description': 'Targeted sequencing of 341 cancer genes from 117 patient-derived PDTCs and ATCs', 'publicStudy': True, 'pmid': '26878173', 'citation': 'Landa et al. J Clin Invest 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:14:20', 'allSampleCount': 117, 'readPermission': True, 'studyId': 'thyroid_mskcc_2016', 'cancerTypeId': 'thyroid', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Carcinoma (TCGA, Nature 2017)', 'description': 'Whole exome sequencing of 559 esophageal and gastric carcinoma tumors with matched normals.', 'publicStudy': True, 'pmid': '28052061', 'citation': 'TCGA, Nature 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:16:32', 'allSampleCount': 559, 'readPermission': True, 'studyId': 'stes_tcga_pub', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Melanoma (MSK, JCO Precis Oncol 2017)', 'description': 'Targeted sequencing of pre-treatment 66 Melanoma tumor samples. PubMed', 'publicStudy': True, 'pmid': '32913971', 'citation': 'Catalanotti et al. JCO Precis Oncol 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:25:49', 'allSampleCount': 66, 'readPermission': True, 'studyId': 'skcm_vanderbilt_mskcc_2015', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer (MSK, JCO Precis Oncol 2017)', 'description': 'IMPACT sequencing of 504 prostate cancer tumor/normal pairs.', 'publicStudy': True, 'pmid': '28825054', 'citation': 'Abida et al. JCO Precis Oncol 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:26:19', 'allSampleCount': 504, 'readPermission': True, 'studyId': 'prad_mskcc_2017', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (SMMU, Eur Urol 2017)', 'description': 'Whole-genome and transcriptome sequencing of 65 Prostate Adenocarcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '28927585', 'citation': 'Shancheng et al. Eur Urol 2017', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:26:54', 'allSampleCount': 65, 'readPermission': True, 'studyId': 'prad_eururol_2017', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'SUMMIT - Neratinib Basket Study (Multi-Institute, Nature 2018)', 'description': 'MSK-IMPACT sequencing of 86 patients with HER2- and HER3-mutant cancers', 'publicStudy': True, 'pmid': '29420467', 'citation': 'Hyman et al. Nature 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:29:22', 'allSampleCount': 141, 'readPermission': True, 'studyId': 'summit_2018', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (MSK/DFCI, Nature Genetics 2018)', 'description': 'Whole exome Sequencing of 1013 prostate cancer samples and their matched normals.', 'publicStudy': True, 'pmid': '29610475', 'citation': 'Armenia et al. Nat Genet 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:29:54', 'allSampleCount': 1013, 'readPermission': True, 'studyId': 'prad_p1000', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'TMB and Immunotherapy (MSK, Nat Genet 2019)', 'description': 'Genomic and survival data from 1661 tumor-normal pairs from 1661 patients with various cancer types sequenced with the MSK-IMPACT assay.', 'publicStudy': True, 'pmid': '30643254', 'citation': 'Samstein et al. Nat Genet 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:41:14', 'allSampleCount': 1661, 'readPermission': True, 'studyId': 'tmb_mskcc_2018', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Prostate Adenocarcinoma (SU2C/PCF Dream Team, PNAS 2019)', 'description': 'Whole exome sequencing of 444 castrate resistant prostate cancer tumor/normal pairs. SU2C-PCF Dream Team: Precision Therapy for Advanced Prostate Cancer.', 'publicStudy': True, 'pmid': '31061129', 'citation': 'Abida et al. PNAS 2019', 'groups': '', 'status': 0,

'importDate': '2023-12-11 10:41:54', 'allSampleCount': 444, 'readPermission': True, 'studyId': 'prad_su2c_2019', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer (MSK, Cell Metab 2020)', 'description': 'MSK-IMPACT Sequencing of 18 prostate cancer tumor/normal pairs.', 'publicStudy': True, 'pmid': '31564440', 'citation': 'Granlund et al. Cell Metab 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 10:54:56', 'allSampleCount': 18, 'readPermission': True, 'studyId': 'prad_msk_2019', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (MSK, Eur Urol 2020)', 'description': 'Targeted sequencing of 1465 prostate adenocarcinoma tumor/normal pairs via MSK-IMPACT.', 'publicStudy': True, 'pmid': '32317181', 'citation': 'Nguyen et al. Eur Urol 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-11 10:55:27', 'allSampleCount': 1465, 'readPermission': True, 'studyId': 'prad_cdk12_mskcc_2020', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Myoepithelial Carcinomas of Soft Tissue (WCM, CSH Molecular Case Studies 2022)', 'description': 'Whole-exome sequencing of 12 Myoepithelial Carcinomas of Soft Tissue from two patients.', 'publicStudy': True, 'pmid': '36577525', 'citation': 'Cyrta et al. 2022 Cold Spring Harb Mol Case Stud 8: a006227', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:02:52', 'allSampleCount': 12, 'readPermission': True, 'studyId': 'stmyec_wcm_2022', 'cancerTypeId': 'stmyec', 'referenceGenome': 'hg19'}, {'name': 'Uterine Carcinosarcoma (Johns Hopkins, Nat Commun 2014)', 'description': 'Whole exome sequencing (WXS) of 22 uterine carcinosarcoma/uterine malignant mixed Mullerian (UCS) tumors with matched normals. <A HREF="http://www.nature.com/ncomms/2014/140919/ncomms6006/extref/ncomms6006-s1.pdf">', 'publicStudy': True, 'pmid': '25233892', 'citation': 'Jones et al. Nat Commun 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:29:02', 'allSampleCount': 22, 'readPermission': True, 'studyId': 'ucs_jhu_2014', 'cancerTypeId': 'ucs', 'referenceGenome': 'hg19'}, {'name': 'Uterine Corpus Endometrial Carcinoma (TCGA, Nature 2013)', 'description': 'Whole exome sequencing of 373 endometrial carcinoma tumors with matched normals. TCGA Uterine Corpus Endometrial Carcinoma project; raw data at the <A HREF="https://tcga-data.nci.nih.gov/docs/publications/ucec_2013/">NCI</A>.', 'publicStudy': True, 'pmid': '23636398', 'citation': 'TCGA, Nature 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:29:45', 'allSampleCount': 373, 'readPermission': True, 'studyId': 'ucec_tcga_pub', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Uveal Melanoma (QIMR, Oncotarget 2016)', 'description': 'Whole-genome or whole-exome sequencing of tumor/normal pairs from 28 uveal melanoma samples.', 'publicStudy': True, 'pmid': '26683228', 'citation': 'Johansson et al. Oncotarget 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:34:01', 'allSampleCount': 28, 'readPermission': True, 'studyId': 'um_qimr_2016', 'cancerTypeId': 'um', 'referenceGenome': 'hg19'}, {'name': 'Unclassified Renal Cell Carcinoma (MSK, Nature 2016)', 'description': 'Targeted sequencing of 62 high-grade primary Unclassified Renal Cell Carcinoma tumor samples with matched normals.', 'publicStudy': True, 'pmid': '27713405', 'citation': 'Chen et al. Nat Commun 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:34:33', 'allSampleCount': 62, 'readPermission': True, 'studyId': 'urcc_mskcc_2016', 'cancerTypeId': 'urcc', 'referenceGenome': 'hg19'}, {'name': 'Upper Tract Urothelial Cancer (MSK, Eur Urol 2015)', 'description': 'Next-generation sequencing (MSK-IMPACT) on all protein-coding exons of 300 cancer associated genes of 85 Upper Tract Urothelial Carcinoma tumor samples and paired normals.', 'publicStudy': True, 'pmid': '26278805', 'citation': 'Sfakianos et al. Eur Urol 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:35:05', 'allSampleCount': 85, 'readPermission': True, 'studyId': 'utuc_mskcc_2015', 'cancerTypeId': 'utuc', 'referenceGenome': 'hg19'}, {'name': "Pediatric Wilms' Tumor (TARGET, 2018)", 'description': 'Whole-exome sequencing of 657 Wilms\' tumor samples. Comprehensive profiling of 657 Wilms\' Tumor samples. <p>TARGET data is intended exclusively for biomedical research using pediatric data (i.e., the research objectives cannot be accomplished using data from adults) that focus on the development of more effective treatments, diagnostic tests, or prognostic markers for childhood cancers. Moreover, TARGET data can be used for research relevant to the biology, causes, treatment and late complications of treatment of pediatric cancers, but is not intended for the sole purposes of methods and/or tool development (please see <a

href="https://ocg.cancer.gov/programs/target/using-target-data">Using TARGET Data section of the OCG website). If you are interested in using TARGET data for publication or other research purposes, you must follow the TARGET Publication Guidelines.</p>', 'publicStudy': True, 'groups': 'NCI-TARGET;PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:35:37', 'allSampleCount': 657, 'readPermission': True, 'studyId': 'wt_target_2018_pub', 'cancerTypeId': 'wt', 'referenceGenome': 'hg19'}, {'name': 'Endometrial Cancer (MSK, 2018)', 'description': 'MSK-IMPACT sequencing of 197 advanced-staged endometrial cancer tumor samples with matched normals, from 189 patients treated at MSK.', 'publicStudy': True, 'pmid': '30068706', 'citation': 'Soumerai et al. Clin Cancer Res. 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:37:21', 'allSampleCount': 197, 'readPermission': True, 'studyId': 'ucec_msk_2018', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Uterine Clear Cell Carcinoma (NIH, Cancer 2017)', 'description': 'Whole exome sequencing of paired tumor-normal DNAs from 16 cases of clear cell endometrial tumors.', 'publicStudy': True, 'pmid': '28485815', 'citation': 'Le Gallo et al. Cancer 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:37:55', 'allSampleCount': 16, 'readPermission': True, 'studyId': 'uccc_nih_2017', 'cancerTypeId': 'uccc', 'referenceGenome': 'hg19'}, {'name': 'Squamous Cell Carcinoma of the Vulva (CUK, Exp Mol Med 2018)', 'description': 'Whole exome sequencing of tumor/normal pairs from 15 vulvar squamous cell carcinomas.', 'publicStudy': True, 'pmid': '29422544', 'citation': 'Han et al. Exp Mol Med 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:38:27', 'allSampleCount': 15, 'readPermission': True, 'studyId': 'vsc_cuk_2018', 'cancerTypeId': 'vsc', 'referenceGenome': 'hg19'}, {'name': 'Upper Tract Urothelial Carcinoma (Cornell/Baylor/MDACC, Nat Commun 2019)', 'description': 'Whole exome sequencing (37 samples) and RNA-seq analysis (32 samples) of 47 upper tract urothelial carcinoma patients.', 'publicStudy': True, 'pmid': '31278255', 'citation': 'Robinson et al. Nat Commun 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:39:00', 'allSampleCount': 47, 'readPermission': True, 'studyId': 'utuc_cornell_baylor_mdacc_2019', 'cancerTypeId': 'utuc', 'referenceGenome': 'hg19'}, {'name': 'Upper Tract Urothelial Carcinoma (MSK, Nat Commun 2020)', 'description': 'Targeted Sequencing of 119 upper tract urothelial carcinoma tumor/normal pairs.', 'publicStudy': True, 'pmid': '32332851', 'citation': 'Kwanghee et al. Nat Commun 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:39:36', 'allSampleCount': 119, 'readPermission': True, 'studyId': 'utuc_msk_2019', 'cancerTypeId': 'utuc', 'referenceGenome': 'hg19'}, {'name': 'Upper Tract Urothelial Carcinoma PDX (MSK, Nat Commun 2020)', 'description': 'MSK-IMPACT sequencing of 34 upper tract urothelial patients and the matching PDX or PDC generated from 17 patient tumors.', 'publicStudy': True, 'pmid': '32332851', 'citation': 'Kwanghee et al. Nat Commun 2020', 'groups': '', 'status': 0, 'importDate': '2023-12-11 11:40:09', 'allSampleCount': 78, 'readPermission': True, 'studyId': 'utuc_pdx_msk_2019', 'cancerTypeId': 'utuc', 'referenceGenome': 'hg19'}, {'name': 'Uterine Sarcoma/Mesenchymal (MSK, Clin Cancer Res 2020)', 'description': 'Targeted Sequencing of 108 Uterine Sarcoma/Mesenchymal tumor/normal pairs from 107 patients.', 'publicStudy': True, 'pmid': '32299819', 'citation': 'Hensley et al. Clin Cancer Res 2020', 'groups': 'DONOGHUM;CHAVANS;PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:40:43', 'allSampleCount': 108, 'readPermission': True, 'studyId': 'usarc_msk_2020', 'cancerTypeId': 'usarc', 'referenceGenome': 'hg19'}, {'name': 'Upper Tract Urothelial Carcinoma (IGBMC, Genome Biology 2021)', 'description': 'Whole-exome sequencing of 30 upper-tract urothelial carcinoma patients and their matched normals.', 'publicStudy': True, 'pmid': '33397444', 'citation': 'Xiaoping et al. Genome Biology 2021', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:41:15', 'allSampleCount': 30, 'readPermission': True, 'studyId': 'utuc_igbmc_2021', 'cancerTypeId': 'utuc', 'referenceGenome': 'hg19'}, {'name': 'Endometrial Carcinoma (CPTAC, Cell 2020)', 'description': 'Proteogenomic Characterization of Endometrial Carcinoma. Generated by CPTAC.', 'publicStudy': True, 'pmid': '32059776', 'citation': 'Yongchao Dou et al. 2020 Cell.', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 11:41:50', 'allSampleCount': 81, 'readPermission': True, 'studyId': 'ucec_cptac_2020', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'},

