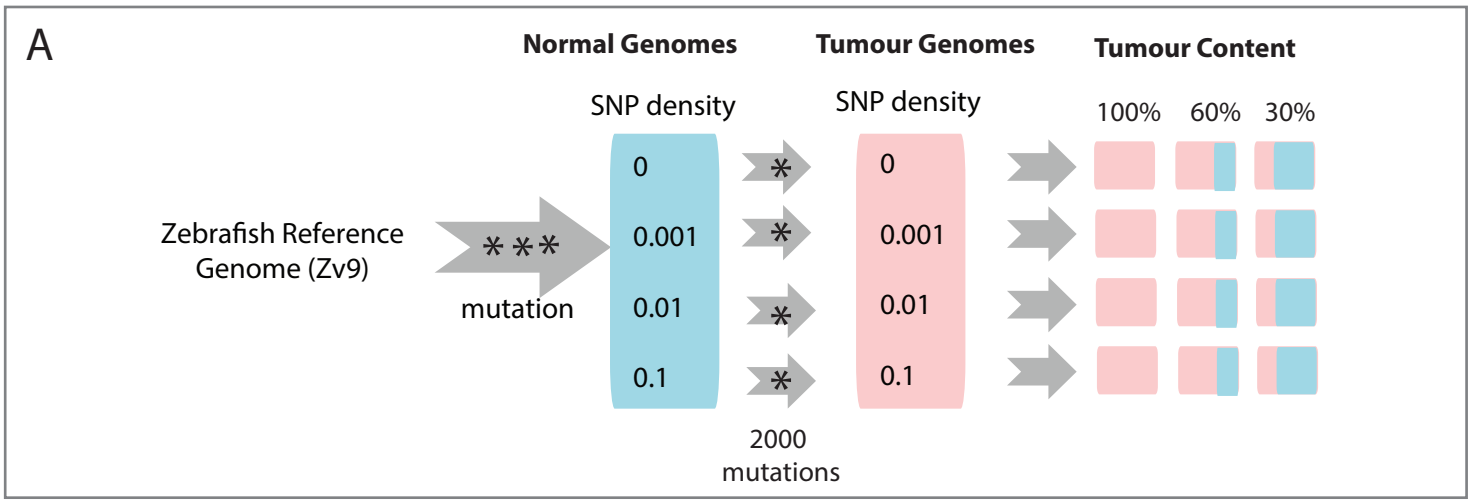
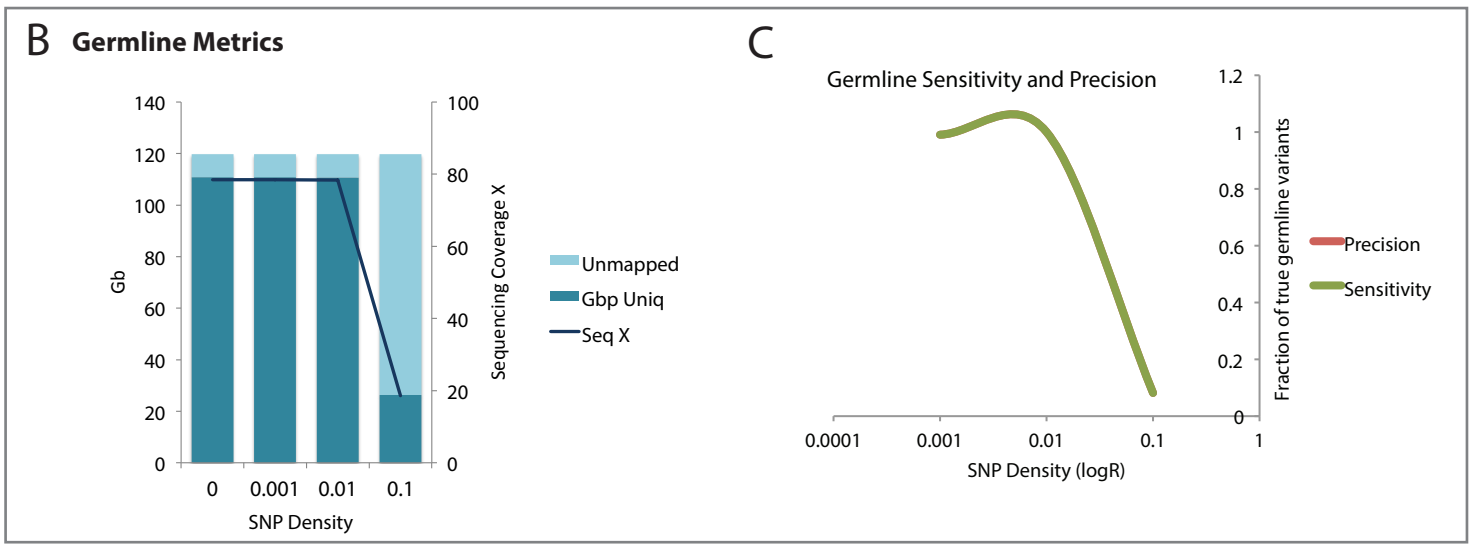
Figure S1


