



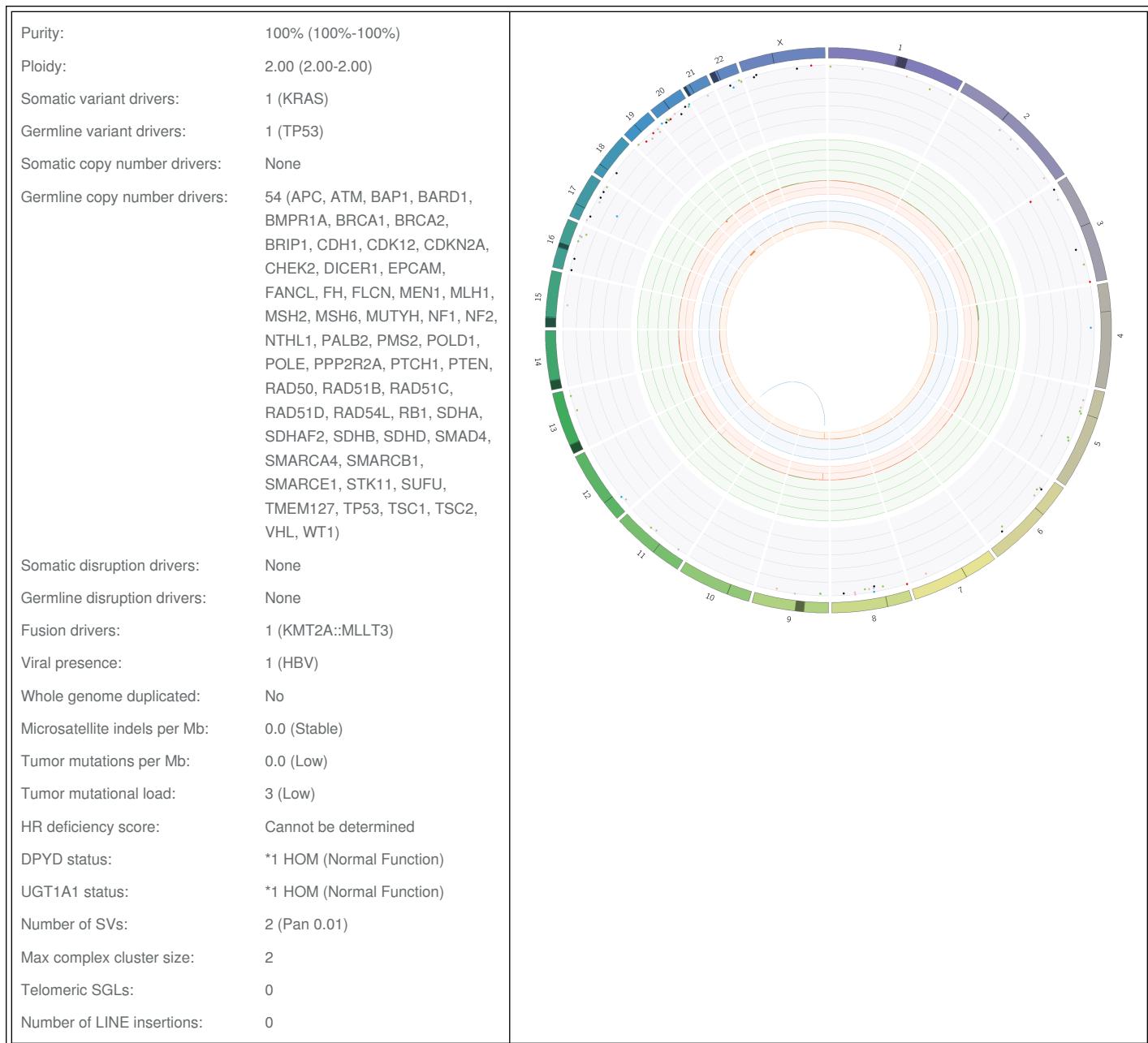
ORANGE Report (Research Use Only)

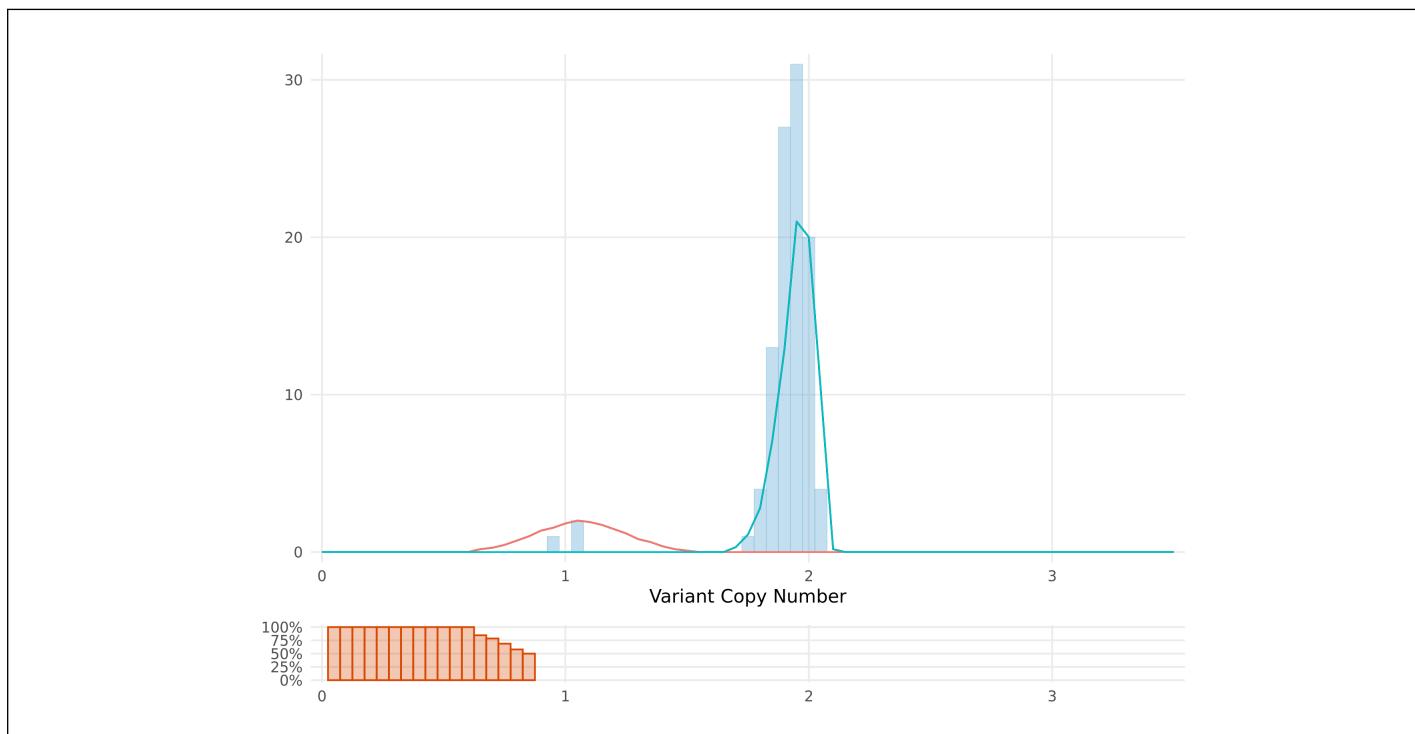
SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

CONFIGURED PRIMARY TUMOR
cancer (DOID 162)

CUPPA CANCER TYPE
Breast: Other (31%)

QC
PASS







Somatic Findings

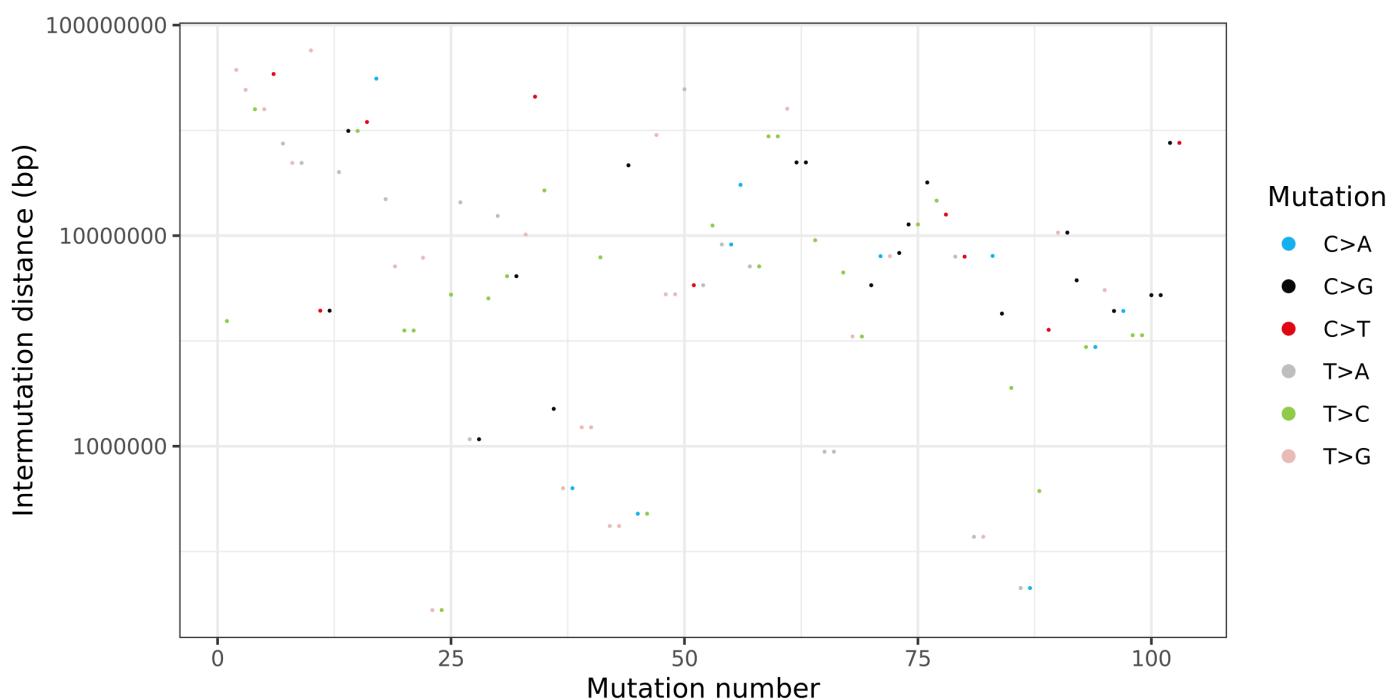
Driver variants (1)

