Table S1 Genomic alterations of the three ACC lesions.

Sample	Test id	Type	Gene	Gene.ID	AAChange	Chr.start	Chr.end	Ref
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	Mutant	PIK3R1	PIK3R1:NM	c.201dup(p.I68Yfs*8)	5:6758818	5:6758818	-
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	Mutant	LYN	LYN:NM_00	c.1079G>A(p.R360Q)	8:5691093	8:5691093	G
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	Mutant	SPOP	SPOP:NM_(	c.361C>T(p.R121W)	17:476964	17:476964	G
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	Mutant	SETD2	SETD2:NM_	c.4929C>G(p.N1643K)	3:4714303	3:4714303	G
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	Mutant	FBXW7	FBXW7:NM	c.1034C>T(p.T345I)	4:1532493	4:1532493	G
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	CNV	MCL1	.	.	.	.	.
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	MS	.	.	MSS	.	.	.
LLL	FB20090248-A3A8AA9XNF1-A001L000KA6W	TMB	.	.	.	.	.	.
RML	FB20090249-A3A8AA9XNF1-A001L000KA6W	Mutant	PIK3R1	PIK3R1:NM	c.201dup(p.I68Yfs*8)	5:6758818	5:6758818	-
RML	FB20090249-A3A8AA9XNF1-A001L000KA6W	MS	.	.	MSS	.	.	.
RML	FB20090249-A3A8AA9XNF1-A001L000KA6W	TMB	.	.	.	.	.	.
RLL	FB20090250-A3A8AA9XNF1-A001L000KA6W	MS	.	.	MSS	.	.	.
RLL	FB20090250-A3A8AA9XNF1-A001L000KA6W	TMB	.	.	.	.	.	.
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	DPYD	DPYD:NM_(	c.1627A>G(p.I543V)	1:9798139	1:9798139	T
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	ERCC1	ERCC1:NM_	c.354T>C(p.N118=)	19:459236	19:459236	A
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	ERCC2	ERCC2:NM_	c.2251A>C(p.K751Q)	19:458549	19:458549	T
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	NQO1	NQO1:NM_	c.559C>T(p.P187S)	16:697451	16:697451	G
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	TYMS 6bp	TYMS:NM_(	c.*450_*455delAAGTTA	18:673444	18:673449	TTAAAG
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	UGT1A1	UGT1A1:NM	c.211G>A(p.G71R)	2:2346691	2:2346691	G
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	SNP	GSTT1	.	.	.	.	.
Blood	PB20090247-C5C8AA9XNF1-A001L000KA6W	TMB	.	.	.	.	.	.

Alt	Hom.Het	ExonicFunc	rsID	AF	CopyNumb	Remarks	targetlevel	chemolevel	Rtlevel	ACMG	FilterCondi
T	het	frameshift_variant	.	29.75%	.	.	level3	.	.	.	.
A	het	missense_variant	rs2018956(	10.83%	.	.	level4	.	.	.	.
A	het	missense_variant	.	7.88%	.	.	level4	.	.	.	.
C	het	missense_variant	.	7.56%	.	.	level4	.	.	.	.
A	het	missense_variant	.	7.12%	.	.	level4	.	.	.	.
.	.	.	.	.	2.0894	.	level3	level2	level1	.	.
.	.	.	.	42.31%	.	.	.	.	.	.	.
.	.	.	.	41.51%	6.3	.	.	.	.	.	.
T	het	frameshift_variant	.	23.71%	.	.	level3	.	.	.	.
.	.	.	.	9.62%	.	.	.	.	.	.	.
.	.	.	.	76.60%	2.1	.	.	.	.	.	.
.	.	.	.	38.46%	.	.	.	.	.	.	.
.	.	.	.	100%	0	.	.	.	.	.	.
C	hom	missense_variant	rs1801159	100.00%	.	.	.	level1	.	.	.
G	hom	synonymous_variant	rs11615	99.93%	.	.	.	level1	.	.	.
G	het	missense_variant	rs13181	51.82%	.	.	.	level1	.	.	.
A	hom	missense_variant	rs1800566	99.94%	.	.	.	level1	.	.	.
-	hom	3_prime_UTR_variant	rs1512643(	84.56%	.	.	.	level1	.	.	.
A	het	missense_variant	rs4148323	49.16%	.	.	.	level1	.	.	.
.	hom	.	.	.	.	.	.	level1	.	.	.
.	.	.	.	85.95%	1.1	.	.	.	.	.	.