A
Normal Genomes
Tumour Genomes
Tumour Content
SNP density
SNP density
100%
60%
30%
Zebrafish Reference Genome (Zv9)
mutation
0
0.001
0.01
0.1
0
0.001
0.01
0.1
2000 mutations


B Germline Metrics
Gb
Sequencing Coverage X
Unmapped
Gbp Uniq
Seq X
SNP Density
C
Germline Sensitivity and Precision
Fraction of true germline variants
Precision
Sensitivity
SNP Density (logR)

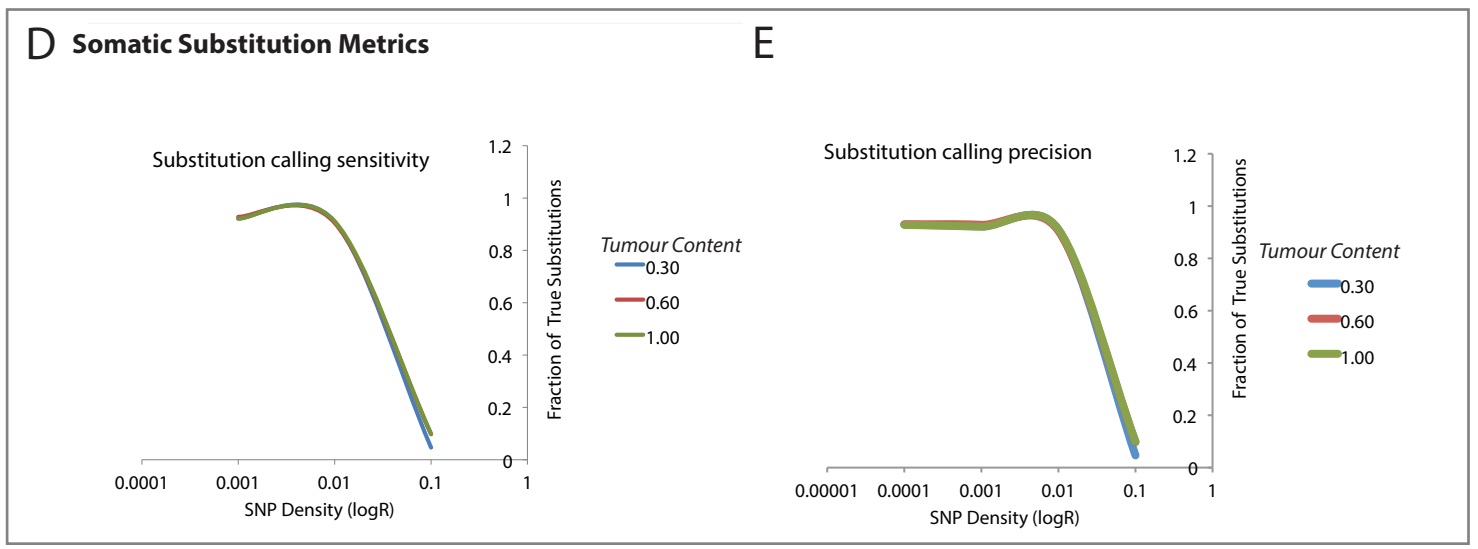
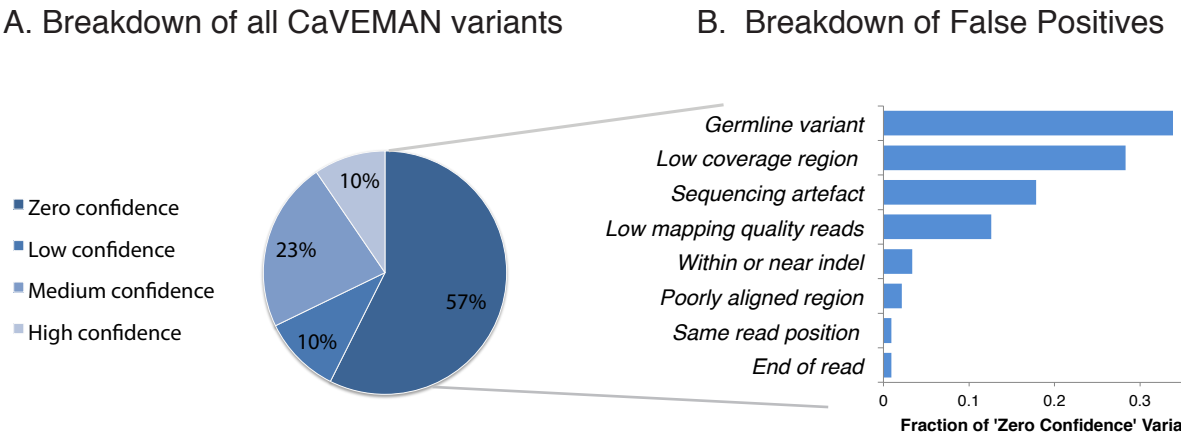

