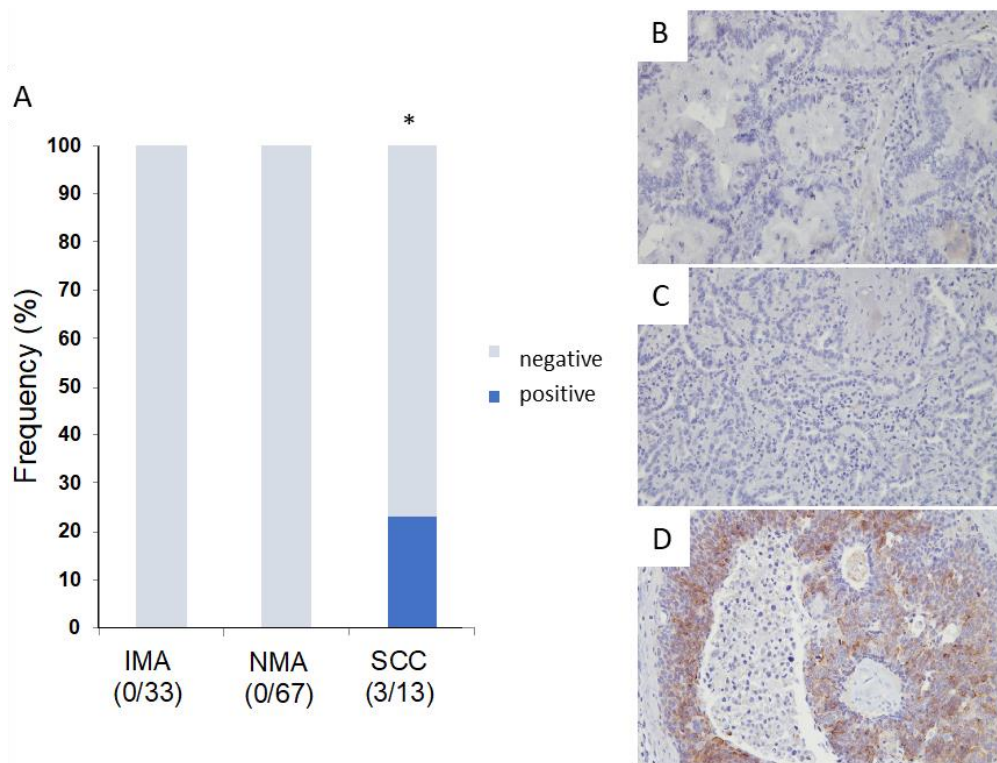


## Supplementary Materials: Genomic Characteristics of Invasive Mucinous Adenocarcinomas of the Lung and Potential Therapeutic Targets of B7-H3

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**Figure S1.** Immunostaining for VTCN-1 in IMA, NMA, and squamous cell carcinoma. (A) V-set domain-containing T-cell inhibitor 1 (VTCN1) was detected in some patients with squamous cell carcinoma, but not in patients with invasive mucinous adenocarcinoma (IMA) or nonmucinous adenocarcinoma (NMA). \*,  $p < 0.05$ , compared to IMA or NMA. (B–D) Representative VTCN1 immunostaining in IMA (B), NMA (C), and squamous cell carcinoma (D).

Table S1. Clinical characteristics of the patients.

