

SUPPLEMENT TABLE 1: Antibody information

Target	IHC			Western Blot		
	Company	Cat #	Dilution	Company	Cat #	Dilution
RB1	Cell Signaling	9309	1:1600	Cell Signaling	9309	1:1000
INSM1	Santa Cruz	sc-271408	1:400	Santa Cruz	sc-271408	1:500
YAP1	Cell Signaling	14074	1:400	Cell Signaling	4912	1:1000
ASCL1 (MASH1)	BD Pharmingen	556604	1:100	BD Pharmingen	556604	1:100
NEUROD1	Abcam	205300	1:500	Cell Signaling	4373	1:1000
POU2F3	Sigma	HPA019652	1:800	Sigma	HPA019652	1:500
ACTB				Sigma	A5441	1:10k
CCND1				Cell Signaling	55506	1:1000
CDK2				Santa Cruz	6248	1:1000
CDK4				Cell Signaling	12790	1:1000
CDK6				Cell Signaling	3136	1:1000
E2F1				Santa Cruz	251	1:1000
CDKN2A				Cell Signaling	4824	1:1000
pRB1-Ser780				Cell Signaling	8180	1:1000

SUPPLEMENT TABLE 2 : *RB1* LOF signature genes from Chen et al (reference 23)

Low expression in <i>RB1</i> -loss: Enriched in wt <i>RB1</i>	High expression in <i>RB1</i> -loss: Low in wt <i>RB1</i>
ALDH18A1	ACYP1
APOBEC3C	AKAP5
ARAP3	BTF3L4
ARPC1B	CAMK2N2
ARPC2	CAND2
AUP1	CCNE2
BAZ2A	CDKAL1
BECN1	CDKN2A
BMS1	CDKN2C
CAB39L	CLSPN
CCND1	COCH
CDADC1	CPE
CDK6	DAND5
CIB1	DCHS1
COG3	DEK
CTSB	DONSON
DDX21	EID2B
DDX54	ELF2
DGKA	FAM111B
DNAJA2	FANCL
DNPEP	FBLN7
DYRK4	GKAP1
E2F4	GLRB
ECD	GPR137C
EDEM1	H2AFV
EEF1D	HSD17B6
EIF3A	ID4
EIF3D	IQCC
ELF1	JAKMIP1
EPB41L2	KCND2
ESD	KCTD16
ETV4	KIAA1841
FNDC3A	KLHL2
GHITM	LHX2
GLUD1	MESP1
GSTO1	MNS1
GTF2F2	NEURL1B
H6PD	OSCP1
HIF1AN	PCSK1
HMGA2	PDIK1L
HMGXB3	PIK3R3
HOXB13	POU4F1
HPS6	RAD1
IGF2BP2	RIBC2

IKBKE	RNASEH2A
IMP4	RTN3
INTS6	SH3GL2
ITM2B	SLC36A4
KPNA3	SPSB4
LDB1	STMN1
LIF	TCTEX1D2
LRCH1	TEX9
M6PR	TIGD7
MCCC2	TTLL7
MED4	TXNDC16
MIPEP	UBR7
MMS19	UCHL1
MPG	USP1
MRPL35	ZBTB8A
MRPS31	ZNF254
MTHFD1L	ZNF347
MTRF1	ZNF367
NAB2	ZNF43
NADSYN1	ZNF528
NEK3	ZNF606
NIP7	ZNF610
NOB1	ZSCAN16
NOP16	ZSCAN18
NPAS2	
NUDT15	
NUFIP1	
OAF	
OGFR	
PDCD6IP	
PDE12	
PHF11	
PLD2	
POLD4	
POMP	
PUS1	
PVT1	
RB1	
RBM19	
RFT1	
RHBDF2	
RNF123	
RNF6	
RPL22L1	
SEC23IP	
SEC24C	

SETDB2	
SFT2D1	
SLC12A9	
SLC25A15	
SLC25A30	
SMAD3	
SMO	
SMURF1	
SMYD5	
SNHG4	
SPRY4	
STAT6	
SUCLA2	
SUGT1	
TBC1D22A	
TCOF1	
THG1L	
TM9SF3	
TNFRSF10B	
TOP1MT	
TPCN2	
TPT1	
TRADD	
WBP4	
WDFY2	
WDR59	
XPNPEP1	
XPO4	