D Somatic Substitution Metrics
Substitution calling sensitivity
Fraction of True Substitutions
Tumour Content
0.30
0.60
1.00
SNP Density (logR)
E
Substitution calling precision
Fraction of True Substitutions
Tumour Content
0.30
0.60
1.00
SNP Density (logR)

Figure S2



Comparison of callers for ZD8a

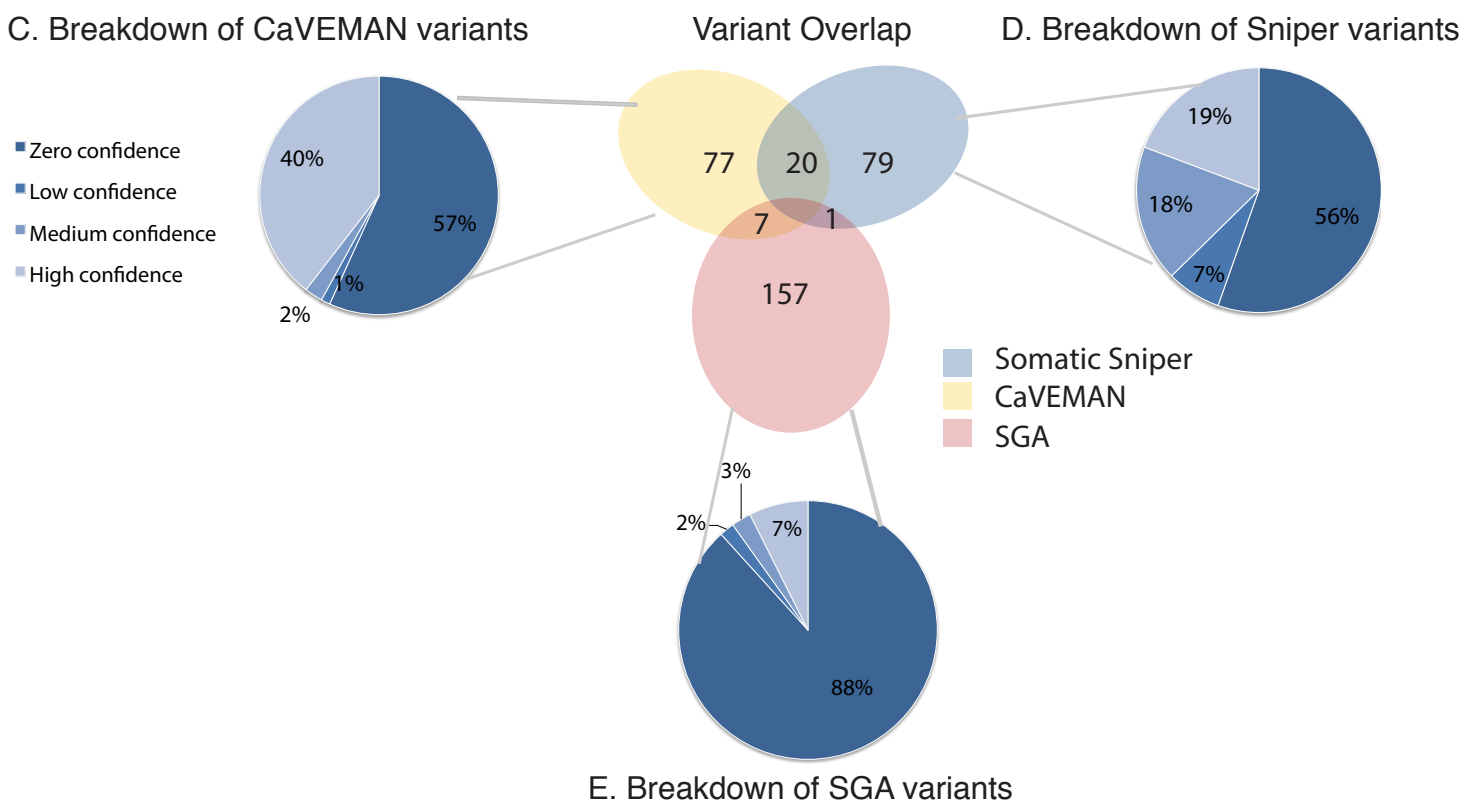


Figure S3

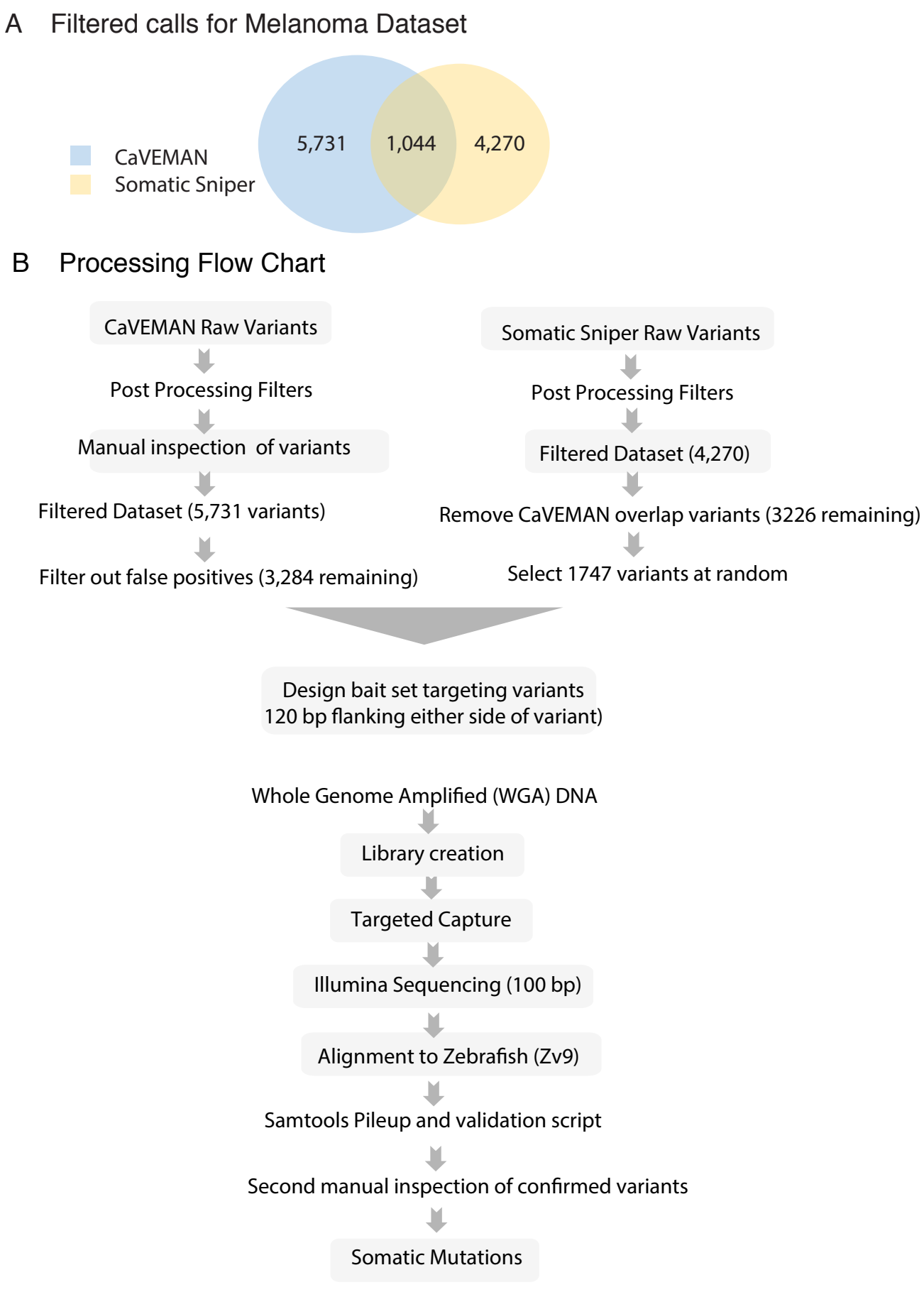

A Filtered calls for Melanoma Dataset
CaVEMAN
Somatic Sniper
5,731
1,044
4,270
B Processing Flow Chart
CaVEMAN Raw Variants
Post Processing Filters
Manual inspection of variants
Filtered Dataset (5,731 variants)
Filter out false positives (3,284 remaining)
Somatic Sniper Raw Variants
Post Processing Filters
Filtered Dataset (4,270)
Remove CaVEMAN overlap variants (3226 remaining)
Select 1747 variants at random
Design bait set targeting variants
120 bp flanking either side of variant)
Whole Genome Amplified (WGA) DNA
Library creation
Targeted Capture
Illumina Sequencing (100 bp)
Alignment to Zebrafish (Zv9)
Samtools Pileup and validation script
Second manual inspection of confirmed variants
Somatic Mutations

