Supplementary Table S4

Slide number	Pt#	Tumor #	Gene	Chromosome	Chr position	Mutated Codon	Identified by NGS		Verified by Sanger	
							DP	Baseline	DP	Baseline
1	Pt37	DP2	KRAS	chr12	25398285	Ggt/Tgt	G12C	WT	G12C	WT
2	Pt37	DP3	PTEN	chr10	89653819	AG->A	rameshift 40 onwar	WT	WT	WT
3	Pt37	DP3	ARHGEF25	chr12	58007078	gGa/gAa	G154E	WT	G154E	WT
4	Pt37	DP3	USH2A	chr1	216380710	tGg/tTg	W1074L	WT	W1074L	WT
5	Pt37	DP3	VN1R4	chr19	53770061	aTG/aAA	M286K	WT	M286K	WT
6	Pt37	DP3	MAP4K1	chr19	39086591	Gtg/Ttg	V723L	WT	V723L	WT
7	Pt37	DP3	EPHA7	chr6	94068081	tCt/tGt	S294C	WT	S294C	WT
8	Pt37	DP4	RAD18	chr3	8977557	tCa/tTa	S296L	WT	S296L	WT
9	Pt37	DP4	GRIN3A	chr9	104432691	gCc/gTc	A668V	WT	A668V	WT
10	Pt37	DP5	KRAS	chr12	25398285	Ggt/Tgt	G12C	WT	G12C	WT
11	Pt37	DP6	LRP1B	chr2	141359094	gCa/gAa	A2305E	WT	A2305E	WT
12	Pt37	DP6	KRAS	chr12	25398285	Ggt/Tgt	G12C	WT	G12C	WT
13	Pt37	DP6	SP100	chr2	231371028	aaG/aaT	K627N	WT	K627N	WT
14	Pt37	DP6	ISL1	chr5	50683518	aGg/aTg	R138M	WT	R138M	WT
15	Pt37	DP6	MAML2	chr11	95712165	Gat/Tat	D1140Y	WT	D1140Y	WT
16	Pt37	DP6	KLHL24	chr3	183368362	gAa/gGa	E73G	WT	E73G	WT
17	Pt37	DP9	PARP11	chr12	3931133	Gaa/Taa	E152*	WT	E152*	WT
18	Pt37	DP9	POLR3A	chr10	79782142	Gaa/Aaa	E216K	WT	E216K	WT
19	Pt37	DP9	LCOR	chr10	98715632	Ccc/Tcc	P419S	WT	P419S	WT
20	Pt37	DP9	CRIP3	chr6	43274195	cCc/cTc	P130L	WT	P130L	WT
21	Pt37	DP9	DCHS1	chr11	6648424	aCg/aTg	T1949M	WT	T1949WT	WT
22	Pt37	DP9	GRIN3B	chr19	1008683	Gct/Act	A845T	WT	A845WT	WT
23	Pt37	DP9	CIC	chr19	42793430	gCg/gTg	A411V	WT	A411V	WT
24	Pt40	DP2	CACNA2D1	chr7	81746474	Agt/Tgt	S138C	WT	S138C	WT
25	Pt40	DP2	PYGB	chr20	25269059	A->G	SPLICE	WT	SPLICE	WT
26	Pt40	DP2	PTK2	chr8	141745451	atG/atT	M665I	WT	M665I	WT
27	Pt40	DP2	AKT3	chr1	243859016	Gaa/Aaa	E17K	WT	E17K	WT
28	Pt15	DP1	DISP1	chr1	223177285	aCc/aTc	T849I	WT	T849I	WT
29	Pt15	DP1	PLD2	chr17	4719981	Ggc/Cgc	G508R	WT	G508R	WT
