



# ORANGE Report (Research Use Only)

SAMPLE

Test

PLATINUM VERSION

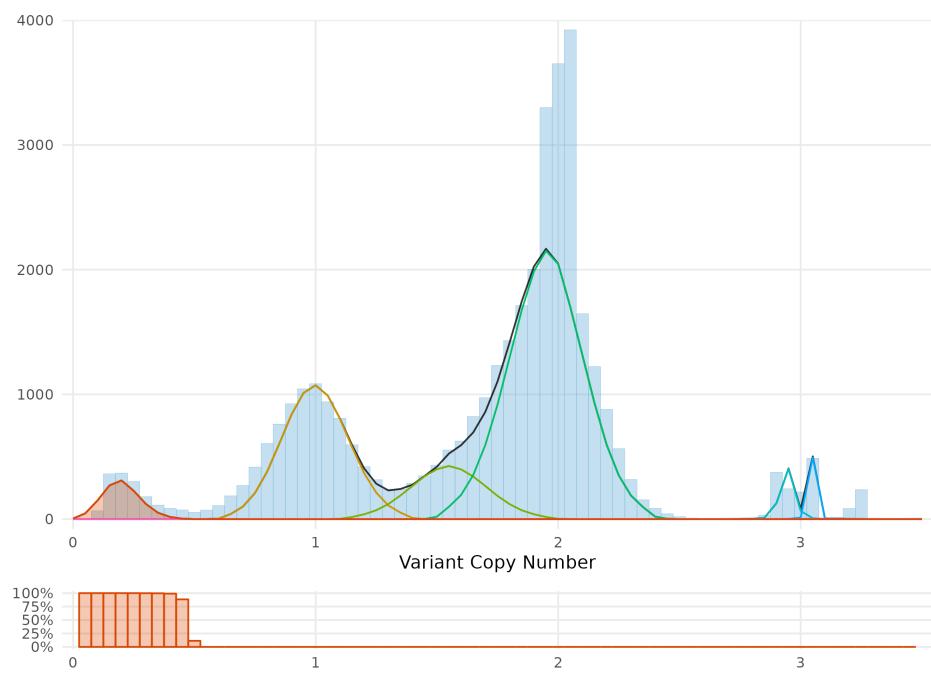
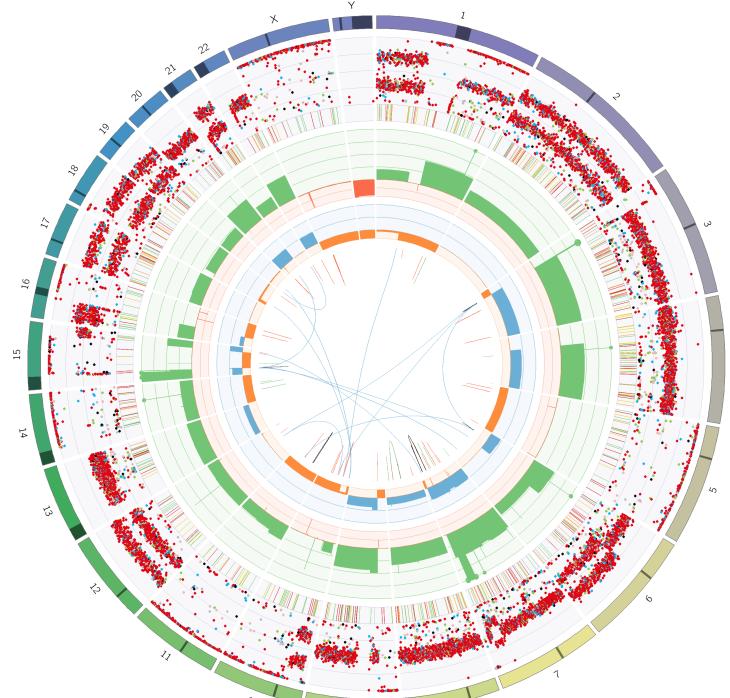
6.0

CONFIGURED PRIMARY TUMOR  
skin melanoma (DOID 8923)

CUPPA CANCER TYPE  
Skin: Melanoma (100%)

QC  
PASS

Purity:	99% (97%-100%)
Ploidy:	3.10 (3.05-3.15)
Somatic variant drivers:	6 (BRAF, CDKN2A, TERT)
Germline variant drivers:	None
Somatic copy number drivers:	1 (PTEN)
Germline copy number drivers:	None
Somatic disruption drivers:	None
Germline disruption drivers:	None
Fusion drivers:	None
Viral presence:	None
Whole genome duplicated:	Yes
Microsatellite indels per Mb:	0.1 (Stable)
Tumor mutations per Mb:	13.7 (High)
Tumor mutational load:	184 (High)
HR deficiency score:	0.0 (Proficient)
DPYD status:	*1 HOM (Normal Function)
UGT1A1 status:	*1 HOM (Normal Function)
Number of SVs:	86 (Pan 0.22   Skin 0.34)
Max complex cluster size:	8
Telomeric SGLs:	0
Number of LINE insertions:	0