Figure S4

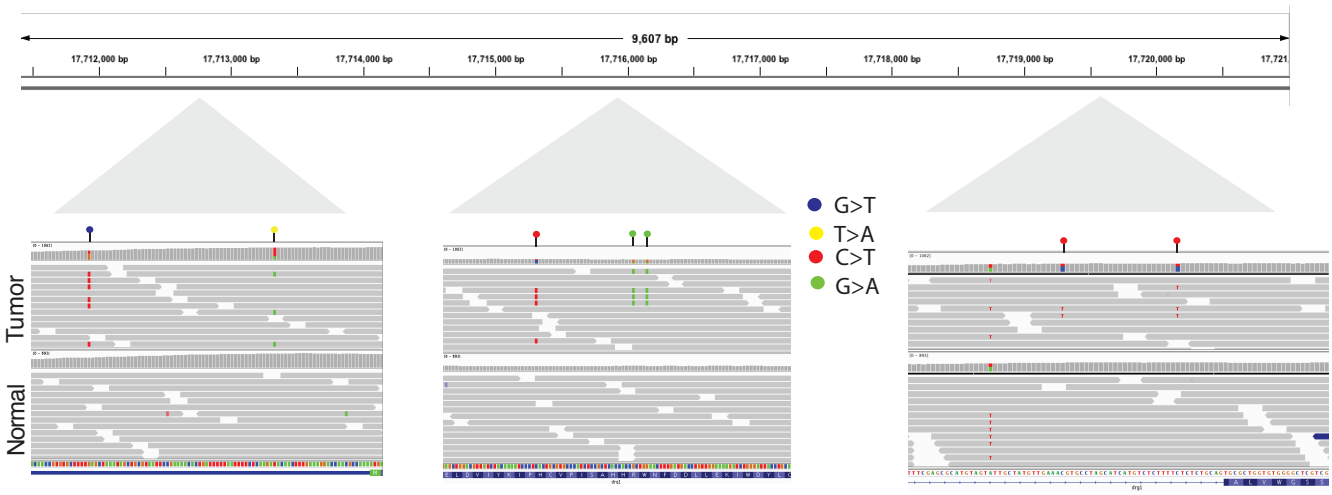

9,607 bp
17,712,000 bp
17,713,000 bp
17,714,000 bp
17,715,000 bp
17,716,000 bp
17,717,000 bp
17,718,000 bp
17,719,000 bp
17,720,000 bp
17,721
Tumor
Normal
G>T
T>A
C>T
G>A

