Supplementary Materials

Whole-Exome and RNA-Sequencing Analyses of Acinic Cell Carcinomas of the Breast

Beca et al.

SUPPLEMENTARY METHODS

Subjects and samples

Following Institutional Review Boards approval formalin-fixed paraffin embedded tissue blocks of acinic cell carcinomas (ACCs) of the breast were retrieved from the archives of the Department of Pathology of the Nottingham City Hospital/Nottingham University Hospitals NHS Trust. Estrogen receptor (ER) and HER2 status was evaluated following the ASCO/CAP guidelines[1, 2]. Informed consent was obtained according to the the protocol approved by the local Institutional Review Board (IRB). Cases were reviewed by three pathologists (E.P., E.G-R. and J.S.R.F.), classified as breast ACCs following the criteria put forward by the World Health Organization[3], and graded according to the Nottingham grading system[4]. Immunohistochemical assessment of MLH1 expression was performed on a Leica Bond III automated stainer platform (Leica, Buffalo Grove, IL) using the anti-MLH1 monoclonal antibody (clone ES05; catalogue #: 26408; Leica Biosystems, Newcastle, UK) at a 1:500 dilution for 30 minutes following EDTA-based high pH epitope retrieval. The standard platform-associated polymeric detection kit (Refine, Leica) was used as secondary reagent. Positive and negative controls were included in each slide run. For MLH1 immunohistochemical analysis, a case was considered interpretable if MLH1 expression could be detected in stromal and/or inflammatory cells (i.e. internal positive control).

Whole-exome sequencing analysis

DNA samples derived from microdissected tumor and normal tissue from ACCs were subjected to whole-exome sequencing (WES) at the Integrated Genomics Operations (IGO) of Memorial Sloan Kettering Cancer Center (MSKCC) using validated protocols, as previously described.[5, 6] Reads were aligned to the reference human genome GRCh37 using the Burrows-Wheeler Aligner (BWA, v.0.7.10)[7]. Local realignment, duplicate removal, and base quality recalibration were performed using the Genome Analysis Toolkit (GATK, v3.1.1).[8] Sequencing

data were analyzed as previously described.[5, 6] In brief, somatic single nucleotide variants (SNVs) were detected by MuTect (v1.0.0)[9], small insertion and deletion (indels) by Strelka (v.2.0.15),[10] VarScan2 (v.2.3.7),[11] Lancet (v1.0.0)[12] and Scalpel (v0.5.53)[13]. SNVs and indels with a >1% global minor allele frequency in ExAC[14] were excluded. We additionally filtered for the FFPE pooled normal passenger mutations by 1) removing mutations with > 1% global minor allele frequency in gnomAD[15], 2) removing the mutations with a normal locus depth of less than 10 and 3) include only mutation in both gnomAD and ExAC. ABSOLUTE (v1.0.6)[16] was employed to determine the cancer cell fraction (CCF) of each mutation. FACETS[17] was used to determine copy number alterations and whether genes harboring a somatic mutation were targeted by loss of heterozygosity as previously described[5, 6]. Large-scale state transitions (LST) score[18], NtAI score[19] and Myriad score[20] were calculated as genomic features of homologous recombination DNA repair deficiency as previously described[21]. Mutations affecting hotspot codons were annotated according to Chang et al.[22] Mutational signatures were defined using Sigma Multivariate Analysis (SigMA)[23] using all synonymous and non-synonymous mutations. Microsatellite instability was quantified using MSIsensor[24], as previously described[25].

RNA-sequencing and fusion gene identification

RNA extracted from all three ACCs included in this study was subjected to RNA-sequencing at MSK's IGO using validated protocols[26, 27]. In brief, paired-end RNA-sequencing was performed with 2x100 bp cycles on an Illumina HiSeq2000. We identified read pairs supporting fusion transcripts using INTEGRATE[28], deFuse[29] and FusionCatcher[30]. Fusion genes and read-through candidates that were detected in a set of 297 normal samples from The Cancer Genome Atlas (TCGA)[31] were excluded to account for alignment artifacts and normal transcriptional variants. Remaining candidate fusions were annotated using OncoFuse[32] to define their oncogenic potential. Additionally, the presence of candidate fusion

genes was inferred on the tumor fusion gene data portal[33], which comprises a list of 20,731 fusion genes across 33 cancer types (n=9,950).

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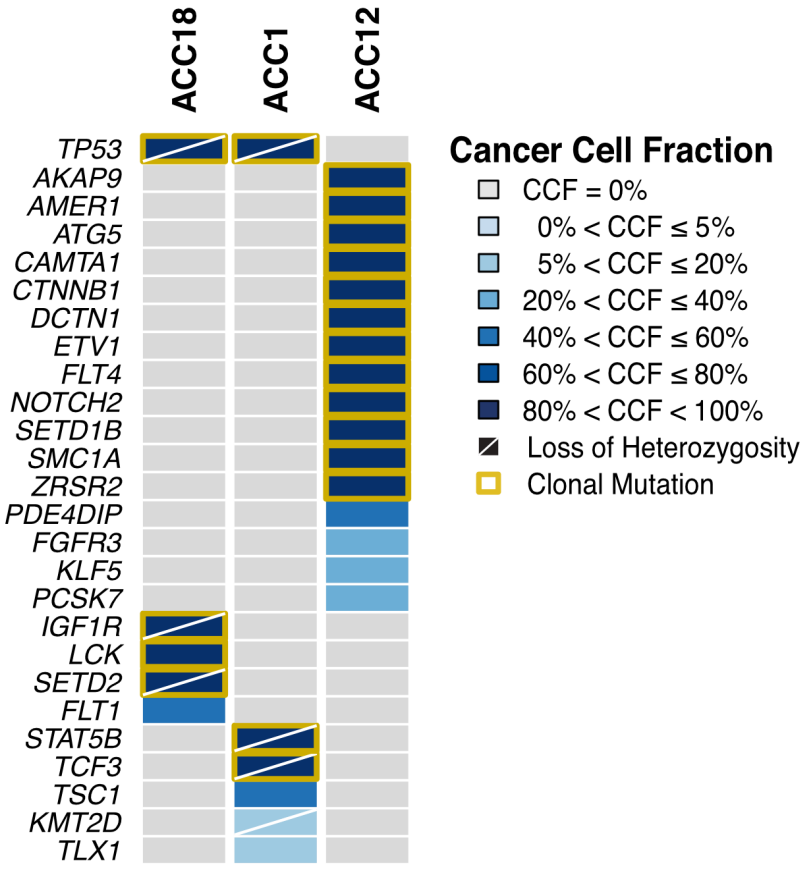
Supplementary Figure 1



Supplementary Figure 1. Cancer cell fractions of non-synonymous somatic mutations affecting cancer-related genes identified in the Acinic Cell Carcinomas (ACCs) of the breast by whole-exome sequencing. Cancer cell fractions (CCFs) and clonality of non-synonymous somatic mutations affecting cancer related genes identified in ACCs (n=3) using whole-exome sequencing. Clonal mutations are depicted by a yellow box.

Supplementary Table 1. Clinicopathologic characteristics of the Acinic Cell Carcinomas of the breast included in this study

Case ID	Age at diagnosis (years)	Growth pattern	Tubule formation	Nuclear pleomorphism	Mitotic count	Histologic grade*	ER status	HER2 status (IHC/FISH)
ACC1	49	MIcroglandular	1	3	1	1	Negative	Negative
ACC12	42	Microglandular	2	2	1	1	Negative	Negative
ACC18	N/A	Microglandular and hypernephroid	1	1	1	1	Negative	Negative

*Nottingham grading system. ER, estrogen receptor; FISH, fluorescence *in situ* hybridization; IHC, immunohistochemistry; N/A, not available.

Supplementary Table 2: Fusion genes identified by RNA-sequencing analysis of Acinic Cell Carcinomas of the breast

Case ID	Fusion Caller	5' Gene	3' Gene	5' Mapping	3' Mapping	Fusion Type	Crossing Reads	Encompassing Reads	In Frame	Driver Probability (Oncofuse)	TCGA fusion data portal
ACC1T	STAR-Integrate	*PIK3AP1*	*CRTAC1*	chr10: 98376396-	chr10: 99771094-	Intra-Chromosomal	4	11	No	0.03893	Absent
ACC1T	STAR-Integrate, Defuse	*SLC12A2*	*PRRC1*	chr5: 127450371+	chr5: 126859150+	Intra-Chromosomal	1	7	No	0.28698	Absent
ACC1T	STAR-Integrate	*ZNF432*	*ZNF841*	chr19: 52543737-	chr19: 52570859-	Intra-Chromosomal	1	7	No	0.83258	Absent
ACC1T	STAR-Integrate	*PTGES3L-AARSD1*	*BRCA1*	chr17: 41116123-	chr17: 41258550-	Intra-Chromosomal	1	4	No	0.52748	Absent
ACC1T	STAR-Integrate	*PRRC2C*	*GORAB*	chr1: 171454873+	chr1: 170508350+	Intra-Chromosomal	1	2	No	0.02169	Absent
ACC1T	STAR-Integrate	*TC2N*	*FBLN5*	chr14: 92302712-	chr14: 92403542-	Intra-Chromosomal	1	2	No	0.19163	Present (Breast cancer, 2/1119)
ACC1T	Defuse	*JMJD1C*	*REEP3*	chr10: 65140239-	chr10: 65281495-	Intra-Chromosomal	7	13	No	0.07933	Absent
ACC1T	Defuse	*URI1*	*LTBP4*	chr19: 30453087+	chr19: 41111646-	Intra-Chromosomal	7	9	No	0.0232	Absent

Supplementary Table 3: Whole-exome sequencing statistics.