{'name': 'Endometrial Carcinoma MSI (MSK, Clin Cancer Res 2022)', 'description': 'Clinical and genetic features of microsatellite instability-high endometrial cancers harboring germline or somatic mutations in MMR genes or MLH1 promoter hypermethylation.', 'publicStudy': True, 'pmid': '35849120', 'groups': '', 'status': 0, 'importDate': '2023-12-11 11:43:25', 'allSampleCount': 181, 'readPermission': True, 'studyId': 'ucec_ccr_msk_2022', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (British Columbia, Nature 2012)', 'description': 'Whole genome/exome sequencing analysis of 65 breast cancer samples', 'publicStudy': True, 'pmid': '22495314', 'citation': 'Shah et al. Nature', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-11 13:31:05', 'allSampleCount': 65, 'readPermission': True, 'studyId': 'brca_bccrc', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Mixed cfDNA (MSK, Nature Medicine 2019)', 'description': "Targeted sequencing of 248 samples from 124 patients' cfDNA/WBC and tumor/normal pairs.", 'publicStudy': True, 'pmid': '31768066', 'citation': 'Razavi et al. Nature Medicine 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-11 13:31:43', 'allSampleCount': 248, 'readPermission': True, 'studyId': 'cfdna_msk_2019', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Non-CDH1 Invasive Lobular Carcinoma (MSK, 2023)', 'description': 'Targeted Sequencing of breast Invasive Lobular Carcinoma tumors and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2023-12-11 16:10:48', 'allSampleCount': 25, 'readPermission': True, 'studyId': 'ilc_msk_2023', 'cancerTypeId': 'breast', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (Columbia University/MSK, Cell 2018)', 'description': 'Targeted sequencing of 130 bladder cancer tumors, organoids and xenografts and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '29625057', 'citation': 'Lee, Suk Hyung et al. Cell 2018', 'groups': '', 'status': 0, 'importDate': '2023-12-11 16:31:13', 'allSampleCount': 130, 'readPermission': True, 'studyId': 'bladder_columbia_msk_2018', 'cancerTypeId': 'bladder', 'referenceGenome': 'hg19'}, {'name': 'Colon Cancer (Sidra-LUMC AC-ICAM, Nat Med 2023)', 'description': 'Whole exome and transcriptome sequencing of 348 Colon Cancers and their matched normals from Sidra-LUMC AC-ICAM.', 'publicStudy': True, 'pmid': '37202560', 'citation': 'Roelands et al, Nat Med 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-11 16:31:50', 'allSampleCount': 348, 'readPermission': True, 'studyId': 'coad_silu_2022', 'cancerTypeId': 'coad', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK/TCGA, 2020)', 'description': 'Whole-exome or targeted sequencing of 476 muscle-invasive bladder tumor/normal pairs via TCGA or MSK-IMPACT sequencing.', 'publicStudy': True, 'pmid': '30290956', 'citation': 'Pietzak et al. Eur Urol 2019', 'groups': '', 'status': 0, 'importDate': '2023-12-13 14:56:08', 'allSampleCount': 476, 'readPermission': True, 'studyId': 'blca_msk_tcga_2020', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'MSK Make-an-IMPACT Rare Cancers (MSK, Clin Cancer Res 2023)', 'description': 'Targeted sequencing of 167 patients with Histiocytosis and Germ Cell Tumors using MSK-IMPACT assay.', 'publicStudy': True, 'pmid': '36862133', 'citation': 'Seyram A et al. Clin Cancer Res 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 15:59:47', 'allSampleCount': 184, 'readPermission': True, 'studyId': 'makeanimpact_ccr_2023', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Rhabdomyosarcomas (MSK, JCO Precis Oncol 2023)', 'description': 'Targeted sequencing of 24 cases with extremity rhabdomyosarcoma tumors and their matched normals (MSK Cohort) via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37315267', 'citation': 'de Wardin et al. JCO Precis Oncol 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:08:26', 'allSampleCount': 24, 'readPermission': True, 'studyId': 'rms_msk_2023', 'cancerTypeId': 'rms', 'referenceGenome': 'hg19'}, {'name': 'Rhabdomyosarcomas (MSK, NPJ Precis Oncol 2023)', 'description': 'Sequential targeted sequencing on 20 rhabdomyosarcoma tumors and their matched normals from the MSK cohort using MSK-IMPACT.', 'publicStudy': True, 'pmid': '37730754', 'citation': 'Wardin et at. NPJ Precis Oncol 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:12:29', 'allSampleCount': 42, 'readPermission': True, 'studyId': 'soft_tissue_msk_2023', 'cancerTypeId': 'rms', 'referenceGenome': 'hg19'}, {'name': 'Sarcoma (MSK, J Pathol 2023)', 'description': 'Targeted sequencing of 82 radiation-associated sarcomas and their matched normals via MSK-IMPACT.',

'publicStudy': True, 'pmid': '37350195', 'citation': 'Josephine K et al. J Pathol 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:16:36', 'allSampleCount': 82, 'readPermission': True, 'studyId': 'sarcoma_msk_2023', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Esophagogastric Cancer (MSK, Clin Cancer Res 2023)', 'description': 'Whole exome sequencing of 64 esophagogastric cancers and their matched normal samples.', 'publicStudy': True, 'pmid': '37406106', 'citation': 'Steven B et al. Clin Cancer Res 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:20:47', 'allSampleCount': 64, 'readPermission': True, 'studyId': 'egc_trap_ccr_msk_2023', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinoma (MSK, JCO Precis Oncol 2023)', 'description': 'Targeted sequencing of 51 hepatocellular carcinoma patients and their matched normal samples via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37769223', 'citation': 'Darren et al. JCO Precis Oncol 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:25:46', 'allSampleCount': 90, 'readPermission': True, 'studyId': 'hcc_jcopo_msk_2023', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Endometrial Cancer (MSK, Cancer Discovery 2023)', 'description': 'Targeted sequencing of 1882 endometrial cancers and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37651310', 'citation': 'Weigelt et al. Cancer Discovery 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:29:58', 'allSampleCount': 1882, 'readPermission': True, 'studyId': 'ucec_ancestry_cds_msk_2023', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Ewing Sarcoma (MSK, 2023)', 'description': 'Targeted Sequencing of 290 Ewing sarcoma tumor/normal pairs via MSK-IMPACT platform.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2023-12-29 16:34:28', 'allSampleCount': 290, 'readPermission': True, 'studyId': 'es_dsrct_msk_2023', 'cancerTypeId': 'es', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (MSK, Clin Cancer Res 2023)', 'description': 'Targeted sequencing of 526 bladder tumors and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37682528', 'citation': 'Guercio et al. Clin Cancer Res. 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:40:18', 'allSampleCount': 526, 'readPermission': True, 'studyId': 'bladder_msk_2023', 'cancerTypeId': 'bladder', 'referenceGenome': 'hg19'}, {'name': 'Non-Small Cell Lung Cancer Brain Metastasis (MSK, Nat Commun 2023)', 'description': 'Targeted sequencing of 322 NSCLC brain metastasis and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37591896', 'citation': 'Anna et al. Nat Commun 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:44:32', 'allSampleCount': 322, 'readPermission': True, 'studyId': 'bm_nsclc_mskcc_2023', 'cancerTypeId': 'nsclc', 'referenceGenome': 'hg19'}, {'name': 'Cervical Cancer (MSK, Clin Cancer Res 2023)', 'description': 'Targeted sequencing of 177 cervical tumors and their matched normal samples via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37643132', 'citation': 'Friedman et al. Clin Cancer Res 2023', 'groups': '', 'status': 0, 'importDate': '2023-12-29 16:48:43', 'allSampleCount': 177, 'readPermission': True, 'studyId': 'cervix_msk_2023', 'cancerTypeId': 'cervix', 'referenceGenome': 'hg19'}, {'name': 'Adrenocortical Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Adrenocortical Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/ACC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 09:11:57', 'allSampleCount': 92, 'readPermission': True, 'studyId': 'acc_tcga', 'cancerTypeId': 'acc', 'referenceGenome': 'hg19'}, {'name': 'Bladder Urothelial Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Bladder Urothelial Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/BLCA/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 09:29:58', 'allSampleCount': 413, 'readPermission': True, 'studyId': 'blca_tcga', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer Xenografts (British Columbia, Nature 2015)', 'description': 'Whole genome/targeted sequencing to evaluate the clonal dynamics in 116 breast cancer patient xenografts.', 'publicStudy': True, 'pmid': '25470049', 'citation': 'Eirew et al. Nature 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 09:55:04', 'allSampleCount': 117, 'readPermission': True, 'studyId': 'brca_bccrc_xenograft_2014', 'cancerTypeId':