DP(ref:alt)	NormalID	NormalAF	NormalDP(	Hotspot	Strand	CLNSIG	CLNREVSTA	CLNDNINCL	CLINID	BRCAClass	CosmicID	Cosmic.Occ
605(425:18	BC2009024	0.00%	54(54:0)	NHS	.	.	.	.	.	.	.	.
360(321:39	BC2009024	0.00%	79(79:0)	NHS	.	.	.	.	.	.	.	.
571(526:45	BC2009024	0.00%	124(124:0)	NHS	.	Uncertain_s	no_assertio	.	694168	.	COSM2698	1(biliary_tr
357(330:27	BC2009024	0.00%	46(46:0)	NHS	.	.	.	.	.	.	.	.
674(626:48	BC2009024	0.00%	112(112:0)	NHS	.	.	.	.	.	.	COSM6993	1(oesophag
.	.	.	.	.	.	.	.	.	.	.	.	.
52	.	.	.	.	.	.	.	.	.	.	.	.
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329(251:78	BC2009024	0.00%	54(54:0)	NHS	.	.	.	.	.	.	.	.
52	.	.	.	.	.	.	.	.	.	.	.	.
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52	.	.	.	.	.	.	.	.	.	.	.	.
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1664(0:166	BC2009024	100.00%	107(0:107)	NHS	.	Benign/Like	criteria_prc	.	100092	.	COSM3747	1(liver);1(la
1401(1:140	BC2009024	100.00%	79(0:79)	NHS	.	drug_respo	reviewed_b	.	225945	.	.	.
1507(726:7	BC2009024	53.66%	41(19:22)	NHS	.	Benign	criteria_prc	.	134105	.	COSM4132	45(haemato
1709(1:170	BC2009024	100.00%	85(0:85)	NHS	.	drug_respo	reviewed_b	.	16809	.	COSM1480	1(breast);1(
1101(170:9	BC2009024	92.31%	65(5:60)	NHS	.	drug_respo	reviewed_b	.	375663	.	.	.
1957(995:9	BC2009024	49.57%	117(59:58)	NHS	.	drug_respo	reviewed_b	.	12280	.	COSM4415	1(haematop
.	.	.	.	.	.	.	.	.	.	.	.	.
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HGMD_clas	Variant_effe	InterVar_Cl	1000g	1000gEAS	ExAC_ALL	ExAC_EAS	gnomAD_e	gnomAD_e	gnomAD_g	gnomAD_g	GS_ALL	SIFT.score
.	.	Likely path	.	.	.	.	.	.	.	.	.	.
.	.	Uncertain s	.	.	4.71E-05	0	4.47E-05	0	.	.	.	0.353
.	.	Uncertain s	.	.	.	.	.	.	.	.	.	0.001
.	.	Uncertain s	.	.	.	.	.	.	.	.	.	0.028
.	.	Uncertain s	.	.	.	.	.	.	.	.	.	0.001
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DFP	?/.	Benign	0.184904	0.2659	0.1915	0.2531	0.1968	0.2528	0.1754	0.2427	0.462789	0.111
.	-/.	Benign	0.66893	0.7381	0.5159	0.7385	0.499	0.7342	0.5425	0.7413	0.916168	.
DFP	-/.	Benign	0.236621	0.0764	0.3269	0.0759	0.3262	0.0746	0.3203	0.0749	0.165098	0.59
DFP	.	Uncertain s	0.288938	0.4187	0.2501	0.4515	0.2521	0.4567	0.2066	0.4625	0.689478	0.176
DFP	.	Benign	0.492013	0.6944	.	.	.	.	0.3854	0.6977	0.84089	.
DFP	+/+	Uncertain s	0.034345	0.1379	0.0223	0.1557	0.0221	0.1539	0.0149	0.1434	0.338751	0.041
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SIFT.pred	PolyPhen.s	PolyPhen.p	CADD_phre	GERP++_RS	OMIM_Inhe	OMIM_Link	InterVar_A(	Chr.start_r	Chr.end_ru	VCFKEY	HGVS3aa	HGVSg
.	.	.	.	.	Autosomal	https://ww	PVS1; PM2	5:6758818	5:6758818	5,6758818	c.201dup(p	5:g.675881
T	0.005	B	23.3	5.52	.	.	PM1; PM2	8:5691093	8:5691093	8,5691093	c.1079G>A	8:g.569109
D	0.948	D	33	4.5	.	.	PM1; PM2;	17:476964	17:476964	17,476964	c.361C>T(p	17:g.47696
D	0.999	D	23.6	0.798	Autosomal	https://ww	PM1; PM2	3:4714303	3:4714303	3,4714303	c.4929C>G	3:g.47143C
D	1	D	29.2	6.05	.	.	PM1; PM2;	4:1532493	4:1532493	4,1532493	c.1034C>T(	4:g.153249
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.	.	.	.	.	Autosomal	https://ww	PVS1; PM2	5:6758818	5:6758818	5,6758818	c.201dup(p	5:g.675881
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T	0	B	9.639	-3.13	Autosomal	https://ww	PM1; BA1; I	1:9798139	1:9798139	1,9798139	c.1627A>G	1:g.979813
.	.	.	.	.	Autosomal	https://ww	BA1; BS1; B	19:459236	19:459236	19,459236	c.354T>C(p	19:g.45923
T	0.001	B	10.56	4.29	Autosomal	https://ww	BA1; BS1; B	19:458549	19:458549	19,458549	c.2251A>C(	19:g.45854
T	0.999	D	32	5.41	.	.	PM1; BP1	16:697451	16:697451	16,697451	c.559C>T(p	16:g.69745
.	.	.	.	.	.	.	BA1; BS1	18:673447	18:673452	18,673443	c.*450_*45	18:g.67344
D	0.625	P	23.7	5.14	;Autosomal	https://ww	BS1	2:2346691	2:2346691	2,2346691	c.211G>A(p	2:g.234669
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BrkpFusion	BrkptType	TumorRefer	TumorSplit	TumorVaria	TumorSplit	Cosmic_Fus	CC_Tumour	Orientation	Column1
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