VARIANT	VCN	CN	MACN	BIALLELIC	HOTSPOT	DL	CL	PHASE ID	RNA DEPTH
KRAS p.G13C	2.0	2.0	1.0	26%	Yes	100%	100%		0/0

Other potentially relevant variants (0)

NONE

Kataegis plot



Driver amps/dels (0)

NONE

Potentially interesting near-driver amps (0)

NONE

Other regions with amps (0)

NONE

Regions with deletions in genes in other autosomal regions (0)

NONE



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SAMPLE
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2.1

Potentially interesting chromosomal rearrangements

CHROMOSOMAL REARRANGEMENT	DETECTED?
1q trisomy	No
1p19q co-deletion	No

Driver fusions (1)

FUSION	DETAILS
KMT2A::MLLT3	5' End KMT2A Exon 9 (ENST00000534358) 3' Start MLLT3 Exon 5 (ENST00000380338) Junction CN 1.0 RNA support chr11:118484975-chr9:20414425, 18 split / 0 realig. / 10 discord. fragments, 44 / 18 depth Phasing Inframe Reported type (DL) KNOWN_PAIR (High) Unreported reason(s) - Chain links (terminated?) 0 (No) Domains kept - Domains lost YEATS

Other potentially interesting fusions (1)

FUSION	DETAILS
MLLT3::KMT2A	5' End MLLT3 Exon 4 (ENST00000380338) 3' Start KMT2A Exon 11 (ENST00000534358) Junction CN 1.0 RNA support None Phasing Inframe Reported type (DL) NONE (NA) Unreported reason(s) Not a known fusion pair Chain links (terminated?) 0 (No) Domains kept - Domains lost -

Potentially interesting in-frame fusions in case no high drivers detected

High driver likelihood events are detected in this sample, therefore this section is empty

Driver viruses (1)

VIRUS	QC STATUS	TYPE	INT	% COVERED	MEAN COV	EXP CLON COV	DRIVER
Hepatitis B virus	NO_ABNORMALITIES	HBV	2	100%	15.0	0.0	High

Other viral presence (0)

NONE



Homozygous disruptions (0)

NONE

Driver gene disruptions (0)

NONE

Other potentially interesting gene disruptions (0)

NONE

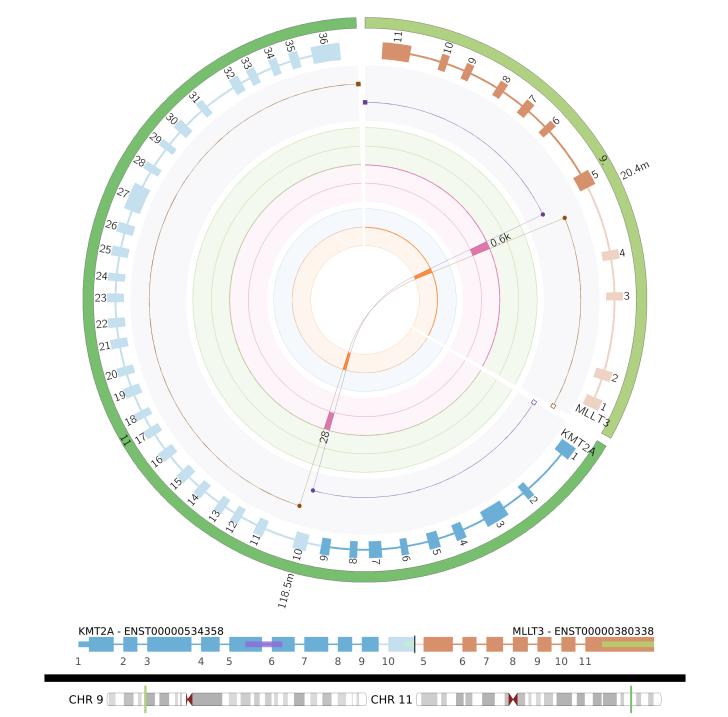
Potentially interesting LOH events (0)

NONE

Signature allocations (7)

SIGNATURE	ETIOLOGY	ALLOCATION	PERCENT
Sig3	Defective HR	47.6	46%
Sig9	Polymerase eta somatic hypermutation activity	33.8	33%
Sig12	Unknown	9.3	9%
Sig17	Unknown	5.1	5%
Sig28	Unknown	4.1	4%
Sig21	Defective DNA mismatch repair	3.1	3%
MISALLOC	-	41.3	40%

Structural driver plots (1)





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SAMPLE
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PLATINUM VERSION
2.1

Germline Findings

Driver variants (1)

VARIANT	VCN	CN	MACN	RNA DEPTH	BIALLELIC	HOTSPOT	GENOTYPE
TP53 p.Y163C	0.9	2.0	1.0	0/0	No	Yes	HET

Other potentially relevant variants (0)

NONE

Potentially pathogenic germline deletions (54)

LOCATION	GENE	TYPE	CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
chr10q23.2	BMPR1A	full loss	0.0	0.0	NA	NA	0.00	0.0
chr10q23.31	PTEN	full loss	0.0	0.0	NA	NA	0.00	0.0
chr10q24.32	SUFU	full loss	0.0	0.0	NA	NA	0.00	0.0
chr11p13	WT1	full loss	0.0	0.0	NA	NA	0.06	0.0
chr11q12.2	SDHAF2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr11q13.1	MEN1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr11q22.3	ATM	full loss	0.0	0.0	NA	NA	0.00	0.0
chr11q23.1	SDHD	full loss	0.0	0.0	NA	NA	0.00	0.0
chr12q24.33	POLE	full loss	0.0	0.0	NA	NA	0.00	0.0
chr13q13.1	BRCA2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr13q14.2	RB1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr14q24.1	RAD51B	full loss	0.0	0.0	NA	NA	0.00	0.0
chr14q32.13	DICER1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr16p12.2	PALB2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr16p13.3	NTHL1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr16p13.3	TSC2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr16q22.1	CDH1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17p11.2	FLCN	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17p13.1	TP53	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q11.2	NF1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q12	CDK12	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q12	RAD51D	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q21.2	SMARCE1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q21.31	BRCA1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q22	RAD51C	full loss	0.0	0.0	NA	NA	0.00	0.0
chr17q23.2	BRIP1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr18q21.2	SMAD4	full loss	0.0	0.0	NA	NA	0.00	0.0
chr19p13.2	SMARCA4	full loss	0.0	0.0	NA	NA	0.00	0.0
chr19p13.3	STK11	full loss	0.0	0.0	NA	NA	0.00	0.0
chr19q13.33	POLD1	full loss	0.0	0.0	NA	NA	0.00	0.0

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Potentially pathogenic germline deletions (54)

CONTINUED FROM THE PREVIOUS PAGE

LOCATION	GENE	TYPE	CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
chr1p34.1	MUTYH	full loss	0.0	0.0	NA	NA	0.00	0.0
chr1p34.1	RAD54L	full loss	0.0	0.0	NA	NA	0.00	0.0
chr1p36.13	SDHB	full loss	0.0	0.0	NA	NA	0.00	0.0
chr1q43	FH	full loss	0.0	0.0	NA	NA	0.00	0.0
chr22q11.23	SMARCB1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr22q12.1	CHEK2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr22q12.2	NF2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr2p16.1	FANCL	full loss	0.0	0.0	NA	NA	0.00	0.0
chr2p16.3	MSH2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr2p16.3	MSH6	full loss	0.0	0.0	NA	NA	0.00	0.0
chr2p21	EPCAM	full loss	0.0	0.0	NA	NA	0.01	0.0
chr2q11.2	TMEM127	full loss	0.0	0.0	NA	NA	0.00	0.0
chr2q35	BARD1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr3p21.1	BAP1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr3p22.2	MLH1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr3p25.3	VHL	full loss	0.0	0.0	NA	NA	0.00	0.0
chr5p15.33	SDHA	full loss	0.0	0.0	NA	NA	0.00	0.0
chr5q22.2	APC	full loss	0.0	0.0	NA	NA	0.00	0.0
chr5q31.1	RAD50	full loss	0.0	0.0	NA	NA	0.00	0.0
chr7p22.1	PMS2	full loss	0.0	0.0	NA	NA	0.00	0.0
chr8p21.2	PPP2R2A	full loss	0.0	0.0	NA	NA	0.00	0.0
chr9p21.3	CDKN2A	full loss	0.0	0.0	NA	NA	0.00	0.0
chr9q22.32	PTCH1	full loss	0.0	0.0	NA	NA	0.00	0.0
chr9q34.13	TSC1	full loss	0.0	0.0	NA	NA	0.00	0.0

Potentially pathogenic germline LOH events (0)

NONE

Potentially pathogenic germline homozygous disruptions (0)

NONE

Potentially pathogenic germline gene disruptions (0)

NONE

Genes with missed variant likelihood > 1% (412)

GENE	MVLH	GENE	MVLH	GENE	MVLH	GENE	MVLH
ABCB1	100.0%	ABL1	100.0%	ACVR1	100.0%	ACVR1B	100.0%

THE TABLE CONTINUES ON THE NEXT PAGE



Genes with missed variant likelihood > 1% (412)