Case	Histology	Cluster analysis	Cluster	Age	sex	Smoking	Brinkman index	Tumor size(mm)	T-N-M	p-Stage	Surgical procedure	Adjuvant Tx	Outcome
1	IMA	Performed	B	67	female	never	0	32	2a-0-0	IB	lobectomy	-	24m no rec
2	IMA	Performed	B	74	male	past	1080	10	1a-0-0	IA1	lobectomy	-	33m no rec
3	IMA	Performed	C	70	male	past	760	22	1c-0-0	IA3	lobectomy	-	33m no rec
4	IMA	Performed	C	74	female	never	0	11	1b-0-0	IA2	wedge resection	-	22m no rec
5	IMA	Performed	C	71	male	past	200	11	1b-0-0	IA2	lobectomy	-	26m no rec
6	IMA	Performed	C	83	female	never	0	20	1b-0-0	IA2	lobectomy	-	19m no rec
7	IMA	Performed	C	72	female	never	0	31	2a-0-0	IB	lobectomy	+	14m no rec
8	IMA	Performed	C	63	male	never	0	80	4-0-0	IIIA	lobectomy	+	31m no rec
9	IMA	Performed	C	49	female	never	0	40	2a-0-0	IB	lobectomy	+	37m no rec
10	IMA	Performed	C	70	male	past	1200	10	1a-0-0	IA1	lobectomy	-	13m no rec
11	IMA	Performed	excluded	74	male	current	600	50	2b-0-0	IIA	lobectomy	-	33m no rec
12	IMA	Performed	excluded	76	male	past	60	10	1a-0-0	IA1	lobectomy	-	14m no rec
13	IMA	-	-	77	female	never	0	28	1c-0-0	IA3	lobectomy	-	6m no rec
14	IMA	-	-	73	male	past	1200	60	2b-0-0	IIA	lobectomy	+	10m no rec
15	IMA	-	-	71	female	never	0	25	1c-0-0	IA3	lobectomy	-	36m no rec
16	IMA	-	-	68	male	past	960	15	1b-0-0	IA2	lobectomy	-	20m no rec
17	IMA	-	-	90	male	past	1000	30	1c-0-0	IA3	lobectomy	-	6m death
18	IMA	-	-	84	female	never	0	90	4-0-0	IIIA	lobectomy	-	1m death
19	IMA	-	-	69	male	current	600	120	4-0-0	IIIA	pneumonectomy	+	18m rec
20	IMA	-	-	78	male	never	0	50	2a-0-0	IB	lobectomy	+	24m no rec
21	Ad	Performed	A	67	male	past	580	20	2a-0-1a	IV	lobectomy	+	32m no rec
22	Ad	Performed	A	74	male	current	1000	35	2a-0-0	IB	lobectomy	+	9m death
23	Ad	Performed	A	58	male	current	340	28	1b-2-0	IIIA	lobectomy	+	30m no rec
24	Ad	Performed	A	49	male	past	400	15	1a-0-0	IA	lobectomy	-	24m no rec
25	Ad	Performed	A	60	male	past	990	12	2b-3-0	IIIB	wedge resection	+	12m rec
26	Ad	Performed	A	73	male	current	1100	20	2a-0-0	IB	wedge resection	-	15m no rec
27	Ad	Performed	B	63	female	never	0	25	1b-0-0	IA	lobectomy	-	34m no rec
28	Ad	Performed	B	75	female	never	0	20	1a-0-0	IA	lobectomy	-	32m no rec
29	Ad	Performed	B	61	female	never	0	14	1a-0-0	IA	wedge resection	-	17m rec
30	Ad	Performed	B	54	female	never	0	16	1a-2-0	IIIA	lobectomy	+	7m rec
31	Ad	Performed	B	75	male	current	825	12	1a-0-0	IA	lobectomy	-	30m no rec
32	Ad	Performed	B	67	male	past	800	32	2a-0-0	IB	lobectomy	-	1m death
33	Ad	Performed	B	59	female	past	700	35	2a-0-0	IB	lobectomy	+	29m no rec
34	Ad	Performed	B	70	female	never	0	35	2a-0-0	IB	lobectomy	-	29m no rec
35	Ad	Performed	B	82	male	past	150	20	1b-0-0	IA	lobectomy	-	27m no rec
36	Ad	Performed	B	55	male	past	700	17	1a-0-0	IA	segmentectomy	-	25m no rec
37	Ad	Performed	B	72	male	past	300	10	1a-0-0	IA	segmentectomy	-	23m no rec
38	Ad	Performed	B	72	male	past	150	10	is-0-0	0	wedge resection	-	23m no rec
39	Ad	Performed	B	74	female	never	0	8	1a-0-0	IA	wedge resection	-	22m no rec
40	Ad	Performed	B	68	female	never	0	10	1a-0-0	IA	lobectomy	-	24m no rec
41	Ad	Performed	B	64	male	never	0	35	2a-0-0	IB	lobectomy	+	25m no rec
42	Ad	Performed	B	63	male	past	740	25	1a-0-0	IA	lobectomy	-	23m no rec
43	Ad	Performed	B	85	female	never	0	30	2a-0-0	IB	lobectomy	+	24m no rec
44	Ad	Performed	B	73	male	past	1800	8	is-0-0	0	pneumonectomy	+	16m no rec