30	Pt15	DP1	MCM10	chr10	13225081	cCc/cTc	P361L	WT	P361L	WT
31	Pt15	DP1	WNT10A	chr2	219754991	gGg/gAg	G221E	WT	G221E	WT
32	Pt15	DP1	GRIA2	chr4	158283949	A ->T	SPLICE	WT	SPLICE	WT
33	Pt15	DP1	DDIT4L	chr4	101108952	tTt/tAt	F155Y	WT	F155Y	WT
34	Pt15	DP1	POLR3A	chr10	79769683	tCa/tTa	S570L	WT	S570L	WT
35	Pt15	DP1	PPP1R3A	chr7	113519116	aaA/aaC	K677N	WT	K677N	WT
36	Pt24	DP1	PIK3R2	chr19	18278061	Aac/Gac	N561D	WT	N561D	WT
37	Pt24	DP2	PKHD1	chr6	51524534	Ccc/Gcc	P3464A	WT	P3464A	WT
38	Pt24	DP2	RBM38	chr20	55982618	Tac/Aac	Y146N	WT	Y146N	WT
39	Pt24	DP3	KAT2A	chr17	40269731	Acc/Gcc	T465A	WT	T465A	WT
40	Pt16	DP1	KLHDC3	chr6	42986425	cGg/cAg	R263Q	WT	R263Q	WT
41	Pt16	DP1	DLG1	chr3	196910678	aTg/aGg	M1R	WT	M1R	WT
42	Pt23	DP1	EPHB2	ch1	23111369	gGc/gAc	G204D	WT	G204D	WT
43	Pt23	DP1	EPHA4	chr2	222428700	Atc/Gtc	I192V	WT	I192V	WT
44	Pt23	DP1	NCOR2	chr12	124957548	Cga/Tga	R181*	WT	R181*	WT
45	Pt23	DP1	PIK3CA	chr3	178921567	gAc/gGc	D350G	WT	D350G	WT
46	Pt23	DP1	PIK3CA	chr3	178936092	gAg/gGg	E545G	WT	E545G	WT
47	Pt23	DP2	NRAS	chr1	115256530	Caa/Aaa	Q61K	WT	Q61K	WT
48	Pt23	DP2	RPTOR	chr17	78831696	gAc/gGc	D502G	WT	D502G	WT
49	Pt23	DP2	ATR	chr3	142177906	aTg/aCg	M2466T	WT	M2466T	WT
50	Pt23	DP2	ARID1A	chr1	27106559	cGg/cAg	R2057Q	WT	R2057Q	WT
51	Pt23	DP2	SIVA1	chr14	105222163	T->C	SPLICE	WT	SPLICE	WT
52	Pt23	DP2	CHAMP1	chr13	115091637	Tca/Cca	S774P	WT	S774P	WT
53	Pt43	DP1	PTEN	chr10	89692915	AATG->A	M134Del	WT	M134Del	WT
54	Pt43	DP1	PLEKHG3	chr14	65208817	tCg/tAg	S805*	WT	S805*	WT

55	Pt43	DP2	PTEN	chr10	89692915	AATG->A	M134Del	WT	M134Del	WT
56	Pt43	DP2	FZD10	chr12	130648773	aCg/aTg	T429M	WT	T429M	WT
57	Pt43	DP2	MEK1	chr15	66729153	Tgc/Agc	C121S	WT	<mark>C121WT</mark>	WT
58	Pt17	DP1	NRAS	chr14	65208817	Ggt/Cgt	G13R	WT	G13R	WT
59	Pt17	DP1	FANCA	chr16	89831380	cCt/cTt	P899L	WT	P899L	WT
60	Pt17	DP1	PTPRR	chr12	71033034	gAg/gGg	E390G	WT	E390G	WT
61	Pt26	DP2	RBM19	chr12	114400215	aAg/aTg	K14M	WT	K14M	WT