'brca', 'referenceGenome': 'hg19'}, {'name': 'The Metastatic Breast Cancer Project (Archived, 2020)', 'description': 'The Metastatic Breast Cancer Project (www.mbcproject.org) is an ongoing patient-driven initiative. This dataset release is derived from 237 samples, including both primary and/or metastatic tumor specimens (FFPE) from 180 patients who developed metastatic breast cancer. 237 samples have undergone whole-exome sequencing (along with matched germline whole-exome sequencing) and 146 of those samples have also undergone RNA-sequencing. This study includes genomic data, patient-reported data (prepended as PRD), medical record data (MedR), and pathology report data (PATH). All annotations have been de-identified. As these data were generated in a research laboratory, not a clinical laboratory, they are for research purposes only and cannot be used to inform clinical decision-making. For questions about these data, including how to cite, please visit www.mbcproject.org/data-release or direct questions to data@mbcproject.org.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-01-19 10:11:47', 'allSampleCount': 237, 'readPermission': True, 'studyId': 'brca_mbcproject_wagle_2017', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Acute Myeloid Leukemia (TARGET, 2018)', 'description': 'Whole genome or whole exome sequencing on 333 TARGET-AML samples. Comprehensive profiling of TARGET-AML samples. <p>TARGET data is intended exclusively for biomedical research using pediatric data (i.e., the research objectives cannot be accomplished using data from adults) that focus on the development of more effective treatments, diagnostic tests, or prognostic markers for childhood cancers. Moreover, TARGET data can be used for research relevant to the biology, causes, treatment and late complications of treatment of pediatric cancers, but is not intended for the sole purposes of methods and/or tool development (please see Using TARGET Data section of the OCG website). If you are interested in using TARGET data for publication or other research purposes, you must follow the TARGET Publication Guidelines.</p>', 'publicStudy': True, 'groups': 'NCI-TARGET;PUBLIC', 'status': 0, 'importDate': '2024-01-19 10:57:48', 'allSampleCount': 1025, 'readPermission': True, 'studyId': 'aml_target_2018_pub', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Bladder Cancer (TCGA, Cell 2017)', 'description': 'Whole-exome sequencing of 412 muscle-invasive bladder tumors and matched normal samples.', 'publicStudy': True, 'pmid': '28988769', 'citation': 'Robertson et al. Cell 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 11:18:03', 'allSampleCount': 413, 'readPermission': True, 'studyId': 'blca_tcga_pub_2017', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Urothelial Carcinoma (Cornell/Trento, Nat Gen 2016)', 'description': 'Whole-exome sequencing of 72 tumor samples (with 32 matched normals) in Urothelial Carcinoma.', 'publicStudy': True, 'pmid': '27749842', 'citation': 'Faltas and Prandi, Nature Genetics 2016', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 11:48:12', 'allSampleCount': 72, 'readPermission': True, 'studyId': 'blca_cornell_2016', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Urothelial Carcinoma (BCAN/HCRN, Nat Commun 2022)', 'description': 'Urothelial Cancer-GENOmic analysis to improve patient outcomes and research.', 'publicStudy': True, 'pmid': '36333289', 'citation': 'Damrauer et al. Nat Commun. 2022', 'groups': '', 'status': 0, 'importDate': '2024-01-19 12:11:05', 'allSampleCount': 192, 'readPermission': True, 'studyId': 'blca_bcan_hcrn_2022', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'The Angiosarcoma Project (Provisional, July 2020)', 'description': 'The Angiosarcoma Project (www.ascproject.org) is an ongoing patient-driven initiative. This provisional dataset is currently derived from 83 samples, including tumor specimens (FFPE and cfDNA) from 62 angiosarcoma patients subjected to WES (along with matched germline WES). This study includes genomic data, patient-reported data (pre-pended as PRD), medical record data (MedR), and pathology report data (PATH). As these data were generated in a research laboratory, not a clinical laboratory, they are for research purposes only and cannot be used to inform clinical decision-making. For questions about these data, including how to cite, please visit www.ascproject.org/data-release or direct questions to data@ascproject.org.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-19 12:47:32', 'allSampleCount': 83,

'readPermission': True, 'studyId': 'angs_painter_2020', 'cancerTypeId': 'angs', 'referenceGenome': 'hg19'}, {'name': 'The Metastatic Breast Cancer Project (Provisional, December 2021)', 'description': 'The Metastatic Breast Cancer Project (www.mbcproject.org) is an ongoing patient-driven initiative. This dataset release is derived from 379 samples, including both primary and/or metastatic tumor specimens (FFPE) from 301 patients who developed metastatic breast cancer. 379 samples have undergone whole-exome sequencing (along with matched germline whole-exome sequencing) and 157 of those samples have also undergone RNA-sequencing. This study includes genomic data, patient-reported data (prepended as PRD), medical record data (MedR), and pathology report data (PATH). All annotations have been de-identified. As these data were generated in a research laboratory, not a clinical laboratory, they are for research purposes only and cannot be used to inform clinical decision-making. For questions about these data, including how to cite, please visit www.mbcproject.org/data-release or direct questions to data@mbcproject.org.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-01-19 13:10:16', 'allSampleCount': 379, 'readPermission': True, 'studyId': 'brca_mbcproject_2022', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Breast Invasive Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/BRCA/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 09:23:04', 'allSampleCount': 1108, 'readPermission': True, 'studyId': 'brca_tcga', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Cervical Squamous Cell Carcinoma and Endocervical Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/CESC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 10:04:11', 'allSampleCount': 310, 'readPermission': True, 'studyId': 'cesc_tcga', 'cancerTypeId': 'cesc', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Cholangiocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/CHOL/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 10:27:40', 'allSampleCount': 51, 'readPermission': True, 'studyId': 'chol_tcga', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Lymphoid Neoplasm Diffuse Large B-cell Lymphoma (TCGA, Firehose Legacy)', 'description': 'TCGA Lymphoid Neoplasm Diffuse Large B-cell Lymphoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/DLBC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 11:04:10', 'allSampleCount': 48, 'readPermission': True, 'studyId': 'dlbc_tcga', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Esophageal Carcinoma . Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/ESCA/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 11:24:28', 'allSampleCount': 186, 'readPermission': True, 'studyId': 'esca_tcga', 'cancerTypeId': 'esca', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma Multiforme (TCGA, Firehose Legacy)', 'description': 'TCGA Glioblastoma Multiforme. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/GBM/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 11:53:05', 'allSampleCount': 619, 'readPermission': True, 'studyId': 'gbm_tcga', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (TCGA, Cell 2015)', 'description': 'Whole-exome sequencing of 817 Breast Invasive Carcinoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) Breast Invasive Carcinoma Project.',

'publicStudy': True, 'pmid': '26451490', 'citation': 'TCGA, Cell 2015', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 12:47:51', 'allSampleCount': 818, 'readPermission': True, 'studyId': 'brca_tcga_pub2015', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (TCGA, Nature 2012)', 'description': 'Whole exome sequencing in 224 of the 276 colorectal carcinoma tumor/normal pairs. The Cancer Genome Atlas (TCGA) Colorectal Cancer project.', 'publicStudy': True, 'pmid': '22810696', 'citation': 'TCGA, Nature 2012', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-20 13:23:35', 'allSampleCount': 276, 'readPermission': True, 'studyId': 'coadread_tcga_pub', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Glioma (GLASS Consortium, Nature 2019)', 'description': 'Whole genome or whole exome sequencing analysis of temporally separated diffuse glioma tumor/normal pairs from 222 adult patients.', 'publicStudy': True, 'pmid': '31748746', 'citation': 'Barthel & Johnson et al. Nature 2019', 'groups': '', 'status': 0, 'importDate': '2024-01-20 13:47:11', 'allSampleCount': 444, 'readPermission': True, 'studyId': 'difg_glass_2019', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Esophagogastric Cancer (MSK, J Natl Cancer Inst 2023)', 'description': 'Targeted sequencing of 902 patients with early-onset and average-onset esophagogastric cancers and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37699004', 'citation': 'Melissa A et al. J Natl Cancer Inst 2023', 'groups': '', 'status': 0, 'importDate': '2024-01-20 14:12:38', 'allSampleCount': 902, 'readPermission': True, 'studyId': 'egc_msk_2023', 'cancerTypeId': 'stomach', 'referenceGenome': 'hg19'}, {'name': 'Mature T and NK Neoplasms (MSK, Blood Adv 2023)', 'description': 'Targeted sequencing of 132 Mature T and NK Neoplasms and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37078708', 'citation': 'William T et al. Blood Adv 2023', 'groups': '', 'status': 0, 'importDate': '2024-01-23 00:15:24', 'allSampleCount': 132, 'readPermission': True, 'studyId': 'mtnn_msk_2022', 'cancerTypeId': 'mtnn', 'referenceGenome': 'hg19'}, {'name': 'Acute Myeloid Leukemia (TCGA, Firehose Legacy)', 'description': 'TCGA Acute Myeloid Leukemia. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/LAML/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 09:49:19', 'allSampleCount': 200, 'readPermission': True, 'studyId': 'laml_tcga', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Clear Cell Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Kidney Renal Clear Cell Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/KIRC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 10:29:46', 'allSampleCount': 538, 'readPermission': True, 'studyId': 'kirc_tcga', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Chromophobe (TCGA, Firehose Legacy)', 'description': 'TCGA Kidney Chromophobe. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/KICH/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 10:56:43', 'allSampleCount': 113, 'readPermission': True, 'studyId': 'kich_tcga', 'cancerTypeId': 'chrcc', 'referenceGenome': 'hg19'}, {'name': 'Brain Lower Grade Glioma (TCGA, Firehose Legacy)', 'description': 'TCGA Brain Lower Grade Glioma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/LGG/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 11:18:45', 'allSampleCount': 530, 'readPermission': True, 'studyId': 'lgg_tcga', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Liver Hepatocellular Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Liver Hepatocellular Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/LIHC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 11:44:44', 'allSampleCount': 379, 'readPermission': True, 'studyId': 'lihc_tcga', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (TCGA,

Firehose Legacy)', 'description': 'TCGA Lung Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/LUAD/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 12:12:38', 'allSampleCount': 586, 'readPermission': True, 'studyId': 'luad_tcga', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Squamous Cell Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Lung Squamous Cell Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/LUSC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 12:48:11', 'allSampleCount': 511, 'readPermission': True, 'studyId': 'lusc_tcga', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg19'}, {'name': 'Mesothelioma (TCGA, Firehose Legacy)', 'description': 'TCGA Mesothelioma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/MESO/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 13:34:30', 'allSampleCount': 87, 'readPermission': True, 'studyId': 'meso_tcga', 'cancerTypeId': 'plmeso', 'referenceGenome': 'hg19'}, {'name': 'Ovarian Serous Cystadenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Ovarian Serous Cystadenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/OV/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 14:13:01', 'allSampleCount': 617, 'readPermission': True, 'studyId': 'ov_tcga', 'cancerTypeId': 'hgsoc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Papillary Cell Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Kidney Renal Papillary Cell Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/KIRP/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 14:54:35', 'allSampleCount': 293, 'readPermission': True, 'studyId': 'kirp_tcga', 'cancerTypeId': 'prcc', 'referenceGenome': 'hg19'}, {'name': 'Acute Myeloid Leukemia (TCGA, NEJM 2013)', 'description': 'Whole-genome or whole-exome sequencing analysis of 200 adult de novo AML tumor/normal pairs. TCGA Acute Myeloid Leukemia Project; raw data at the <A HREF="https://tcga-data.nci.nih.gov/tcga/tcgaCancerDetails.jsp?diseaseType=LAML&diseaseName=Acute%20Myeloid%20Leukemia">NCI</A>.', 'publicStudy': True, 'pmid': '23634996', 'citation': 'TCGA, NEJM 2013', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 15:18:43', 'allSampleCount': 200, 'readPermission': True, 'studyId': 'laml_tcga_pub', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Acral Melanoma (TGEN, Genome Res 2017)', 'description': 'Whole exome sequencing and transcriptome analysis of 34 Acral Melanoma patients (33 with matched normals).', 'publicStudy': True, 'pmid': '28373299', 'citation': 'Liang et al. Genome Res 2017', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 15:41:06', 'allSampleCount': 38, 'readPermission': True, 'studyId': 'mel_tsam_liang_2017', 'cancerTypeId': 'mel', 'referenceGenome': 'hg19'}, {'name': 'Mature B-cell malignancies (MD Anderson Cancer Center)', 'description': 'We performed targeted deep sequencing of 380 recurrently mutated genes across a cohort of 755 mature B-cell malignancies to define conserved and disease-specific patterns of genomic alterations.PubMed', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-01-23 16:02:56', 'allSampleCount': 760, 'readPermission': True, 'studyId': 'mbn_mdacc_2013', 'cancerTypeId': 'mbn', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Melanoma (DFCI, Nature Medicine 2019)', 'description': 'Whole-exome sequencing of 144 pre-treatment samples from 144 patients with metastatic melanoma treated with anti-PD1 ICB.', 'publicStudy': True, 'pmid': '31792460', 'citation': 'Liu et al. Nature Medicine 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-23 16:40:12', 'allSampleCount': 144, 'readPermission': True, 'studyId': 'mel_dfci_2019', 'cancerTypeId': 'mel', 'referenceGenome': 'hg19'}, {'name': 'Meningioma (University of Toronto, Nature 2021)', 'description': 'Meningioma DNA somatic