45	Ad	Performed	B	78	male	past	330	15	1a-0-0	IA	lobectomy	-	16m no rec
46	Ad	Performed	B	75	male	past	800	17	is-0-0	0	lobectomy	-	18m no rec
47	Ad	Performed	C	77	male	current	1120	35	2a-0-0	IB	lobectomy	-	33m no rec
48	Ad	Performed	C	67	male	past	500	15	1a-0-0	IA	wedge resection	+	32m no rec
49	Ad	Performed	C	71	male	current	800	10	1a-0-0	IA	lobectomy	-	2m death
50	Ad	Performed	C	69	male	past	2520	20	2a-1-0	IIA	lobectomy	+	22m no rec
51	Ad	Performed	Excluded	63	female	never	0	4	is-0-0	0	wedge resection	-	34m no rec
52	Ad	Performed	Excluded	59	female	never	0	25	2a-0-0	IB	lobectomy	-	15m rec
53	Ad	Performed	Excluded	74	male	current	800	10	1a-0-0	IA	lobectomy	+	32m no rec
54	Ad	Performed	Excluded	78	female	never	0	10	1a-0-0	IA	lobectomy	-	30m no rec
55	Ad	Performed	Excluded	64	female	past	172	25	1a-0-0	IA	lobectomy	-	29m no rec
56	Ad	Performed	Excluded	49	female	never	0	15	1a-0-0	IA	lobectomy	-	29m no rec
57	Ad	Performed	Excluded	82	male	past	550	25	1b-0-0	IA	lobectomy	-	27m no rec
58	Ad	Performed	Excluded	55	male	past	525	32	1b-0-0	IA	lobectomy	-	25m no rec
59	Ad	Performed	Excluded	71	male	current	1020	30	2a-0-0	IB	lobectomy	+	4m rec
60	Ad	Performed	Excluded	65	male	past	360	25	1a-0-0	IA	segmentectomy	-	24m no rec
61	Ad	Performed	Excluded	79	male	past	1640	13	is-0-0	0	lobectomy	-	13m no rec
62	Ad	Performed	Excluded	67	female	never	0	20	1a-0-0	IA	lobectomy	-	17m no rec
63	Ad	Performed	Excluded	67	female	never	0	25	2a-0-0	IB	lobectomy	-	17m no rec
64	Sq	Performed	A	68	male	past	1860	20	1a-0-0	IA	lobectomy	-	32m no rec
65	Sq	Performed	A	82	male	past	1100	60	2b-1-0	IIA	lobectomy	-	24m death
66	Sq	Performed	A	73	male	past	1800	33	2a-0-0	IB	pneumonectomy	+	16m no rec
67	Sq	Performed	A	77	male	past	675	20	2b-1-0	IIIB	lobectomy	+	14m no rec
68	Sq	Performed	B	78	male	current	1700	60	2a-2-0	IIIA	lobectomy	-	11m death
69	Sq	Performed	C	79	male	past	1640	27	1b-0-0	IA	lobectomy	-	13m no rec
70	Sq	Performed	Excluded	72	male	current	1500	140	3-2-0	IIIA	lobectomy	-	1m death
71	Sq	Performed	Excluded	81	male	past	870	35	2a-0-0	IB	lobectomy	-	31m no rec
72	Sq	Performed	Excluded	57	male	past	1060	60	2b-1-0	IIIB	lobectomy	+	29m no rec
73	Sq	Performed	Excluded	57	male	past	1060	15	2a-0-0	IB	wedge resection	+	29m no rec
74	Sq	Performed	Excluded	79	female	never	0	90	3-0-0	IIIB	lobectomy	-	12m death
75	Sq	Performed	Excluded	69	male	past	920	35	3-0-0	IIIB	lobectomy	+	19m death
76	Sq	Performed	Excluded	75	male	current	1080	32	3-0-0	IIIB	lobectomy	+	23m no rec
77	small	Performed	A	77	male	past	675	20	2a-0-0	IB	lobectomy	+	12m rec
78	small	Performed	Excluded	64	male	past	1200	35	2a-0-0	IB	lobectomy	+	29m no rec
79	small	Performed	Excluded	73	male	current	1100	18	2a-0-0	IB	lobectomy	-	13m no rec
80	other	Performed	Excluded	68	male	past	90	35	2a-0-1a	IV	lobectomy	+	31m no rec
81	other	Performed	A	83	male	current	2520	110	3-0-0	IIIB	lobectomy	-	4m death
82	other	Performed	A	67	male	past	1800	40	2a-2-0	IIIA	Incisional biopsy	+	2m rec
83	other	Performed	C	54	male	current	600	50	2a-0-1a	IV	lobectomy	+	4m death
84	other	Performed	C	78	female	current	780	47	3-0-0	IIIB	lobectomy	-	19m no rec
85	other	Performed	Excluded	60	female	never	0	30	1b-0-0	IB	lobectomy	-	23m rec
86	other	Performed	A	74	male	past	1350	28	1b-0-0	IA	lobectomy	-	29m death

Table S2. Mutations in IMA specimens.