Case ID	Tissue type (Sample ID)	Total reads	Mean target coverage (X)	Target bases 2X	Target bases 50X	Target bases 100X
ACC1	Tumor (ACC1-T)	316,773,539	276.31	99.84	97.27	88.57
	Normal (ACC1-N)	108,277,019	22.01	99.53	02.40	00.01
ACC12	Tumor (ACC12-T)	267,776,663	107.52	99.73	87.51	54.14
	Normal (ACC12-N)	181,406,979	90.96	99.80	74.66	39.57
ACC18	Tumor (ACC18-T)	268,448,663	226.98	99.82	97.26	87.97
	Normal (ACC18-N)	158,170,351	115.07	99.79	74.66	39.57

Supplementary Table 4: Non-synonymous somatic mutations identified in the Acinic Cell Carcinomas of the breast by whole-exome sequencing.

Sample ID	Gene symbol	Aminoacid change	Chromosome	Genomic position	Reference allele	Alternate allele	Type of mutation	Depth at mutation (X)	Mutant allele fraction	HOTSPOT	Cancer Cell Fraction (CCF)	Probability of mutation being clonal	Upper bound of 95% confidence interval for CCF	Lower bound of 95% confidence interval for CCF	Clonal status	Mutation Taster	CHASM (breast)	PROVEAN	FATHMM	Loss of heterozygosity (LOH)	Pathogenicity	Cancer Gene Census	Kandoth et al	Cancer5000-S genes (Lawrence et al)
ACC12T	LRRC47	p.P567R	1	3697704	G	C	Missense	104	23.1%	.	93.0%	0.77127	1	0.618570358	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	CAMTA1	p.T959M	1	7737755	C	T	Missense	84	26.2%	.	100.0%	0.83882	1	0.659513351	Clonal	D	Passenger	D	T	.	Passenger	Yes	No	No
ACC12T	RERE	p.D484G	1	8424895	T	C	Missense	65	24.6%	.	100.0%	0.78715	1	0.584067686	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	UBE4B	p.N459I	1	10179608	A	T	Missense	80	21.3%	.	86.0%	0.68133	0.988853263	0.533304445	Clonal	D	Driver	N	T	.	Likely pathogenic	No	No	No
ACC12T	MFN2	p.F537V	1	12065881	T	G	Missense	76	19.7%	.	80.0%	0.59617	0.984096687	0.484617606	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	C1orf134	p.G18E	1	16555986	C	T	Missense	45	11.1%	.	45.0%	0.12729	0.891671533	0.194139096	Subclonal	N	Passenger	.	.	.	Passenger	No	No	No
ACC12T	CROCC	p.R903S	1	17275018	C	A	Missense	8	37.5%	.	100.0%	0.77209	1	0.326804072	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	GRHL3	p.P480H	1	24671406	C	A	Missense	47	53.2%	.	100.0%	0.94827	1	0.830192839	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SZT2	p.R2677Q	1	43908539	G	A	Missense	125	4.8%	.	19.0%	0	0.40300711	0.086327562	Subclonal	D	Passenger	N	.	.	Passenger	No	No	No
ACC12T	CCDC17	p.E7Q	1	46089563	C	G	Missense	69	56.5%	.	100.0%	0.92667	1	0.887632462	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	BEND5	p.R198H	1	49224724	C	T	Missense	97	18.6%	.	75.0%	0.47836	0.975482438	0.480098987	Subclonal	D	Passenger	N	.	.	Passenger	No	No	No
ACC12T	CC2D1B	p.H680Y	1	52821892	G	A	Missense	36	47.2%	.	100.0%	0.94593	1	0.75456527	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	TTC22	p.A400V	1	55247427	G	A	Missense	59	28.8%	.	100.0%	0.84613	1	0.64930179	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	PROK1	p.X24_splice	1	110993912	T	C	Splice Site	83	12.0%	.	49.0%	0.03966	0.829153407	0.266895099	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACC12T	NOTCH2	p.P2359A	1	120458270	G	C	Missense	58	58.6%	.	100.0%	0.89747	1	0.87576987	Clonal	D	Passenger	N	D	.	Likely pathogenic	Yes	No	No
ACC12T	PDE4DIP	p.M534I	1	144917502	C	T	Missense	156	14.1%	.	57.0%	0.01633	0.821082936	0.380348347	Subclonal	D	Passenger	.	T	.	Passenger	Yes	No	No
ACC12T	PRPF3	p.D249E	1	150307424	C	G	Missense	91	18.7%	.	76.0%	0.49976	0.977224994	0.476335584	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	LINGO4	p.R301Q	1	151774279	C	T	Missense	72	45.8%	.	100.0%	0.95557	1	0.850915465	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	KIAA0907	p.R168W	1	155896910	G	A	Missense	113	23.9%	.	97.0%	0.80476	1	0.650974033	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	OR10J5	p.G16E	1	159505751	C	T	Missense	81	30.9%	.	94.0%	0.83174	1	0.636804105	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	IGSF9	p.R637G	1	159900134	G	C	Missense	59	15.3%	.	62.0%	0.30633	0.952975858	0.327957906	Subclonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ZNF648	p.R406C	1	182025930	G	A	Missense	61	36.1%	.	100.0%	0.86889	1	0.753441227	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	KIF21B	p.R130W	1	200977956	G	A	Missense	135	36.3%	.	100.0%	0.58139	1	0.863615511	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	C1orf198	p.S134N	1	230979626	C	T	Missense	111	27.0%	.	100.0%	0.87219	1	0.718562011	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	WDFY4	p.S1001R	10	49984932	A	C	Missense	93	32.3%	.	100.0%	0.88589	1	0.775505638	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	C10orf90	p.R152H	10	128193314	C	T	Missense	135	28.9%	.	100.0%	0.90254	1	0.779371755	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	CD151	p.C243R	11	838157	T	C	Missense	165	7.3%	.	29.0%	0	0.492465282	0.16623282	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	C11orf89	p.P81L	11	1911573	G	A	Missense	108	45.4%	.	100.0%	0.9569	1	0.892132139	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	WEE1	p.A577T	11	9608345	G	A	Missense	71	25.4%	.	100.0%	0.81	1	0.614624459	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	F2	p.K517E	11	46751006	A	G	Missense	54	51.9%	.	100.0%	0.95456	1	0.842818315	Clonal	N	Passenger	N	D	.	Passenger	No	No	No
ACC12T	TMEM109	p.R217*	11	60689554	C	T	Nonsense	50	8.0%	.	32.0%	0.02168	0.752130507	0.126802228	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACC12T	P2RY2	p.P189S	11	72945769	C	T	Missense	183	24.0%	.	97.0%	0.83695	1	0.715905721	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	PCSK7	p.S550R	11	117079654	A	T	Missense	133	8.3%	.	33.0%	0.00002	0.570307875	0.185579883	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	OR10G9	p.K295Q	11	123894602	A	C	Missense	71	7.0%	.	29.0%	0.00149	0.620826377	0.121251915	Subclonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	PKNOX2	p.T84M	11	125255470	C	T	Missense	25	56.0%	.	100.0%	0.92603	1	0.738922082	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	WNT5B	p.R262W	12	1755122	C	T	Missense	167	28.1%	.	100.0%	0.90915	1	0.79372208	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	BCAT1	p.E360K	12	24985659	C	T	Missense	59	49.2%	.	100.0%	0.95895	1	0.842107346	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SHMT2	p.R236H	12	57626348	G	A	Missense	87	5.7%	.	23.0%	0.00006	0.511683027	0.097828269	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ALX1	p.R64L	12	85674230	G	T	Missense	53	47.2%	.	100.0%	0.95465	1	0.817082265	Clonal	D	Driver	N	D	.	Likely pathogenic	No	No	No