copy number, somatic point mutations, DNA methylation, RNA abundance, protein abundance', 'publicStudy': True, 'pmid': '34433969', 'citation': 'Farshad et al. Nature 2021', 'groups': 'PRIVATE', 'status': 0, 'importDate': '2024-01-23 17:07:43', 'allSampleCount': 121, 'readPermission': True, 'studyId': 'mng_utoronto_2021', 'cancerTypeId': 'mng', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Adenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Pancreatic Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/PAAD/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 09:19:36', 'allSampleCount': 186, 'readPermission': True, 'studyId': 'paad_tcga', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Pheochromocytoma and Paraganglioma (TCGA, Firehose Legacy)', 'description': 'TCGA Pheochromocytoma and Paraganglioma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/PCPG/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 09:45:29', 'allSampleCount': 184, 'readPermission': True, 'studyId': 'pcpg_tcga', 'cancerTypeId': 'mnet', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Prostate Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/PRAD/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 10:09:35', 'allSampleCount': 501, 'readPermission': True, 'studyId': 'prad_tcga', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Sarcoma (TCGA, Firehose Legacy)', 'description': 'TCGA Sarcoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/SARC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 10:41:22', 'allSampleCount': 265, 'readPermission': True, 'studyId': 'sarc_tcga', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Stomach Adenocarcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/STAD/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 11:10:35', 'allSampleCount': 478, 'readPermission': True, 'studyId': 'stad_tcga', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Testicular Germ Cell Cancer (TCGA, Firehose Legacy)', 'description': 'TCGA Testicular Germ Cell Cancer. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/TGCT/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 11:48:12', 'allSampleCount': 156, 'readPermission': True, 'studyId': 'tgct_tcga', 'cancerTypeId': 'nsgct', 'referenceGenome': 'hg19'}, {'name': 'Thymoma (TCGA, Firehose Legacy)', 'description': 'TCGA Thymoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/THYM/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 12:12:42', 'allSampleCount': 124, 'readPermission': True, 'studyId': 'thym_tcga', 'cancerTypeId': 'thym', 'referenceGenome': 'hg19'}, {'name': 'Thyroid Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Thyroid Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/THCA/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 12:35:44', 'allSampleCount': 516, 'readPermission': True, 'studyId': 'thca_tcga', 'cancerTypeId': 'thpa', 'referenceGenome': 'hg19'}, {'name': 'Uterine Corpus Endometrial Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Uterine Corpus Endometrial Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/UCEC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 14:22:20', 'allSampleCount': 549,

'readPermission': True, 'studyId': 'ucec_tcga', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Uterine Carcinosarcoma (TCGA, Firehose Legacy)', 'description': 'TCGA Uterine Carcinosarcoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/UCS/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 15:07:19', 'allSampleCount': 57, 'readPermission': True, 'studyId': 'ucs_tcga', 'cancerTypeId': 'ucs', 'referenceGenome': 'hg19'}, {'name': 'Uveal Melanoma (TCGA, Firehose Legacy)', 'description': 'TCGA Uveal Melanoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/UVM/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 15:32:33', 'allSampleCount': 80, 'readPermission': True, 'studyId': 'uvm_tcga', 'cancerTypeId': 'um', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Rhabdoid Tumor (TARGET, 2018)', 'description': 'Whole-genome sequencing 72 patients with Rhabdoid Tumor. Comprehensive profiling of 72 patients with Rhabdoid Tumor. <p>TARGET data is intended exclusively for biomedical research using pediatric data (i.e., the research objectives cannot be accomplished using data from adults) that focus on the development of more effective treatments, diagnostic tests, or prognostic markers for childhood cancers. Moreover, TARGET data can be used for research relevant to the biology, causes, treatment and late complications of treatment of pediatric cancers, but is not intended for the sole purposes of methods and/or tool development (please see Using TARGET Data section of the OCG website). If you are interested in using TARGET data for publication or other research purposes, you must follow the TARGET Publication Guidelines.</p>', 'publicStudy': True, 'groups': 'NCI-TARGET;PUBLIC', 'status': 0, 'importDate': '2024-01-24 15:57:09', 'allSampleCount': 72, 'readPermission': True, 'studyId': 'rt_target_2018_pub', 'cancerTypeId': 'mrt', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer (DKFZ, Cancer Cell 2018)', 'description': 'Whole genome and transcriptome sequencing of tumor/normal pairs from 292 prostate cancer patients.', 'publicStudy': True, 'pmid': '30537516', 'citation': 'Gerhauser et al. Cancer Cell 2018', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 16:20:06', 'allSampleCount': 324, 'readPermission': True, 'studyId': 'prostate_dkfz_2018', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Preclinical Testing Consortium (CHOP, Cell Rep 2019)', 'description': "Whole-exome sequencing of 261 patient derived xenografts (PDXs) samples from high-risk childhood cancers (with no matched normals). Website: PPTC", 'publicStudy': True, 'pmid': '31693904', 'citation': 'Rotika et al. Cell Rep 2019', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-01-24 16:44:53', 'allSampleCount': 261, 'readPermission': True, 'studyId': 'pptc_2019', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Gastric Cancer (OncoSG, 2018)', 'description': 'Whole-genome sequencing of 147 gastric cancer tumors with matched normals. Courtesy of OncoSG.', 'publicStudy': True, 'pmid': '29670109', 'citation': 'Guo et al. Nat Commun 2018', 'groups': '', 'status': 0, 'importDate': '2024-01-24 17:12:07', 'allSampleCount': 147, 'readPermission': True, 'studyId': 'stad_oncosg_2018', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Pan-cancer Analysis of Advanced and Metastatic Tumors (BCGSC, Nature Cancer 2020)', 'description': 'Whole-genome and transcriptome sequencing of 570 advanced and metastatic cancers and their matched normals.', 'publicStudy': True, 'pmid': '35121966', 'citation': 'Pleasance et al. Nature Cancer 2020', 'groups': '', 'status': 0, 'importDate': '2024-01-24 17:45:47', 'allSampleCount': 570, 'readPermission': True, 'studyId': 'pog570_bcgsc_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Colorectal Cancer (MSK, Cancer Cell 2018)', 'description': 'Targeted sequencing of 1134 metastatic colorectal tumor/normal pairs.', 'publicStudy': True, 'pmid': '29316426', 'citation': 'Yaeger et al. Cancer Cell 2018', 'groups': '', 'status': 0, 'importDate': '2024-02-21 12:02:44', 'allSampleCount': 1134, 'readPermission': True,

'studyId': 'crc_msk_2017', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'BRAF Fusions - IMPACT Clinical Sequencing Cohort (MSKCC)', 'description': 'Targeted sequencing of 105 clinical cases via MSK-IMPACT to characterize the structure and impact of BRAF fusions on clinical course in a tumor-agnostic approach.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-03-27 13:07:30', 'allSampleCount': 105, 'readPermission': True, 'studyId': 'braf_msk_impact_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Breast Cancer (METABRIC, Nature 2012 & Nat Commun 2016)', 'description': 'Targeted sequencing of 2509 primary breast tumors with 548 matched normals.', 'publicStudy': True, 'pmid': '27161491,30867590,22522925', 'citation': 'Pereira et al. Nat Commun 2016, Rueda et al. Nature 2019, Curtis et al. Nature 2012', 'groups': '', 'status': 0, 'importDate': '2024-04-22 12:02:38', 'allSampleCount': 2509, 'readPermission': True, 'studyId': 'brca_metabric', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'BRAF Fusions - ARCHER Clinical Sequencing Cohort (MSKCC)', 'description': 'Targeted sequencing of 107 clinical cases via ARCHER to characterize the structure and impact of BRAF fusions on clinical course in a tumor-agnostic approach.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-04-24 04:41:45', 'allSampleCount': 107, 'readPermission': True, 'studyId': 'braf_msk_archer_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Glioma (GLASS Consortium)', 'description': 'Whole genome or whole exome sequencing analysis of temporally separated diffuse glioma tumor/normal pairs from 329 adult patients. The data provided is based on the May 31, 2022 version and can be accessed at Synapse.', 'publicStudy': True, 'pmid': '35649412,38117484', 'citation': 'Varn et al. Cell 2022, Malta et al. Cancer Res. 2023', 'groups': '', 'status': 0, 'importDate': '2024-04-25 12:35:12', 'allSampleCount': 693, 'readPermission': True, 'studyId': 'difg_glass', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinoma (MSK, 2024)', 'description': 'Targeted sequencing of 1370 Hepatobiliary Cancer samples and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-05-17 04:01:22', 'allSampleCount': 1370, 'readPermission': True, 'studyId': 'hcc_msk_2024', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Cancer (CAS Shanghai, Cancer Cell 2020)', 'description': 'Whole-exome sequencing of 146 colorectal tumor/normal pairs from a chinese cohort, covering 70 metastatic and 76 non-metastatic colorectal cancer patients.', 'publicStudy': True, 'pmid': '32888432', 'citation': 'Li et al. Cancer Cell 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-05-20 12:01:21', 'allSampleCount': 146, 'readPermission': True, 'studyId': 'coadread_cass_2020', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Mature B-Cell Neoplasms (Simon Fraser University, Blood 2023)', 'description': 'Comprehensive whole-genome sequencing of 297 Burrkitt Lymphoma (BL) and diffuse large B-cell lymphoma (DLBCL) samples and their matched normals.', 'publicStudy': True, 'pmid': '36201743', 'citation': 'Thomas et al. Blood 2023', 'groups': '', 'status': 0, 'importDate': '2024-05-20 12:10:40', 'allSampleCount': 297, 'readPermission': True, 'studyId': 'mbn_sfu_2023', 'cancerTypeId': 'mbn', 'referenceGenome': 'hg38'}, {'name': 'Pre-cancer Colorectal Polyps (HTAN Vanderbilt, Cell 2021)', 'description': 'Whole-exome sequencing and single-cell transcriptomics analysis of 61 pre-malignant colorectal polyps (discovery and validation sets) and their matched normal colon tissues.', 'publicStudy': True, 'pmid': '34910928', 'citation': 'Chen et al. Cell 2021', 'groups': '', 'status': 0, 'importDate': '2024-05-20 12:17:09', 'allSampleCount': 61, 'readPermission': True, 'studyId': 'crc_hta11_htan_2021', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'IDH-mutated Diffuse Glioma (MSK, Clin Cancer Res 2024)', 'description': 'Targeted sequencing of 73 IDH-mutated low-grade gliomas and their matched normal pairs via MSK-IMPACT. The data is available on Synapse.', 'publicStudy': True, 'pmid': '37910594', 'citation': 'Ankush et al. Clin Cancer Res 2024', 'groups': '', 'status': 0, 'importDate': '2024-05-20 12:20:29', 'allSampleCount': 73, 'readPermission': True, 'studyId': 'difg_msk_2023', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Anaplastic Thyroid