Patients	Gene	Function	Protein	Position	Reference	Tumor Variant	allele fraction	Patients	Gene	Function	Protein	Position	Reference	Tumor Variant	allele fraction
Case 1	CTNNB1	Wnt	p.Leu427Phe	chr3:41275113	C	T	72%	Case 10	KRAS	RTK/RAS/RAF	p.Gly12Val	chr12:25398280	GCCAC	GCCAC/GCCAA	37%
	TP53	TP53/ Cell Cycle	p.Gly115Val	chr17:7578469	C	A	69%		SMARCA4	Chromatin	p.Phe1059Ser	chr19:11136983	T	T/C	27%
	KMT2D	Epigenetic	p.Pro3145Ser	chr12:49431706	G	A	27%		RBM10	Splicing	p.Trp936Ter	chrX:47045731	G	G/A	21%
	AKT3	RTK/RAS/RAF	p.Trp410Cys	chr1:243708833	C	A	26%		COBL	Other	p.Glu481Ala	chr7:51098571	T	T/G	20%
Case 2	SETD2	Epigenetic	p.Gln97Ter	chr3:47165837	G	A	22%	RASA1	RTK/RAS/RAF	p.Gln1034His	chr5:86686658	A	A/C	18%	
	KRAS	RTK/RAS/RAF	p.Gly12Val	chr12:25398284	C	A	35%	RASA1	RTK/RAS/RAF	p.Gln1035Pro	chr5:86686660	A	A/C	17%	
Case 3	ATM	TP53/ Cell Cycle	p.Leu2629fs	chr11:108203577	CTTATA	C	34%	SMAD4	TGFb-SMAD	p.Thr197Ala	chr18:48581285	A	A/G	17%	
	U2AF1	Splicing	p.Ser34Phe	chr21:44524456	G	G/A	33%	ATM	TP53/ Cell Cycle	p.Leu942Phe	chr11:108139322	C	C/T	17%	
	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	32%	MGA	Transcription	p.Lys2262Thr	chr15:42042590	A	A/C	17%	
	KMT2D	Epigenetic	p.Arg2645Ter	chr12:49433620	G	G/A	6%	MGA	Transcription	p.Phe665Cys	chr15:41989202	T	T/G	15%	
Case 4	SOX2	Transcription	p.Met294Ile	chr3:181431030	G	G/A	4%	NOTCH2	NOTCH	p.Val1686Ala	chr1:120465015	A	A/G	15%	
	SMAD4	TGFb-SMAD	spliceite_3	chr18:48591977	G	G/A	54%	TSC1	RTK/RAS/RAF	p.Leu92Phe	chr9:135801061	T	T/G	14%	
	KRAS	RTK/RAS/RAF	p.Gly12Arg	chr12:25398280	GCCACC	GCCACC/GCCACG	44%	KMT2A	Epigenetic	p.Cys3962Ser	chr11:18392852	T	T/A	14%	
	ATM	TP53/ Cell Cycle	p.Gln201Ter	chr11:108114784	C	C/T	40%	KMT2A	Epigenetic	p.Cys3962delinsTrpThr	chr11:18392854	TGG	TGG/GAC	14%	
Case 5	FGFR3	RTK/RAS/RAF	p.Ala636Thr	chr4:1807841	G	G/A	12%	ERBB3	RTK/RAS/RAF	p.Asp857Ala	chr12:56491678	A	A/C	13%	
	SOX2	Transcription	p.Met294Ile	chr3:181431030	G	G/A	6%	TSC1	RTK/RAS/RAF	p.Pro362Leu	chr9:135786445	G	G/A	13%	
	MGA	Transcription	p.Leu28Val	chr15:41961174	T	T/G	4%	ERBB3	RTK/RAS/RAF	p.Glu448Asp	chr12:56487198	A	A/C	12%	
	KRAS	RTK/RAS/RAF	p.Gly12Ala	chr12:25398280	GCCAC	GCCAC/GCCAG	35%	TSC2	RTK/RAS/RAF	p.Cys519Ser	chr16:2114384	T	T/A	12%	