ACC12T	NTN4	p.N239D	12	96131793	T	C	Missense	142	26.1%	.	100.0%	0.87327	1	0.732525923	Clonal	N	Passenger	N	T	.	Passenger	No	No	Yes
ACC12T	TUBA3C	p.V437M	13	19748047	C	T	Missense	71	12.7%	.	51.0%	0.09091	0.87773244	0.272505822	Subclonal	N	Passenger	N	D	.	Passenger	No	No	No
ACC12T	ZMYM5	p.D59V	13	20426145	T	A	Missense	71	12.7%	.	51.0%	0.09091	0.87773244	0.272505822	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	POMP	p.R91C	13	29246482	C	T	Missense	93	5.4%	.	22.0%	0.00002	0.479814202	0.091230479	Subclonal	D	Passenger	D	.	.	Passenger	No	No	No
ACC12T	DIAPH3	p.P596L	13	60545158	G	A	Missense	22	54.5%	.	100.0%	0.92797	1	0.70478624	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	KLF5	p.G429D	13	73649936	G	A	Missense	197	6.1%	.	25.0%	0	0.414027891	0.138282106	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	TRAV34	p.G110R	14	22676016	G	A	Missense	8	37.5%	.	100.0%	0.77209	1	0.326804072	Clonal	.	Passenger	.	.	.	Passenger	No	No	No
ACC12T	SFTA3	p.P54A	14	36946277	G	C	Missense	70	54.3%	.	100.0%	0.94812	1	0.882184492	Clonal	N	Passenger	D	.	.	Passenger	No	No	No
ACC12T	AREL1	p.M618T	14	75136413	A	G	Missense	63	28.6%	.	100.0%	0.84879	1	0.656609563	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ATXN3	p.G306R	14	92537354	C	G	Missense	55	50.9%	.	100.0%	0.9566	1	0.841164765	Clonal	P	Passenger	N	T	.	Passenger	No	No	No
ACC12T	IGHV3-9	p.Y114H	14	106552299	A	G	Missense	20	95.0%	.	100.0%	0.00122	1	0.828467066	Subclonal	.	Passenger	.	.	.	Passenger	No	No	No
ACC12T	UBE3A	p.Q729R	15	25599778	T	C	Missense	49	38.8%	.	100.0%	0.89389	1	0.742913399	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	MAP1A	p.A2717V	15	43821962	C	T	Missense	97	24.7%	.	100.0%	0.81898	1	0.649740506	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SPG11	p.R2161W	15	44861700	G	A	Missense	20	40.0%	.	100.0%	0.87428	1	0.569301114	Clonal	D	Driver	D	D	.	Likely pathogenic	No	No	No
ACC12T	SRL	p.R341H	16	4242554	C	T	Missense	164	6.7%	.	27.0%	0	0.465344901	0.149453192	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	CCDC113	p.R81H	16	58287915	G	A	Missense	115	20.9%	.	84.0%	0.65542	0.987546426	0.570095261	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	DHX38	p.G259D	16	72132837	G	A	Missense	99	20.2%	.	82.0%	0.61382	0.985223214	0.531844456	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SPG7	p.A401P	16	89598921	G	C	Missense	24	16.7%	.	67.0%	0.50639	0.977136326	0.254316798	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	DLG4	p.A690T	17	7095249	C	T	Missense	91	5.5%	.	22.0%	0.00002	0.489957634	0.093197975	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	PFAS	p.P132H	17	8158830	C	A	Missense	34	23.5%	.	95.0%	0.71447	1	0.44803285	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	CASC3	p.Q672H	17	38325627	G	C	Missense	57	36.8%	.	100.0%	0.87371	1	0.750269744	Clonal	D	Passenger	D	.	.	Passenger	No	No	No
ACC12T	TBKBP1	p.R160H	17	45775986	G	A	Missense	46	50.0%	.	100.0%	0.95378	1	0.81160306	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ITGB4	p.E957*	17	73738749	G	T	Nonsense	182	26.4%	.	100.0%	0.89397	1	0.770630262	Clonal	A	.	.	.	.	Passenger	No	No	No
ACC12T	NOTUM	p.A385V	17	79912162	G	A	Missense	50	16.0%	.	65.0%	0.39512	0.965965934	0.329956002	Subclonal	D	Passenger	D	.	.	Passenger	No	No	No
ACC12T	DCC	p.E1414G	18	51053116	A	G	Missense	48	22.9%	.	93.0%	0.7224	1	0.49545562	Clonal	D	Driver	D	T	.	Likely pathogenic	No	No	No
ACC12T	PPAP2C	p.R284W	19	281468	G	A	Missense	83	47.0%	.	100.0%	0.96171	1	0.872609509	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	PRAM1	p.V76F	19	8564466	C	A	Missense	27	22.2%	.	90.0%	0.67005	0.988292041	0.381263636	Clonal	P	Passenger	N	T	.	Passenger	No	No	No
ACC12T	OR1M1	p.V69I	19	9204125	G	A	Missense	71	7.0%	.	21.0%	0.00001	0.466531814	0.090186697	Subclonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACC12T	CACNA1A	p.P1177R	19	13397340	G	C	Missense	19	78.9%	.	100.0%	0.32816	1	0.780339475	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ILVBL	p.R275H	19	15230319	C	T	Missense	28	39.3%	.	100.0%	0.88849	1	0.637951659	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	CPAMD8	p.S523Y	19	17091465	G	T	Missense	100	6.0%	.	24.0%	0.00002	0.50024921	0.109708106	Subclonal	D	Passenger	.	.	.	Passenger	No	No	No
ACC12T	KIRREL2	p.G38W	19	36348297	G	T	Missense	60	41.7%	.	100.0%	0.92201	1	0.800304103	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	ZNF793	p.R330Q	19	38028549	G	A	Missense	89	5.6%	.	23.0%	0.00004	0.500578249	0.095385221	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	FAM98C	p.S205L	19	38896042	C	T	Missense	66	53.0%	.	100.0%	0.95414	1	0.871683168	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	GSK3A	p.A399T	19	42736738	C	T	Missense	87	17.2%	.	70.0%	0.37671	0.964684196	0.42776432	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	NTN5	p.X274_splice	19	49167550	C	T	Splice Site	51	13.7%	.	56.0%	0.23824	0.937439486	0.271729176	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACC12T	PPFIA3	p.R1021Q	19	49651973	G	A	Missense	87	5.7%	.	23.0%	0.00006	0.511683027	0.097828269	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	CD37	p.I71T	19	49840235	T	C	Missense	123	26.8%	.	100.0%	0.87634	1	0.729244406	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	NLRP2	p.A801T	19	55501424	G	A	Missense	45	53.3%	.	100.0%	0.94703	1	0.824422721	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ZNF444	p.A310V	19	56671515	C	T	Missense	33	24.2%	.	98.0%	0.7273	1	0.456479995	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SIX3	p.A72P	2	45169457	G	C	Missense	31	12.9%	.	52.0%	0.30987	0.951623229	0.204258948	Subclonal	N	Passenger	N	D	.	Passenger	No	No	No
ACC12T	DCTN1	p.R1049Q	2	74592252	C	T	Missense	22	63.6%	.	100.0%	0.86024	1	0.751358919	Clonal	D	Passenger	N	T	.	Passenger	Yes	No	No
ACC12T	ARHGEF4	p.N188D	2	131785652	A	G	Missense	22	18.2%	.	74.0%	0.55757	0.981210971	0.271623581	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	TTN	p.T23021I	2	179442000	G	A	Missense	87	25.3%	.	100.0%	0.82388	1	0.645513038	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ANKRD44	p.K877N	2	197863103	C	A	Missense	46	10.9%	.	44.0%	0.11155	0.881754189	0.190060114	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SPAG16	p.R437H	2	214794779	G	A	Missense	66	30.3%	.	100.0%	0.86661	1	0.693097629	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SPEG	p.R512H	2	220313415	G	A	Missense	54	25.9%	.	100.0%	0.79911	1	0.579964495	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SNED1	p.G1183R	2	242009574	G	A	Missense	43	16.3%	.	66.0%	0.43679	0.970626375	0.319249626	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	NOP56	p.R381*	20	2637177	C	T	Nonsense	63	23.8%	.	96.0%	0.76474	1	0.560931006	Clonal	A	.	.	.	.	Passenger	No	No	No