SUPPLEMENT TABLE 3: H scores for all SCLC cases analyzed by IHC*

	PID	# cores	Site	RB	INSM1	ASCL1	NEUROD1	POU2F3	YAP1
TMA 0035	326	2	node	120	50	50	na	na	120
	553	4	brain	0	190	60	35	0	60
	551	2	node	5	180	40	na	na	0
	425	2	node	0	190	0	na	na	0
	424	2	node	0	190	170	20	na	10
	550	2	node	10	190	160	0	0	5
	549	2	lung	180	190	180	0	0	0
	548	2	brain	0	190	160	na	na	0
	543	2	lung	0	180	170	0	0	0
	541	2	lung	140	10	0	10	?	160
	458	2	lung	0	120	0	na	na	5
	519	2	lung	5	180	190	0	0	0
	556	2	lung	0	160	140	15	0	0
	482	2	lung	5	190	190	0	0	10
	557	2	pleura	0	190	20	na	na	0
	558	2	spine	0	20	5	0	0	0
	559	2	pleura	120	190	190	na	na	0
	475	2	brain	0	90	0	na	0	0
	555	4	brain	0	190	180	20	0	0
TMA 0047	48	1	lung	0	0	na	na	na	na
	277	2	trachea	na	na	na	na	na	na
	217	2	node	0	3	0	0	na	0
	?	2	node	0	270	270	60	30	3
	420	2	node	0	0	15	150	0	90
	246	4	mediastinum	180	0	90	240	0	0
	200	2	lung	0	10	na	na	na	na
	243	2	lung	90	240	0	0	0	0
	268	2	lung	0	150	na	na	na	na
	270	2	neck	0	240	225	0	0	0
	302	2	lung	0	120	na	na	na	na
	408	2	bronchus	0	40	na	na	0	0
	343	2	node	0	5	na	na	na	na
	374	2	bronchus	0	5	na	na	na	na
	394	2	lung	0	60	0	0	0	0
	283	2	node	0	0	0	na	0	0
	340	4	node	0	60	0	10	0	0
	508	2	diaphragm	3	240	na	na	na	na
	598	2	adrenal	0	240	270	15	3	60
	636	2	pleura	100	270	160	255	0	0
	639	4	node	0	285	na	na	na	na

	Cases		
Positives (H Score at least 20)	#	total evaluable	%
RB1	9	62	14.5
INSM1	51	62	82.2
ASCL1	36	51	70.5
NEUROD1	16	41	39
POU2F3	1	42	2.3
YAP1	7	53	20.7
RB1/YAP1	3	9	33.3
RB1/INSM1	7	9	77.7
RB1/ASCL1	7	9	77.7
RB1/NEUROD1	3	7	42.8
ASCL1/NEUROD1	13	31	41.9

Site	
brain	20
lung	16
node	13
bronchus	4
pleura	3
spine	2
trachea	1
mediastinum	1
neck	1
diaphragm	1
adrenal	1
liver	1

	649	2	bronchus	0	225	na	na	na	na
	665	2	brain	0	210	195	1	0	1
	669	2	brain	0	285	294	75	0	0
	671	2	lung	0	180	na	na	na	na
	677	2	bronchus	15	120	20	0	0	0
	693	2	lung	0	255	35	10	0	0
	697	2	lung	0	270	0	na	na	0
	703	2	spine	0	180	270	40	0	0
	662	2	node	0	60	0	0	0	0
	737	2	liver	na	na	195	2	0	0
TMA 0048	?	4	brain	0	180	na	160	6	0
	?	2	brain	0	0	0	30	0	0
	527	4	brain	15	50	110	0	0	2
	?	2	brain	0	0	na	na	0	0
	776	4	brain	225	120	40	0	15	6
	?	4	brain	0	70	40	285	0	0
	?	6	brain	10	270	270	240	0	0
	603	2	brain	0	85	180	0	0	70
	655	6	brain	0	270	285	3	0	4
Multiple TMAs	552	2	brain	5	190	180	0	0	0
	471	6	brain	180	285	270	270	0	40
	554	8	brain	5	255	270	0	0	0
	589	6	brain	0	270	190	285	6	30
	460	4	brain	0	240	180	180	0	0
	* All RB1 positives case highlighted in yellow								
	na = no tissue available for analysis								

SUPPLEMENT TABLE 4: PATIENT CHARACTERISTICS OF IHC (N=64) COHORT (8 missing)