CONTINUED FROM THE PREVIOUS PAGE

GENE	MVLH	GENE	MVLH	GENE	MVLH	GENE	MVLH
ACVR2A	100.0%	AJUBA	100.0%	AKT1	100.0%	AKT2	100.0%
AKT3	100.0%	ALB	100.0%	ALK	100.0%	AMER1	100.0%
APC	100.0%	AR	100.0%	ARAF	100.0%	ARHGAP35	100.0%
ARID1A	100.0%	ARID1B	100.0%	ARID2	100.0%	ARID5B	100.0%
ASXL1	100.0%	ATM	100.0%	ATP1A1	100.0%	ATP2B3	100.0%
ATR	100.0%	ATRX	100.0%	AXIN1	100.0%	AXIN2	100.0%
AXL	100.0%	B2M	100.0%	BAP1	100.0%	BARD1	100.0%
BCL2	100.0%	BCL9L	100.0%	BCOR	100.0%	BIRC3	100.0%
BMPR1A	100.0%	BMPR2	100.0%	BRAF	100.0%	BRCA1	100.0%
BRCA2	100.0%	BRD7	100.0%	BRIP1	100.0%	BTK	100.0%
CACNA1D	100.0%	CALR	100.0%	CARD11	100.0%	CASP8	100.0%
CASZ1	100.0%	CBFB	100.0%	CBL	100.0%	CBLB	100.0%
CCND1	100.0%	CD58	100.0%	CD79A	100.0%	CD79B	100.0%
CDC73	100.0%	CDH1	100.0%	CDH10	100.0%	CDK12	100.0%
CDK4	100.0%	CDK6	100.0%	CDKN1A	100.0%	CDKN1B	100.0%
CDKN2A	100.0%	CDKN2B	100.0%	CDKN2C	100.0%	CEBPA	100.0%
CHD4	100.0%	CHEK1	100.0%	CHEK2	100.0%	CIC	100.0%
CNOT3	100.0%	COL2A1	100.0%	CREBBP	100.0%	CRLF2	100.0%
CRNL1	100.0%	CSF1R	100.0%	CSF3R	100.0%	CTCF	100.0%
CTNNA1	100.0%	CTNNB1	100.0%	CUL3	100.0%	CUX1	100.0%
CXCR4	100.0%	CYLD	100.0%	CYP2D6	100.0%	CYP3A4	100.0%
CYP3A5	100.0%	DAXX	100.0%	DDR2	100.0%	DDX3X	100.0%
DGCR8	100.0%	DICER1	100.0%	DNM2	100.0%	DNMT3A	100.0%
DPYD	100.0%	DROSHA	100.0%	EED	100.0%	EEF1A1	100.0%
EGFR	100.0%	ELF3	100.0%	EML4	100.0%	EP300	100.0%
EPAS1	100.0%	EPCAM	100.0%	EPHA2	100.0%	EPOR	100.0%
ERBB2	100.0%	ERBB3	100.0%	ERBB4	100.0%	ERCC2	100.0%
ERF	100.0%	ERG	100.0%	ESR1	100.0%	ETNK1	100.0%
ETS2	100.0%	EZH2	100.0%	FANCA	100.0%	FANCC	100.0%
FANCD2	100.0%	FANCF	100.0%	FANCL	100.0%	FANCM	100.0%
FAT1	100.0%	FAT4	100.0%	FBXO11	100.0%	FBXW7	100.0%
FGFR1	100.0%	FGFR2	100.0%	FGFR3	100.0%	FGFR4	100.0%
FH	100.0%	FLCN	100.0%	FLT1	100.0%	FLT3	100.0%
FLT4	100.0%	FNTB	100.0%	FOSL2	100.0%	FOXA1	100.0%
FOXA2	100.0%	FOXL2	100.0%	FOXP1	100.0%	FOXQ1	100.0%
FUBP1	100.0%	G6PD	100.0%	GATA1	100.0%	GATA2	100.0%
GATA3	100.0%	GNA11	100.0%	GNAQ	100.0%	GNAS	100.0%
GPS2	100.0%	GRIN2A	100.0%	GSTP1	100.0%	GTF2I	100.0%
H1-2	100.0%	H3-3A	100.0%	H3-3B	100.0%	H3C13	100.0%

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with missed variant likelihood > 1% (412)

CONTINUED FROM THE PREVIOUS PAGE

GENE	MVLH	GENE	MVLH	GENE	MVLH	GENE	MVLH
H3C2	100.0%	H3C3	100.0%	HDAC2	100.0%	HIF1A	100.0%
HLA-A	2.2%	HLA-B	2.2%	HLA-C	2.3%	HNF1A	100.0%
HNRNPA2B1	100.0%	HOXB13	100.0%	HOXC13	100.0%	HRAS	100.0%
IDH1	100.0%	IDH2	100.0%	IGLL5	100.0%	IKBKB	100.0%
IKZF1	100.0%	IL6ST	100.0%	IL7R	100.0%	IRS2	100.0%
JAK1	100.0%	JAK2	100.0%	JAK3	100.0%	JMJD4	100.0%
KANSL1	100.0%	KCNJ5	100.0%	KDM5C	100.0%	KDM6A	100.0%
KDR	100.0%	KEAP1	100.0%	KIT	100.0%	KLF4	100.0%
KLF5	100.0%	KMT2A	97.8%	KMT2B	100.0%	KMT2C	100.0%
KMT2D	100.0%	KNSTRN	100.0%	KRAS	80.7%	KRT5	100.0%
KRTAP5-5	100.0%	LATS1	100.0%	LATS2	100.0%	LRIG2	100.0%
LRIG3	100.0%	LRP1B	100.0%	LZTR1	100.0%	MAP2K1	100.0%
MAP2K2	100.0%	MAP2K4	100.0%	MAP2K7	100.0%	MAP3K1	100.0%
MAP3K13	100.0%	MAP3K21	100.0%	MAX	100.0%	MED12	100.0%
MEN1	100.0%	MET	100.0%	MGA	100.0%	MGMT	100.0%
MITF	100.0%	MLH1	100.0%	MLH3	100.0%	MPL	100.0%
MRE11	100.0%	MSH2	100.0%	MSH3	100.0%	MSH6	100.0%
MST1R	100.0%	MTAP	100.0%	MTHFR	100.0%	MTOR	100.0%
MUTYH	100.0%	MYD88	100.0%	MYOD1	100.0%	NBN	100.0%
NCOA2	100.0%	NCOR1	100.0%	NF1	100.0%	NF2	100.0%
NFE2L2	100.0%	NFKBIE	100.0%	NIPBL	100.0%	NOTCH1	100.0%
NOTCH2	100.0%	NOTCH3	100.0%	NOTCH4	100.0%	NPAP1	100.0%
NPM1	100.0%	NRAS	100.0%	NRG1	100.0%	NSD1	100.0%
NSD2	100.0%	NT5C2	100.0%	NTHL1	100.0%	NTRK1	100.0%
NTRK2	100.0%	NTRK3	100.0%	OR11H1	100.0%	OR4N2	100.0%
PALB2	100.0%	PAX5	100.0%	PBRM1	100.0%	PDGFRA	100.0%
PDGFRB	100.0%	PDYN	100.0%	PHF6	100.0%	PHOX2B	100.0%
PIK3CA	100.0%	PIK3CB	100.0%	PIK3R1	100.0%	PIK3R2	100.0%
PIM1	100.0%	PLCG1	100.0%	PML	100.0%	PMS1	100.0%
PMS2	100.0%	POLD1	100.0%	POLE	100.0%	POT1	100.0%
PPM1D	100.0%	PPP1R15A	100.0%	PPP2R1A	100.0%	PPP2R2A	100.0%
PPP6C	100.0%	PRDM1	100.0%	PREX2	100.0%	PRKACA	100.0%
PRKAR1A	100.0%	PRKD1	100.0%	PSIP1	100.0%	PTCH1	100.0%
PTCH2	100.0%	PTEN	100.0%	PTK2	100.0%	PTK6	100.0%
PTPN11	100.0%	PTPN13	100.0%	PTPRB	100.0%	RABAC1	100.0%
RAC1	100.0%	RACGAP1	100.0%	RAD21	100.0%	RAD50	100.0%
RAD51	100.0%	RAD51B	100.0%	RAD51C	100.0%	RAD51D	100.0%
RAD54L	100.0%	RAF1	100.0%	RARG	100.0%	RASA1	100.0%
RB1	100.0%	RBM10	100.0%	RET	100.0%	RHOA	100.0%

THE TABLE CONTINUES ON THE NEXT PAGE



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Genes with missed variant likelihood > 1% (412)

CONTINUED FROM THE PREVIOUS PAGE

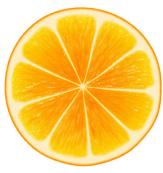
GENE	MVLH	GENE	MVLH	GENE	MVLH	GENE	MVLH
RHOB	100.0%	RNF43	100.0%	ROS1	100.0%	RPL10	100.0%
RPL22	100.0%	RPL5	100.0%	RPS6KA3	100.0%	RUNX1	100.0%
RXRA	100.0%	SDHA	100.0%	SDHAF2	100.0%	SDHB	100.0%
SDHC	100.0%	SDHD	100.0%	SERPINB3	100.0%	SERPINB4	100.0%
SETBP1	100.0%	SETD2	100.0%	SF3B1	100.0%	SH2B3	100.0%
SIX1	100.0%	SIX2	100.0%	SLCO1B1	100.0%	SMAD2	100.0%
SMAD3	100.0%	SMAD4	100.0%	SMARCA2	100.0%	SMARCA4	100.0%
SMARCB1	100.0%	SMARCC1	100.0%	SMARCC2	100.0%	SMARCD1	100.0%
SMARCE1	100.0%	SMC3	100.0%	SMO	100.0%	SMTNL2	100.0%
SOCs1	100.0%	SOX9	100.0%	SPEN	100.0%	SPOP	100.0%
SPRED1	100.0%	SPTAN1	100.0%	SRC	100.0%	SRSF2	100.0%
STAG2	100.0%	STAT3	100.0%	STAT5B	100.0%	STK11	100.0%
SUFU	100.0%	SUZ12	100.0%	TBL1XR1	100.0%	TBX3	100.0%
TCF12	100.0%	TCF7L2	100.0%	TERT	100.0%	TET2	100.0%
TG	100.0%	TGFBR1	100.0%	TGFBR2	100.0%	TGIF1	100.0%
TMEM127	100.0%	TMEM30A	100.0%	TNFAIP3	100.0%	TNFRSF14	100.0%
TOP2A	100.0%	TP53	66.0%	TP63	100.0%	TPMT	100.0%
TRAF7	100.0%	TRIM51	100.0%	TSC1	100.0%	TSC2	100.0%
TSHR	100.0%	TYMS	100.0%	U2AF1	100.0%	UBR5	100.0%
UGT1A8	100.0%	USP28	100.0%	USP8	100.0%	USP9X	100.0%
VHL	100.0%	WEE1	100.0%	WT1	100.0%	XPO1	100.0%
XRCC1	100.0%	ZBTB20	100.0%	ZBTB7B	100.0%	ZFHX3	100.0%
ZFP36L1	100.0%	ZFP36L2	100.0%	ZFX	100.0%	ZIM3	100.0%
ZMYM3	100.0%	ZNF750	100.0%	ZNRF3	100.0%	ZRSR2	100.0%