ACC12T	ATRN	p.N877D	20	3562866	A	G	Missense	57	42.1%	.	100.0%	0.92737	1	0.795490042	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ACTL10	p.Q186R	20	32255860	A	G	Missense	43	9.3%	.	38.0%	0.06988	0.841024057	0.148229414	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	DLGAP4	p.R365C	20	35064605	C	T	Missense	79	6.3%	.	26.0%	0.0003	0.561105761	0.108362299	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	CYYR1	p.A81V	21	27852683	G	A	Missense	66	10.6%	.	43.0%	0.03583	0.809456111	0.209392722	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	TIAM1	p.P220L	21	32638630	G	A	Missense	184	6.0%	.	24.0%	0	0.41574949	0.132302236	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ITSN1	p.R403C	21	35144529	C	T	Missense	88	20.5%	.	83.0%	0.63588	0.986470642	0.524105416	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	BRWD1	p.R1397I	21	40581928	C	A	Missense	60	23.3%	.	94.0%	0.74829	1	0.541977913	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	FOXRED2	p.V510I	22	36892110	C	T	Missense	105	28.6%	.	100.0%	0.88546	1	0.738928781	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	CDC42EP1	p.S260P	22	37964429	T	C	Missense	51	21.6%	.	87.0%	0.68308	0.988961011	0.474234337	Clonal	P	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SHANK3	p.G1671S	22	51169507	G	A	Missense	36	50.0%	.	100.0%	0.9481	1	0.772031076	Clonal	N	Passenger	.	T	.	Passenger	No	No	No
ACC12T	BTD	p.F496V	3	15686849	T	G	Missense	99	27.3%	.	100.0%	0.86751	1	0.706377121	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	GALNT15	p.R118H	3	16217011	G	A	Missense	66	71.2%	.	100.0%	0.04056	1	0.915461992	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	DAZL	p.A2V	3	16646005	G	A	Missense	121	5.8%	.	23.0%	0	0.459093156	0.111262261	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	CTNNB1	p.I327T	3	41268742	T	C	Missense	64	48.4%	.	100.0%	0.96007	1	0.849209098	Clonal	D	Passenger	D	T	.	Passenger	Yes	Yes	Yes
ACC12T	CTNNB1	p.K335I	3	41268766	A	T	Missense	73	45.2%	Yes	100.0%	0.95268	1	0.849371112	Clonal	D	Driver	D	T	.	Likely pathogenic	Yes	Yes	Yes
ACC12T	FYCO1	p.R949H	3	46007980	C	T	Missense	88	25.0%	.	100.0%	0.81831	1	0.640966095	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	BSN	p.A1502T	3	49691493	G	A	Missense	91	15.4%	.	62.0%	0.19467	0.930070637	0.375404241	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	PXK	p.R349*	3	58383392	C	T	Nonsense	50	16.0%	.	65.0%	0.39512	0.965965934	0.329956002	Subclonal	A	.	.	.	.	Passenger	No	No	No
ACC12T	ROBO2	p.R73Q	3	77147273	G	A	Missense	109	13.8%	.	56.0%	0.05095	0.857167394	0.340916082	Subclonal	N	Driver	D	T	.	Likely pathogenic	No	No	No
ACC12T	NXPE3	p.P90S	3	101520253	C	T	Missense	101	12.9%	.	52.0%	0.03469	0.831772597	0.306975308	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	NPHP3	p.R724H	3	132415575	C	T	Missense	36	25.0%	.	100.0%	0.74882	1	0.487338413	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	FGFR3	p.A341T	4	1805509	G	A	Missense	110	5.5%	.	22.0%	0	0.456365153	0.099162102	Subclonal	D	Driver	D	T	.	Likely pathogenic	Yes	Yes	Yes
ACC12T	HTT	p.S3078N	4	3241590	G	A	Missense	38	36.8%	.	100.0%	0.87724	1	0.675385603	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC12T	SLC25A31	p.A10V	4	128651729	C	T	Missense	135	5.9%	.	24.0%	0	0.450858175	0.119327773	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	HSPA9	p.R578*	5	137892552	G	A	Nonsense	113	5.3%	.	21.0%	0	0.444622579	0.096123311	Subclonal	A	.	.	.	.	Passenger	No	No	No
ACC12T	PCDHGA11	p.A131T	5	140801185	G	A	Missense	86	7.0%	.	28.0%	0.0003	0.578262519	0.128366465	Subclonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACC12T	GRK6	p.C260Y	5	176860955	G	A	Missense	80	25.0%	.	100.0%	0.81138	1	0.626085588	Clonal	D	Driver	D	T	.	Likely pathogenic	No	No	No
ACC12T	FLT4	p.A786T	5	180047659	C	T	Missense	109	35.8%	.	100.0%	0.7633	1	0.834655222	Clonal	D	Passenger	D	T	.	Passenger	Yes	No	No
ACC12T	PRR3	p.P144L	6	30529872	C	T	Missense	67	32.8%	.	100.0%	0.87472	1	0.7315558	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	GLTSCR1L	p.T870M	6	42832553	C	T	Missense	139	23.7%	.	96.0%	0.81132	1	0.674400118	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	GTPBP2	p.G98D	6	43594068	C	T	Missense	132	8.3%	.	34.0%	0.00003	0.574662929	0.187099393	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	AARS2	p.R611Q	6	44272191	C	T	Missense	86	47.7%	.	100.0%	0.96394	1	0.87952192	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	HTR1B	p.S197L	6	78172531	G	A	Missense	99	6.1%	.	25.0%	0.00002	0.505285307	0.110803506	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	ATG5	p.H257Q	6	106634472	A	C	Missense	84	29.8%	.	100.0%	0.87942	1	0.7244131	Clonal	D	Passenger	D	.	.	Passenger	No	No	No
ACC12T	SFT2D1	p.G71S	6	166743017	C	T	Missense	72	27.8%	.	100.0%	0.85024	1	0.66525842	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ETV1	p.F289I	7	13949263	A	T	Missense	99	33.3%	.	100.0%	0.87362	1	0.797433152	Clonal	D	Passenger	N	T	.	Passenger	Yes	No	No
ACC12T	AKAP9	p.Q2400K	7	91708645	C	A	Missense	93	24.7%	.	100.0%	0.81579	1	0.643086012	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	MUC3A	p.E364K	7	100552339	G	A	Missense	88	12.5%	.	51.0%	0.04373	0.838285244	0.284791985	Subclonal	N	Passenger	.	T	.	Passenger	No	No	No
ACC12T	PLOD3	p.E147K	7	100859507	C	T	Missense	124	25.0%	.	100.0%	0.84195	1	0.690634111	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	PRRT4	p.A668T	7	127991608	C	T	Missense	36	25.0%	.	100.0%	0.74882	1	0.487338413	Clonal	N	Passenger	N	.	.	Passenger	No	No	No
ACC12T	TRBV7-1	p.R4S	7	142032050	G	C	Missense	44	13.6%	.	55.0%	0.27066	0.944602598	0.255031684	Subclonal	.	Passenger	.	.	.	Passenger	No	No	No
ACC12T	NOBOX	p.Y624*	7	144094537	G	T	Nonsense	45	44.4%	.	100.0%	0.94221	1	0.774302446	Clonal	D		.	.	.	Passenger	No	No	No
ACC12T	STMN4	p.D101E	8	27098667	A	C	Missense	76	56.6%	.	100.0%	0.92419	1	0.896923245	Clonal	D	Passenger	N	.	.	Passenger	No	No	No
ACC12T	IZUMO3	p.R209Q	9	24543321	C	T	Missense	46	10.9%	.	44.0%	0.11155	0.881754189	0.190060114	Subclonal	.	Passenger	N	T	.	Passenger	No	No	No
ACC12T	PIP5K1B	p.X67_splice	9	71491591	A	G	Splice Site	108	32.4%	.	100.0%	0.88604	1	0.798647971	Clonal	D	.	.	.	.	Passenger	No	No	No