Case 6	CDKN2A	TP53/ Cell Cycle	p.Trp15Ter	chr9:21974782	C	C/T	26%	ARID1A	Chromatin	p.Asn472Ser	chr1:27057707	A	A/G	12%	
	PIK3CA	RTK/RAS/RAF	p.His1047Leu	chr3:178952085	A	A/T	25%	FGFR2	RTK/RAS/RAF	p.Tyr780Cys	chr10:123239501	T	T/C	12%	
	FGFR3	RTK/RAS/RAF	p.Ala636Thr	chr4:1807841	G	G/A	8%	MET	RTK/RAS/RAF	p.Leu90fs	chr7:116339405	GC	GC/G	11%	
	PIK3CA	RTK/RAS/RAF	p.His1047Leu	chr3:178952085	A	A/T	39%	COBL	Other	p.Gln1004Lys	chr7:51095783	G	G/T	11%	
Case 7	NFE2L2	Oxidative	p.Leu30Phe	chr2:178098957	G	G/A	18%	KMT2D	Epigenetic	p.Val4078Ala	chr12:49426255	A	A/G	10%	
	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	18%	KMT2D	Epigenetic	p.Val4078fs	chr12:49426258	AG	AG/A	10%	
	MAP2K1	RTK/RAS/RAF	p.Lys168Arg	chr15:66735682	A	A/G	11%	EP300	Transcription	p.Met1989Thr	chr22:41573681	T	T/C	10%	
	TP53	TP53/ Cell Cycle	p.Arg280Thr	chr17:7577094	GGTCTCT	GTCTCT/GGTCTCG	9%	KMT2A	Epigenetic	p.Glu970Gly	chr11:18344783	A	A/G	7%	
Case 8	ATM	TP53/ Cell Cycle	p.Glu953Lys	chr11:108141809	G	G/A	8%	COBL	Other	p.Thr403Lys	chr7:51111278	G	G/T	6%	
	NOTCH2	NOTCH	p.Leu1689Phe	chr1:120465007	T	T/A	7%	NOTCH2	NOTCH	p.Ala862Val	chr1:120491644	G	G/A	6%	
	KMT2D	Epigenetic	p.Asp632Glu	chr12:49445570	G	G/C	6%	EPHA7	Other	p.Asp356Glu	chr6:94066691	G	G/C	5%	
	MGA	Transcription	p.Arg3038Trp	chr15:42059392	C	C/T	5%	KMT2D	Epigenetic	p.Thr5101Asn	chr12:49420447	G	G/T	5%	
Case 9	STK11	RTK/RAS/RAF	p.Pro221Leu	chr19:1220644	C	C/T	37%	SETD2	Epigenetic	p.Asp699Asn	chr3:47164031	C	C/T	5%	
	NOTCH1	NOTCH	p.Glu794Ter	chr9:139407560	C	C/A	5%	ARID2	Chromatin	p.Met877Ile	chr12:46244537	G	G/A	5%	
Case 10	CUL3	Oxidative	p.Ser585Cys	chr2:225360637	G	G/C	23%	MAP2K1	RTK/RAS/RAF	p.Gly77Ala	chr15:66727514	G	G/C	4%	
	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	23%	KMT2D	Epigenetic	p.Ala5100Pro	chr12:49420451	C	C/G	4%	
	NOTCH1	NOTCH	p.Gly1434Ser	chr9:139400048	C	C/T	5%	SETD2	Epigenetic	p.Arg620Ter	chr3:47164268	G	G/A	4%	
	KRAS	RTK/RAS/RAF	p.Gly12Cys	chr12:25398280	GCCACC	GCCACC/GCCACA	71%	Case 11	KRAS	RTK/RAS/RAF	p.Gly12Cys	chr12:25398280	GCCACC	GCCACC/GCCACA	56%
Case 9	EGFR	RTK/RAS/RAF	p.Ala16Val	chr7:55087017	C	C/T	23%	Case 12	KMT2A	Epigenetic	p.Cys3962Ser	chr11:18392852	T	T/A	4%