Figure S5

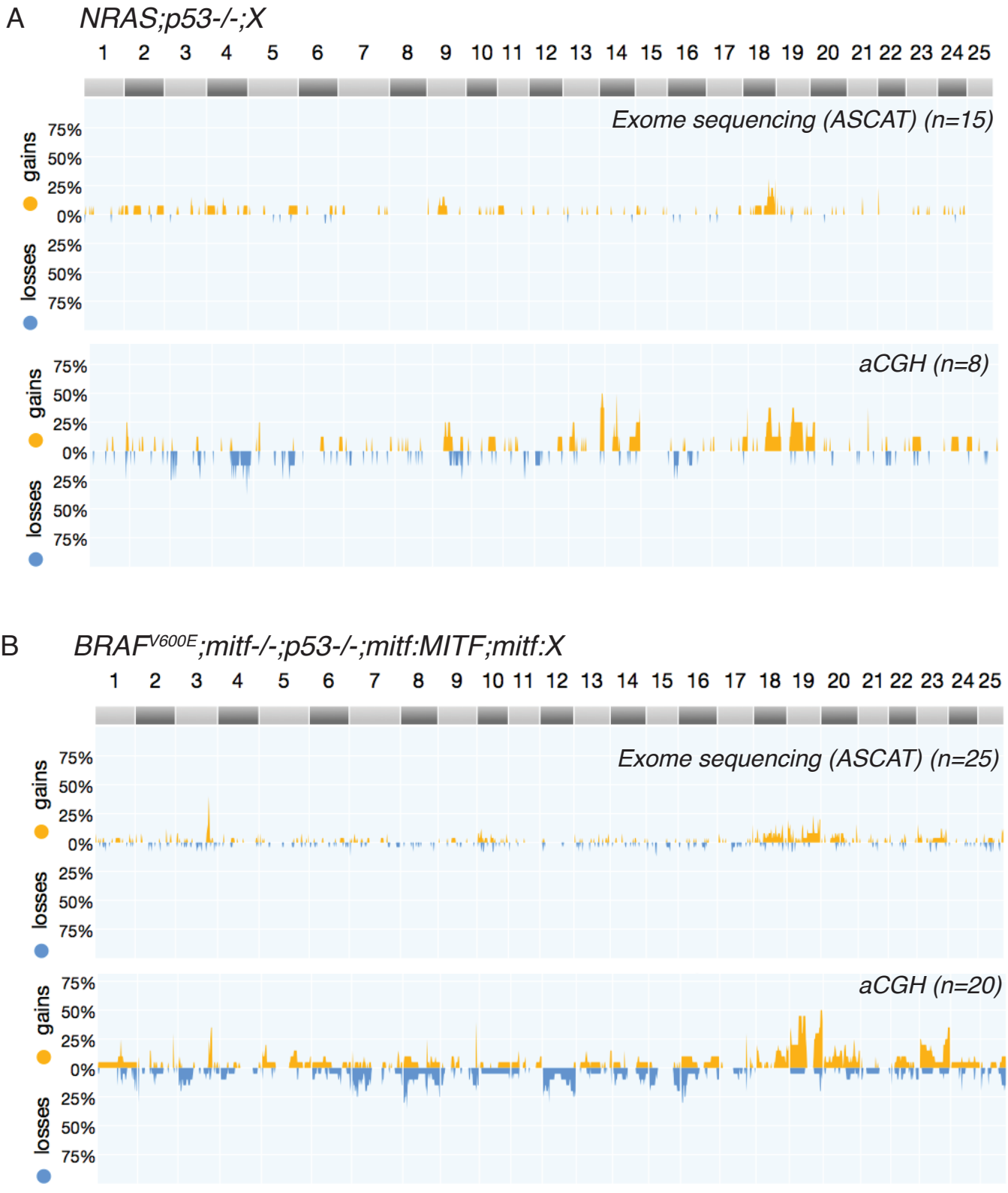

A
NRAS;p53-/-;X
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
Exome sequencing (ASCAT) (n=15)
gains
losses
75%
50%
25%
0%
aCGH (n=8)
B
BRAF^V600E;mitf-/-;p53-/-;mitf:MITF;mitf:X
Exome sequencing (ASCAT) (n=25)
aCGH (n=20)

Figure S6

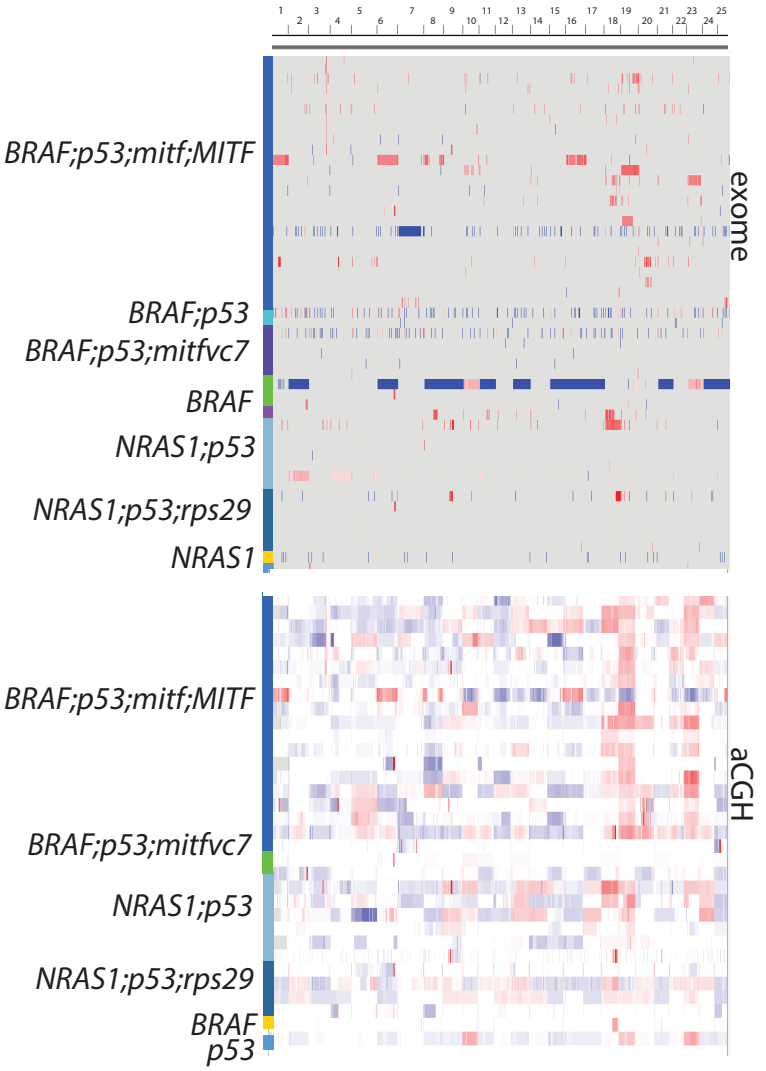

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25
BRAF;p53;mitf;MITF
BRAF;p53
BRAF;p53;mitfvc7
BRAF
NRAS1;p53
NRAS1;p53;rps29
NRAS1
exome
BRAF;p53;mitf;MITF
BRAF;p53;mitfvc7
NRAS1;p53
NRAS1;p53;rps29
BRAF
p53
aCGH