ACC12T	GALNT12	p.T289K	9	101594188	C	A	Missense	126	29.4%	.	100.0%	0.90112	1	0.777653117	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	PALM2-AKAP2	p.P631T	9	112899715	C	A	Missense	73	47.9%	.	100.0%	0.96178	1	0.862556279	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	C5	p.A1155V	9	123744144	G	A	Missense	40	22.5%	.	91.0%	0.6999	0.989811851	0.455304492	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC12T	ENG	p.V539A	9	130580469	A	G	Missense	105	19.0%	.	77.0%	0.51164	0.97825911	0.504002878	Subclonal	N	Passenger	N	D	.	Passenger	No	No	No
ACC12T	SPTAN1	p.R547H	9	131344825	G	A	Missense	58	22.4%	.	91.0%	0.71791	1	0.51483433	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	QRFP	p.R135W	9	133768823	G	A	Missense	28	50.0%	.	100.0%	0.94097	1	0.725534212	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC12T	CACNA1B	p.G31V	9	140772477	G	T	Missense	14	28.6%	.	100.0%	0.72832	1	0.353766924	Clonal	D	Passenger	N	D	.	Likely pathogenic	No	No	No
ACC12T	ZRSR2	p.R126Q	23	15822298	G	A	Missense	102	23.5%	.	95.0%	0.78666	1	0.6274392	Clonal	D	Passenger	N	D	.	Likely pathogenic	Yes	No	No
ACC12T	CCDC120	p.A627T	23	48926087	G	A	Missense	81	19.8%	.	80.0%	0.5938	0.983959629	0.493392034	Subclonal	D	Passenger	.	.	.	Passenger	No	No	Yes
ACC12T	MAGIX	p.A55V	23	49020235	C	T	Missense	15	33.3%	.	100.0%	0.78778	1	0.427891848	Clonal	D	Passenger	.	T	.	Passenger	No	No	No
ACC12T	MAGIX	p.R164C	23	49021411	C	T	Missense	93	20.4%	.	83.0%	0.63251	0.986288494	0.530675058	Clonal	D	Passenger	.	T	.	Passenger	No	No	No
ACC12T	SMC1A	p.G1119V	23	53409234	C	A	Missense	50	26.0%	.	100.0%	0.79403	1	0.567538663	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	Yes	Yes
ACC12T	ITIH6	p.A368V	23	54785404	G	A	Missense	44	29.5%	.	100.0%	0.83001	1	0.606760099	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	AMER1	p.R353*	23	63412110	G	A	Nonsense	73	20.5%	.	83.0%	0.64481	0.986950153	0.501626339	Clonal	A	.	.	.	.	Likely pathogenic	Yes	No	No
ACC12T	HEPH	p.G620S	23	65417719	G	A	Missense	11	36.4%	.	100.0%	0.79179	1	0.389163428	Clonal	N	Passenger	N	D	.	Passenger	No	No	No
ACC12T	RAB40AL	p.I216S	23	102192893	T	G	Missense	32	9.4%	.	38.0%	0.13699	0.891777679	0.131785679	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	PRRG3	p.R19C	23	150868515	C	T	Missense	65	7.7%	.	31.0%	0.00475	0.674164716	0.132884907	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC12T	TKTL1	p.Q25*	23	153524285	C	T	Nonsense	33	39.4%	.	100.0%	0.89637	1	0.673591862	Clonal	N	.	.	.	.	Passenger	No	No	No
ACC18ACC	PINK1	p.A208P	1	20964569	G	C	Missense	129	10.1%	.	41.0%	0.00026	0.668482705	0.24060979	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	LCK	p.D77N	1	32740635	G	A	Missense	289	33.9%	.	100.0%	0.85473	1	0.842624082	Clonal	D	Passenger	N	T	.	Passenger	Yes	No	No
ACC18ACC	DMRTB1	p.E207V	1	53927188	A	T	Missense	378	33.3%	.	100.0%	0.85904	1	0.854122325	Clonal	D	Passenger	N	.	.	Passenger	No	No	No
ACC18ACC	SELP	p.V197L	1	169582824	C	A	Missense	347	3.5%	.	14.0%	0	0.237968547	0.07638427	Subclonal	D	Passenger	N	T	.	Passenger	No	No	Yes
ACC18ACC	RGSL1	p.L925H	1	182517556	T	A	Missense	92	5.4%	.	22.0%	0.00001	0.489176755	0.092987907	Subclonal	.	Passenger	D	.	.	Passenger	No	No	No
ACC18ACC	IFIT2	p.S405L	10	91066927	C	T	Missense	308	4.5%	.	14.0%	0	0.226137294	0.079765367	Subclonal	N	Passenger	D	.	.	Passenger	No	No	No
ACC18ACC	ATRNL1	p.R1277H	10	117486792	G	A	Missense	286	29.7%	.	92.0%	0.60618	1	0.751756617	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	OR51F2	p.R237*	11	4843324	C	T	Nonsense	317	33.4%	.	100.0%	0.84897	1	0.842182427	Clonal	D	.	.	.	.	Passenger	No	No	No
ACC18ACC	MPPED2	p.I5T	11	30601907	A	G	Missense	252	4.4%	.	13.0%	0	0.230726164	0.071201229	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	NAALAD2	p.F175Y	11	89883690	T	A	Missense	160	38.8%	.	100.0%	0.85855	1	0.8511228	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	CDON	p.N908S	11	125859582	T	C	Missense	190	3.2%	.	10.0%	0	0.20207975	0.04082677	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	FAM118B	p.N228K	11	126124316	C	A	Missense	425	3.1%	.	9.0%	0	0.154640051	0.050765821	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	ZBTB44	p.Q112E	11	130131435	G	C	Missense	200	27.5%	.	85.0%	0.38	0.983202285	0.664040092	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	OR2AP1	p.S249F	12	55968944	C	T	Missense	185	31.4%	.	97.0%	0.71909	1	0.750806402	Clonal	N	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	CCDC41	p.G697A	12	94702605	C	G	Missense	367	30.0%	.	92.0%	0.62668	1	0.776949751	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	MYO1H	p.V885I	12	109881331	G	A	Missense	86	5.8%	.	12.0%	0	0.264057887	0.04850463	Subclonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACC18ACC	RCBTB1	p.E251Q	13	50125565	C	G	Missense	167	7.8%	.	24.0%	0	0.391887096	0.137614936	Subclonal	D	Passenger	N	D	.	Likely pathogenic	No	No	No
ACC18ACC	LRRC16B	p.S240R	14	24524948	C	A	Missense	91	12.1%	.	37.0%	0.00006	0.623736558	0.208490801	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	CLEC14A	p.V64M	14	38725038	C	T	Missense	152	36.2%	.	100.0%	0.84182	1	0.814261308	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	SYNE2	p.N1848I	14	64489487	A	T	Missense	102	17.6%	.	37.0%	0	0.540993102	0.23409009	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	MTHFD1	p.D472E	14	64898354	C	G	Missense	113	22.1%	.	46.0%	0	0.63369764	0.317188637	Subclonal	D	Driver	D	T	loh	Likely pathogenic	No	No	No
ACC18ACC	PPP4R4	p.Y325S	14	94707130	A	C	Missense	13	46.2%	.	100.0%	0.68919	1	0.492239916	Clonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACC18ACC	BEGAIN	p.T22A	14	101012950	T	C	Missense	301	32.2%	.	99.0%	0.7985	1	0.814224351	Clonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	IGF1R	p.I628M	15	99459248	C	G	Missense	395	63.0%	.	100.0%	0.97888	1	0.979510245	Clonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACC18ACC	GNPTG	p.V30L	16	1402138	G	C	Missense	55	43.6%	.	91.0%	0.66372	1	0.632889886	Clonal	D	Passenger	N	D	loh	Likely pathogenic	No	No	No
ACC18ACC	SEC14L5	p.R292C	16	5046949	C	T	Missense	144	33.3%	.	100.0%	0.77662	1	0.762656773	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC18ACC	TP53	p.I195T	17	7578265	A	G	Missense	119	47.9%	Yes	100.0%	0.83572	1	0.786020158	Clonal	D	Passenger	D	D	loh	Likely pathogenic	Yes	Yes	Yes
ACC18ACC	FMNL1	p.X162_splice	17	43311099	G	A	Splice Site	148	7.4%	.	15.0%	0	0.262365169	0.08278988	Subclonal	D	.	.	.	loh	Likely pathogenic	No	No	No

