S1 Table. Somatic hotspot mutations and germline polymorphisms used for SGZ validation

A. Somatic hotspot mutations in Fig 3A

Gene	Mutation	Germline calls	Somatic calls
AKT1	E17K	8	106
BRAF	V600†	12	398
BRAF	D594†	0	56
EGFR	S768I	0	16
EGFR	L858R	5	143
ERBB2	S310F	3	66
IDH1	R132H	13	144
KRAS	G13†	12	281
KRAS	G12†	82	2196
KRAS	Q61†	6	218
MAP2K1	K57†	0	22
NRAS	G13†	2	35
NRAS	G12†	7	79
NRAS	Q61†	20	279
PIK3CA	E542†	12	286
PIK3CA	H1047†	20	507
PIK3CA	E545†	13	493

† Includes all missense mutations of the codon

B. Germline polymorphisms in Fig 3A

Gene	Mutation	Germline calls	Somatic calls
GATA2	P161A	350	7
MAP3K1	S939C	638	55
NTRK1	G18E	365	3
BRCA2	K3326*	288	5
FANCF	A186V	275	2
PNRC1	A152V	268	5
GPR124	V1146A	244	10
TSC1	K587R	217	2
ZNF217	M410V	218	5
CREBBP	N1978S	183	3
BRIP1	V193I	179	2
CTCF	P315S	140	0
APC	I1307K	140	2
NOTCH2	R91L	141	6
RPTOR	A862T	128	3
ESR1	H6Y	125	3

TSHR	V721F	92	1
FAT3	A3418S	77	1
RAD52	S346*	59	1
PIK3C2G	*1446S	45	1