Cancers (GATCI, Cell Reports 2024)', 'description': 'Whole-genome or whole-exome sequencing of 190 anaplastic thyroid carcinoma (ATC) and co-occurring differentiated thyroid carcinoma (DTC) samples.', 'publicStudy': True, 'pmid': '38412093', 'citation': 'Zeng, Peter Y F et al. Cell reports', 'groups': '', 'status': 0, 'importDate': '2024-05-20 12:24:05', 'allSampleCount': 190, 'readPermission': True, 'studyId': 'thyroid_gatci_2024', 'cancerTypeId': 'thyroid', 'referenceGenome': 'hg38'}, {'name': 'Prostate Cancer (MSK, Science 2022)', 'description': 'Targeted sequencing and whole exome sequencing of 35 prostate cancer tumors, organoids and cell lines via MSK-IMPACT.', 'publicStudy': True, 'pmid': '35617398', 'citation': 'Tang et al. Science 2022', 'groups': '', 'status': 0, 'importDate': '2024-05-28 12:06:24', 'allSampleCount': 47, 'readPermission': True, 'studyId': 'prad_organoids_msk_2022', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Chronic Lymphocytic Leukemia (Broad, Nature Genetics 2022)', 'description': 'Whole genome and whole exome sequencing of 1,154 samples from 1,148 patients with Chronic Lymphocytic Leukemia and monoclonal B cell lymphocytosis and their matched normals.', 'publicStudy': True, 'pmid': '35927489', 'citation': 'Knisbacher et al. Nature 2022', 'groups': '', 'status': 0, 'importDate': '2024-05-29 12:01:47', 'allSampleCount': 1154, 'readPermission': True, 'studyId': 'cll_broad_2022', 'cancerTypeId': 'cllsll', 'referenceGenome': 'hg19'}, {'name': 'MSK ctDNA Sequencing Cohort (MSK,2024)', 'description': 'Targeted sequencing of clinical cases via MSK-ACCES.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-06-11 12:01:24', 'allSampleCount': 5567, 'readPermission': True, 'studyId': 'msk_ctdna_vte_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Ovarian Cancer - MSK SPECTRUM (MSK, Nature 2022)', 'description': 'Multi-region, multi-modal profiling of 42 untreated high-grade serous ovarian cancer (HGSOC) tumor/normal pairs. This study reports an integrative analysis of mutational processes and their impact on the tumor microenvironment using single-cell RNA sequencing, whole-genome sequencing, targeted sequencing (MSK-IMPACT), digital histopathology and multiplexed immunofluorescence. The study is part of a prospective research program to understand the spatio-temporal determinants of HGSOC evolution, treatment and response (MSK SPECTRUM: Memorial Sloan Kettering - SPatio-temporal Evolution in Cancer TRaced Using Multimodalities).', 'publicStudy': True, 'pmid': '36517593', 'citation': 'VÃ¡zquez-GarcÃ\xada, Uhlitz et al. Nature 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-06-13 12:01:47', 'allSampleCount': 82, 'readPermission': True, 'studyId': 'msk_spectrum_tme_2022', 'cancerTypeId': 'ovary', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer (MSK 2024)', 'description': 'Targeted sequencing of 2257 prostate cancer patient samples and their matched normals via MSK-IMPACT platform.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-06-20 10:26:44', 'allSampleCount': 2260, 'readPermission': True, 'studyId': 'prostate_msk_2024', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Metastatic Breast Cancer (AURORA US Network, Nat Cancer 2023)', 'description': 'Retrospective Tissue Collection; an initiative of the Breast Cancer Research Foundation', 'publicStudy': True, 'pmid': '36585450', 'citation': 'Garcia-Recio et al. Nat Cancer 2023', 'groups': '', 'status': 0, 'importDate': '2024-06-25 12:02:53', 'allSampleCount': 163, 'readPermission': True, 'studyId': 'brca_aurora_2023', 'cancerTypeId': 'brca', 'referenceGenome': 'hg38'}, {'name': 'Rectal Cancer (MSK,Nature Medicine 2019)', 'description': 'MSK-IMPACT targeted sequencing of matched rectal cancer tumor and tumoroid samples.', 'publicStudy': True, 'pmid': '31591597', 'citation': 'Ganesh et al. Nat Med 2019', 'groups': 'SELCUKLS;SAUVEC;ZHENGY1;SMITHJ5;PUBLIC;SANCHEZF', 'status': 0, 'importDate': '2024-06-28 04:01:50', 'allSampleCount': 339, 'readPermission': True, 'studyId': 'rectal_msk_2019', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Endometrial Carcinoma cfDNA (MSK, Clin Cancer Res 2022)', 'description': 'High-sensitivity mutation analysis of cell-free DNA for disease monitoring in endometrial cancer.', 'publicStudy': True, 'pmid': '36007103', 'citation': 'Ashley et al. Clin Cancer Res 2023', 'groups': '', 'status': 0, 'importDate': '2024-06-28 04:04:45', 'allSampleCount': 44, 'readPermission': True, 'studyId': 'ucec_ccr_cfdna_msk_2022', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Cancer Therapy and Clonal Hematopoiesis (MSK, Blood Adv 2023)', 'description': 'Targeted sequencing of 47,532 patient samples with mixed

tumor types and their matched normals to identify clonal hematopoiesis mutations using MSK-IMPACT.', 'publicStudy': True, 'pmid': '38147626', 'citation': 'Stonestrom et al. Blood Adv 2024', 'groups': '', 'status': 0, 'importDate': '2024-06-28 04:07:35', 'allSampleCount': 42714, 'readPermission': True, 'studyId': 'msk_ch_2023', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (OncoSG, Nat Genet 2020)', 'description': 'Whole-exome and transcriptome sequencing of 305 east asian lung adenocarcinomas with matched normals. Courtesy of OncoSG. Lung Cancer Consortium Singapore (LCCS).', 'publicStudy': True, 'pmid': '32015526', 'citation': 'Chen et al. Nat Genet 2020', 'groups': '', 'status': 0, 'importDate': '2024-06-28 12:01:53', 'allSampleCount': 305, 'readPermission': True, 'studyId': 'luad_oncosg_2020', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Neuroendocrine Tumors (MSK, 2023)', 'description': 'Targeted sequencing of 65 Pancreatic Neuroendocrine tumors/normal pairs via MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-07-03 12:05:23', 'allSampleCount': 65, 'readPermission': True, 'studyId': 'panet_msk_erc_2023', 'cancerTypeId': 'pancreas', 'referenceGenome': 'hg19'}, {'name': 'Primary CNS Lymphoma - Ibrutinib Long Term Follow Up (MSK, 2024)', 'description': 'A Phase II study assessing Long-Term Response to Ibrutinib Monotherapy in recurrent or refractory CNS Lymphoma.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-07-08 12:01:20', 'allSampleCount': 86, 'readPermission': True, 'studyId': 'pcnsl_msk_2024', 'cancerTypeId': 'pcnsl', 'referenceGenome': 'hg19'}, {'name': 'Adrenocortical Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Adrenocortical Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 04:03:47', 'allSampleCount': 92, 'readPermission': True, 'studyId': 'acc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'acc', 'referenceGenome': 'hg19'}, {'name': 'Bladder Urothelial Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Bladder Urothelial Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 04:11:18', 'allSampleCount': 411, 'readPermission': True, 'studyId': 'blca_tcga_pan_can_atlas_2018', 'cancerTypeId': 'blca', 'referenceGenome': 'hg19'}, {'name': 'Breast Invasive Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Breast Invasive Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 04:36:55', 'allSampleCount': 1084, 'readPermission': True, 'studyId': 'brca_tcga_pan_can_atlas_2018', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Cervical Squamous Cell Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Cervical Squamous Cell Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,296250

49,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:01:13', 'allSampleCount': 297, 'readPermission': True, 'studyId': 'cesc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'cesc', 'referenceGenome': 'hg19'}, {'name': 'Cholangiocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Cholangiocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:19:30', 'allSampleCount': 36, 'readPermission': True, 'studyId': 'chol_tcga_pan_can_atlas_2018', 'cancerTypeId': 'chol', 'referenceGenome': 'hg19'}, {'name': 'Diffuse Large B-Cell Lymphoma (TCGA, PanCancer Atlas)', 'description': 'Diffuse Large B-Cell Lymphoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:23:39', 'allSampleCount': 48, 'readPermission': True, 'studyId': 'dlbc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg19'}, {'name': 'Esophageal Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Esophageal Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:28:52', 'allSampleCount': 182, 'readPermission': True, 'studyId': 'esca_tcga_pan_can_atlas_2018', 'cancerTypeId': 'esca', 'referenceGenome': 'hg19'}, {'name': 'Glioblastoma Multiforme (TCGA, PanCancer Atlas)', 'description': 'Glioblastoma Multiforme TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:38:49', 'allSampleCount': 592, 'readPermission': True, 'studyId': 'gbm_tcga_pan_can_atlas_2018', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg19'}, {'name': 'Head and Neck Squamous Cell Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Head and Neck Squamous Cell Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-10 05:48:41', 'allSampleCount': 523, 'readPermission': True, 'studyId': 'hnsc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Colorectal Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid':

'29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:04:59', 'allSampleCount': 594, 'readPermission': True, 'studyId': 'coadread_tcga_pan_can_atlas_2018', 'cancerTypeId': 'coadread', 'referenceGenome': 'hg19'}, {'name': 'Kidney Chromophobe (TCGA, PanCancer Atlas)', 'description': 'Kidney Chromophobe TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:29:03', 'allSampleCount': 65, 'readPermission': True, 'studyId': 'kich_tcga_pan_can_atlas_2018', 'cancerTypeId': 'chrcc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Clear Cell Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Kidney Renal Clear Cell Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:33:31', 'allSampleCount': 512, 'readPermission': True, 'studyId': 'kirc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg19'}, {'name': 'Kidney Renal Papillary Cell Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Kidney Renal Papillary Cell Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:42:41', 'allSampleCount': 283, 'readPermission': True, 'studyId': 'kirp_tcga_pan_can_atlas_2018', 'cancerTypeId': 'prcc', 'referenceGenome': 'hg19'}, {'name': 'Acute Myeloid Leukemia (TCGA, PanCancer Atlas)', 'description': 'Acute Myeloid Leukemia TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:49:57', 'allSampleCount': 200, 'readPermission': True, 'studyId': 'laml_tcga_pan_can_atlas_2018', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Brain Lower Grade Glioma (TCGA, PanCancer Atlas)', 'description': 'Brain Lower Grade Glioma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 04:54:48', 'allSampleCount': 514, 'readPermission': True, 'studyId': 'lgg_tcga_pan_can_atlas_2018', 'cancerTypeId': 'difg', 'referenceGenome': 'hg19'}, {'name': 'Liver Hepatocellular Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Liver Hepatocellular Carcinoma TCGA PanCancer data. The original data is <a

href="https://gdc.cancer.gov/about-data/publications/pancanatlas">here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 05:06:30', 'allSampleCount': 372, 'readPermission': True, 'studyId': 'lihc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Lung Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 05:20:01', 'allSampleCount': 566, 'readPermission': True, 'studyId': 'luad_tcga_pan_can_atlas_2018', 'cancerTypeId': 'luad', 'referenceGenome': 'hg19'}, {'name': 'Lung Squamous Cell Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Lung Squamous Cell Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 05:46:50', 'allSampleCount': 487, 'readPermission': True, 'studyId': 'lusc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg19'}, {'name': 'Mesothelioma (TCGA, PanCancer Atlas)', 'description': 'Mesothelioma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 06:10:55', 'allSampleCount': 87, 'readPermission': True, 'studyId': 'meso_tcga_pan_can_atlas_2018', 'cancerTypeId': 'plmeso', 'referenceGenome': 'hg19'}, {'name': 'Ovarian Serous Cystadenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Ovarian Serous Cystadenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 06:17:16', 'allSampleCount': 585, 'readPermission': True, 'studyId': 'ov_tcga_pan_can_atlas_2018', 'cancerTypeId': 'hgsoc', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Pancreatic Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 12:03:44', 'allSampleCount': 184, 'readPermission': True, 'studyId':

'paad_tcga_pan_can_atlas_2018', 'cancerTypeId': 'paad', 'referenceGenome': 'hg19'}, {'name': 'Pheochromocytoma and Paraganglioma (TCGA, PanCancer Atlas)', 'description': 'Pheochromocytoma and Paraganglioma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 12:12:11', 'allSampleCount': 178, 'readPermission': True, 'studyId': 'pcpg_tcga_pan_can_atlas_2018', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Prostate Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Prostate Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 12:17:27', 'allSampleCount': 494, 'readPermission': True, 'studyId': 'prad_tcga_pan_can_atlas_2018', 'cancerTypeId': 'prad', 'referenceGenome': 'hg19'}, {'name': 'Sarcoma (TCGA, PanCancer Atlas)', 'description': 'Sarcoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 12:31:59', 'allSampleCount': 255, 'readPermission': True, 'studyId': 'sarc_tcga_pan_can_atlas_2018', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Skin Cutaneous Melanoma (TCGA, PanCancer Atlas)', 'description': 'Skin Cutaneous Melanoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 12:49:16', 'allSampleCount': 448, 'readPermission': True, 'studyId': 'skcm_tcga_pan_can_atlas_2018', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg19'}, {'name': 'Stomach Adenocarcinoma (TCGA, PanCancer Atlas)', 'description': 'Stomach Adenocarcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 13:15:12', 'allSampleCount': 440, 'readPermission': True, 'studyId': 'stad_tcga_pan_can_atlas_2018', 'cancerTypeId': 'stad', 'referenceGenome': 'hg19'}, {'name': 'Testicular Germ Cell Tumors (TCGA, PanCancer Atlas)', 'description': 'Testicular Germ Cell Tumors TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11