ACC18ACC	RGS9	p.H479Y	17	63221147	C	T	Missense	54	35.2%	.	73.0%	0.23892	0.959543443	0.489829024	Subclonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACC18ACC	CACNG4	p.Y186F	17	65026693	A	T	Missense	204	3.9%	.	8.0%	0	0.152400536	0.036628207	Subclonal	D	Passenger	D	D	loh	Likely pathogenic	No	No	No
ACC18ACC	RECQL5	p.F29Y	17	73662552	A	T	Missense	381	3.4%	.	14.0%	0	0.229670029	0.077020567	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	RECQL5	p.F26C	17	73662561	A	C	Missense	392	3.3%	.	14.0%	0	0.223557802	0.074511131	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	SLC25A10	p.G113A	17	79682732	G	C	Missense	338	3.0%	.	12.0%	0	0.214085323	0.061423402	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	ZNF236	p.G231E	18	74587478	G	A	Missense	313	3.8%	.	12.0%	0	0.198095457	0.063010406	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACC18ACC	CELF5	p.R435Q	19	3290346	G	A	Missense	189	32.3%	.	100.0%	0.76416	1	0.77213611	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	F2RL3	p.V343L	19	17001301	G	C	Missense	333	3.0%	.	9.0%	0	0.162933641	0.045311026	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	SLC27A1	p.P559R	19	17612121	C	G	Missense	75	6.7%	.	21.0%	0	0.447996592	0.085785053	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	APLP1	p.A574D	19	36369983	C	A	Missense	181	30.4%	.	94.0%	0.66013	1	0.726928857	Clonal	D	Passenger	N	D	.	Likely pathogenic	No	No	No
ACC18ACC	NLRP7	p.V251M	19	55451436	C	T	Missense	311	28.0%	.	86.0%	0.35351	0.981815158	0.711450053	Subclonal	N	Passenger	D	D	.	Passenger	No	No	No
ACC18ACC	AMER3	p.G549S	2	131521290	G	A	Missense	49	40.8%	.	100.0%	0.77033	1	0.713675957	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	TTN	p.M2595I	2	179637906	C	G	Missense	66	19.7%	.	61.0%	0.07528	0.916620109	0.361937401	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	PLCL1	p.P23T	2	198669890	C	A	Missense	47	25.5%	.	79.0%	0.38797	0.983121079	0.454763397	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	ASB18	p.G242R	2	237123382	C	T	Missense	17	41.2%	.	100.0%	0.65307	1	0.504793513	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC18ACC	KCNG1	p.R326C	20	49621142	G	A	Missense	167	37.1%	.	100.0%	0.85917	1	0.836834814	Clonal	D	Passenger	N	D	.	Likely pathogenic	No	No	No
ACC18ACC	APOL1	p.E159Q	22	36661309	G	C	Missense	404	3.2%	.	13.0%	0	0.216886042	0.072315694	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	PHF21B	p.L213P	22	45309895	A	G	Missense	84	14.3%	.	58.0%	0.0732	0.912945494	0.337395749	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	KLHDC7B	p.V489M	22	50988060	G	A	Missense	557	6.8%	.	28.0%	0	0.371936902	0.20006247	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	SETD2	p.R448L	3	47164783	C	A	Missense	150	61.3%	.	100.0%	0.45533	1	0.920565838	Clonal	D	Passenger	N	T	loh	Passenger	No	Yes	Yes
ACC18ACC	KIF9	p.Q588H	3	47282451	T	A	Missense	147	48.3%	.	100.0%	0.85847	1	0.811925135	Clonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACC18ACC	PPM1M	p.T66S	3	52282388	C	G	Missense	182	25.3%	.	53.0%	0	0.663321223	0.401639337	Subclonal	D	Driver	D	T	loh	Likely pathogenic	No	No	No
ACC18ACC	DLG1	p.E381D	3	196857519	T	G	Missense	82	6.1%	.	19.0%	0	0.411317991	0.078109925	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	UBA6	p.M844K	4	68490893	A	T	Missense	122	37.7%	.	100.0%	0.83808	1	0.808954664	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	LSM11	p.G79D	5	157170994	G	A	Missense	81	13.6%	.	28.0%	0	0.468733563	0.157273523	Subclonal	D	Passenger	N	.	loh	Passenger	No	No	No
ACC18ACC	ABHD16A	p.D510E	6	31655435	G	C	Missense	221	3.2%	.	13.0%	0	0.256104611	0.05905678	Subclonal	D	Passenger	N	.	.	Passenger	No	No	No
ACC18ACC	MCM3	p.L487Q	6	52141115	A	T	Missense	111	31.5%	.	97.0%	0.68861	1	0.696733875	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	THEMIS	p.L29V	6	128221993	G	C	Missense	281	2.8%	.	9.0%	0	0.165381607	0.040462895	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	AKAP12	p.I683V	6	151671573	A	G	Missense	306	29.1%	.	90.0%	0.52302	0.989988621	0.740550642	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	SLC22A2	p.R207C	6	160671634	G	A	Missense	166	34.3%	.	100.0%	0.81691	1	0.795980613	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC18ACC	SAMD9	p.I1084V	7	92732161	T	C	Missense	302	5.6%	.	17.0%	0	0.267529514	0.104235724	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	POMK	p.A13V	8	42958729	C	T	Missense	333	3.9%	.	12.0%	0	0.197649519	0.065634105	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	RIPK2	p.S33*	8	90770386	C	A	Nonsense	472	12.1%	.	49.0%	0	0.620996172	0.380682238	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACC18ACC	KLF9	p.H193N	9	73002850	G	T	Missense	293	4.8%	.	15.0%	0	0.237603273	0.083423752	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACC18ACC	TMEFF1	p.G48C	9	103235968	G	T	Missense	199	30.2%	.	93.0%	0.6463	1	0.730804792	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	TMEFF1	p.G48V	9	103235969	G	T	Missense	196	29.6%	.	91.0%	0.60109	1	0.715755175	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	TTC16	p.R827W	9	130493541	A	T	Missense	122	28.7%	.	88.0%	0.53577	1	0.645497866	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	SEC16A	p.S1127R	9	139368687	A	T	Missense	107	7.5%	.	23.0%	0	0.428994967	0.114408845	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC18ACC	HUWE1	p.R150P	23	53672318	C	G	Missense	90	22.2%	.	69.0%	0.11777	0.941772083	0.453133892	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	P2RY10	p.R90W	23	78216285	C	T	Missense	258	26.7%	.	100.0%	0.84272	1	0.820563292	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACC18ACC	USP26	p.L901R	23	132159547	A	C	Missense	206	4.4%	.	18.0%	0	0.325676065	0.090625439	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACC12T	MEGF6	p.A749Pfs*223	1	3418428	GC	G	Frame-shift deletion	149	25.5%	.	100.0%	0.86545	1	0.72651417	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	ZBTB7B	p.G110Vfs*19	1	154987358	CG	C	Frame-shift deletion	63	20.6%	.	84.0%	0.64957	0.987204282	0.483014169	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	GPR161	p.G517Afs*13	1	168054868	GC	G	Frame-shift deletion	146	26.7%	.	100.0%	0.88574	1	0.750068291	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	RASSF5	p.D39Tfs*127	1	206681043	GC	G	Frame-shift deletion	38	28.9%	.	100.0%	0.81168	1	0.568255076	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	CACNB2	p.K645Nfs*29	10	18828598	CA	C	Frame-shift deletion	112	18.8%	.	76.0%	0.4714	0.975021614	0.502026503	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	WDFY4	p.W2960Gfs*74	10	50178274	GGT	G	Frame-shift deletion	66	21.2%	.	86.0%	0.67657	0.988620253	0.504741114	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	HMX3	p.P23Hfs*100	10	124895626	GC	G	Frame-shift deletion	15	33.3%	.	100.0%	0.78778	1	0.427891848	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	DGKZ	p.A39Lfs*23	11	46387915	TC	T	Frame-shift deletion	51	19.6%	.	79.0%	0.60224	0.984421545	0.426064446	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	OR8I2	p.C178Lfs*2	11	55861307	A	AT	Frame-shift insertion	91	12.1%	.	37.0%	0.00014	0.616501876	0.205893106	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	MYEOV	p.W272Gfs*66	11	69063723	TG	T	Frame-shift deletion	72	18.1%	.	73.0%	0.48253	0.975593348	0.430148968	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	ANKK1	p.P193Lfs*39	11	113265742	TC	T	Frame-shift deletion	99	21.2%	.	86.0%	0.68016	0.988793029	0.561087128	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	C1QTNF5	p.A195Pfs*3	11	119210189	GC	G	Frame-shift deletion	151	23.2%	.	94.0%	0.79274	1	0.66983919	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	OAF	p.E46del	11	120082119	CGAG	C	In-Frame deletion	64	17.2%	.	