Figure S7

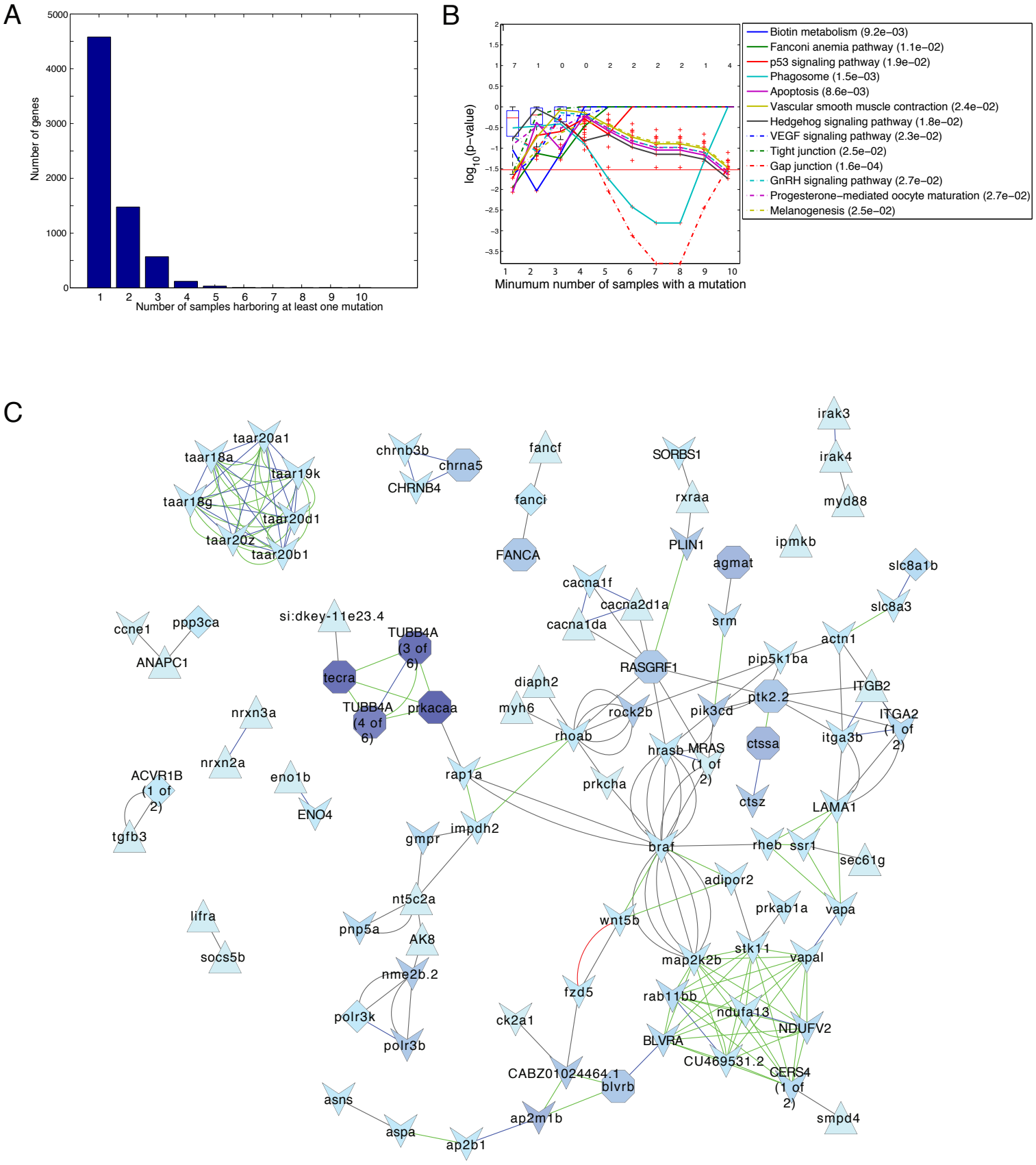
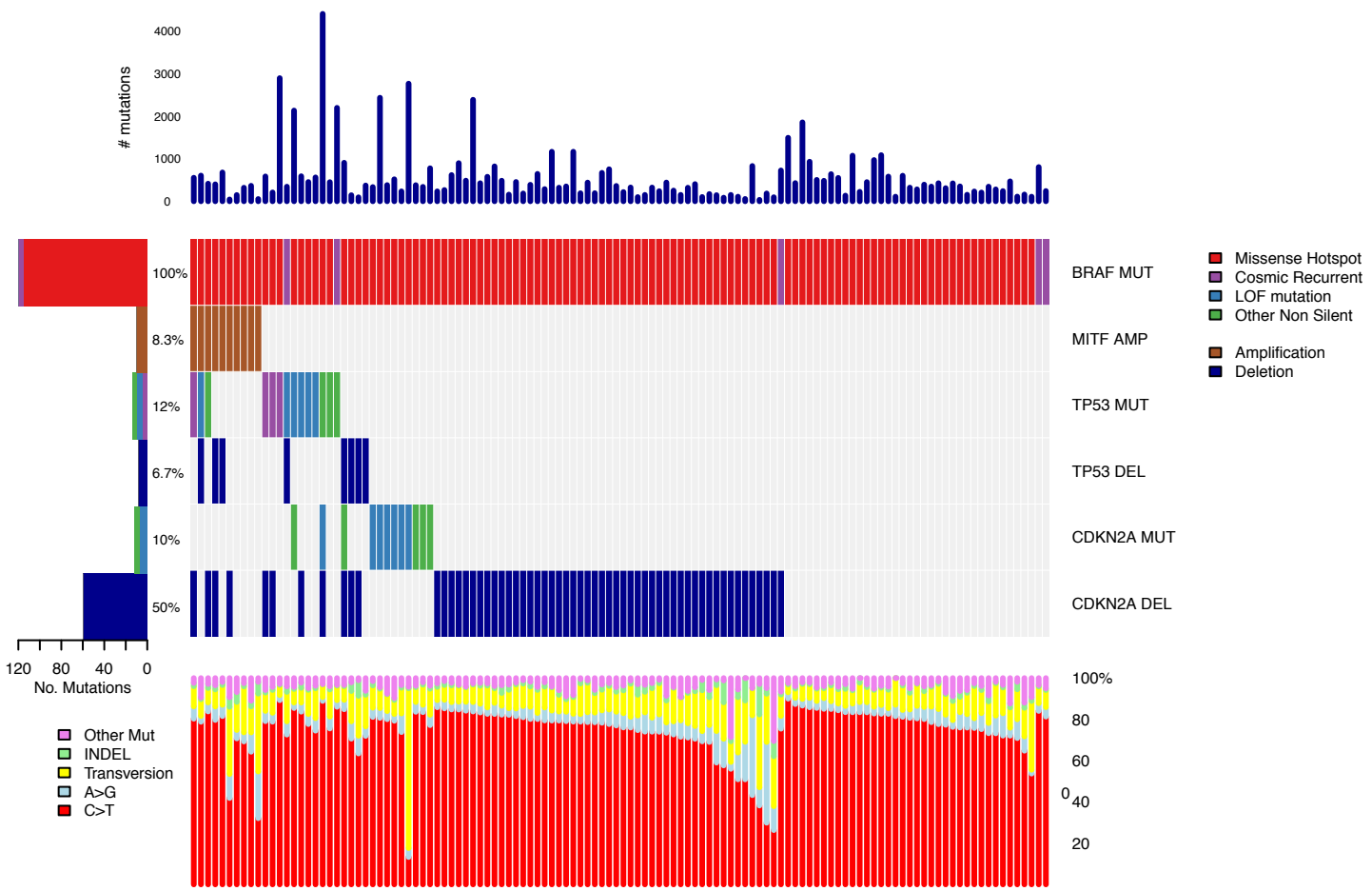