## Somatic Findings

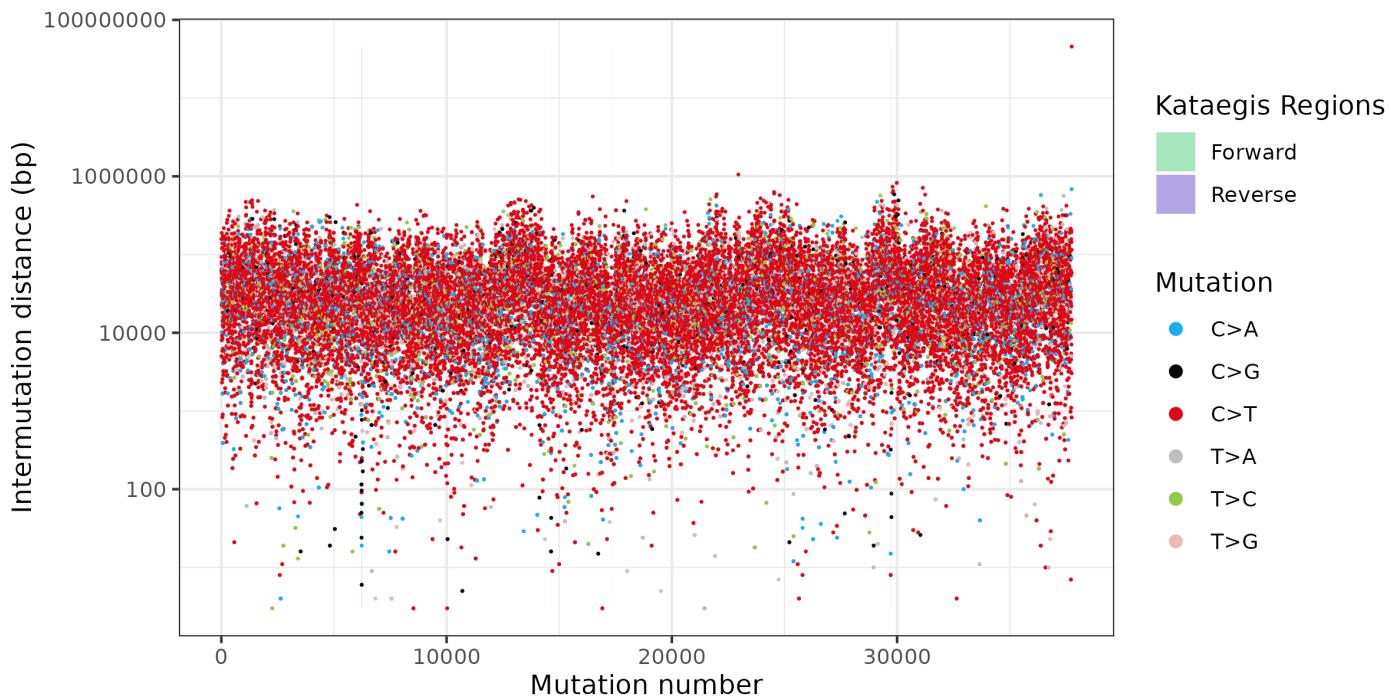
### Driver variants (7)

VARIANT	VCN	CN	MACN	BIALLELIC	HOTSPOT	DL	CL	PHASE ID	RNA DEPTH
BRAF p.V600E	4.1	6.0	2.0	2%	Yes	100%	100%		NA
CDKN2A p.A68fs	2.0	2.0	0.0	100%	Near	100%	100%		NA
CDKN2A (alt) p.G83fs	2.0	2.0	0.0	100%	Near	100%	100%		NA
TERT c.-125_-124delCCinsTT	1.7	2.0	0.0	92%	Yes	100%	100%	4304	NA
HDAC2 p.R409*	0.9	2.9	1.0	2%	No	34%	100%		NA
SF3B1 p.P718L	2.0	3.0	1.0	2%	No	15%	100%		NA
TP63 p.M499I	1.8	4.0	2.0	2%	No	0%	100%		NA

### Other potentially relevant variants (2)

VARIANT	VCN	CN	MACN	BIALLELIC	HOTSPOT	DL	CL	PHASE ID	RNA DEPTH
ALB c.1059-52dupT	1.8	3.9	1.9	2%	No		100%		NA
STK19 p.D89N	2.0	3.8	1.8	2%	Yes		100%		NA

## Kataegis plot



### Driver amps/dels (1)

LOCATION	GENE	TYPE	CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
10q23.31	PTEN	partial loss	0.0	NA	NA	NA	NA	NA

### Potentially interesting near-driver amps (0)

NONE



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### Other regions with amps (1)

LOCATION	GENE	TYPE	CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
3p24.2	CFL1P7	full gain	12.1	NA	NA	NA	NA	NA

### Regions with deletions in genes in other autosomal regions (1)

LOCATION	GENE	TYPE	CN	TPM	PERC (TYPE)	FC (TYPE)	PERC (DB)	FC (DB)
16q21	CNOT1	partial loss	0.0	NA	NA	NA	NA	NA

### Potentially interesting chromosomal rearrangements

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

### Driver fusions (0)

NONE
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### Other potentially interesting fusions (0)

NONE
------

### 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 (0)

NONE
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### Other viral presence (0)

NONE
------

### Homozygous disruptions (0)

NONE
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### Driver gene disruptions (2)

LOCATION	GENE	RANGE	TYPE	CLUSTER ID	JUNCTION CN	UNDISRUPTED CN
10	PTEN	Intron 5 Upstream	DEL	73	2.0	0.0
10	PTEN	Intron 6 Downstream	DEL	73	2.0	0.0