62	Pt26	DP2	IRS1	chr2	227660544	Ggg/Agg	G971R	WT	<mark>G971WT</mark>	WT
63	Pt38	DP1	CENPF	chr1	214816068	Gag/Aag	E1463K	WT	E1463K	WT
64	Pt38	DP1	PLAGL1	chr6	144269167	cAg/cCg	Q36P	WT	Q36P	WT
65	Pt38	DP1	CDH2	chr18	25573568	Aca/Tca	T352S	WT	T352S	WT
66	Pt38	DP1	CACNA1C	chr12	2760862	atG/atT	M1323I	WT	M1323I	WT
67	Pt38	DP1	DOCK6	chr19	11363460	Gaa/Caa	E103Q	WT	E103Q	WT
68	Pt38	DP1	PIK3CG	chr7	106526655	gTg/gAg	V983E	WT	V983E	WT
69	Pt14	DP1	NRAS	chr1	115256530	Caa/Aaa	Q61K	WT	Q61K	WT
70	Pt14	DP2	PIWIL1	chr12	130839450	Cgt/Tgt	R397C	WT	R397C	WT
71	Pt14	DP2	NRAS	chr1	115256529	cAa/cGa	Q61R	WT	Q61R	WT
72	Pt9	DP2	SLC30A9	chr4	41732064	cAa/cCa	Q209P	WT	Q209P	WT
73	Pt9	DP2	C16orf46	chr16	79654881	Ttt/Ctt	F61L	WT	F61L	WT
74	Pt9	DP2	NKTR	chr3	42654733	Gaa/Aaa	E845K	WT	E845K	WT
75	Pt9	DP2	MYBPC2	chr19	55659565	Ggc/Agc	G1127S	WT	G1127S	WT
76	Pt9	DP2	HMHA1	chr19	1025160	gAt/gTt	D299V	WT	D299V	WT
77	Pt9	DP2	SLC29A2	chr11	65887554	Atg/Gtg	M434V	WT	M434V	WT
78	Pt9	DP2	HEATR5B	chr2	37163970	cGa/cAa	R31Q	WT	R31Q	WT
79	Pt9	DP2	AFAP1	chr4	7853245	Gag/Aag	E208K	WT	E208K	WT
80	Pt9	DP2	NXPH1	chr7	8757709	Gtt/Ttt	V201F	WT	V201F	WT
81	Pt9	DP2	PAK7	chr20	9471265	Agt/Tgt	S658C	WT	S658C	WT
82	Pt9	DP2	RBM34	chr1	235311717	A ->G	SPLICE	WT	SPLICE	WT
83	Pt9	DP2	SRSF6	chr20	42088781	Gac/Aac	D164N	WT	D164N	WT
84	Pt9	DP2	DVL2	chr17	7131012	tCc/tTc	S398F	WT	S398F	WT
85	Pt9	DP2	PLA2G4D	chr15	42371799	cAg/cTg	Q418L	WT	Q418	WT
86	Pt9	DP3	RC3H2	chr9	124682716	cAc/cGc	H313R	WT	H313R	WT
87	Pt9	DP3	SYT17	chr16	19102801	aCc/aAc	T261N	WT	T261N	WT
88	Pt9	DP3	RMI1	chr9	86617359	ttG/ttT	L486F	WT	L486F	WT
89	Pt9	DP3	WNK1	chr12	841536	Gga/Aga	G660R	WT	G660R	WT
90	Pt9	DP3	TRPV4	chr12	108710829	aCt/aTt	T656I	WT	T656I	WT
91	Pt9	DP3	AK5	chr1	77760178	Cct/Tct	P438S	WT	P438S	WT
92	Pt22	DP1	MEK1	chr15	66727455	aaG/aaC	K57N	WT	K57N	WT
93	Pt22	DP1	PHLPP1	chr18	60506029	Aaa/Gaa	K596E	WT	K596E	WT
