A

Mutation type	Count
Frame Shift Deletion	196
Frame Shift Insertion	33
In Frame Deletion	27
In Frame Insertion	6
Missense Mutation	4350
Nonsense Mutation	240
Nonstop Mutation	5
Silent	1644
Splice Site	215
Total	**6716**

B

rank	gene	Nbase	nmut	npat	nsite	nsil	n1	n2	n3	n4	n5	n6	p_ns_s	p	q
1	BRAF	894038	240	240	6	1	0	1	1	234	4	0	<1.00E-15	<1.00E-15	<1.81E-11
2	NRAS	235555	34	34	2	0	0	0	27	7	0	0	8.81E-06	2.78E-15	2.51E-11
3	HRAS	260728	14	14	2	0	0	0	11	3	0	0	0.094	1.88E-14	1.13E-10
4	EIF1AX	177141	7	6	5	0	0	4	0	1	2	0	0.207	1.18E-11	5.34E-08
5	PPM1D	627291	5	5	5	0	0	1	0	0	4	0	0.7	4.73E-07	0.00171
6	KRAS	276486	4	4	3	0	0	0	1	3	0	0	0.414	3.19E-06	0.00861
7	CHEK2	636843	5	5	5	0	0	0	1	3	1	0	0.333	3.33E-06	0.00861
8	S100A7	126228	3	3	3	0	0	0	0	3	0	0	0.679	1.75E-05	0.0396
9	TMSB15A	58621	2	2	2	0	0	1	0	1	0	0	0.592	4.91E-05	0.0987
10	SLA	332301	3	3	3	0	0	0	1	0	2	0	0.755	7.82E-05	0.141
11	MSI1	314867	3	3	3	0	1	0	0	1	1	0	0.502	0.000108	0.178
12	NUP93	1021878	4	4	2	0	0	1	0	0	3	0	0.118	0.000135	0.2
13	ADO	143305	2	2	2	0	0	0	0	2	0	0	0.648	0.000143	0.2
14	BRIX1	363547	3	3	3	0	0	1	1	1	0	0	0.411	0.000191	0.234
15	SAMD1	179676	2	2	2	0	1	0	1	0	0	0	0.451	0.000206	0.234
16	EFCAB1	259309	2	2	2	0	1	0	0	0	1	0	0.73	0.000213	0.234
17	C11orf87	235800	3	3	3	0	2	0	0	1	0	0	0.301	0.000228	0.234
18	SLC25A45	358159	3	3	3	1	1	1	1	0	0	0	0.704	0.000233	0.234
19	CD163	1408189	4	4	4	0	2	1	1	0	0	0	0.228	0.000319	0.299
20	DNAH9	5334405	9	9	9	1	2	3	1	3	0	0	0.139	0.000335	0.299

C

Summary of BRAF Variants

Alteration	Protein change	# tumours	Size of cohort	% of cohort
All		254	402	63.18%
SSNV	V600E	235	402	58.46%
SSNV	K601E	1	402	0.25%
indels		3	402	0.75%
fusions		13	482	2.70%
focal deletions		2	495	0.40%

D

Summary of RAS Variants

Alteration	Protein change	# tumours	Size of cohort	% of cohort
NRAS	Q61R	34	402	8.46%
All HRAS		14	402	3.48%
HRAS	Q61R	11	402	2.74%
HRAS	Q61K	3	402	0.75%
All KRAS		4	402	1.00%
KRAS	Q61R	1	402	0.25%
KRAS	Q61K	1	402	0.25%
KRAS	G12V	1	402	0.25%
KRAS	Q61K	1	402	0.25%

E

	BRAF-mutant				RAS-mutant			
	# positve	# total	% posiitve	p-value*	# positve	# total	% posiitve	p-value*
CT	191	239	79.92%	2.07E-08	20	49	40.82%	1.19E-05
FV	17	239	7.11%	1.16E-17	29	49	59.18%	1.44E-09
TCV	28	239	11.72%	1.23E-05	0	49	0.00%	2.19E-02
OV	3	239	1.26%	6.80E-01	0	49	0.00%	1.00E+00
Missing	8	247	3.24%	0.432688	3	52	5.77%	0.446869

	CT				FV				TCV			
	# positve	# total	% posiitve	p-value*	# positve	# total	% posiitve	p-value*	# positve	# total	% posiitve	p-value*
BRAF-mutant	191	268	71.27%	2.07E-08	17	83	20.48%	1.16E-17	28	29	96.55%	1.23E-05
RAS-mutant	20	268	7.46%	1.19E-05	29	83	34.94%	1.44E-09	0	29	0.00%	2.19E-02