### Other potentially interesting gene disruptions (0)

NONE
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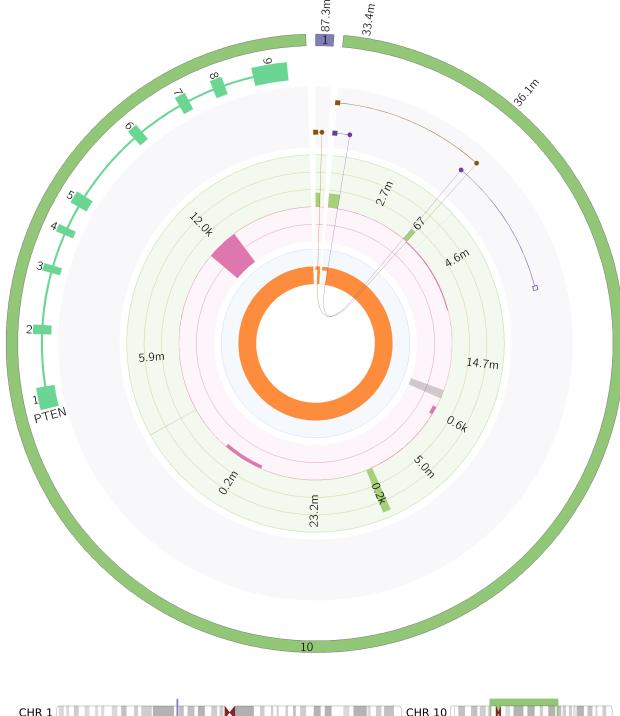
## Potentially interesting LOH events (0)

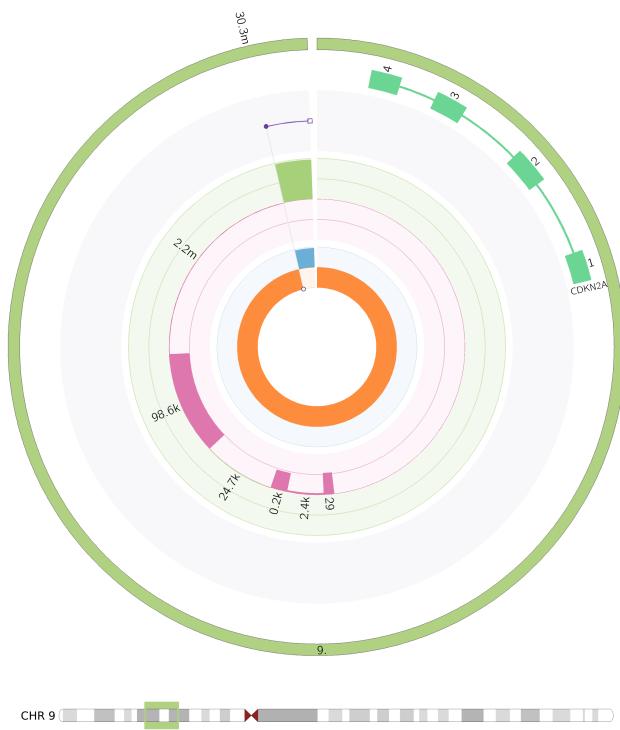
NONE

## Signature allocations (12)

SIGNATURE	ETIOLOGY	ALLOCATION	PERCENT
Sig7	Ultraviolet light exposure	23350.7	62%
Sig2	APOBEC activity	3749.5	10%
Sig8	Unknown	2056.2	5%
Sig18	Reactive oxygen species	2012.6	5%
Sig4	Tobacco smoking	2011.8	5%
Sig11	Temozolomide treatment	1263.2	3%
Sig12	Unknown	1121.8	3%
Sig17	Unknown	1109.9	3%
Sig28	Unknown	526.6	1%
Sig24	Aflatoxin exposure	309.0	1%
Sig20	Unknown	241.7	1%
MISALLOC	-	4610.5	12%

## Structural driver plots (3)







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### Germline Findings

#### Driver variants (0)

NONE

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#### Other potentially relevant variants (3)

VARIANT	VCN	CN	MACN	RNA DEPTH	BIALLELIC	HOTSPOT	GENOTYPE
CYP2D6 c.506-1G>A splice	1.8	4.0	2.0	NA	No	Yes	HET
CYP3A4 c.522-191C>T	2.4	4.0	2.0	NA	No	Yes	HET
CYP3A4 upstream	4.0	4.0	2.0	NA	Yes	Yes	HOM

#### Potentially pathogenic germline deletions (0)

NONE

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#### Potentially pathogenic germline LOH events (0)

NONE

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#### Potentially pathogenic germline homozygous disruptions (0)

NONE

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#### Potentially pathogenic germline gene disruptions (0)

NONE

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#### Genes with missed variant likelihood > 1% (0)

NONE

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### Germline CN aberrations (0)

NONE

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### Pharmacogenetics (2)

GENE	HAPLOTYPE	GENOTYPE	FUNCTION	LINKED DRUGS	SOURCE
DYPD	*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*01:01	210	1609	NA	2.0	NONE
A*01:01	211	1609	NA	1.8	NONE
B*08:01	217	753	NA	1.8	NONE
B*40:02	196	726	NA	2.0	NONE
C*03:04	213	772	NA	2.0	NONE
C*07:01	225	772	NA	1.8	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