94	Pt22	DP2	PHLPP1	chr18	60506029	Aaa/Gaa	K596E	WT	K596E	WT
95	Pt22	DP2	SMYD3	chr1	246490606	gGc/gAc	G84D	WT	G84D	WT
96	Pt22	DP3	DNMT3B	chr20	31395591	tAc/tGc	Y732C	WT	Y732C	WT
97	Pt22	DP3	PLCG1	chr20	39788273	cGc/cAc	R82H	WT	R82H	WT
98	Pt22	DP3	WISP1	chr8	134225107	Gcc/Acc	A24T	WT	A24T	WT
99	Pt22	DP3	SSH3	chr11	67079188	Gtt/Ttt	V604F	WT	V604F	WT
100	Pt22	DP3	KDM5C	chrX	53247034	Cac/Tac	H156Y	WT	H156Y	WT
101	Pt22	DP3	SSH1	chr12	109186093	aAc/aGc	N621S	WT	N621S	WT
102	Pt22	DP3	MAPK6	chr15	52356287	tAc/tGc	Y419C	WT	Y419C	WT
103	Pt22	DP3	FBXW2	chr9	123550211	aTa/aCa	I109T	WT	I109T	WT
104	Pt18	DP2	AKT1	chr14	105243048	Cag/Aag	Q79K	WT	Q79K	WT
105	Pt44	DP2	PREX2	chr8	68939530	aGa/aTa	R172I	WT	R172I	WT
106	Pt39	DP1	TLR3	chr4	187004767	Cgc/Tgc	R643C	WT	<mark>R643WT</mark>	WT
107	Pt40	DP1	MAGED1	chrX	51638235	caG/caC	Q44H	WT	Q44H	WT
108	Pt35	DP1	PTCH1	chr9	98268704	Gag/Aag	E127K	WT	E127K	WT

Yellow highlights indicate lack of NGS validation by Sanger.

Primers

Forward	Reverse
AAGGTACTGGTGGAGTATTTG	GTACTCATGAAAATGGTCAGAG
TGAACTCTTGTCTTTTCAGG	ATCAAATGAACTGTATCCCC
CAAACATTGTCTCAGTGTGG	CAGAGCCTTCTTCTTCTGTT
ACAACAGCATTTATCCTCAA	GCATCCTTGGATGGTT
TTAATGACTCTACTGCAGGC	GCACATTGATAGGAGCAATC
CGGTTTTAAGAACTGTGAGC	AACTGGGGAGATTGATGATG
TTTGCAGACACGGAAATAAC	GTGCAAGTTTGCTGTATCAT
GGAAGGCTGGCTTATCATAG	CAAGTCTCTCACTTCTGGTG
AACCTTCCAGTCCAACATTT	ATGGCAGTCACTTCCTTTAG
AAGGTACTGGTGGAGTATTTG	GTACTCATGAAAATGGTCAGAG
TTCCAGCATGGTATTGTCTC	TGTGGAGAAATGGTTGATGA
AAGGTACTGGTGGAGTATTTG	GTACTCATGAAAATGGTCAGAG
TCTCATTGCATGATGGTCAA	CATGATGAATTTCTGGGCAC
GGAAATGCTGTTTACTTGGG	ATTTAACTGCAGGCAAACAC
GCAGTTACTTTCTGCTTTCC	TTTTCAAGGAACTGACCACA
ACTAATATTGGGACGCAGAC	GTGATCTTCACCTTTCCAGT
TTACAGAGCACCTCTTTCAC	GAAGGGCTAAGTTCTTGACA
AGATCATCTTCATTGGTGCC	TAAACTGTCAGGCTCTTTCC
GGAAGCAATCTCAGTGGTTA	CTGTACACACAAGTCAATGC
GCCAATTTCTGCCTAATGAC	GATGAAAAGGAAGCAGGAGA
GTAAGAGTCCACAGTAGTGC	CTTTCCAGCTGAGGATAGAG