70.0%	0.43507	0.970842697	0.391266172	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	PLEKHG6	p.E671del	12	6436756	GGAA	G	In-Frame deletion	91	20.9%	.	85.0%	0.66115	0.987831124	0.540652694	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	KLHL42	p.C399Vfs*44	12	27950768	TG	T	Frame-shift deletion	99	26.3%	.	100.0%	0.85222	1	0.686129606	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	B4GALNT1	p.G88Afs*24	12	58025102	GC	G	Frame-shift deletion	76	21.1%	.	85.0%	0.67097	0.988333181	0.520904555	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	SETD1B	p.H8Tfs*27	12	122242657	AC	A	Frame-shift deletion	55	50.9%	.	100.0%	0.9566	1	0.841164765	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	SETD8	p.A171Lfs*36	12	123879807	GA	G	Frame-shift deletion	81	21.0%	.	85.0%	0.66787	0.988174734	0.527934956	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	RNF6	p.L593Yfs*2	13	26788240	TA	T	Frame-shift deletion	118	16.9%	.	69.0%	0.26107	0.947974893	0.450071451	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	DACH1	p.S164_S165dup	13	72440428	G	GCTGCTA	In-Frame insertion	28	14.3%	.	58.0%	0.39511	0.965219805	0.223834051	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	SLITRK5	p.S36Rfs*26	13	88327746	CT	C	Frame-shift deletion	77	15.6%	.	63.0%	0.26072	0.945299474	0.365007797	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	TLE3	p.S593del	15	70346831	CAGG	C	In-Frame deletion	100	19.0%	.	77.0%	0.51438	0.978436559	0.496970352	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	FAM92B	p.P241Lfs*18	16	85133775	AG	A	Frame-shift deletion	96	15.6%	.	63.0%	0.19861	0.931830116	0.388035104	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	GSE1	p.L239Sfs*38	16	85688511	TC	T	Frame-shift deletion	117	25.6%	.	100.0%	0.85236	1	0.697056127	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	CDH15	p.H513Tfs*9	16	89258217	GC	G	Frame-shift deletion	84	14.3%	.	58.0%	0.13709	0.908214176	0.334439449	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	PELP1	p.L798Cfs*14	17	4575893	AG	A	Frame-shift deletion	42	21.4%	.	87.0%	0.67067	0.988336041	0.439903728	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	XYLT2	p.G529Afs*78	17	48433966	AC	A	Frame-shift deletion	128	21.9%	.	89.0%	0.72019	1	0.612547569	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	CNDP1	p.L20dup	18	72223591	G	GTGC	In-Frame insertion	38	39.5%	.	100.0%	0.90083	1	0.702542078	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	ZNF382	p.E461Kfs*84	19	37118175	CG	C	Frame-shift deletion	57	17.5%	.	71.0%	0.47755	0.974972467	0.38695114	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	SIPA1L3	p.D915Mfs*34	19	38610393	CG	C	Frame-shift deletion	118	29.7%	.	100.0%	0.89877	1	0.773237421	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	SEMA4C	p.F239del	2	97530769	TGAA	T	In-Frame deletion	130	15.4%	.	62.0%	0.09404	0.89637594	0.407803844	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	KLHL41	p.K72Rfs*3	2	170366495	GA	G	Frame-shift deletion	98	19.4%	.	78.0%	0.55076	0.981109025	0.506322109	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	MYO3B	p.S438Wfs*23	2	171242714	GGA	G	Frame-shift deletion	60	10.0%	.	40.0%	0.0351	0.802269394	0.186650143	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	JAG1	p.N1187Tfs*25	20	10620244	TG	T	Frame-shift deletion	195	22.1%	.	89.0%	0.73222	1	0.665748591	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	BRPF1	p.R955Gfs*33	3	9786130	GC	G	Frame-shift deletion	99	22.2%	.	90.0%	0.73301	1	0.589112009	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	SCAP	p.K394del	3	47463992	GTTC	G	In-Frame deletion	97	13.4%	.	54.0%	0.05791	0.859575079	0.32018732	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	AARS2	p.T871Nfs*21	6	44269188	G	GT	Frame-shift insertion	75	21.3%	.	86.0%	0.68446	0.989009878	0.526430392	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	NCOA7	p.E102Rfs*23	6	126196060	TA	T	Frame-shift deletion	49	22.4%	.	91.0%	0.71004	1	0.488389004	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	HIVEP2	p.P995Sfs*2	6	143092893	G	GA	Frame-shift insertion	77	16.9%	.	68.0%	0.37306	0.963938614	0.403578745	Subclonal	.	.	.	.	.	.	No	No	No
ACC12T	PTN	p.V42*	7	136938376	CT	C	Frame-shift deletion	76	36.8%	.	100.0%	0.84268	1	0.795541655	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	MAGEB2	p.G84Rfs*8	23	30236940	T	TA	Frame-shift insertion	55	20.0%	.	81.0%	0.61981	0.985504304	0.446960404	Clonal	.	.	.	.	.	.	No	No	No
ACC12T	PNMA3	p.R11Gfs*5	23	152225442	TC	T	Frame-shift deletion	118	16.9%	.	69.0%	0.26107	0.947974893	0.450071451	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	DNAJC11	p.G207Dfs*31	1	6712898	TC	T	Frame-shift deletion	443	23.3%	.	95.0%	0.70823	1	0.783916198	Clonal	.	.	.	.	.	.	No	No	No
ACC18ACC	ATP1A2	p.R421Lfs*17	1	160098809	TGTCTCGAATTGCTG	T	Frame-shift deletion	220	17.3%	.	53.0%	0.00001	0.698923868	0.391467864	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	FLT1	p.S1247_T1248de	13	28880886	AGTGCTG	A	In-Frame deletion	136	18.4%	.	57.0%	0.00194	0.788712771	0.389323855	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	SPTBN1	p.K226Qfs*7	2	54845238	AACTAAAGAAATCTAACGCAC	A	Frame-shift deletion	278	12.2%	.	38.0%	0	0.507368433	0.269345663	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	C5orf42	p.Y703Ffs*10	5	37226567	AATAACTTCAGGTTGAAGAATGT	A	Frame-shift deletion	293	5.5%	.	17.0%	0	0.263112344	0.100161478	Subclonal	.	.	.	.	loh	.	No	No	No
ACC18ACC	HIST1H1T	p.K67_Y75del	6	26108096	CGTAGCCAGCAGCGGCCAATGCCTTCTT	C	In-Frame deletion	636	14.2%	.	58.0%	0	0.692548954	0.471110542	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	TJP2	p.D969Mfs*25	9	71863070	TG	T	Frame-shift deletion	193	12.4%	.	38.0%	0	0.545472569	0.25743321	Subclonal	.	.	.	.	.	.	No	No	No
ACC18ACC	KLHL34	p.P511Sfs*76	23	21674358	AACGTGCGGTGCCCATGGGT	A	Frame-shift deletion	218	14.2%	.	44.0%	0	0.596056057	0.310067707	Subclonal	.	.	.	.	.	.	No	No	No
ACCV1T	ANKRD65	p.R357*	1	1354611	G	A	Nonsense	377	25.7%	.	67.0%	0	0.789545275	0.559560526	Subclonal	D	.	.	.	loh	Likely pathogenic	No	No	No
ACCV1T	ZBTB7B	p.Q217E	1	154987683	C	G	Missense	517	3.5%	.	13.0%	0	0.191687597	0.074668517	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	NAV1	p.X1135_splice	1	201763005	T	G	Splice Site	216	6.9%	.	25.0%	0	0.398075499	0.149595771	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACCV1T	ENAH	p.Q146K	1	225707266	G	T	Missense	141	9.9%	.	36.0%	0	0.573234453	0.213001493	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	LYST	p.E1851A	1	235938295	T	G	Missense	74	8.1%	.	37.0%	0.00634	0.756874566	0.171916704	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	RYR2	p.L459F	1	237617773	C	T	Missense	302	5.0%	.	23.0%	0	0.366038709	0.135344013	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACCV1T	RYR2	p.P1124L	1	237730023	C	T	Missense	374	32.1%	.	100.0%	0.0032	1	0.933858298	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	TLX1	p.A326V	10	102896654	C	T	Missense	751	3.6%	.	13.0%	0	0.182655401	0.084178614	Subclonal	D	Passenger	N	D	.	Likely pathogenic	Yes	No	No
ACCV1T	RBMXL2	p.G262S	11	7111135	G	A	Missense	867	18.6%	.	67.0%	0	0.765385748	0.577848846	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	NLRP10	p.K636R	11	7981252	T	C	Missense	192	13.5%	.	49.0%	0.00002	0.686228156	0.335620331	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	STK33	p.M290L	11	8474372	T	G	Missense	115	7.8%	.	28.0%	0	0.509087063	0.147115925	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	COPB1	p.K450Q	11	14501125	T	G	Missense	122	9.0%	.	33.0%	0	0.553333341	0.180968259	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	NELL1	p.W608*	11	21581772	G	A	Nonsense	233	5.2%	.	19.0%	0	0.312872397	0.102839983	Subclonal	A	.	.	.	.	Passenger	No	No	No