13:34:20', 'allSampleCount': 149, 'readPermission': True, 'studyId': 'tgct_tcga_pan_can_atlas_2018', 'cancerTypeId': 'testis', 'referenceGenome': 'hg19'}, {'name': 'Thyroid Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Thyroid Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 13:38:41', 'allSampleCount': 500, 'readPermission': True, 'studyId': 'thca_tcga_pan_can_atlas_2018', 'cancerTypeId': 'thpa', 'referenceGenome': 'hg19'}, {'name': 'Thymoma (TCGA, PanCancer Atlas)', 'description': 'Thymoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 13:43:54', 'allSampleCount': 123, 'readPermission': True, 'studyId': 'thym_tcga_pan_can_atlas_2018', 'cancerTypeId': 'thym', 'referenceGenome': 'hg19'}, {'name': 'Uterine Corpus Endometrial Carcinoma (TCGA, PanCancer Atlas)', 'description': 'Uterine Corpus Endometrial Carcinoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,30643250,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 13:49:05', 'allSampleCount': 529, 'readPermission': True, 'studyId': 'ucec_tcga_pan_can_atlas_2018', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Uterine Carcinosarcoma (TCGA, PanCancer Atlas)', 'description': 'Uterine Carcinosarcoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 14:32:52', 'allSampleCount': 57, 'readPermission': True, 'studyId': 'ucs_tcga_pan_can_atlas_2018', 'cancerTypeId': 'ucs', 'referenceGenome': 'hg19'}, {'name': 'Uveal Melanoma (TCGA, PanCancer Atlas)', 'description': 'Uveal melanoma TCGA PanCancer data. The original data is here. The publications are here.', 'publicStudy': True, 'pmid': '29625048,29596782,29622463,29617662,29625055,29625050,29617662,32214244,29625049,29850653', 'citation': 'TCGA, Cell 2018', 'groups': 'PUBLIC;PANCAN', 'status': 0, 'importDate': '2024-07-11 14:38:13', 'allSampleCount': 80, 'readPermission': True, 'studyId': 'uvm_tcga_pan_can_atlas_2018', 'cancerTypeId': 'um', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Adenocarcinoma (MSK, 2024)', 'description': 'Targeted sequencing of 2336 pancreatic adenocarcinoma samples and their matched normals via MSK-IMPACT platform.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-07-16 12:01:47', 'allSampleCount': 2336, 'readPermission': True, 'studyId': 'pdac_msk_2024', 'cancerTypeId': 'pancreas', 'referenceGenome': 'hg19'}, {'name': 'ERBB2-mutant Endometrial cancer (MSK,2024)', 'description': 'Targeted sequencing of 69 uterine carcinoma tumor and normal pairs via

MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-07-17 04:01:27', 'allSampleCount': 69, 'readPermission': True, 'studyId': 'ucs_msk_2024', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg19'}, {'name': 'Adrenocortical Carcinoma (TCGA, GDC)', 'description': 'TCGA Adrenocortical Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 14:48:59', 'allSampleCount': 92, 'readPermission': True, 'studyId': 'acc_tcga_gdc', 'cancerTypeId': 'acc', 'referenceGenome': 'hg38'}, {'name': 'Bladder Urothelial Carcinoma (TCGA, GDC)', 'description': 'TCGA Bladder Urothelial Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 14:52:50', 'allSampleCount': 413, 'readPermission': True, 'studyId': 'blca_tcga_gdc', 'cancerTypeId': 'blca', 'referenceGenome': 'hg38'}, {'name': 'Invasive Breast Carcinoma (TCGA, GDC)', 'description': 'TCGA Invasive Breast Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:07:36', 'allSampleCount': 1103, 'readPermission': True, 'studyId': 'brca_tcga_gdc', 'cancerTypeId': 'brca', 'referenceGenome': 'hg38'}, {'name': 'Cervical Squamous Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Cervical Squamous Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:39:33', 'allSampleCount': 309, 'readPermission': True, 'studyId': 'cesc_tcga_gdc', 'cancerTypeId': 'cesc', 'referenceGenome': 'hg38'}, {'name': 'Cholangiocarcinoma (TCGA, GDC)', 'description': 'TCGA Cholangiocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:48:06', 'allSampleCount': 51, 'readPermission': True, 'studyId': 'chol_tcga_gdc', 'cancerTypeId': 'chol', 'referenceGenome': 'hg38'}, {'name': 'Diffuse Large B-Cell Lymphoma, NOS (TCGA, GDC)', 'description': 'TCGA Diffuse Large B-Cell Lymphoma, NOS. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:49:34', 'allSampleCount': 48, 'readPermission': True, 'studyId': 'dlbclnos_tcga_gdc', 'cancerTypeId': 'dlbclnos', 'referenceGenome': 'hg38'}, {'name': 'Esophageal Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Esophageal Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:51:27', 'allSampleCount': 186, 'readPermission': True, 'studyId': 'esca_tcga_gdc', 'cancerTypeId': 'esca', 'referenceGenome': 'hg38'}, {'name': 'Glioblastoma Multiforme (TCGA, GDC)', 'description': 'TCGA Glioblastoma Multiforme. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 15:58:24', 'allSampleCount': 610, 'readPermission': True, 'studyId': 'gbm_tcga_gdc', 'cancerTypeId': 'gbm', 'referenceGenome': 'hg38'}, {'name': 'Head and Neck Squamous Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Head and Neck Squamous Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:04:42', 'allSampleCount': 530, 'readPermission': True, 'studyId': 'hnsc_tcga_gdc', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg38'}, {'name': 'Chromophobe Renal Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Chromophobe Renal Cell Carcinoma. Source data from GDC and generated in Jul

2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:21:53', 'allSampleCount': 66, 'readPermission': True, 'studyId': 'chrcc_tcga_gdc', 'cancerTypeId': 'chrcc', 'referenceGenome': 'hg38'}, {'name': 'Renal Clear Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Renal Clear Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:24:30', 'allSampleCount': 537, 'readPermission': True, 'studyId': 'ccrcc_tcga_gdc', 'cancerTypeId': 'ccrcc', 'referenceGenome': 'hg38'}, {'name': 'Papillary Renal Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Papillary Renal Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:29:41', 'allSampleCount': 292, 'readPermission': True, 'studyId': 'prcc_tcga_gdc', 'cancerTypeId': 'prcc', 'referenceGenome': 'hg38'}, {'name': 'Acute Myeloid Leukemia (TCGA, GDC)', 'description': 'TCGA Acute Myeloid Leukemia. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:33:39', 'allSampleCount': 200, 'readPermission': True, 'studyId': 'aml_tcga_gdc', 'cancerTypeId': 'aml', 'referenceGenome': 'hg38'}, {'name': 'Diffuse Glioma (TCGA, GDC)', 'description': 'TCGA Diffuse Glioma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:35:17', 'allSampleCount': 530, 'readPermission': True, 'studyId': 'difg_tcga_gdc', 'cancerTypeId': 'difg', 'referenceGenome': 'hg38'}, {'name': 'Hepatocellular Carcinoma (TCGA, GDC)', 'description': 'TCGA Hepatocellular Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:40:34', 'allSampleCount': 379, 'readPermission': True, 'studyId': 'hcc_tcga_gdc', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg38'}, {'name': 'Lung Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Lung Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 16:50:04', 'allSampleCount': 571, 'readPermission': True, 'studyId': 'luad_tcga_gdc', 'cancerTypeId': 'luad', 'referenceGenome': 'hg38'}, {'name': 'Lung Squamous Cell Carcinoma (TCGA, GDC)', 'description': 'TCGA Lung Squamous Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 17:12:43', 'allSampleCount': 503, 'readPermission': True, 'studyId': 'lusc_tcga_gdc', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg38'}, {'name': 'Pleural Mesothelioma (TCGA, GDC)', 'description': 'TCGA Pleural Mesothelioma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 17:33:01', 'allSampleCount': 87, 'readPermission': True, 'studyId': 'plmeso_tcga_gdc', 'cancerTypeId': 'plmeso', 'referenceGenome': 'hg38'}, {'name': 'High-Grade Serous Ovarian Cancer (TCGA, GDC)', 'description': 'TCGA High-Grade Serous Ovarian Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 17:35:20', 'allSampleCount': 602, 'readPermission': True, 'studyId': 'hgsoc_tcga_gdc', 'cancerTypeId': 'hgsoc', 'referenceGenome': 'hg38'}, {'name': 'Pancreatic Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Pancreatic Adenocarcinoma. Source

data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 17:55:24', 'allSampleCount': 186, 'readPermission': True, 'studyId': 'paad_tcga_gdc', 'cancerTypeId': 'paad', 'referenceGenome': 'hg38'}, {'name': 'Miscellaneous Neuroepithelial Tumor (TCGA, GDC)', 'description': 'TCGA Miscellaneous Neuroepithelial Tumor. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 17:58:32', 'allSampleCount': 184, 'readPermission': True, 'studyId': 'mnet_tcga_gdc', 'cancerTypeId': 'mnet', 'referenceGenome': 'hg38'}, {'name': 'Prostate Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Prostate Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 18:00:25', 'allSampleCount': 501, 'readPermission': True, 'studyId': 'prad_tcga_gdc', 'cancerTypeId': 'prad', 'referenceGenome': 'hg38'}, {'name': 'Rectal Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Rectal Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 18:05:31', 'allSampleCount': 171, 'readPermission': True, 'studyId': 'read_tcga_gdc', 'cancerTypeId': 'read', 'referenceGenome': 'hg38'}, {'name': 'Cutaneous Melanoma (TCGA, GDC)', 'description': 'TCGA Cutaneous Melanoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 18:20:50', 'allSampleCount': 473, 'readPermission': True, 'studyId': 'skcm_tcga_gdc', 'cancerTypeId': 'skcm', 'referenceGenome': 'hg38'}, {'name': 'Stomach Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Stomach Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 18:41:41', 'allSampleCount': 443, 'readPermission': True, 'studyId': 'stad_tcga_gdc', 'cancerTypeId': 'stad', 'referenceGenome': 'hg38'}, {'name': 'Non-Seminomatous Germ Cell Tumor (TCGA, GDC)', 'description': 'TCGA Non-Seminomatous Germ Cell Tumor. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 18:58:02', 'allSampleCount': 156, 'readPermission': True, 'studyId': 'nsgct_tcga_gdc', 'cancerTypeId': 'nsgct', 'referenceGenome': 'hg38'}, {'name': 'Papillary Thyroid Cancer (TCGA, GDC)', 'description': 'TCGA Papillary Thyroid Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:05:14', 'allSampleCount': 515, 'readPermission': True, 'studyId': 'thpa_tcga_gdc', 'cancerTypeId': 'thpa', 'referenceGenome': 'hg38'}, {'name': 'Thymoma (TCGA, GDC)', 'description': 'TCGA Thymoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:08:06', 'allSampleCount': 124, 'readPermission': True, 'studyId': 'thym_tcga_gdc', 'cancerTypeId': 'thym', 'referenceGenome': 'hg38'}, {'name': 'Endometrial Carcinoma (TCGA, GDC)', 'description': 'TCGA Endometrial Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:10:06', 'allSampleCount': 548, 'readPermission': True, 'studyId': 'ucec_tcga_gdc', 'cancerTypeId': 'ucec', 'referenceGenome': 'hg38'}, {'name': 'Uterine Carcinosarcoma/Uterine Malignant Mixed Mullerian