TATTCACCCTACAAAACCCC	TTTCTAAGACCCCAGACAGA
TAGCGCCACTCTCTACTTTA	CAATGCTCACCAATGACATC
AGAGCATGGTATTCCAACAG	TGACTCCAACATTGAGGAAA
GCTTTTCTGGAAACTGAGGT	CTTCCATCCCATTCTGACTC
CGGGACTAAGTTATTACGGG	TACTCGAGTGCCTAGAAGAA
ATGCTCTAACAACCATCTGA	AACCTCTATGCTAAGGGACT
GGTTCCTTGCCTTAACTGTA	TGATAGCTCTCTTGATGCAC
ACCCTCTGTTTCATTCTTCC	CTCTCATCCCACTCTCAGTA
GCATAACCTACAGTTCAAAA	CTGGAGGTAGACTAATACAAA
CAAACTGAAGGCCTGTGG	AGGTGGTATGCTGATCCA
TGTTGTTTCATGGTAGCTGT	AGAAAGCTAAACGTGCACTA
GGGGTTTCTTATTTAGGGCA	GCAAACTAAACTTGGTTGCT
TCCACTCACAGGAATCATTG	TTGTTTCAATTCACGCTGTT
AATGCCATGATCAGCTAGAG	GGGATTGGAGCTAGTAACAG
TCCTTGAGAAAACCCTGGA	TTTAAGGGGTCTCGGGG
ATTTGGTTTTGGCCAATCTG	CCATTTGGGCAATTCAGAAG
TGGCTTCAAACTCTCAATCA	CGTATGGGTACTGGTCATAG
TGACATGGAACTCGATGATG	CTCATTCACTCCTTCCCAAA
TCTTTGACACCAGAACTGAG	TAGGACAAAAACTACCCACG
GCAGTCAATAAAGCTGTGTC	CTAATCGACCTCACTTCCTG
ACTATGAGGCTGACTTTGAC	CAGTTCTATGCATTTGCAGG
TAATTACTCGCACTAAGCCC	GACAAAGAGCGTTTCATCAG
TCCAATAAACGTAAAGGGCA	GGTTGTACAGACTGGGGG
TTGGTTCTTTCCTGTCTCTG	TCCACAAATATCAATTTACAACCA
TATGTCTTAGATTGGTTCTTTCCTGTCTC	TCTGCTTTATTTATTCCAATAGGTATGG
GCTTGAATAGTTAGATGCTTATTTAACCTTG	GCTCTATCTTCCCTAGTGTGGTAACCTC
TATGTGCTGAAGATAGCACC	TTTACCCCAGAAGAGAGGAA
TCTCTCCATCCTAATACGCA	AAAGAACTTCGCCAGTGTAT
GTCTGTGTGTCCAATACCAT	AATCAGGTCCACATTGTTGT
GGTTCATGTGAGGCTAGAAA	GATAACAGGAGCCTTCTGAG
AGCGTGGAAAAGGAAAGTAT	AGTCACATAGACAGAGACCA
CCGTATAGCGTAAATTCCCA	TCAGATCCAGGAAGAGGAAA
AGGACTGGTAAGAAACTCCA	TGGTAGACCTTGTTCTTGAC

CCGTATAGCGTAAATTCCCA TCAGATCCAGGAAGAGGAAA
TCCTGGTCCTCTACTACTTC TCTGGTTGTTCATTTTGCAC
CCTGTTTCTCCTCCCTCTACC ACACCCACCAGGAATACTGC
TAAAGTACTGTAGATGTGGCTCGCC ACAGAATATGGGTAAAGATGATCCGAC
TTCTTAAGAGCTGCACATGA AAACTTGCGCAATGAAGAAA
TACACAAGGAGCTGGAAATC TTAATCACGTGCCTAGTGTG
CATCACAAAGTGAAGAGGGA GCTGGAACCTGTTGTAACTA
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TGAACAACCAAATGAACAGC GGTTTCTTTCCTGGTCAGAT
ACAACAAGACGGTCACATAA GCTTGAGACTGCATGTAAAC
AGAAATGTCCGAGTTAGCAG CTCTCTAGACAAGGACCAGA