	ARID1A	Chromatin	p.Trp1844Ter	chr1:27105920	G	G/A	22%	Case 13	ERBB2	RTK/RAS/RAF	p.Trp614Arg	chr17:37873675	T	T/C	5%
	AKT1	RTK/RAS/RAF	p.Cys296Gly	chr14:105239659	A	A/C	8%	Case 14	KRAS	RTK/RAS/RAF	p.Gly12Val	chr12:25398280	GCCAC	GCCAC/GCCAA	18%
	FGFR3	RTK/RAS/RAF	p.Gly192Asp	chr4:1803223	G	G/A	6%	Case 15	MGA	Transcription	p.Met1236Ile	chr15:42021412	G	G/A	4%
	KMT2D	Epigenetic	p.Asp1749Glu	chr12:49437723	A	A/C	6%	Case 16	U2AF1	Splicing	p.Ser34Phe	chr2:144524456	G	G/A	29%
	SMARCA4	Chromatin	p.Leu724Phe	chr19:11121103	C	C/T	4%	Case 17	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	26%
	TSC2	RTK/RAS/RAF	p.Ala1238Thr	chr16:2131697	G	G/A	4%	Case 18	SMAD4	TGFb-SMAD	p.Pro298Ser	chr18:48584814	C	C/T	24%
	KRAS	RTK/RAS/RAF	p.Gly12Cys	chr12:25398280	GCCACC	GCCACC/GCCACA	56%	RBM10	Splicing	p.Arg831Leu	chrX:47044971	G	G/T	77%	
	TP63	NOTCH	p.Ser38Ala	chr3:189455578	T	T/G	32%	KEAP1	Oxidative	p.Glu149Lys	chr19:10610265	C	C/T	71%	
	ARID1A	Chromatin	p.Trp1844Ter	chr1:27105920	G	G/A	19%	KRAS	RTK/RAS/RAF	p.Gly12Cys	chr12:25398280	GCCACC	GCCACC/GCCACA	66%	
Case 11	KMT2D	Epigenetic	p.Thr2314Ile	chr12:49434612	G	G/A	4%	Case 19	ARID1A	Chromatin	p.Gly1469fs	chr1:27101116	A	A/AC	38%
	STK11	RTK/RAS/RAF	p.Trp15Ter	chr9:21974782	C	C/T	26%	Case 20	STK11	RTK/RAS/RAF	p.Arg297Ser	chr19:1221976	G	G/T	28%
	SMARCA4	Chromatin	p.Phe1059Ser	chr19:11136983	T	T/C	4%	Case 20	KRAS	RTK/RAS/RAF	p.Gly12Val	chr12:25398280	GCCAC	GCCAC/GCCAA	19%
	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	72%	Case 20	SMARCA4	Chromatin	p.Phe1059Ser	chr19:11136983	T	T/C	4%
Case 12	ATM	TP53/ Cell Cycle	p.Leu2544Pro	chr11:108202607	T	T/C	59%	Case 20	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	29%
	KRAS	RTK/RAS/RAF	p.Gly12Asp	chr12:25398280	GCCAC	GCCAC/GCCAT	29%	Case 20	PIK3CA	RTK/RAS/RAF	p.Asn370Ser	chr3:178922340	A	A/G	21%
	PIK3CA	RTK/RAS/RAF	p.Asn370Ser	chr3:178922340	A	A/G	21%	Case 20	KMT2D	Epigenetic	p.Asp2622Asn	chr12:49433689	C	C/T	14%
	SOX2	Transcription	p.Ser295Phe	chr3:181431032	C	C/T	5%	Case 20	SOX2	Transcription	p.Ser295Phe	chr3:181431032	C	C/T	5%
Case 13	SOX2	Transcription	p.Met294Ile	chr3:181431030	G	G/A	4%	Case 20	SOX2	Transcription	p.Met294Ile	chr3:181431030	G	G/A	4%

Table S3. Pathways affected in IMA and NMA by mutations with allele fractions  $\geq 20\%$ .