Germline CN aberrations (0)

NONE

Pharmacogenetics (2)

GENE	HAPLOTYPE	GENOTYPE	FUNCTION	LINKED DRUGS	SOURCE
DPYD	*1	HOM	Normal Function	5-Fluorouracil;Capecitabine;Tegafur	PHARMGKB
UGT1A1	*1	HOM	Normal Function	Irinotecan	PHARMGKB



Immunology

HLA QC

QC Status: PASS

HLA Alleles (6)

ALLELE	REF FRAGS	TUMOR FRAGS	RNA FRAGS	TUMOR CN	SOMATIC #MUTATIONS
A*03:01	71	141	0	1.0	NONE
A*03:01	71	141	0	1.0	NONE
B*07:02	60	119	0	1.0	NONE
B*07:02	60	119	0	1.0	NONE
C*07:02	64	128	0	1.0	NONE
C*07:02	64	128	0	1.0	NONE

Genetic Immune Escape

ESCAPE MECHANISM	DETECTED?
HLA-1 loss-of-function	No
Antigen presentation pathway inactivation	No
IFN gamma pathway inactivation	No
(Potential) PD-L1 overexpression	No
CD58 inactivation	No
Epigenetics driven immune escape via SETDB1	No



RNA Findings

QC	TOTAL FRAGMENTS	NON-DUPLICATE FRAGMENTS	DUPLICATE RATE
FAIL_LOW_COVERAGE	405323	380003	6%

The RNA QC status of this sample is not a pass. All presented RNA data should be interpreted with caution

Genes with high expression (0)

NONE

Genes with low expression (307)