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## Cohort Comparison

## Probabilities by classifier

### Cancer group (strips) and subtype (label)

## **SNV96: Mutational signatures**

## **EVENT: Feature contributions**

## DNA COMBINED: Training set performance

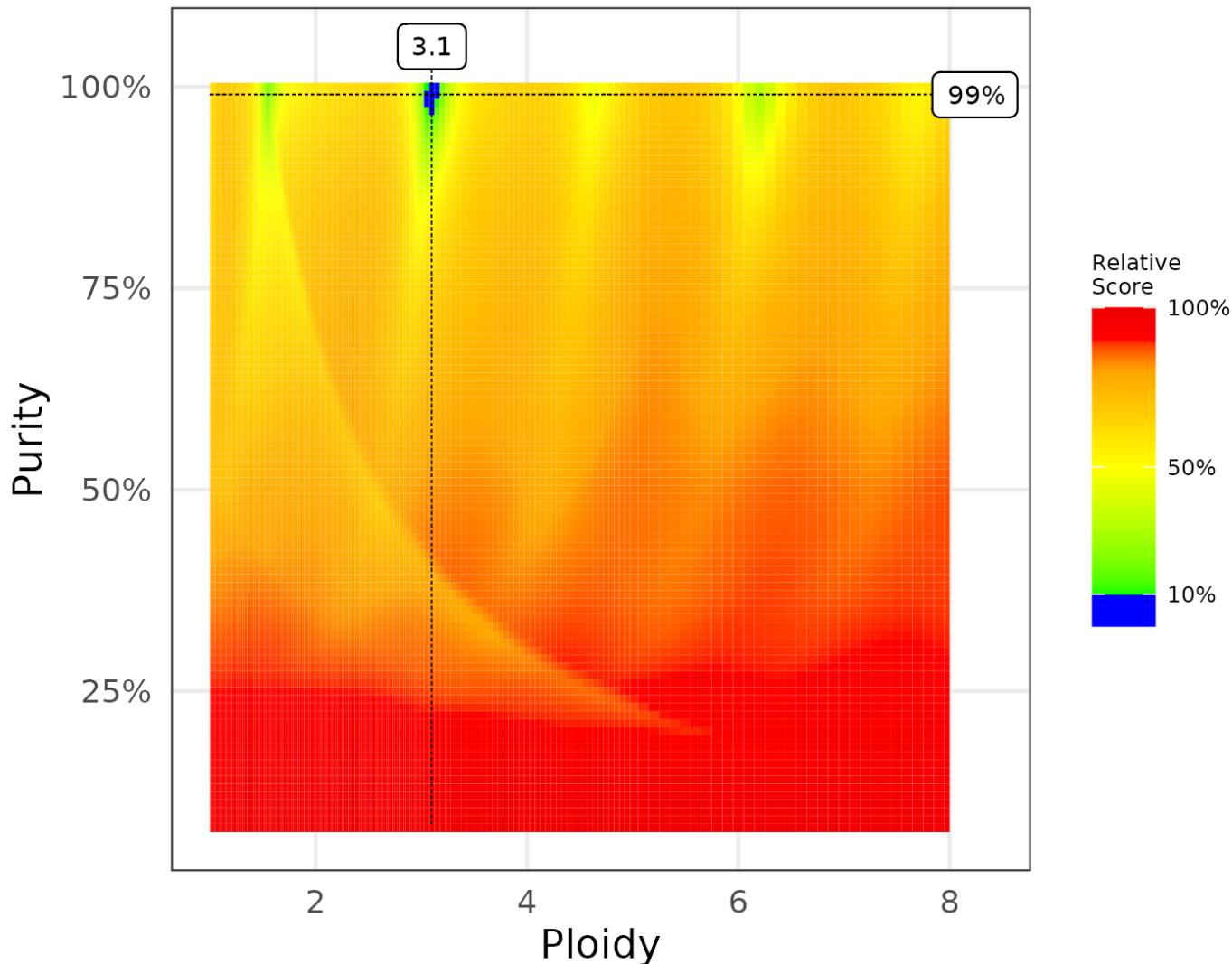
	Total no. of samples	128	9	66	80	59	47	37	157	183	908	159	138	58	837	349	85	320	131	341	372	10	26	101	44	277	254	78	56	216	77	12	18	56	46	118	607	408	49	71	241	1.00
training set	Recall (prop. of total correct)	0.74	0.33	0.95	0.76	0.85	0.57	0.43	0.68	0.7	0.94	0.96	0.94	0.74	0.96	0.85	0.61	0.91	0.54	0.96	0.88	0.5	0.27	0.66	0.77	0.94	0.91	0.65	0.84	0.99	0.91	0.75	0.67	0.79	0.74	0.8	0.99	0.99	0.73	0.73	0.88	0.00
	Precision (prop. of predicted correct)	0.77	0.75	0.91	0.77	0.81	0.77	0.35	0.64	0.77	0.91	0.94	0.86	0.91	0.96	0.87	0.83	0.84	0.76	0.93	0.86	0.62	0.47	0.6	0.94	0.95	0.89	0.77	0.85	0.96	0.92	0.64	0.55	0.77	0.79	0.73	0.96	0.96	0.82	0.87	0.92	0.00



## Quality Control

QC	REF GENOME	FIT METHOD	MEAN DEPTH	CONTAMINATION	UNS. SEGMENTS (%)	DELETED GENES
PASS	V37	NORMAL	111	0%	0 (0%)	4

## Purity/Ploidy Scores



## Flagstats

	UNIQUE RC	SECONDARY RC	SUPPLEMENTARY RC	MAPPED PROPORTION
Ref Sample	691880238	0	871753	100%
Tumor Sample	2513301754	0	3179178	100%