	RB1: Positive (N=9)	RB1: Negative (N=47)	p-value
Age: mean (STD)	64.8 (4.1)	67.7 (9.9)	0.454
Sex: Male/Female (0 missing)	6/3	26/21	0.529
Race: White/Black (1 missing)	7/2	36/10	0.974
Smoking: No/Yes (0 missing)	2/7	1/46	0.014
Stage: Extensive/Limited (2 missing)	6/3	37/8	0.29
Stage: (6 missing)			
1,2	2	3	
3	1	2	0.285
4	6	36	

SUPPLEMENT TABLE 5: PATIENT CHARACTERISTICS OF GENOMIC (N=122) COHORT

	RB1: WT (N=37)	RB1: Mutant (N=85)	p-value
Age: mean (STD)	62.2 (11.4)	65.9 (9.4)	0.089
Sex: Male/Female (0 missing)	21/16	36/49	0.143
Race: White/Black (8 missing)	21/14	61/18	0.059
Smoking: No/Yes (3 missing)	3/33	5/78	0.644
Stage: Extensive/Limited (1 missing)	30/6	61/24	0.178
Stage: (22 missing)			
1,2	0	4	
3	2	7	0.283
4	30	57	

SUPPLEMENT TABLE 7: RB1 stained tumor cores with known *RB1* mutation status

TMA	Type SCLC	PID	<i>RB1</i> Mut status		Platform	Site	RB1 H score
0035	pure	482	mutant	Q384*	FM	lung	5
0047	pure	636	mutant	RB1-USP24 fusion	FM	pleura	100
	cSCLC	508	mutant	RB1 loss exons 9-11	FM	diaphragm	3
	pure	639	mutant	R467*	FM	node	0
	pure	649	wt		FM	bronchus	0
	pure	677	wt		FM	bronchus	15
	pure	693	mutant	G617fs*6	FM	lung	0
0048	cSCLC	776	wt		FM	brain	225

SUPPLEMENT TABLE 8											
Patient 2: RESPONDER											
Sample	Pre-Rx				Post-Rx				Patient 1: NON-RESPONDER		
Platform	TEMPUS xT				TEMPUS xT				FOUNDATTIONONE*CDx		
Site	Lymph node				Blood				Lung		
Biologically Relevant	TP53	p.T125T Splice variant- LOF	90.30%	TP53	p.T125T Splice region variant-LOF	62.10%	TP53	p.T124T Splice region variant-LOF	0.40%	TP53	C124R
	KEAP1	p.E493V Missense- LOF	80.50%							CREBBP	M783fs*21 - subclonal
										BCL2	Amp
										GATA6	Amp
										SOX2	Amp- equivocal
VUS	AXIN1	c.1115C>T p.P372L Splice region variant	87.80%	JAK2	c.3158A>G p.K1053R Missense	68.40%	ALK	c.3421G>A p. D1141N Missense	48.60%	AKT1	Amp
	SYNE1	c.1921C>T p.A6406V Missense	81.30%	ALK	c.3421G>A p.D1141N Missense	49.30%	JAK2	c.3158A>G p.K1053R Missense	47.30%	APC	V2781M
	HSPH1	c.211del p.R71fs Frameshift	79.60%	KMT2A (MLL)	c.212G>T p.G71V Missense	35.30%				ATM	G3029D
	GNAQ	c.606-3C>T Splice region variant	72.90%	EGFR	c.478G>C p.E160Q Missense	32.00%				CSF3R	T486M
	ZNF217	c.1260T>A p.C420* Stop gain	54.70%	PTPN11	c.1448-4G>A Splice region variant	31.80%				ESR1	R269C
	KMT2A (MLL)	c.212G>T p.G71V Missense	53.30%	KMT2A (MLL)	c.8041G>C p.D2681H Missense	19.50%				FLT1	K673E
	PTPN11	c.1448-4G>A Splice region variant	51.00%	PDGFRB	c.2919_2920delinsTT p.VD973VY Missense	0.40%				GABRA6	P49S
	EGFR	c.474_478delinsTGTGC p.NVE158NVQ Missense	47.90%							KMT2A (MLL)	P1987T
	AP2M1	c.1012C>T p.P338S Missense	35.80%							MLL2	K287E, V5400C
	TOP2A	c.2645G>C p.G882A Missense	28.30%							MYCN	A220S, I350T
	KMT2A (MLL)	c.8041G>C p.D2681H Missense	23.50%							NOTCH3	F1358V
										RB1	V84_L88del
									ROS1	W2145C	
									SMAD2	Amp	
									SMAD4	Amp	