A
Number of genes
Number of samples harboring at least one mutation
B
log10(p-value)
Minumum number of samples with a mutation
Biotin metabolism (9.2e−03)
Fanconi anemia pathway (1.1e−02)
p53 signaling pathway (1.9e−02)
Phagosome (1.5e−03)
Apoptosis (8.6e−03)
Vascular smooth muscle contraction (2.4e−02)
Hedgehog signaling pathway (1.8e−02)
VEGF signaling pathway (2.3e−02)
Tight junction (2.5e−02)
Gap junction (1.6e−04)
GnRH signaling pathway (2.7e−02)
Progesterone−mediated oocyte maturation (2.7e−02)
Melanogenesis (2.5e−02)
C
taar20a1
taar18a
taar19k
taar18g
taar20d1
taar20z
taar20b1
chrnb3b
chrna5
CHRNB4
fancf
fanci
FANCA
SORBS1
rxraa
PLIN1
irak3
irak4
myd88
ipmkb
agmat
slc8a1b
slc8a3
cacna1f
cacna2d1a
cacna1da
srm
actn1
ccne1
ppp3ca
ANAPC1
si:dkey-11e23.4
TUBB4A (3 of 6)
tecra
TUBB4A (4 of 6)
prkacaa
RASGRF1
pip5k1ba
diaph2
myh6
rock2b
pik3cd
ptk2.2
ITGB2
ITGA2 (1 of 2)
itga3b
rhoab
ctssa
hrasb
MRAS (1 of 2)
nrxn3a
nrxn2a
ACVR1B (1 of 2)
tgfb3
eno1b
ENO4
rap1a
prkcha
ctsz
LAMA1
impdh2
gmpr
braf
rheb
ssr1
sec61g
adipor2
nt5c2a
pnp5a
AK8
lifra
socs5b
wnt5b
prkab1a
vapa
stk11
vapal
map2k2b
nme2b.2
polr3k
polr3b
fzd5
rab11bb
ndufa13
NDUFV2
ck2a1
BLVRA
CU469531.2
CERS4 (1 of 2)
CABZ01024464.1
blvrb
asns
aspa
ap2b1
ap2m1b
smpd4

Figure S8


mutations
4000
3000
2000
1000
0
100%
8.3%
12%
6.7%
10%
50%
BRAF MUT
MITF AMP
TP53 MUT
TP53 DEL
CDKN2A MUT
CDKN2A DEL
120
80
40
0
No. Mutations
Missense Hotspot
Cosmic Recurrent
LOF mutation
Other Non Silent
Amplification
Deletion
Other Mut
INDEL
Transversion
A>G
C>T
100%
80
60
40
20
0