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
AJUBA	2.0	0.0	NA	NA	0.00	0.0
PRKD1	2.0	0.0	NA	NA	0.00	0.0
MIPOL1	2.0	0.0	NA	NA	0.00	0.0
FANCM	2.0	0.0	NA	NA	0.00	0.0
SAV1	2.0	0.0	NA	NA	0.00	0.0
MAX	2.0	0.0	NA	NA	0.00	0.0
GPHN	2.0	0.0	NA	NA	0.00	0.0
RAD51B	2.0	0.0	NA	NA	0.00	0.0
ZFP36L1	2.0	0.0	NA	NA	0.00	0.0
MLH3	2.0	0.0	NA	NA	0.00	0.0
DICER1	2.0	0.0	NA	NA	0.00	0.0
LZTR1	1.9	0.0	NA	NA	0.00	0.0
SMARCB1	1.9	0.0	NA	NA	0.00	0.0
CHEK2	1.9	0.0	NA	NA	0.00	0.0
ZNRF3	1.9	0.0	NA	NA	0.00	0.0
NF2	1.9	0.0	NA	NA	0.00	0.0
DEPDC5	1.9	0.0	NA	NA	0.00	0.0
EP300	1.9	0.0	NA	NA	0.00	0.0
CYP2D6	1.9	0.0	NA	NA	0.00	0.0
PLXNB2	1.9	0.0	NA	NA	0.00	0.0
RHOB	2.0	0.0	NA	NA	0.00	0.0
DNMT3A	2.0	0.0	NA	NA	0.00	0.0
ASXL2	2.0	0.0	NA	NA	0.00	0.0
FOSL2	2.0	0.0	NA	NA	0.00	0.0
EML4	2.0	0.0	NA	NA	0.00	0.0
ZFP36L2	2.0	0.0	NA	NA	0.00	0.0
MSH2	2.0	0.0	NA	NA	0.00	0.0
MSH6	2.0	0.0	NA	NA	0.00	0.0
FBXO11	2.0	0.0	NA	NA	0.00	0.0
FANCL	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
TMEM127	2.0	0.0	NA	NA	0.00	0.0
ACVR2A	2.0	0.0	NA	NA	0.00	0.0
ITGAV	2.0	0.0	NA	NA	0.00	0.0
PMS1	2.0	0.0	NA	NA	0.00	0.0
CASP8	2.0	0.0	NA	NA	0.00	0.0
BMPR2	2.0	0.0	NA	NA	0.00	0.0
PARD3B	2.0	0.0	NA	NA	0.00	0.0
BARD1	2.0	0.0	NA	NA	0.00	0.0
CUL3	2.0	0.0	NA	NA	0.00	0.0
FANCD2	2.0	0.0	NA	NA	0.00	0.0
VHL	2.0	0.0	NA	NA	0.00	0.0
ATG7	2.0	0.0	NA	NA	0.00	0.0
TGFBR2	2.0	0.0	NA	NA	0.00	0.0
MLH1	2.0	0.0	NA	NA	0.00	0.0
ITGA9	2.0	0.0	NA	NA	0.00	0.0
SETD2	2.0	0.0	NA	NA	0.00	0.0
SMARCC1	2.0	0.0	NA	NA	0.00	0.0
MST1R	2.0	0.0	NA	NA	0.00	0.0
BAP1	2.0	0.0	NA	NA	0.00	0.0
PBRM1	2.0	0.0	NA	NA	0.00	0.0
FHIT	2.0	0.0	NA	NA	0.00	0.0
FOXP1	2.0	0.0	NA	NA	0.00	0.0
CBLB	2.0	0.0	NA	NA	0.00	0.0
ZBTB20	2.0	0.0	NA	NA	0.00	0.0
LSAMP	2.0	0.0	NA	NA	0.00	0.0
ATR	2.0	0.0	NA	NA	0.00	0.0
NAALADL2	2.0	0.0	NA	NA	0.00	0.0
TBL1XR1	2.0	0.0	NA	NA	0.00	0.0
GMDS	2.0	0.0	NA	NA	0.00	0.0
HLA-A	2.0	0.0	NA	NA	0.00	0.0
HLA-C	2.0	0.0	NA	NA	0.00	0.0
HLA-B	2.0	0.0	NA	NA	0.00	0.0
DAXX	2.0	0.0	NA	NA	0.00	0.0
CDKN1A	2.0	0.0	NA	NA	0.00	0.0
NFKBIE	2.0	0.0	NA	NA	0.00	0.0
EYS	2.0	0.0	NA	NA	0.00	0.0
TMEM30A	2.0	0.0	NA	NA	0.00	0.0
PRDM1	2.0	0.0	NA	NA	0.00	0.0
FOXO3	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
HDAC2	2.0	0.0	NA	NA	0.00	0.0
TNFAIP3	2.0	0.0	NA	NA	0.00	0.0
LATS1	2.0	0.0	NA	NA	0.00	0.0
ARID1B	2.0	0.0	NA	NA	0.00	0.0
PRKN	2.0	0.0	NA	NA	0.00	0.0
AFDN	2.0	0.0	NA	NA	0.00	0.0
DOCK8	2.0	0.0	NA	NA	0.00	0.0
SMARCA2	2.0	0.0	NA	NA	0.00	0.0
PTPRD	2.0	0.0	NA	NA	0.00	0.0
PSIP1	2.0	0.0	NA	NA	0.00	0.0
MTAP	2.0	0.0	NA	NA	0.00	0.0
CDKN2A	2.0	0.0	NA	NA	0.00	0.0
CDKN2B	2.0	0.0	NA	NA	0.00	0.0
FANCC	2.0	0.0	NA	NA	0.00	0.0
PTCH1	2.0	0.0	NA	NA	0.00	0.0
TGFBR1	2.0	0.0	NA	NA	0.00	0.0
KLF4	2.0	0.0	NA	NA	0.00	0.0
PPP6C	2.0	0.0	NA	NA	0.00	0.0
SPTAN1	2.0	0.0	NA	NA	0.00	0.0
ASS1	2.0	0.0	NA	NA	0.00	0.0
TSC1	2.0	0.0	NA	NA	0.00	0.0
RXRA	2.0	0.0	NA	NA	0.00	0.0
NOTCH1	2.0	0.0	NA	NA	0.00	0.0
AXIN1	2.0	0.0	NA	NA	0.00	0.0
NTHL1	2.0	0.0	NA	NA	0.00	0.0
TSC2	2.0	0.0	NA	NA	0.00	0.0
TRAF7	2.0	0.0	NA	NA	0.00	0.0
CREBBP	2.0	0.0	NA	NA	0.00	0.0
SOCS1	2.0	0.0	NA	NA	0.00	0.0
PALB2	2.0	0.0	NA	NA	0.00	0.0
BRD7	2.0	0.0	NA	NA	0.00	0.0
CYLD	2.0	0.0	NA	NA	0.00	0.0
CBFB	2.0	0.0	NA	NA	0.00	0.0
CTCF	2.0	0.0	NA	NA	0.00	0.0
CDH1	2.0	0.0	NA	NA	0.00	0.0
ZFHX3	2.0	0.0	NA	NA	0.00	0.0
WWOX	2.0	0.0	NA	NA	0.00	0.0
ANKRD11	2.0	0.0	NA	NA	0.00	0.0
FANCA	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
GPS2	2.0	0.0	NA	NA	0.00	0.0
TP53	2.0	0.0	NA	NA	0.00	0.0
MAP2K4	2.0	0.0	NA	NA	0.00	0.0
NCOR1	2.0	0.0	NA	NA	0.00	0.0
FLCN	2.0	0.0	NA	NA	0.00	0.0
USP22	2.0	0.0	NA	NA	0.00	0.0
NF1	2.0	0.0	NA	NA	0.00	0.0
SUZ12	2.0	0.0	NA	NA	0.00	0.0
RAD51D	2.0	0.0	NA	NA	0.00	0.0
CDK12	2.0	0.0	NA	NA	0.00	0.0
SMARCE1	2.0	0.0	NA	NA	0.00	0.0
STAT5B	2.0	0.0	NA	NA	0.00	0.0
BRCA1	2.0	0.0	NA	NA	0.00	0.0
KANSL1	2.0	0.0	NA	NA	0.00	0.0
RNF43	2.0	0.0	NA	NA	0.00	0.0
RAD51C	2.0	0.0	NA	NA	0.00	0.0
BRIP1	2.0	0.0	NA	NA	0.00	0.0
AXIN2	2.0	0.0	NA	NA	0.00	0.0
PRKAR1A	2.0	0.0	NA	NA	0.00	0.0
SOX9	2.0	0.0	NA	NA	0.00	0.0
ZNF750	2.0	0.0	NA	NA	0.00	0.0
TNFRSF14	2.0	0.0	NA	NA	0.00	0.0
MEGF6	2.0	0.0	NA	NA	0.00	0.0
RPL22	2.0	0.0	NA	NA	0.00	0.0
CASZ1	2.0	0.0	NA	NA	0.00	0.0
MTHFR	2.0	0.0	NA	NA	0.00	0.0
SPEN	2.0	0.0	NA	NA	0.00	0.0
SDHB	2.0	0.0	NA	NA	0.00	0.0
ARID1A	2.0	0.0	NA	NA	0.00	0.0
PTCH2	2.0	0.0	NA	NA	0.00	0.0
MUTYH	2.0	0.0	NA	NA	0.00	0.0
RAD54L	2.0	0.0	NA	NA	0.00	0.0
CDKN2C	2.0	0.0	NA	NA	0.00	0.0
JAK1	2.0	0.0	NA	NA	0.00	0.0
NEGR1	2.0	0.0	NA	NA	0.00	0.0
RPL5	2.0	0.0	NA	NA	0.00	0.0
DPYD	2.0	0.0	NA	NA	0.00	0.0
ATP1A1	2.0	0.0	NA	NA	0.00	0.0
CD58	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
NOTCH2	2.0	0.0	NA	NA	0.00	0.0
ZBTB7B	2.0	0.0	NA	NA	0.00	0.0
SDHC	2.0	0.0	NA	NA	0.00	0.0
CDC73	2.0	0.0	NA	NA	0.00	0.0
ELF3	2.0	0.0	NA	NA	0.00	0.0
JMJD4	2.0	0.0	NA	NA	0.00	0.0
MAP3K21	2.0	0.0	NA	NA	0.00	0.0
FH	2.0	0.0	NA	NA	0.00	0.0
PTPN13	2.0	0.0	NA	NA	0.00	0.0
CCSER1	2.0	0.0	NA	NA	0.00	0.0
TET2	2.0	0.0	NA	NA	0.00	0.0
FAT4	2.0	0.0	NA	NA	0.00	0.0
FBXW7	2.0	0.0	NA	NA	0.00	0.0
IRF2	2.0	0.0	NA	NA	0.00	0.0
FAT1	2.0	0.0	NA	NA	0.00	0.0
SDHA	2.0	0.0	NA	NA	0.00	0.0
DROSHA	2.0	0.0	NA	NA	0.00	0.0
NIPBL	2.0	0.0	NA	NA	0.00	0.0
MAP3K1	2.0	0.0	NA	NA	0.00	0.0
PDE4D	2.0	0.0	NA	NA	0.00	0.0
PIK3R1	2.0	0.0	NA	NA	0.00	0.0
MSH3	2.0	0.0	NA	NA	0.00	0.0
RASA1	2.0	0.0	NA	NA	0.00	0.0
CHD1	2.0	0.0	NA	NA	0.00	0.0
FBXL17	2.0	0.0	NA	NA	0.00	0.0
APC	2.0	0.0	NA	NA	0.00	0.0
RAD50	2.0	0.0	NA	NA	0.00	0.0
CTNNA1	2.0	0.0	NA	NA	0.00	0.0
NSD1	2.0	0.0	NA	NA	0.00	0.0
PMS2	2.0	0.0	NA	NA	0.00	0.0
HNRNPA2B1	2.0	0.0	NA	NA	0.00	0.0
IKZF1	2.0	0.0	NA	NA	0.00	0.0
ABCB1	2.0	0.0	NA	NA	0.00	0.0
CYP3A5	2.0	0.0	NA	NA	0.00	0.0
CUX1	2.0	0.0	NA	NA	0.00	0.0
IMMP2L	2.0	0.0	NA	NA	0.00	0.0
LRRN3	2.0	0.0	NA	NA	0.00	0.0
POT1	2.0	0.0	NA	NA	0.00	0.0
KMT2C	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
PTPRN2	2.0	0.0	NA	NA	0.00	0.0
PPP2R2A	2.0	0.0	NA	NA	0.00	0.0
NBN	2.0	0.0	NA	NA	0.00	0.0
UBR5	2.0	0.0	NA	NA	0.00	0.0
GATA3	2.0	0.0	NA	NA	0.00	0.0
PARD3	2.0	0.0	NA	NA	0.00	0.0
BMPR1A	2.0	0.0	NA	NA	0.00	0.0
PTEN	2.0	0.0	NA	NA	0.00	0.0
SUFU	2.0	0.0	NA	NA	0.00	0.0
TCF7L2	2.0	0.0	NA	NA	0.00	0.0
MGMT	2.0	0.0	NA	NA	0.00	0.0
LINC01001	2.0	0.0	NA	NA	0.00	0.0
FANCF	2.0	0.0	NA	NA	0.00	0.0
AMBRA1	2.0	0.0	NA	NA	0.00	0.0
SDHAF2	2.0	0.0	NA	NA	0.00	0.0
MEN1	2.0	0.0	NA	NA	0.00	0.0
GSTP1	2.0	0.0	NA	NA	0.00	0.0
DLG2	2.0	0.0	NA	NA	0.00	0.0
EED	2.0	0.0	NA	NA	0.00	0.0
MRE11	2.0	0.0	NA	NA	0.00	0.0
BIRC3	2.0	0.0	NA	NA	0.00	0.0
ATM	2.0	0.0	NA	NA	0.00	0.0
SDHD	2.0	0.0	NA	NA	0.00	0.0
USP28	2.0	0.0	NA	NA	0.00	0.0
BCL9L	2.0	0.0	NA	NA	0.00	0.0
CHEK1	2.0	0.0	NA	NA	0.00	0.0
CDKN1B	2.0	0.0	NA	NA	0.00	0.0
ETNK1	2.0	0.0	NA	NA	0.00	0.0
ARID2	2.0	0.0	NA	NA	0.00	0.0
KMT2D	2.0	0.0	NA	NA	0.00	0.0
RACGAP1	2.0	0.0	NA	NA	0.00	0.0
SMARCD1	2.0	0.0	NA	NA	0.00	0.0
ACVR1B	2.0	0.0	NA	NA	0.00	0.0
RARG	2.0	0.0	NA	NA	0.00	0.0
SMARCC2	2.0	0.0	NA	NA	0.00	0.0
PTPRB	2.0	0.0	NA	NA	0.00	0.0
SH2B3	2.0	0.0	NA	NA	0.00	0.0
TBX3	2.0	0.0	NA	NA	0.00	0.0
HNF1A	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
POLE	2.0	0.0	NA	NA	0.00	0.0
LATS2	2.0	0.0	NA	NA	0.00	0.0
FLT1	2.0	0.0	NA	NA	0.00	0.0
BRCA2	2.0	0.0	NA	NA	0.00	0.0
RB1	2.0	0.0	NA	NA	0.00	0.0
SPRED1	2.0	0.0	NA	NA	0.00	0.0
RAD51	2.0	0.0	NA	NA	0.00	0.0
MGA	2.0	0.0	NA	NA	0.00	0.0
B2M	2.0	0.0	NA	NA	0.00	0.0
TCF12	2.0	0.0	NA	NA	0.00	0.0
RNF111	2.0	0.0	NA	NA	0.00	0.0
SMAD3	2.0	0.0	NA	NA	0.00	0.0
PML	2.0	0.0	NA	NA	0.00	0.0
TGIF1	2.0	0.0	NA	NA	0.00	0.0
PTPN2	2.0	0.0	NA	NA	0.00	0.0
ZNF521	2.0	0.0	NA	NA	0.00	0.0
SMAD2	2.0	0.0	NA	NA	0.00	0.0
SMAD4	2.0	0.0	NA	NA	0.00	0.0
PARD6G	2.0	0.0	NA	NA	0.00	0.0
STK11	2.0	0.0	NA	NA	0.00	0.0
MAP2K7	2.0	0.0	NA	NA	0.00	0.0
KEAP1	2.0	0.0	NA	NA	0.00	0.0
DNM2	2.0	0.0	NA	NA	0.00	0.0
SMARCA4	2.0	0.0	NA	NA	0.00	0.0
EPOR	2.0	0.0	NA	NA	0.00	0.0
CEBPA	2.0	0.0	NA	NA	0.00	0.0
KMT2B	2.0	0.0	NA	NA	0.00	0.0
RABAC1	2.0	0.0	NA	NA	0.00	0.0
ERF	2.0	0.0	NA	NA	0.00	0.0
CIC	2.0	0.0	NA	NA	0.00	0.0
ERCC2	2.0	0.0	NA	NA	0.00	0.0
ARHGAP35	2.0	0.0	NA	NA	0.00	0.0
POLD1	2.0	0.0	NA	NA	0.00	0.0
PPP2R1A	2.0	0.0	NA	NA	0.00	0.0
CNOT3	2.0	0.0	NA	NA	0.00	0.0
MACROD2	2.0	0.0	NA	NA	0.00	0.0
ASXL1	2.0	0.0	NA	NA	0.00	0.0
PTK6	2.0	0.0	NA	NA	0.00	0.0
C21orf91	2.0	0.0	NA	NA	0.00	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



ORANGE Report (Research Use Only)