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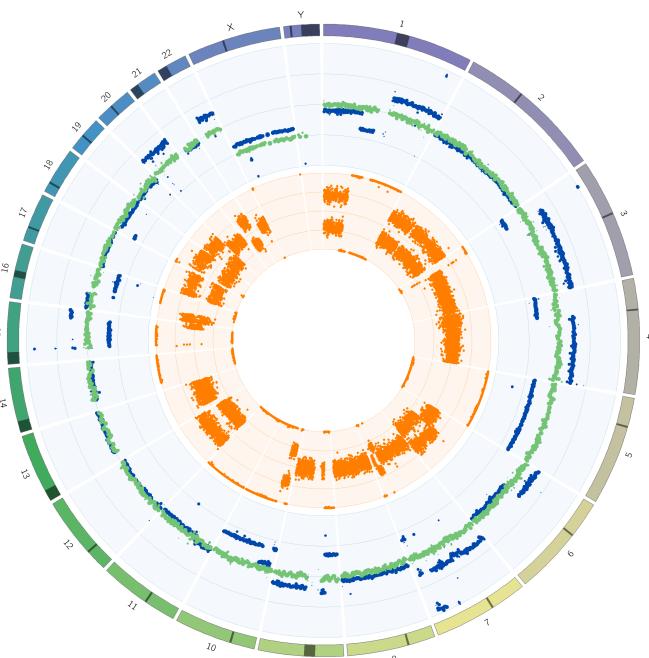
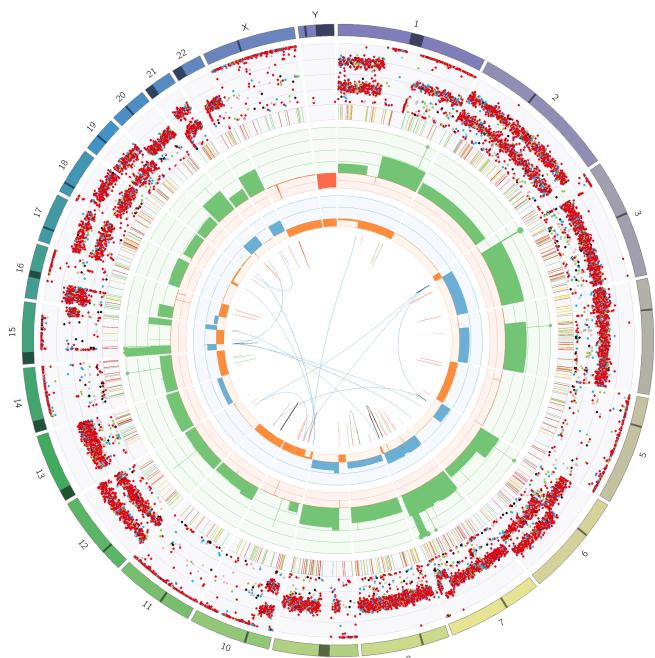
### Coverage Stats

	MEAN COVERAGE	SD COVERAGE	MEDIAN COVERAGE	MAD COVERAGE
Ref Sample	31.3	9.4	32	5
Tumor Sample	107.6	34.9	109	23

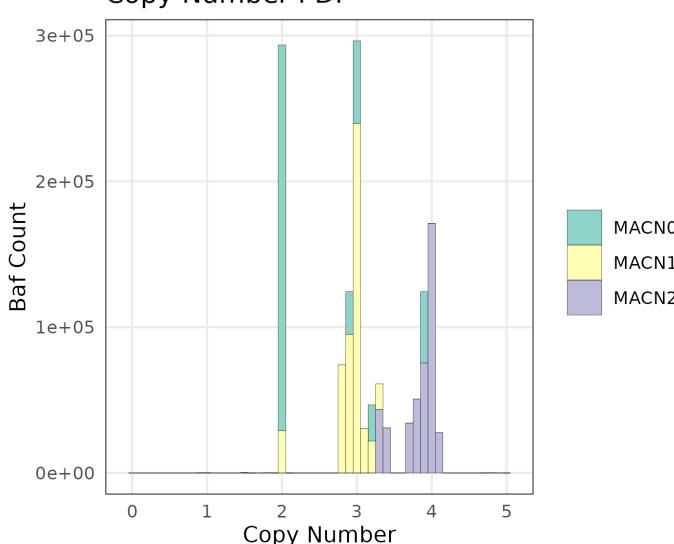
### Excluded Percentages

	ADAPTER	BASEQ	CAPPED	DUPE	MAPQ	OVERLAP	UNPAIRED	TOTAL
Ref Sample	0%	0%	0%	11%	2%	0%	0%	13%
Tumor Sample	0%	0%	0%	15%	2%	1%	0%	18%