GGCTGTCCACTCATTAAAGT AAAGTAAGGCAGACCCTTTC
CTGCAGCAAAAGAAGATCAG GCCCTCCTATTTGAGTTTGA
GTTTTGTGGCTACGACTTTC TAGGTGGGAGGATTACTGAG
GCTTGAATAGTTAGATGCTTATTTAACCTTG GCTCTATCTTCCCTAGTGTGGTAACCTC
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GCTTGAATAGTTAGATGCTTATTTAACCTTG GCTCTATCTTCCCTAGTGTGGTAACCTC
TTTGCTGTTAGCTAGTAGCGC ATTGAGATCACAGACATGCTAG
ACCCACAGTAGGTGCTGCTC AGCAAGCATCACAGTAATGGATCT
AGCAGTGATGATGGAAGGCG AATCGGATGTGGCCTCACCT
AGCCGAAGGTGGTCTGGATG GCAAGGGTCAGCCAGTGTTG
GGAAGACTGTGACGCCGGTA GCATGACGCTCTGTCTGCAG
CCCACAGCACTCCAAGTGGA CAGAGCCCAGACTGGATGGG
ACTCTCAAGTTCCATAAGTGACCCA TCCGTAATGGAGTTAGCCCACA
CAGCCGGAACGTCAGAGGAT CGTAGCCACGGCTCTCCTAG
AGACCTCTGGGACTGGCTGA GCTTGGAGCAGAGCCAGGAT
CCTGCTGGATGTGGTAAGCC GCTCCTCGGGATCATGGTGA
TTCTCATGGCTCATTTTCCA GATCACAGTGTACTGGAGTT
AACATCTGGCAGAGACAAAT AAACATCCAGAAAAGAACGC
GCATTAGGGATGGTGATCTT GGACTGAGAATGGGTCATTT
ATCTGCTAACTCAGAAAGGC GAGACCCATTTACCAGATCG
TTGTTTCCCTGTTGCATCCCT GTATCCCCCACCCTCCCTGA
CTGCTGCACAACCACCTCAC GACACAGTGGCGGGAGAACT
TCATTTGGTTGTCCATCTGT CCTTCCAGGAACTTTTGGTA
CTGAGAACCTCCTGGCCTCC CCCTGGGACTGTGCCTGTAG
CGAGGGTGGCTGGTAGAGTG CGCTCACTAGGCCCTCAGCTT
TTCCTCCCTCCCTCAGTGGA TCTTCTGGAAGGATGCCCGT
GCTTTCTTTCCATGATAGGAGTAC ATCAGTCTTCCTTCTACCCTGG
GGTGATCATATGCAGGAACT ATGCCTGTTTACAGACCAAT
GGTGATCATATGCAGGAACT ATGCCTGTTTACAGACCAAT
AGGGTCTTGAATTTCCTGTC GCAGACAAAATTTGGCAGAA
AGCCTGTGATGACTGAAAAT CTGGCTGGAACTATTCACAT
TCTTCTGGAGTCTAGCTCTT GCATTCCCCTAACTATCCTC
GCGACAATCACTCAAGAAAG ACATCTTACAGCACTCACAG
TACAAGCAGGTAGGGTTCAA GAGTTGTGGATCCTCTTCAG
CACTAGGAAAGAGCAGAGTC ATCTTTAGGCTGCAATGGAA
CAGAATCACCCTGTGAAAGA GACTCTGTGAGAAGGATGTG
ACATAGAAGGTACTCGGTGA CTTTCTTTTCCAGCCAGTTG
ACTACACATGGAGGAAACAC TAAAATGGCTCGATCCTCAG
TGACCTGACGCCGGGCCAG GAGCACTGGGGAGTGAGGATG
CTCTCTGTGAGTGTTTGTGA GCTTTTCCACTGAACATCTG
TCGATTTGCAGCATAACAAC CATGATAGTGAGGTGGAGTG
CTTATTCTCAACTCCGCGAT ACATCCTTGGCATTATGAGC
GACTCCTTTTTCTTTGGACG CTGAGAGCGAAGTTTCAGAG