ACCV1T	MADD	p.L254F	11	47297552	G	C	Missense	312	56.4%	.	100.0%	0.97218	1	0.970582796	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	DAGLA	p.A336T	11	61502352	G	A	Missense	502	3.6%	.	13.0%	0	0.197659572	0.0773977	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	TM7SF2	p.I204L	11	64882191	A	C	Missense	229	21.0%	.	76.0%	0.08434	0.944908384	0.58032342	Subclonal	D	Passenger	N	D	.	Likely pathogenic	No	No	No
ACCV1T	SPA17	p.A124S	11	124564256	G	T	Missense	59	27.1%	.	71.0%	0.15641	0.96105969	0.449493847	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	PIANP	p.R172H	12	6806461	C	T	Missense	161	11.8%	.	31.0%	0	0.458296864	0.196339355	Subclonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACCV1T	KMT2D	p.E731*	12	49445275	C	A	Nonsense	338	6.8%	.	18.0%	0	0.257063646	0.114479612	Subclonal	A	.	.	.	loh	Likely pathogenic	Yes	Yes	Yes
ACCV1T	ZC3H10	p.G30R	12	56514434	G	C	Missense	317	6.0%	.	16.0%	0	0.235345552	0.096085229	Subclonal	D	Passenger	N	.	loh	Passenger	No	No	No
ACCV1T	PARP4	p.F149L	13	25073469	A	C	Missense	39	20.5%	.	54.0%	0.04558	0.896927347	0.277978843	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	HERC2	p.E4804D	15	28357002	C	G	Missense	711	10.4%	.	38.0%	0	0.460289541	0.297634477	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	ISLR2	p.A252T	15	74425849	G	A	Missense	589	19.9%	.	72.0%	0.00016	0.836977307	0.60379287	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	SRRM2	p.A2049G	16	2816675	C	G	Missense	744	3.5%	.	13.0%	0	0.178577998	0.081531899	Subclonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACCV1T	CHST4	p.R130Q	16	71570969	G	A	Missense	578	3.3%	.	12.0%	0	0.178710692	0.071481863	Subclonal	D	Passenger	D	D	loh	Likely pathogenic	No	No	No
ACCV1T	TP53	p.C238Y	17	7577568	C	T	Missense	181	57.5%	Yes	100.0%	0.00012	1	0.940368949	Clonal	D	Passenger	D	D	loh	Likely pathogenic	Yes	Yes	Yes
ACCV1T	RP11-1407O15.2	p.Y438D	17	36352475	A	C	Missense	124	13.7%	.	36.0%	0	0.54119716	0.223997518	Subclonal	D	Passenger	.	T	loh	Passenger	No	No	No
ACCV1T	SEC11C	p.E115A	18	56819914	A	C	Missense	64	21.9%	.	79.0%	0.33029	0.98330121	0.473637673	Subclonal	D	Passenger	.	.	.	Passenger	No	No	No
ACCV1T	TCF3	p.G267V	19	1622075	C	A	Missense	167	46.1%	.	100.0%	0.82621	1	0.881611834	Clonal	N	Passenger	D	T	loh	Passenger	Yes	No	No
ACCV1T	DOCK6	p.P2016S	19	11311039	G	A	Missense	187	7.5%	.	20.0%	0	0.313808787	0.113260372	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACCV1T	IRF2BP1	p.A537V	19	46387423	G	A	Missense	647	3.2%	.	15.0%	0	0.22183036	0.093221054	Subclonal	N	Passenger	N	D	.	Passenger	No	No	No
ACCV1T	NUCB1	p.A26P	19	49404129	G	C	Missense	785	11.3%	.	52.0%	0	0.629547199	0.424333212	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	PRR12	p.P1318A	19	50102802	C	G	Missense	526	4.4%	.	20.0%	0	0.294271792	0.130707005	Subclonal	N	Passenger	N	.	.	Passenger	No	No	No
ACCV1T	CTU1	p.T126K	19	51607450	G	T	Missense	845	40.4%	.	100.0%	0.92288	1	0.931571772	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	PTPRH	p.A877D	19	55697845	G	T	Missense	259	5.0%	.	13.0%	0	0.215047568	0.072419552	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	KCNS3	p.R293Q	2	18113153	G	A	Missense	262	38.9%	.	100.0%	0.03386	1	0.922550972	Clonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACCV1T	TDRD15	p.A1109V	2	21363665	C	T	Missense	266	15.0%	.	54.0%	0.00001	0.712361128	0.401707214	Subclonal	.	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	DQX1	p.R685S	2	74745672	T	A	Missense	176	44.9%	.	100.0%	0.37811	1	0.921671428	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	MYO7B	p.E1324K	2	128382943	G	A	Missense	239	59.8%	.	100.0%	0.92506	1	0.965087388	Clonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	LRP2	p.R2095*	2	170066149	G	A	Nonsense	118	15.3%	.	55.0%	0.0067	0.81916171	0.352646492	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACCV1T	ESPNL	p.A112T	2	239010621	G	A	Missense	706	3.8%	.	18.0%	0	0.249228103	0.116773898	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	TIAM1	p.Y1196C	21	32513711	T	C	Missense	437	15.8%	.	57.0%	0	0.700332303	0.453090774	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACCV1T	CECR2	p.M793I	22	18022274	G	T	Missense	684	21.1%	.	76.0%	0.00089	0.872628789	0.65170684	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	FLNB	p.P1104L	3	58109004	C	T	Missense	284	3.9%	.	10.0%	0	0.173207565	0.052008878	Subclonal	D	Passenger	D	D	.	Likely pathogenic	No	No	No
ACCV1T	MAGI1	p.V157M	3	65479268	C	T	Missense	128	17.2%	.	45.0%	0	0.640380685	0.299861022	Subclonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	ZXDC	p.Q203*	3	126194102	G	A	Nonsense	297	3.7%	.	10.0%	0	0.165686095	0.050163973	Subclonal	A	.	.	.	.	Passenger	No	No	No
ACCV1T	EPHB1	p.R90C	3	134670357	C	T	Missense	335	3.3%	.	9.0%	0	0.146688619	0.042924737	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	VPS8	p.V1358I	3	184766282	G	A	Missense	240	58.8%	.	100.0%	0	1	0.955613806	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	SEMA5A	p.W506L	5	9136698	C	A	Missense	86	19.8%	.	71.0%	0.17917	0.96582364	0.453135585	Subclonal	D	Passenger	D	T	.	Passenger	No	No	No
ACCV1T	KCTD16	p.R13L	5	143586315	G	T	Missense	377	3.2%	.	12.0%	0	0.193442108	0.061458388	Subclonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	MUC22	p.T1447S	6	30997547	A	T	Missense	885	21.5%	.	99.0%	0.78943	1	0.853253639	Clonal	.	Passenger	N	.	.	Passenger	No	No	No
ACCV1T	TMEM217	p.R125I	6	37186433	C	A	Missense	432	13.9%	.	64.0%	0.00034	0.801586303	0.500496126	Subclonal	N	Passenger	D	.	.	Passenger	No	No	No
ACCV1T	MDGA1	p.H597Q	6	37616861	G	T	Missense	454	26.9%	.	100.0%	0.70413	1	0.908165432	Clonal	N	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	NFKBIE	p.C373F	6	44228267	C	A	Missense	500	27.0%	.	100.0%	0.61724	1	0.915895426	Clonal	D	Passenger	D	T	.	Passenger	Yes	No	No
ACCV1T	HDAC2	p.D175E	6	114274555	A	C	Missense	100	21.0%	.	55.0%	0.00134	0.779718454	0.365819165	Subclonal	D	Passenger	D	D	loh	Likely pathogenic	No	No	No
ACCV1T	FAM120B	p.V3M	6	170626485	G	A	Missense	149	8.1%	.	21.0%	0	0.34958284	0.117635016	Subclonal	D	Passenger	N	T	loh	Passenger	No	No	No
ACCV1T	FAM135B	p.L138V	8	139263214	G	C	Missense	329	8.5%	.	48.0%	0.00001	0.670515794	0.330053545	Subclonal	D	Passenger	D	T	loh	Passenger	No	No	No
ACCV1T	LINGO2	p.Q10*	9	27950642	G	A	Nonsense	128	20.3%	.	73.0%	0.14643	0.95989965	0.509624961	Subclonal	D	.	.	.	.	Passenger	No	No	No
ACCV1T	TSC1	p.E878K	9	135772991	C	T	Missense	90	12.2%	.	44.0%	0.00198	0.739151174	0.248163055	Subclonal	D	Passenger	N	T	.	Passenger	Yes	No	Yes
ACCV1T	PHEX	p.R342C	23	22117214	C	T	Missense	360	39.4%	.	100.0%	0.00085	1	0.942995503	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	SYN1	p.A92V	23	47478853	G	A	Missense	211	34.1%	.	100.0%	0.8079	1	0.869319978	Clonal	D	Passenger	N	T	.	Passenger	No	No	No
ACCV1T	CXorf57	p.P635S	23	105883950	C	T	Missense	84	25.0%	.	65.0%	0.03881	0.90582548	0.439068855	Subclonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACCV1T	MAGEC2	p.S219N	23	141291118	C	T	Missense	199	4.5%	.	12.0%	0	0.214249469	0.058216683	Subclonal	N	Passenger	N	T	loh	Passenger	No	No	No
ACCV1T	STAT5B	p.Q368Pfs*9	17	40370235	T	TG	Frame-shift insertion	215	40.9%	.	100.0%	0.83737	1	0.851015517	Clonal	.	.	.	.	loh	.	Yes	No	No
ACCV1T	IGLV3-22	p.P62*	22	23047145	C	CTGATATA	Nonsense	162	48.8%	.	100.0%	0.87	1	0.928872966	Clonal	.	.	.	.	.	.	No	No	No

Supplementary Table 5: Genomic features of Homologous Recombination Deficiency and Microsatellite Instability in the Acinic Cell Carcinomas of the breast included in this study.

Sample	% MSI	LST score	Myriad score	NtAI Score	Indels (n)	Indels (%)	Average indel length (bp)
ACC1	3.19	4	3	5	2	2.11	4
ACC12	10.93	0	0	0	48	17.3	3.22
ACC18	0.35	24	11	23	9	8.82	12.33

%MSI, Microsatellite instability score (MSIsensor score); LST, Large-scale State Transitions; NtAI, Telomere Allelic Imbalance score; indels, insertions or deletions.