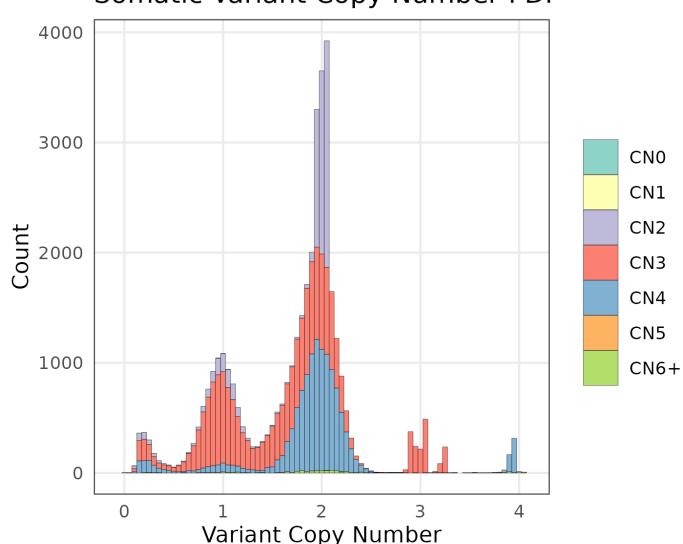
### QC plots



### Copy Number PDF



### Somatic Variant Copy Number PDF





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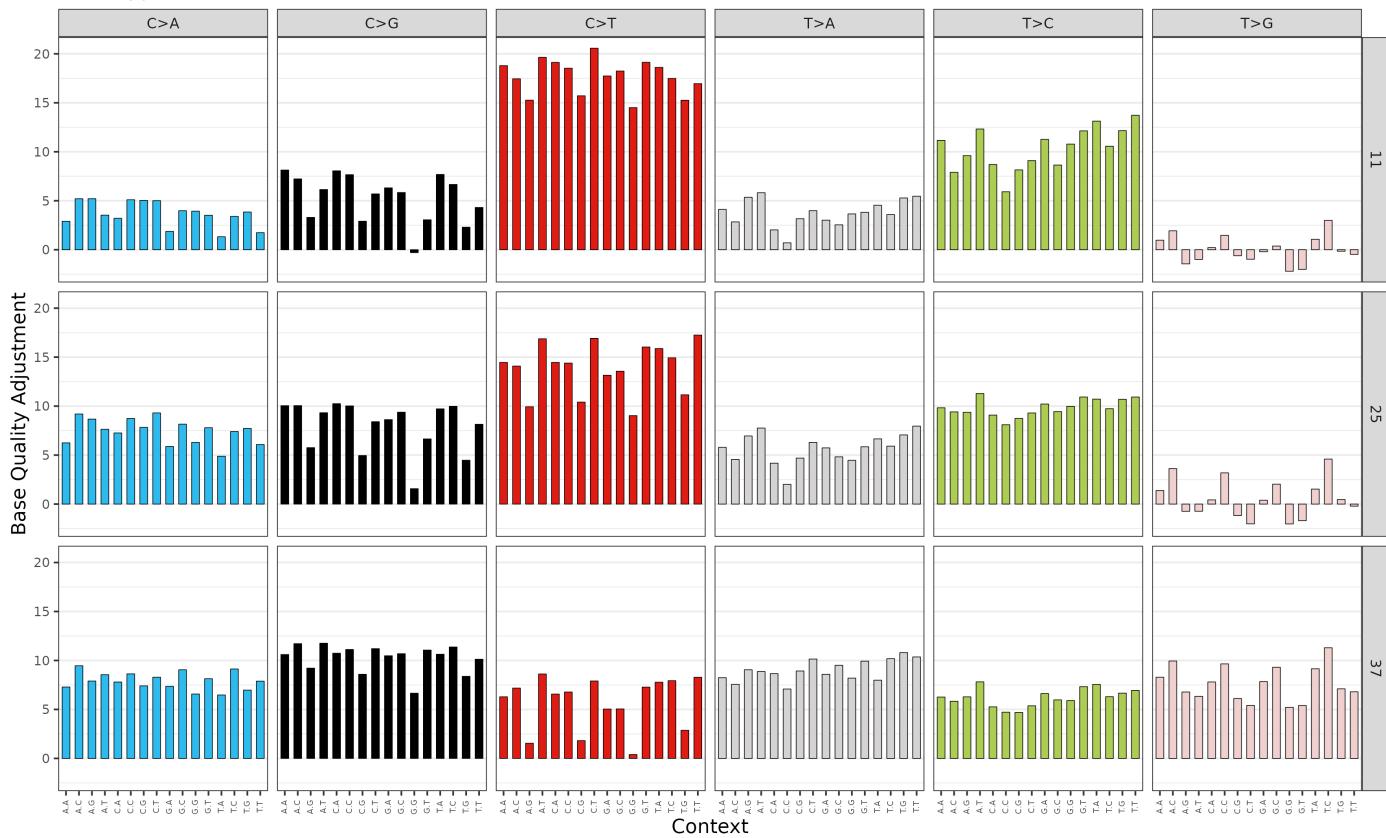
Test