Pathway	IMA (n=20)	NMA (n=43)	p value
RTK/RAS/RAF	16 (80.0%)	30 (69.8%)	0.394
TP53/ Cell Cycle	5 (25.0%)	15 (34.9%)	0.433
Transcription	0 (0.0%)	3 (7.0%)	0.226
NOTCH	0 (0.0%)	3 (7.0%)	0.226
Epigenetic	1 (5.0%)	1 (2.3%)	0.573
Oxidative	3 (15.0%)	4 (9.3%)	0.503
Chromatin	3 (15.0%)	1 (2.3%)	0.055
Splicing	4 (20.0%)	7 (16.3%)	0.717
Wnt	1 (5.0%)	0 (0.0%)	0.139
TGFb-SMAD	3 (15.0%)	2 (4.7%)	0.157
Axon guidance	0 (0.0%)	1 (2.3%)	0.492
Other	0 (0.0%)	1 (2.3%)	0.492

Table S4. Sequencing targets.

No	Gene symbol	Chromosome	Number of Amplicons	Total Bases	Covered Bases	Overall Coverage
1	AKT1	chr14	26	1573	1497	95%
2	AKT2	chr19	27	1576	1543	98%
3	AKT3	chr1	30	1624	1624	100%
4	ARID1A	chr1	76	7058	6023	85%
5	ARID1B	chr6	75	6950	5965	86%
6	ARID2	chr12	71	5718	5643	99%
7	ASCL4	chr12	5	532	382	72%
8	ATM	chr11	147	9791	9439	96%
9	BRAF	chr7	37	2481	2224	90%
10	CDKN2A	chr9	9	962	612	64%
11	COBL	chr7	48	4151	3977	96%
12	CREBBP	chr16	96	7639	7071	93%
13	CTNNB1	chr3	32	2486	2486	100%
14	CUL3	chr2	42	2561	2495	97%
15	EGFR	chr7	60	4189	4135	99%
16	EP300	chr22	90	7555	7182	95%
17	EPHA7	chr6	44	3175	3154	99%
18	ERBB2	chr17	57	4080	3808	93%
19	ERBB3	chr12	59	4440	4374	99%
20	FGFR1	chr8	41	2825	2816	100%
21	FGFR2	chr10	43	2910	2842	98%
22	FGFR3	chr4	34	2752	2215	81%
23	FOXP2	chr7	36	2487	2469	99%
24	HRAS	chr11	11	683	683	100%
25	KEAP1	chr19	24	1925	1845	96%
26	KMT2D	chr12	192	17154	15854	92%
27	KRAS	chr12	10	737	681	92%
28	MAP2K1	chr15	18	1292	1239	96%
29	MET	chr7	59	4427	4396	99%
30	MGA	chr15	110	9428	9345	99%
31	MLL	chr11	144	12279	11875	97%
32	NF1	chr17	136	9161	9023	99%
33	NFE2L2	chr2	23	1868	1826	98%
34	NOTCH1	chr9	99	8008	7078	88%
35	NOTCH2	chr1	101	7809	7539	97%
36	NRAS	chr1	9	610	610	100%
37	PIK3CA	chr3	50	3407	3282	96%
38	PTEN	chr10	18	1302	1223	94%
39	RASA1	chr5	55	3412	3216	94%
40	RB1	chr13	55	3057	2902	95%
41	RBM10	chrX	48	3228	3079	95%
42	RIT1	chr1	13	771	771	100%
43	SETD2	chr3	91	7905	7663	97%
44	SLIT2	chr4	76	4972	4854	98%
45	SMAD4	chr18	24	1769	1715	97%
46	SMARCA4	chr19	74	5399	5055	94%
47	SOX2	chr3	9	964	883	92%
48	STK11	chr19	23	1392	1343	97%
49	TP53	chr17	22	1383	1351	98%
50	TP63	chr3	34	2360	2227	94%

51	TSC1	chr9	49	3705	3603	97%
52	TSC2	chr16	92	5834	5677	97%
53	U2AF1	chr21	15	880	870	99%

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