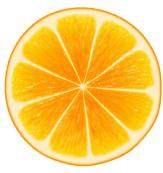
SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
RUNX1	2.0	0.0	NA	NA	0.00	0.0
ETS2	2.0	0.0	NA	NA	0.00	0.0
PPP2R3B	2.1	0.0	NA	NA	0.00	0.0
PUDP	2.1	0.0	NA	NA	0.00	0.0
STS	2.1	0.0	NA	NA	0.00	0.0
WWC3	2.1	0.0	NA	NA	0.00	0.0
ZRSR2	2.1	0.0	NA	NA	0.00	0.0
RPS6KA3	2.1	0.0	NA	NA	0.00	0.0
ZFX	2.1	0.0	NA	NA	0.00	0.0
DMD	2.1	0.0	NA	NA	0.00	0.0
BCOR	2.1	0.0	NA	NA	0.00	0.0
USP9X	2.1	0.0	NA	NA	0.00	0.0
DDX3X	2.1	0.0	NA	NA	0.00	0.0
KDM6A	2.1	0.0	NA	NA	0.00	0.0
RBM10	2.1	0.0	NA	NA	0.00	0.0
KDM5C	2.1	0.0	NA	NA	0.00	0.0
AMER1	2.0	0.0	NA	NA	0.00	0.0
MED12	2.0	0.0	NA	NA	0.00	0.0
ZMYM3	2.0	0.0	NA	NA	0.00	0.0
ATRX	2.0	0.0	NA	NA	0.00	0.0
DIAPH2	2.0	0.0	NA	NA	0.00	0.0
BTK	2.0	0.0	NA	NA	0.00	0.0
STAG2	2.0	0.0	NA	NA	0.00	0.0
TENM1	2.0	0.0	NA	NA	0.00	0.0
SMARCA1	2.0	0.0	NA	NA	0.00	0.0
PHF6	2.0	0.0	NA	NA	0.00	0.0
RPL10	2.0	0.0	NA	NA	0.00	0.0
G6PD	2.0	0.0	NA	NA	0.00	0.0
TP63	2.0	0.0	NA	NA	0.01	0.0
NRG1	2.0	0.0	NA	NA	0.01	0.0
SIX1	2.0	0.0	NA	NA	0.01	0.0
EPCAM	2.0	0.0	NA	NA	0.01	0.0
GRIN2A	2.0	0.0	NA	NA	0.01	0.0
CYP3A4	2.0	0.0	NA	NA	0.01	0.0
TMPRSS2	2.0	0.0	NA	NA	0.01	0.0
LRP1B	2.0	0.0	NA	NA	0.02	0.0
ERBB4	2.0	0.0	NA	NA	0.02	0.0
FOXQ1	2.0	0.0	NA	NA	0.02	0.0
AGBL4	2.0	0.0	NA	NA	0.03	0.0

THE TABLE CONTINUES ON THE NEXT PAGE



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SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Genes with low expression (307)

CONTINUED FROM THE PREVIOUS PAGE

GENE	TUMOR CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
OR4F21	2.0	0.0	NA	NA	0.03	0.0
ATP2B3	2.0	0.0	NA	NA	0.03	0.0
SIX2	2.0	0.0	NA	NA	0.04	0.0
CSMD1	2.0	0.0	NA	NA	0.05	0.0

Known fusions detected in RNA and not in DNA (0)

NONE

Promiscuous fusions detected in RNA and not in DNA (0)

NONE

Potentially interesting novel splice junctions - Skipped exons (0)

NONE

Potentially interesting novel splice junctions - Novel exon/intron (0)

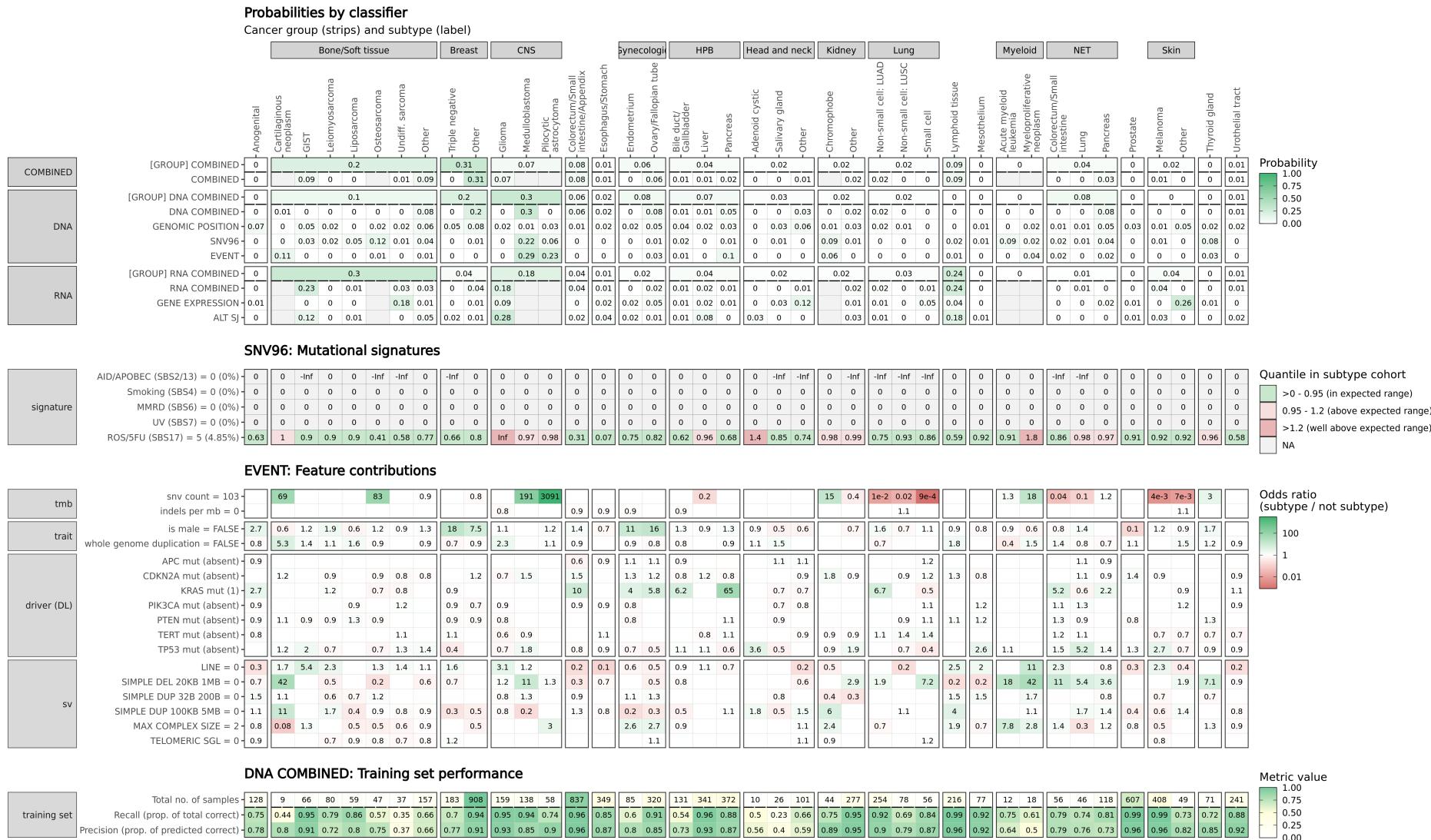
NONE

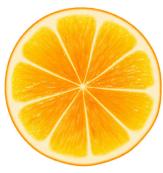


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SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Cohort Comparison

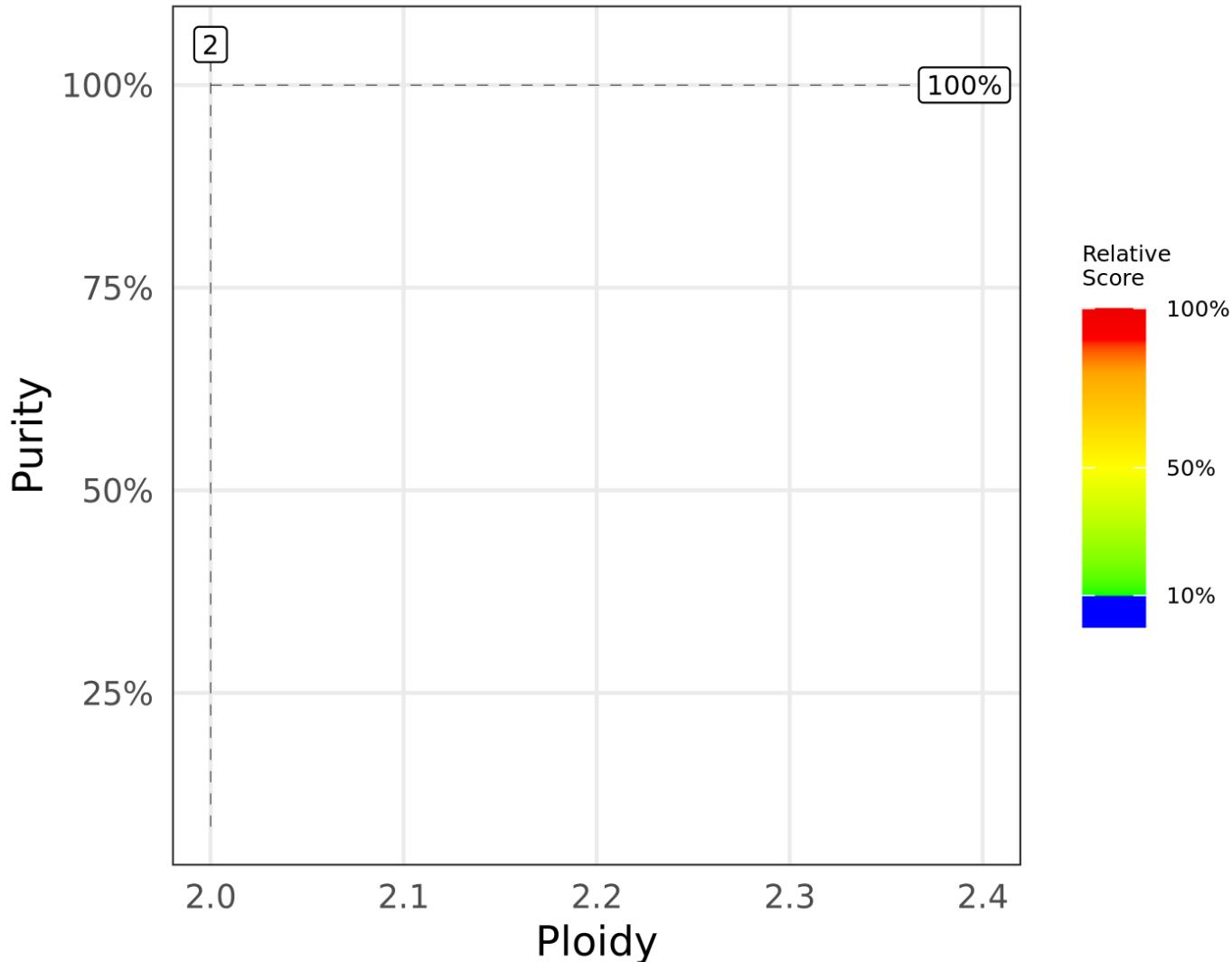




Quality Control

QC	REF GENOME	FIT METHOD	MEAN DEPTH	CONTAMINATION	UNS. SEGMENTS (%)	DELETED GENES
PASS	V38	NORMAL	30	0%	0 (0%)	0

Purity/Ploidy Scores



Flagstats

	UNIQUE RC	SECONDARY RC	SUPPLEMENTARY RC	MAPPED PROPORTION
Ref Sample	419712	0	0	100%
Tumor Sample	420014	0	19	100%