PLATINUM VERSION

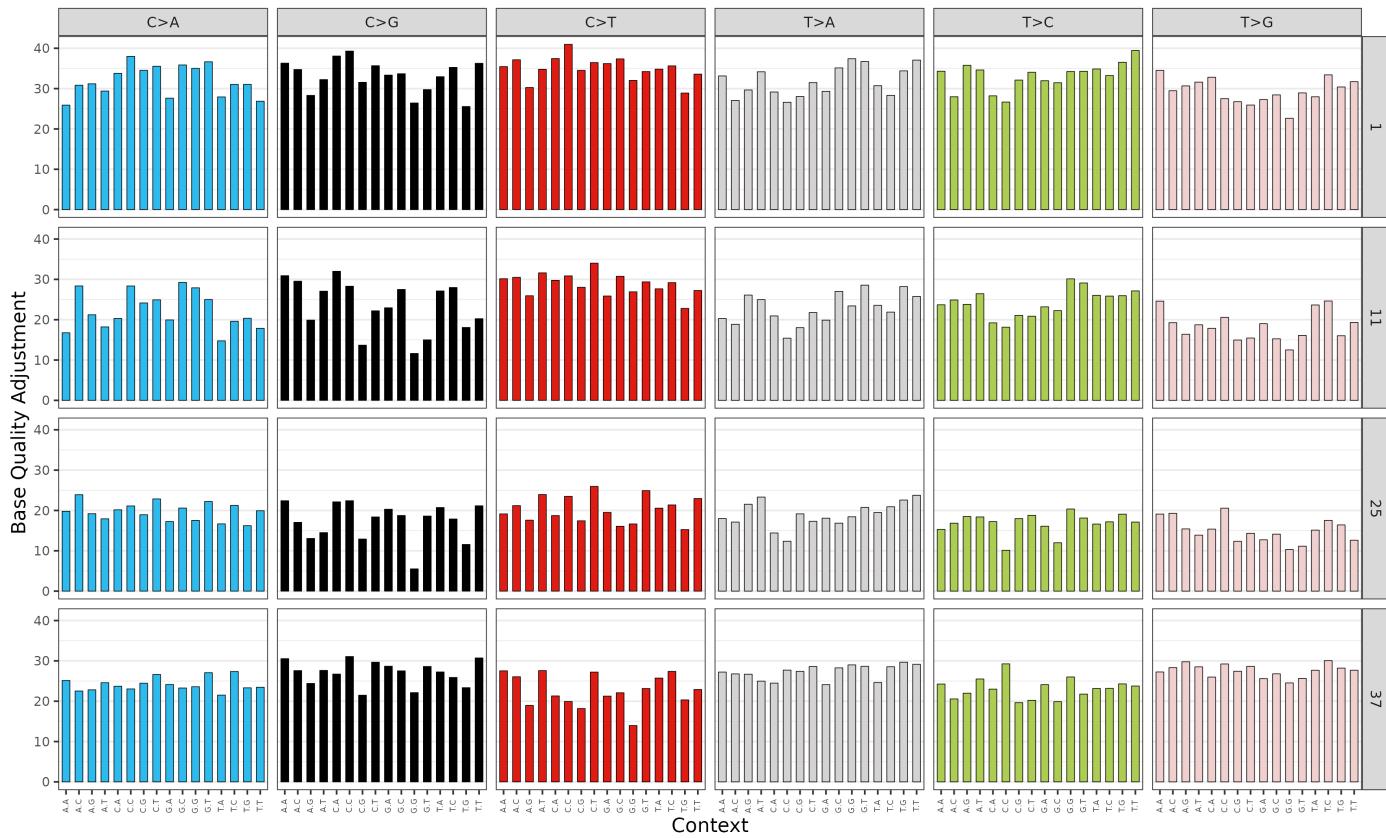
6.0

## Reference Sample BQR plot

Read type: NONE



Read type: SINGLE





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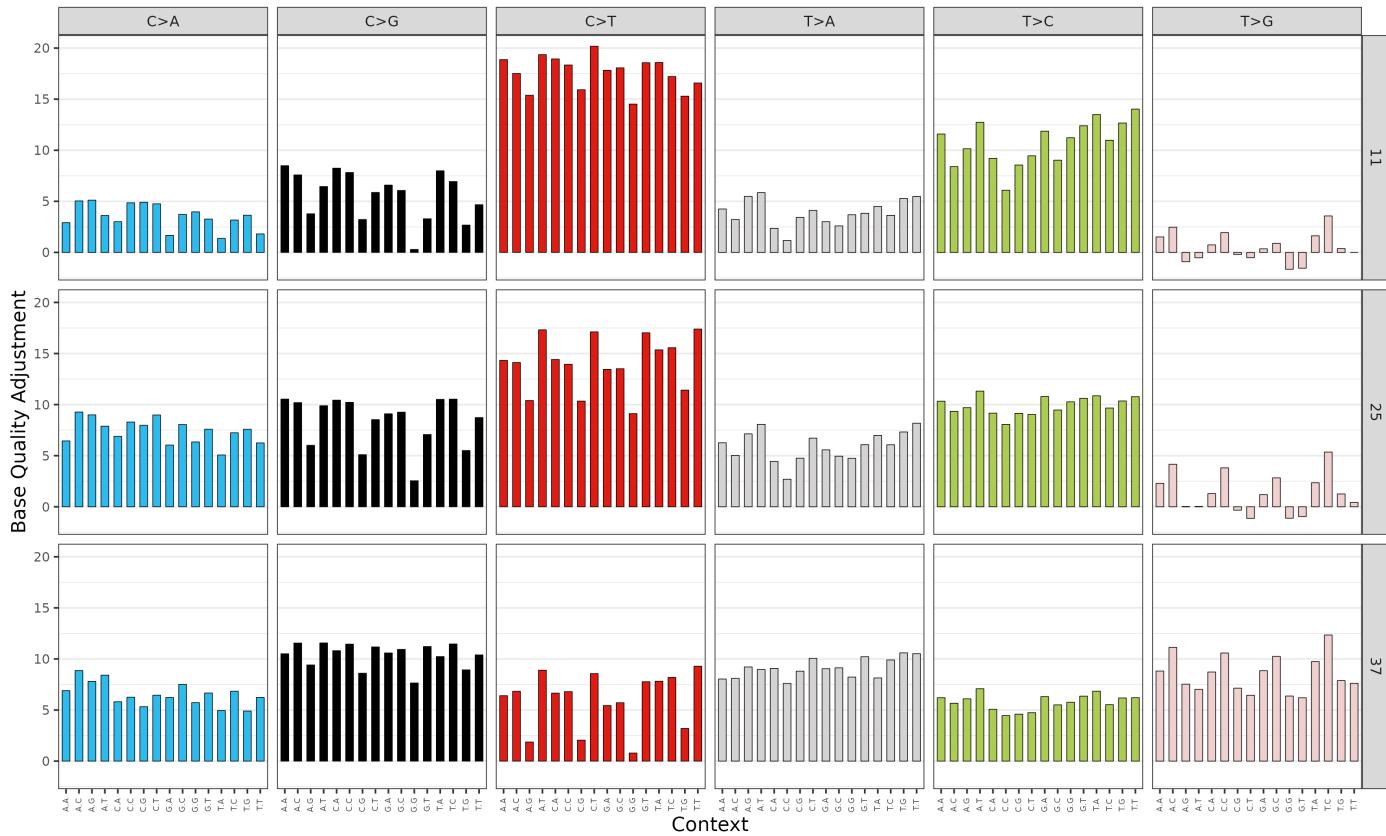
Test