Tumor (TCGA, GDC)', 'description': 'TCGA Uterine Carcinosarcoma/Uterine Malignant Mixed Mullerian Tumor. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:40:35', 'allSampleCount': 57, 'readPermission': True, 'studyId': 'ucs_tcga_gdc', 'cancerTypeId': 'ucs', 'referenceGenome': 'hg38'}, {'name': 'Uveal Melanoma (TCGA, GDC)', 'description': 'TCGA Uveal Melanoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:44:07', 'allSampleCount': 80, 'readPermission': True, 'studyId': 'um_tcga_gdc', 'cancerTypeId': 'um', 'referenceGenome': 'hg38'}, {'name': 'Colon Adenocarcinoma (TCGA, GDC)', 'description': 'TCGA Colon Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-27 19:46:15', 'allSampleCount': 463, 'readPermission': True, 'studyId': 'coad_tcga_gdc', 'cancerTypeId': 'coad', 'referenceGenome': 'hg38'}, {'name': 'Soft Tissue Cancer (TCGA, GDC)', 'description': 'TCGA Soft Tissue Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:07:12', 'allSampleCount': 264, 'readPermission': True, 'studyId': 'soft_tissue_tcga_gdc', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg38'}, {'name': 'CNS/Brain Cancer (CPTAC, GDC)', 'description': 'CPTAC CNS/Brain Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:14:17', 'allSampleCount': 74, 'readPermission': True, 'studyId': 'brain_cptac_gdc', 'cancerTypeId': 'brain', 'referenceGenome': 'hg38'}, {'name': 'Breast Cancer (CPTAC, GDC)', 'description': 'CPTAC Breast Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:16:03', 'allSampleCount': 154, 'readPermission': True, 'studyId': 'breast_cptac_gdc', 'cancerTypeId': 'breast', 'referenceGenome': 'hg38'}, {'name': 'Colon Adenocarcinoma (CPTAC, GDC)', 'description': 'CPTAC Colon Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:17:58', 'allSampleCount': 109, 'readPermission': True, 'studyId': 'coad_cptac_gdc', 'cancerTypeId': 'coad', 'referenceGenome': 'hg38'}, {'name': 'Lung Adenocarcinoma (CPTAC, GDC)', 'description': 'CPTAC Lung Adenocarcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:21:40', 'allSampleCount': 180, 'readPermission': True, 'studyId': 'luad_cptac_gdc', 'cancerTypeId': 'luad', 'referenceGenome': 'hg38'}, {'name': 'Lung Squamous Cell Carcinoma (CPTAC, GDC)', 'description': 'CPTAC Lung Squamous Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:28:50', 'allSampleCount': 90, 'readPermission': True, 'studyId': 'lusc_cptac_gdc', 'cancerTypeId': 'lusc', 'referenceGenome': 'hg38'}, {'name': 'Head and Neck Carcinoma, Other (CPTAC, GDC)', 'description': 'CPTAC Head and Neck Carcinoma, Other. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:32:53', 'allSampleCount': 150, 'readPermission': True, 'studyId': 'ohnca_cptac_gdc', 'cancerTypeId': 'ohnca', 'referenceGenome': 'hg38'}, {'name': 'Ovarian Cancer (CPTAC, GDC)', 'description': 'CPTAC Ovarian

Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:36:26', 'allSampleCount': 113, 'readPermission': True, 'studyId': 'ovary_cptac_gdc', 'cancerTypeId': 'ovary', 'referenceGenome': 'hg38'}, {'name': 'Pancreatic Cancer (CPTAC, GDC)', 'description': 'CPTAC Pancreatic Cancer. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:38:16', 'allSampleCount': 139, 'readPermission': True, 'studyId': 'pancreas_cptac_gdc', 'cancerTypeId': 'pancreas', 'referenceGenome': 'hg38'}, {'name': 'Renal Cell Carcinoma (CPTAC, GDC)', 'description': 'CPTAC Renal Cell Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:40:01', 'allSampleCount': 288, 'readPermission': True, 'studyId': 'rcc_cptac_gdc', 'cancerTypeId': 'rcc', 'referenceGenome': 'hg38'}, {'name': 'Uterine Endometrioid Carcinoma (CPTAC, GDC)', 'description': 'CPTAC Uterine Endometrioid Carcinoma. Source data from GDC and generated in Jul 2024 using <A HREF="https://isb-cgc.appspot.com/bq_meta_search/">ISB-CGC BigQuery tables</A>.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-07-28 10:44:47', 'allSampleCount': 292, 'readPermission': True, 'studyId': 'uec_cptac_gdc', 'cancerTypeId': 'uec', 'referenceGenome': 'hg38'}, {'name': 'Adenoid Cystic Carcinoma of the Breast (MSK, J Pathol. 2015)', 'description': 'Whole exome sequencing of 12 breast AdCCs.', 'publicStudy': True, 'pmid': '26095796', 'citation': 'Martelotto et al. J Pathol 2015', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2024-08-02 12:02:51', 'allSampleCount': 12, 'readPermission': True, 'studyId': 'acbc_mskcc_2015', 'cancerTypeId': 'acbc', 'referenceGenome': 'hg19'}, {'name': 'Atypical Small Cell Lung Cancer (MSK, 2024)', 'description': 'Targeted sequencing of 31 atypical small cell lung cancers and their matched normals via MSK-IMPACT, including structural variant analysis via whole-genome sequencing.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-08-02 12:31:22', 'allSampleCount': 31, 'readPermission': True, 'studyId': 'asclc_msk_2024', 'cancerTypeId': 'lung', 'referenceGenome': 'hg19'}, {'name': 'Pan-cancer analysis of whole genomes (ICGC/TCGA, Nature 2020)', 'description': 'WGS changes cataloged in 2,583 whole-cancer genomes and their matched normal tissues across 38 tumor types. Source data from <A HREF="https://xenabrowser.net/datapages/?cohort=PCAWG%20(specimen%20centric)&addHub=https%3A%2F%2Fpcawg.xenahubs.net&removeHub=https%3A%2F%2Fxena.treehouse.gi.ucsc.edu%3A443">UCSC Xena</A> and <A HREF="https://dcc.icgc.org/releases/PCAWG/">ICGC Data Portal</A>.', 'publicStudy': True, 'pmid': '32025007', 'citation': 'Campbell et al. Nature 2020', 'groups': '', 'status': 0, 'importDate': '2024-08-23 04:42:27', 'allSampleCount': 2922, 'readPermission': True, 'studyId': 'pancan_pcawg_2020', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pancreatic Cancer (MSK, 2024)', 'description': 'Targeted sequencing of 395 pancreatic cases and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-08-30 10:40:31', 'allSampleCount': 395, 'readPermission': True, 'studyId': 'pancreas_msk_2024', 'cancerTypeId': 'pancreas', 'referenceGenome': 'hg19'}, {'name': 'Head and Neck Squamous Cell Carcinoma (TCGA, Firehose Legacy)', 'description': 'TCGA Head and Neck Squamous Cell Carcinoma. Source data from <A HREF="http://gdac.broadinstitute.org/runs/stddata__2016_01_28/data/HNSC/20160128/">GDAC Firehose</A>. Previously known as TCGA Provisional.', 'publicStudy': True, 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-09-05 10:50:14', 'allSampleCount': 530, 'readPermission': True, 'studyId': 'hnsc_tcga', 'cancerTypeId': 'hnsc', 'referenceGenome': 'hg19'}, {'name': 'Gastrointestinal Stromal Tumors (MSK, Clin Cancer Res 2023)', 'description': 'Targeted sequencing of 469 gastrointestinal stromal tumors and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '37477937', 'citation': 'Dermawan et al. Clin Cancer Res 2023', 'groups': '', 'status': 0, 'importDate': '2024-09-07 04:42:45', 'allSampleCount': 469, 'readPermission': True, 'studyId': 'gist_msk_2023', 'cancerTypeId':

'gist', 'referenceGenome': 'hg19'}, {'name': 'Leiomyosarcoma (MSK, Clin Cancer Res 2024)', 'description': 'Targeted sequencing of 470 Leiomyosarcoma samples and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '38488807', 'citation': 'Josephine K et al. Clin Cancer Res 2024', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-09-07 04:54:42', 'allSampleCount': 470, 'readPermission': True, 'studyId': 'lms_msk_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Cancer Cell Line Encyclopedia (Genetech, Nat biotech 2014)', 'description': 'Single-nucleotide polymorphism (SNP) array analysis and RNA sequencing and of 675 mixed human cancer cell lines from the Cancer Cell Line Encyclopedia. Out of the 675 cell lines, the Genetech cohort includes 148 lines that were not investigated in other CCLE studies.', 'publicStudy': True, 'pmid': '25485619', 'citation': 'Klijn, Christiaan et al. Nature biotechnology 2014', 'groups': '', 'status': 0, 'importDate': '2024-09-07 05:11:31', 'allSampleCount': 675, 'readPermission': True, 'studyId': 'ccle_genetech_2014', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Soft Tissue and Bone Sarcoma (MSK, Nat Commun 2022)', 'description': 'Targeted sequencing of 7,494 soft tissue and bone sarcoma samples using the Foundation Medicine platform.', 'publicStudy': True, 'pmid': '35705558', 'citation': 'Gounder et. al. Nat Comm 2022', 'groups': '', 'status': 0, 'importDate': '2024-09-18 04:41:04', 'allSampleCount': 7494, 'readPermission': True, 'studyId': 'sarcoma_msk_2022', 'cancerTypeId': 'soft_tissue', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (DFCI/Orion, 2024)', 'description': 'Combined spatial and targeted genomic analysis of 74 colon and rectal cancers. Preprint can be found here.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-09-26 12:41:00', 'allSampleCount': 74, 'readPermission': True, 'studyId': 'crc_orion_2024', 'cancerTypeId': 'bowel', 'referenceGenome': 'hg19'}, {'name': 'Pediatric Acute Lymphoid Leukemia - Phase II (TARGET, 2018)', 'description': 'Whole genome or whole exome sequencing on 298 Pediatric Acute Lymphoid Leukemia - Phase II samples. Comprehensive profiling of ALL Phase 2 samples. <p>TARGET data is intended exclusively for biomedical research using pediatric data (i.e., the research objectives cannot be accomplished using data from adults) that focus on the development of more effective treatments, diagnostic tests, or prognostic markers for childhood cancers. Moreover, TARGET data can be used for research relevant to the biology, causes, treatment and late complications of treatment of pediatric cancers, but is not intended for the sole purposes of methods and/or tool development (please see Using TARGET Data section of the OCG website). If you are interested in using TARGET data for publication or other research purposes, you must follow the TARGET Publication Guidelines.</p>', 'publicStudy': True, 'groups': 'NCI-TARGET;PUBLIC', 'status': 0, 'importDate': '2024-09-27 12:41:03', 'allSampleCount': 1978, 'readPermission': True, 'studyId': 'all_phase2_target_2018_pub', 'cancerTypeId': 'bll', 'referenceGenome': 'hg19'}, {'name': 'RAD51B Associated Mixed Cancers (MSK, NPJ Breast Cancer 2021)', 'description': 'Targeted sequencing of 19 samples with RAD51B loss-of-function variants and their matched normals. Samples confer susceptibility to hereditary breast and ovarian cancers, resulting in homologous recombination-deficient tumors.', 'publicStudy': True, 'pmid': '34635660', 'citation': 'Setton et al. NPJ Breast Cancer 2021', 'groups': '', 'status': 0, 'importDate': '2024-09-27 17:18:50', 'allSampleCount': 17, 'readPermission': True, 'studyId': 'mixed_msk_tcga_2021', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Cutaneous Squamous Cell Carcinoma (UOW, Front Oncol 2022)', 'description': 'Whole genome sequencing of 25 metastatic cutaneous squamous cell carcinoma and their matched normals. Generated by the Ranson Lab 2022.', 'publicStudy': True, 'pmid': '35982973', 'citation': 'Thind, Amarinder Singh et al. Front Oncol 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-09-27 17:22:24', 'allSampleCount': 25, 'readPermission': True, 'studyId': 'cscc_ranson_2022', 'cancerTypeId': 'cscc', 'referenceGenome': 'hg38'}, {'name': 'Diffuse Large B-Cell Lymphoma (MSK, Haematologica 2024)', 'description': 'Targeted sequencing of 396 diffuse large B-cell lymphoma samples and their

matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '38497151', 'citation': 'Zhu, Meng-Lei et al. Haematologica 2024', 'groups': '', 'status': 0, 'importDate': '2024-09-27 17:30:45', 'allSampleCount': 396, 'readPermission': True, 'studyId': 'mbn_msk_2024', 'cancerTypeId': 'mbn', 'referenceGenome': 'hg19'}, {'name': 'Endometrial and Ovarian Cancer (MSK, Nature Medicine 2024)', 'description': 'Targeted sequencing of 33 endometrial and ovarian tumors and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '38653864', 'citation': 'Friedman, Claire F et al. Nature Medicine 2024', 'groups': '', 'status': 0, 'importDate': '2024-09-27 17:33:29', 'allSampleCount': 33, 'readPermission': True, 'studyId': 'ucec_msk_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Pleural Mesothelioma (MSK, Clin Cancer Res 2024)', 'description': 'Targeted sequencing of 14 genomic near-haploidization (GNH) pleural mesothelioma samples and their matched normals via MSK-IMPACT.', 'publicStudy': True, 'pmid': '38630790', 'citation': 'Yang, Soo-Ryum et al. Clin Cancer Res 2024', 'groups': '', 'status': 0, 'importDate': '2024-09-27 17:35:29', 'allSampleCount': 14, 'readPermission': True, 'studyId': 'plmeso_msk_2024', 'cancerTypeId': 'plmeso', 'referenceGenome': 'hg19'}, {'name': 'Hepatocellular Carcinoma (CLCA, Nature 2024)', 'description': 'The Chinese Liver Cancer Atlas (CLCA) project. Deep whole-genome sequencing of 494 hepatocellular carcinomas and their matched normals. Data from CLC Atlas.', 'publicStudy': True, 'pmid': '38355797', 'citation': 'Chen L et al. Nature 2024', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-09-27 17:37:37', 'allSampleCount': 494, 'readPermission': True, 'studyId': 'hcc_clca_2024', 'cancerTypeId': 'hcc', 'referenceGenome': 'hg19'}, {'name': 'Pediatric European MAPPYACTS Trial (Gustave Roussy, Cancer Discov 2022)', 'description': 'Whole-exome sequencing of 674 pediatric matched normal samples on multiple pathologies driven on mappyacts program and somatic mutation data for 484 single nucleotide alterations reported as potentially actionable, see the README', 'publicStudy': True, 'pmid': '35292802', 'citation': 'Berlanga et al. Cancer Discov 2022', 'groups': '', 'status': 0, 'importDate': '2024-09-28 04:02:02', 'allSampleCount': 178, 'readPermission': True, 'studyId': 'pancan_mappyacts_2022', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg38'}, {'name': 'Nerve Sheath Tumors (Johns Hopkins, 2024)', 'description': 'Whole-exome sequencing of 134 nerve sheath tumor samples with their matched normals. The raw data is contributed by Johns Hopkins University researchers funded by the Neurofibromatosis Therapeutic Acceleration Program (NTAP). The reprocessing of the raw data is managed by the NF Open Science Initiative (NF Data Portal). The original raw data was reprocessed with updated genome build and filtered to remove low confidence variant calls, and any common variants that had a gnomAD allele frequency (for any subpopulation) greater than or equal to 0.0005. (Recent preprint can be found here).', 'publicStudy': True, 'pmid': '32561749', 'citation': 'Pollard et al. Sci Data 2020', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-09-30 12:02:01', 'allSampleCount': 134, 'readPermission': True, 'studyId': 'nst_nfosi_ntap', 'cancerTypeId': 'nst', 'referenceGenome': 'hg38'}, {'name': 'Pituitary Adenoma (MSK, Acta Neuropathologica 2024)', 'description': 'Targeted sequencing of 104 pituitary adenoma samples and their matched normals using MSK-IMPACT.', 'publicStudy': True, 'pmid': '38758238', 'citation': 'Lin, Andrew L et al, Acta Neuropathologica 2024', 'groups': '', 'status': 0, 'importDate': '2024-10-01 04:02:10', 'allSampleCount': 104, 'readPermission': True, 'studyId': 'ptad_msk_2024', 'cancerTypeId': 'ptad', 'referenceGenome': 'hg19'}, {'name': 'MSK CHORD (MSK, 2024)', 'description': 'Targeted sequencing of 25040 tumors from 24950 patients and their matched normals via MSK-IMPACT, along with clinical annotations, some of which are derived from natural language processing (denoted NLP). This data is available under the Creative Commons BY-NC-ND 4.0 license.', 'publicStudy': True, 'groups': '', 'status': 0, 'importDate': '2024-10-02 04:27:56', 'allSampleCount': 25040, 'readPermission': True, 'studyId': 'msk_chord_2024', 'cancerTypeId': 'mixed', 'referenceGenome': 'hg19'}, {'name': 'Triple-Negative Breast Cancer (FUSCC, Cell Research 2020)',

'description': 'Targeted sequencing of 69 refractory metastatic triple-negative breast cancer patients and their matched normal samples as part of the FUTURE trial.', 'publicStudy': True, 'pmid': '32719455', 'citation': 'Jiang, Yi-Zhou et al. Cell Research 2020', 'groups': '', 'status': 0, 'importDate': '2024-10-02 12:01:53', 'allSampleCount': 69, 'readPermission': True, 'studyId': 'brca_fuscc_2020', 'cancerTypeId': 'brca', 'referenceGenome': 'hg19'}, {'name': 'Lung Adenocarcinoma (MSK Mind,Nature Cancer 2022)', 'description': 'Multimodality tools to predict response to PD-(L)1 blockade in patients with lung adenocarcinoma.', 'publicStudy': True, 'pmid': '36038778', 'citation': 'Rami S et al. Nature Cancer 2022', 'groups': '', 'status': 0, 'importDate': '2024-10-17 12:02:04', 'allSampleCount': 247, 'readPermission': True, 'studyId': 'lung_msk_mind_2020', 'cancerTypeId': 'lung', 'referenceGenome': 'hg19'}, {'name': 'Esophageal/Stomach Cancer (MSK, 2020)', 'description': 'Targeted sequencing of 487 Esophageal/stomach cancer tumor-normal pairs via MSK-IMPACT.', 'publicStudy': True, 'pmid': '33795256', 'citation': 'Sihag et al. Clin Cancer Res 2021', 'groups': '', 'status': 0, 'importDate': '2024-10-17 12:04:04', 'allSampleCount': 487, 'readPermission': True, 'studyId': 'egc_mskcc_2020', 'cancerTypeId': 'stomach', 'referenceGenome': 'hg19'}, {'name': 'Rectal Cancer (MSK, Nature Medicine 2022)', 'description': 'DNA and RNA sequencing of 738 primary rectal tumors.', 'publicStudy': True, 'pmid': '35970919', 'citation': 'Walid K et al. Nature Medicine 2022', 'groups': '', 'status': 0, 'importDate': '2024-10-17 12:07:36', 'allSampleCount': 788, 'readPermission': True, 'studyId': 'rectal_msk_2022', 'cancerTypeId': 'bowel', 'referenceGenome': 'hg19'}, {'name': 'Esophagogastric Cancer (MSK, Clin Cancer Res 2022)', 'description': 'Targeted sequencing of 237 esophagogastric tumor/normal pairs via MSK-IMPACT platform.', 'publicStudy': True, 'pmid': '35377946', 'citation': 'Smita et al. Clin Cancer Res 2022', 'groups': '', 'status': 0, 'importDate': '2024-10-17 12:11:52', 'allSampleCount': 237, 'readPermission': True, 'studyId': 'egc_msk_tp53_ccr_2022', 'cancerTypeId': 'egc', 'referenceGenome': 'hg19'}, {'name': 'Gallbladder Cancer (MSK, 2022)', 'description': 'Targeted sequencing of 244 Gallbladder cases via MSK-IMPACT where investigators calculated the Overall survival time for 100 metastatic gallbladder patients.', 'publicStudy': True, 'pmid': '36228155', 'citation': 'Nicolas A et al. Clin Cancer Res 2022', 'groups': '', 'status': 0, 'importDate': '2024-10-17 12:14:21', 'allSampleCount': 244, 'readPermission': True, 'studyId': 'gbc_mskcc_2022', 'cancerTypeId': 'gbc', 'referenceGenome': 'hg19'}, {'name': 'Colorectal Adenocarcinoma (MSK, Nat Commun 2022)', 'description': 'Targeted sequencing of 180 colitis-associated cancers and their matched normals.', 'publicStudy': True, 'pmid': '36611031', 'citation': 'Walid K et al. Nat Commun. 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-10-17 12:16:39', 'allSampleCount': 179, 'readPermission': True, 'studyId': 'bowel_colitis_msk_2022', 'cancerTypeId': 'bowel', 'referenceGenome': 'hg19'}, {'name': 'Papillary Thyroid Carcinoma (TCGA, Cell 2014)', 'description': 'Exome and whole genome sequencing of 496 papillary thyroid carcinoma tumor/normal pairs', 'publicStudy': True, 'pmid': '25417114', 'citation': 'TCGA, Cell 2014', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-10-18 12:02:22', 'allSampleCount': 496, 'readPermission': True, 'studyId': 'thca_tcga_pub', 'cancerTypeId': 'thpa', 'referenceGenome': 'hg19'}, {'name': 'Acute Myeloid Leukemia (OHSU, Cancer Cell 2022)', 'description': 'Whole-exome and transcriptomic sequencing of 942 acute myeloid leukemia samples (with 500 matched normals) from the Beat AML program.', 'publicStudy': True, 'pmid': '35868306', 'citation': 'Bottomly et al. Cancer Cell 2022', 'groups': 'PUBLIC', 'status': 0, 'importDate': '2024-10-18 12:05:39', 'allSampleCount': 942, 'readPermission': True, 'studyId': 'aml_ohsu_2022', 'cancerTypeId': 'aml', 'referenceGenome': 'hg19'}, {'name': 'Prostate Cancer MDA PCa PDX (MD Anderson, Clin Cancer Res 2024)', 'description': 'Targeted sequencing and whole-genome sequencing of 88 MD Anderson Prostate Cancer PDX models derived from 38 patients with tumor.', 'publicStudy': True, 'pmid': '38488813', 'citation': 'Anselmino et al. Clin Cancer Res 2024', 'groups': '', 'status': 0, 'importDate': '2024-10-25 04:09:08', 'allSampleCount': 88, 'readPermission': True, 'studyId': 'prad_msk_mdanderson_2023', 'cancerTypeId': 'prostate', 'referenceGenome': 'hg19'}, {'name': 'Adenoid Cystic Carcinoma Project (J Clin Invest 2019)', 'description': 'Multi-Institute Cohort of 1045 Adenoid Cystic Carcinoma patients.', 'publicStudy': True, 'pmid': '31483290', 'citation': 'Allen et al. J Clin Invest 2019', 'groups': 'ACYC;PUBLIC', 'status': 0, 'importDate': '2024-10-25 15:27:14',

'allSampleCount': 1049, 'readPermission': True, 'studyId': 'acc_2019', 'cancerTypeId': 'acyc', 'referenceGenome': 'hg19'}]

(cbio_ml_pl_env) D:\000_AI_Helper\000_Do_Informatics\Final_info_controller\ InfoProj_CG_PTTD_CTS\pipeline_interface\cbio_ml_pl\cbioportal_api_project>