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SAMPLE
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2.1

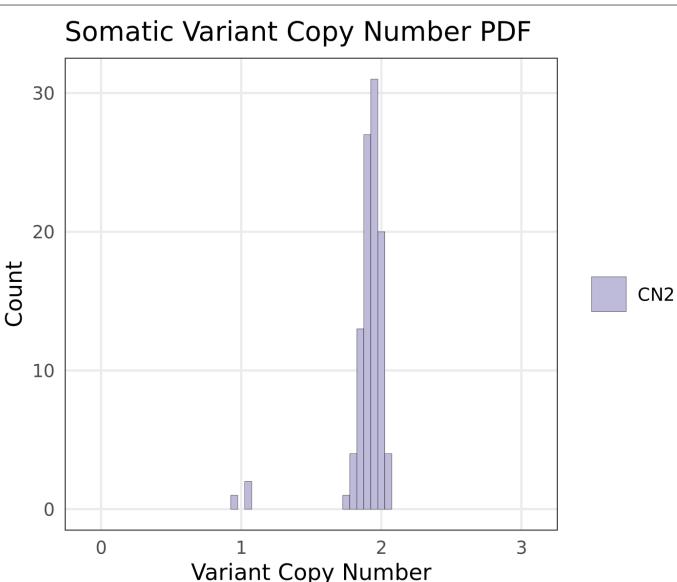
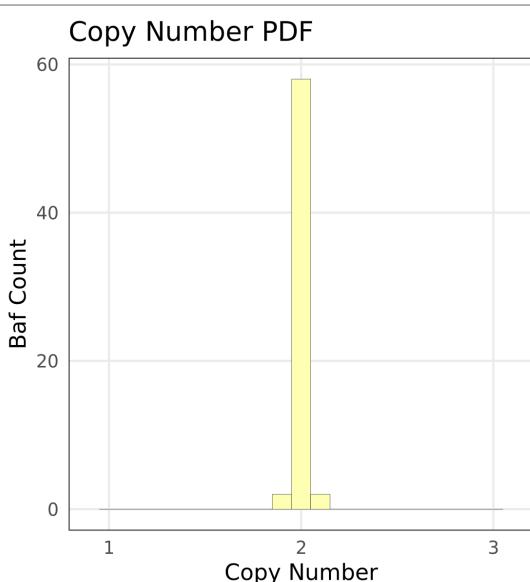
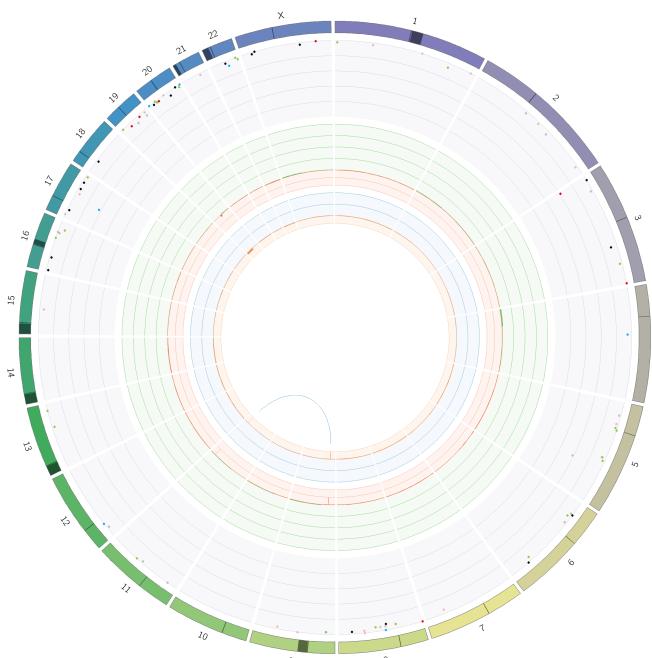
Coverage Stats

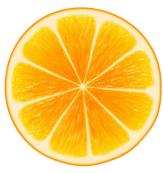
	MEAN COVERAGE	SD COVERAGE	MEDIAN COVERAGE	MAD COVERAGE
Ref Sample	0.0	0.8	0	0
Tumor Sample	0.0	0.8	0	0

Excluded Percentages

	ADAPTER	BASEQ	CAPPED	DUPE	MAPQ	OVERLAP	UNPAIRED	TOTAL
Ref Sample	0%	0%	0%	1%	0%	0%	0%	1%
Tumor Sample	0%	0%	0%	0%	0%	0%	0%	1%