PLATINUM VERSION

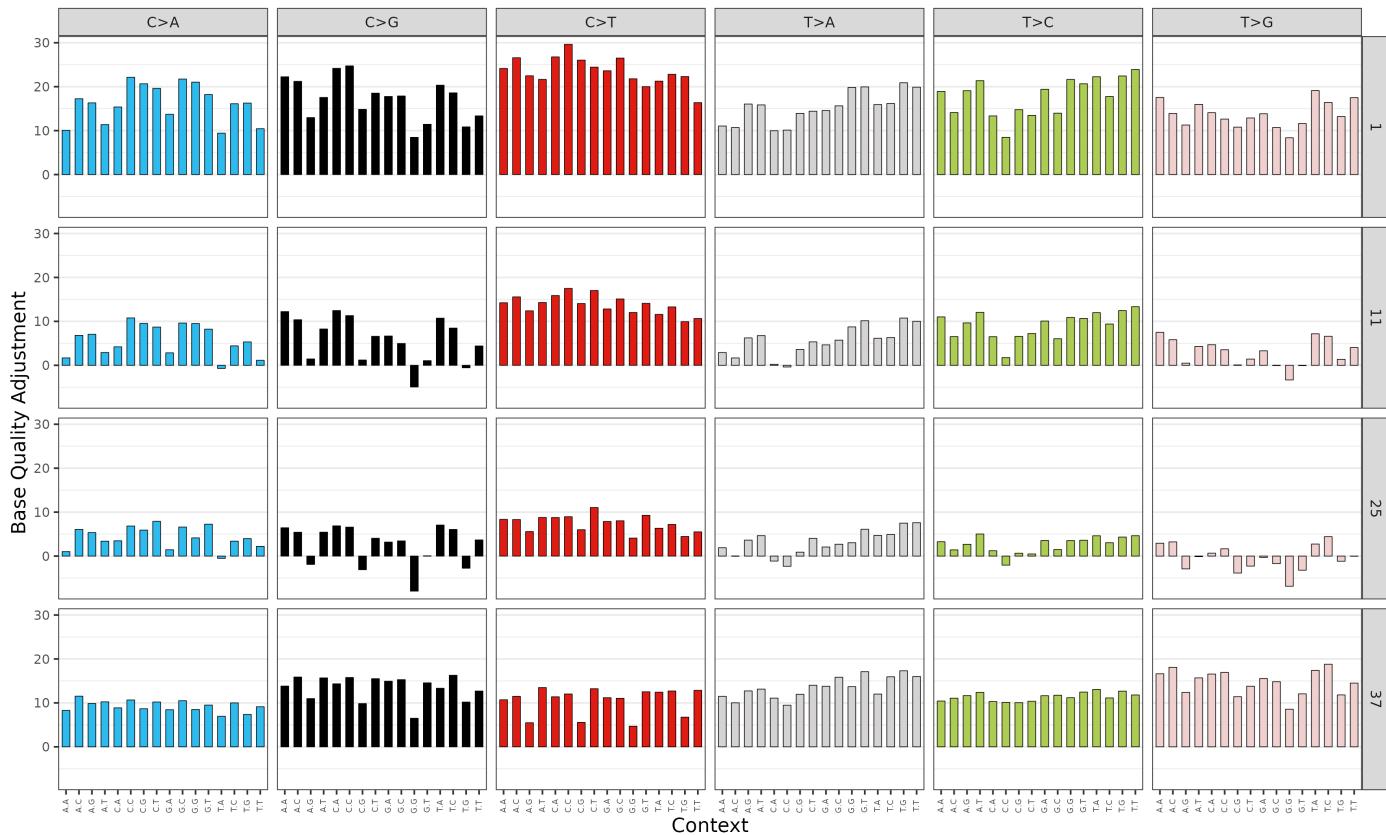
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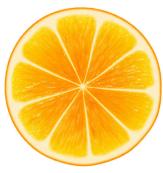
## Tumor Sample BQR plot

Read type: NONE



Read type: SINGLE





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### Tumor Detection Statistics

Tumor maximum diploid proportion	0.02
Number of hotspot mutations	3
Number of hotspot structural variants	0
Sum of small variant allele read counts	2287733
Sum of structural variant tumor fragment counts (excluding single breakends)	6408
Sum of B-allele frequency points in germline diploid regions with tumor ratio < 0.8 OR > 1.2	682755