QC plots



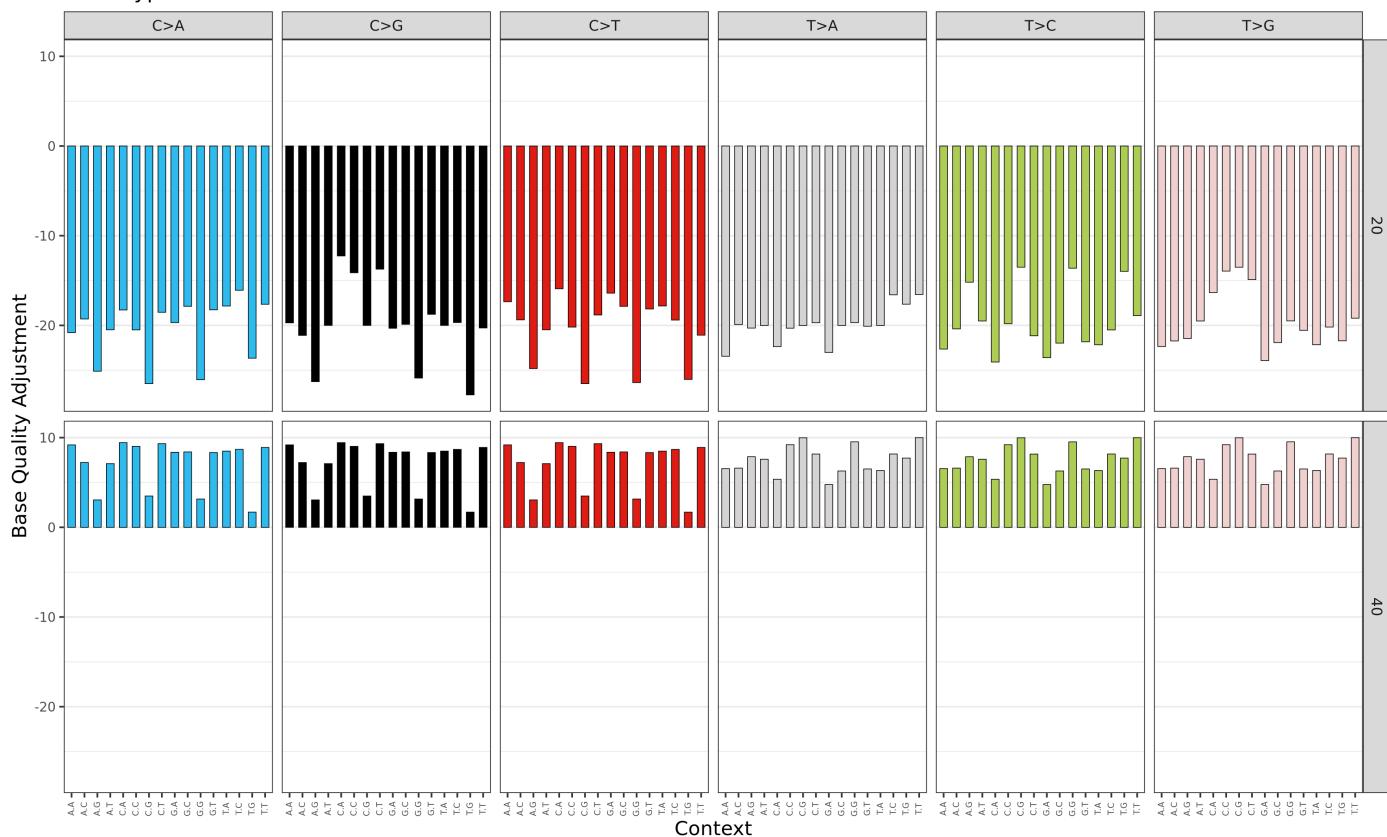


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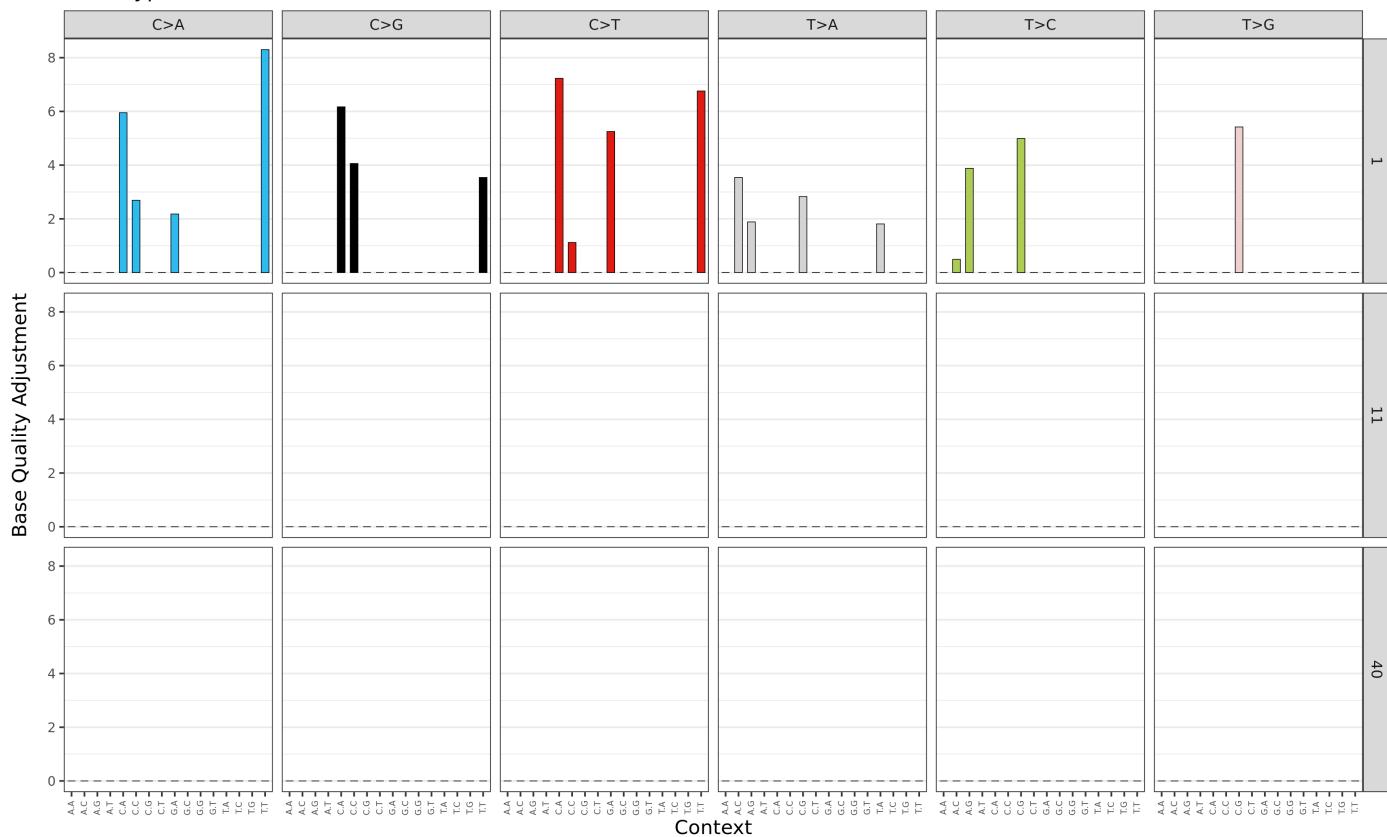
SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

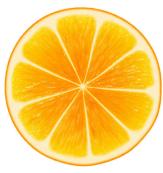
Reference Sample BQR plot

Read type: NONE



Read type: SINGLE



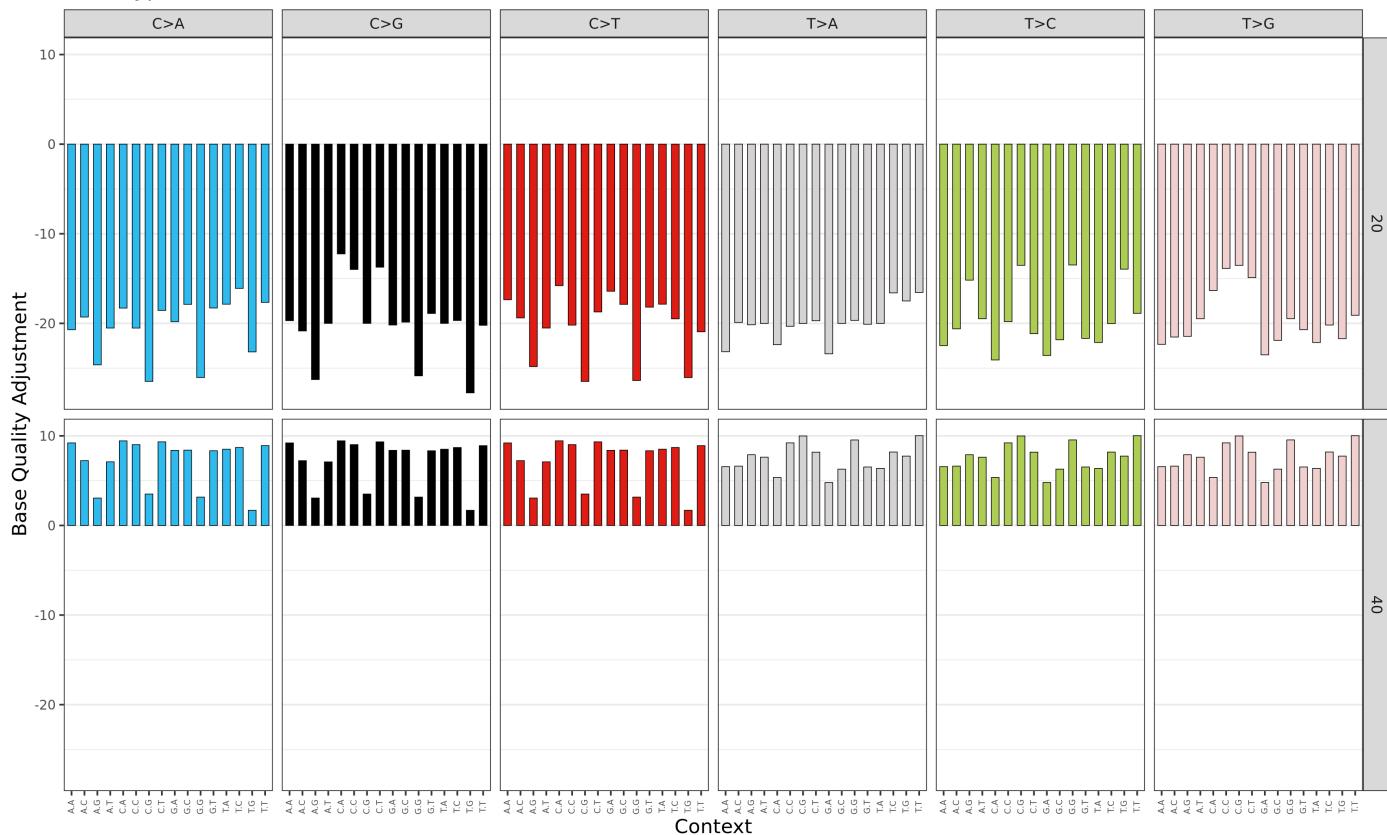


ORANGE Report (Research Use Only)

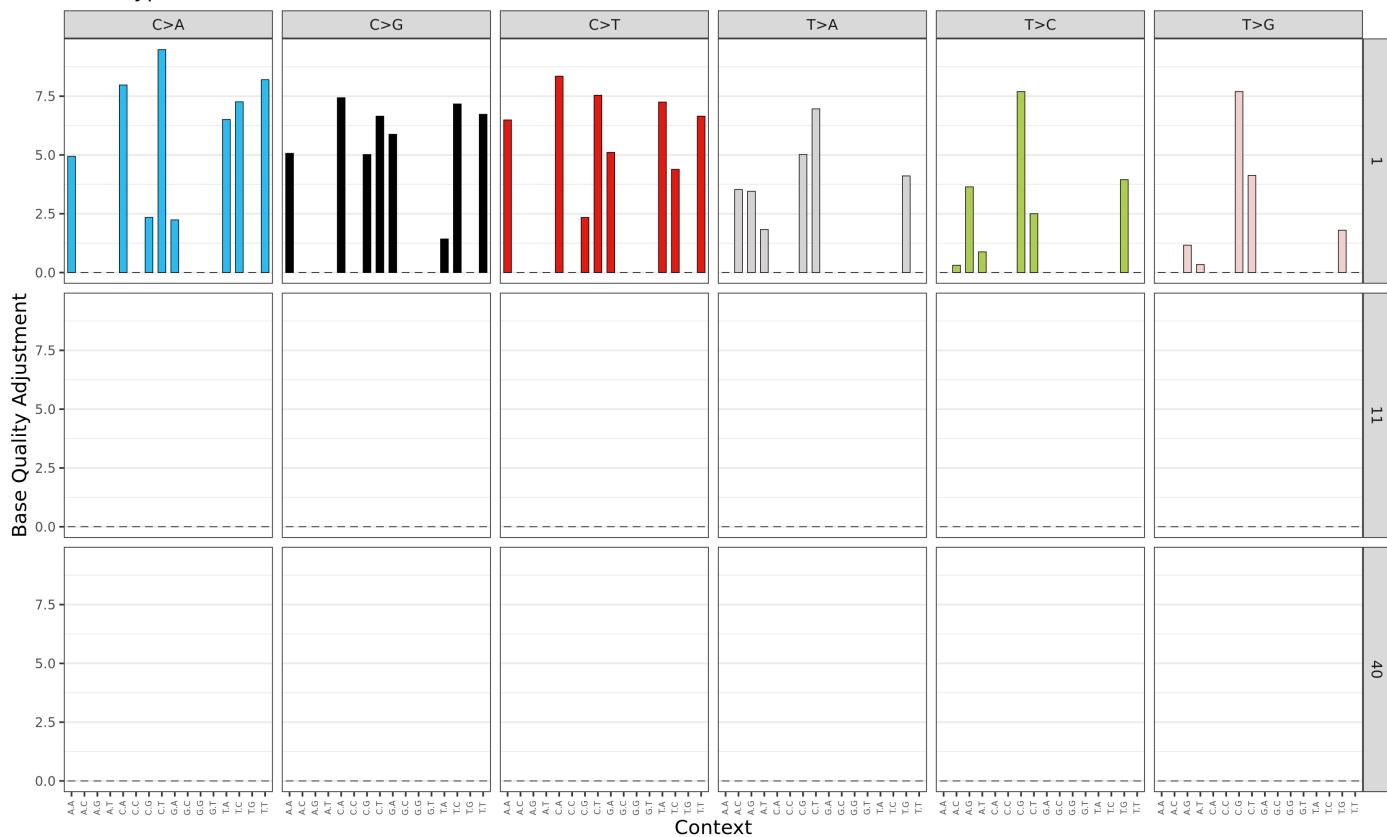
SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

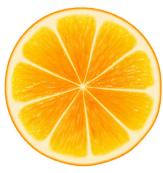
Tumor Sample BQR plot

Read type: NONE



Read type: SINGLE





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SAMPLE
subject_a.tumor
PLATINUM VERSION
2.1

Tumor Detection Statistics

Tumor maximum diploid proportion	1.00
Number of hotspot mutations	1
Number of hotspot structural variants	1
Sum of small variant allele read counts	2922
Sum of structural variant tumor fragment counts (excluding single breakends)	48
Sum of B-allele frequency points in germline diploid regions with tumor ratio < 0.8 OR > 1.2	0