

Supplementary Table S3. Somatic mutations identified in endometrial clear cell carcinomas by targeted massively parallel sequencing

Table with columns: Sample ID, Gene, Chromosome, Position, AA, Effect, Hotspot, Loss of Heterozygosity, Reference Allele, Alternative Allele, Tumor MAF, Normal MAF, Tumor Depth, Normal Depth, Cancer Cell Fraction (ABSOUL), Somatic Probability, 95% Confidence Interval Low, Clonality, Pathogenicity, Mutation Taster, FATHMM, CHASM (Utrons), Cancer Gene, Kanodoth, Lawrence. The table lists 1000 samples and their associated genomic mutations.

CCDS	ALOX12B	17	797679	p.Gly684Asp	missense_variant	C	T	14.37%	0.00%	348	121	0.99	0.8994	0.7274	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ALOX12B	17	797680	p.Asp743Asp	missense_variant	C	A	14.34%	0.00%	569	165	0.99	0.9122	0.7688	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	AMER1	X	6347003	p.Asp133Asp	missense_variant	C	T	15.63%	0.80%	399	125	1.00	0.9310	0.7371	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	AMER1	X	6347012	p.Glu181Val	missense_variant	C	T	12.72%	0.00%	383	164	0.87	0.7835	0.6809	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	APC	5	11214560	p.Asp45Val	missense_variant	C	T	15.76%	0.00%	368	297	1.00	0.9361	0.7670	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	APC	5	11217173	p.Pro61Cys	missense_variant	C	T	14.20%	0.00%	331	207	0.98	0.8769	0.7143	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	APC	5	11217677	p.Ser212Gln	missense_variant	C	T	14.42%	0.00%	384	213	0.99	0.8987	0.7220	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	AR	X	6675210	p.Ser74His	missense_variant	G	T	6.74%	0.00%	178	66	0.96	0.6232	0.2844	Subclonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	AR	X	6675744	p.Asp52Gln	missense_variant	G	A	13.07%	0.00%	523	311	0.99	0.8564	0.6911	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARAF	X	47430740	p.Arg75Gln	missense_variant	G	A	13.07%	0.00%	528	161	0.90	0.8184	0.7072	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ARHGAP26	5	14228144	p.Glu213Gln	missense_variant	G	A	12.89%	0.00%	357	209	0.89	0.8043	0.6998	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARHGAP26	5	14228202	p.Asp21Asp	synonymous_variant	G	A	12.79%	0.00%	349	201	0.97	0.8699	0.6772	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID1A	1	27100888	p.Ser130Ser	synonymous_variant	C	T	4.09%	0.00%	391	128	0.28	0.0000	0.1701	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID1A	1	27109236	p.Arg218Cys	missense_variant	C	T	10.84%	0.00%	369	119	0.74	0.3762	0.5487	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID1B	6	15752445	p.Pro193Leu	missense_variant	C	T	17.00%	0.00%	421	121	1.00	0.9398	0.8198	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID1B	6	15752872	p.Ile209Ile	synonymous_variant	C	A	13.88%	0.00%	351	176	0.94	0.8668	0.6871	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID2	12	4802527	p.Ile12Met	missense_variant	C	G	14.22%	0.00%	206	176	0.98	0.8895	0.6816	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ARID2	12	4802449	p.Val130Val	synonymous_variant	C	T	9.89%	0.00%	491	200	0.99	0.9243	0.8045	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ASXL1	20	31020716	p.Arg338Gln	missense_variant	G	A	15.54%	0.00%	341	209	1.00	0.9258	0.7708	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	108108963	p.Arg417Gln	missense_variant	C	T	16.60%	0.00%	504	432	1.00	0.9540	0.8209	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	108109707	p.Asp417Asp	missense_variant	C	T	11.61%	0.00%	349	209	0.81	0.6253	0.6074	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	108113792	p.Ser584Phe	missense_variant	C	T	14.16%	0.00%	438	275	0.97	0.8990	0.7432	Clonal	Passenger	N	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	10812624	p.Arg592Trp	missense_variant	C	T	14.83%	0.26%	317	216	0.95	0.9169	0.7353	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	108201008	p.Arg2459Gln	missense_variant	C	T	13.31%	0.00%	325	255	0.92	0.8440	0.6722	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATM	11	108203443	p.Arg2598Gln	missense_variant	A	C	13.42%	0.00%	231	194	0.93	0.8431	0.6379	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATR	X	14223599	p.Asp133Cys	missense_variant	G	A	19.75%	0.00%	324	250	1.00	0.9329	0.8651	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATR	X	14227251	p.Arg202Cys	missense_variant	G	G	10.67%	0.00%	319	197	0.75	0.4706	0.5435	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76813003	p.Arg220Asp	missense_variant	T	G	17.04%	0.00%	399	271	1.00	0.9478	0.8335	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76814228	p.Ser213Met	missense_variant	G	T	16.41%	0.00%	463	292	0.93	0.9253	0.8162	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76817189	p.Pro162Leu	missense_variant	G	A	12.49%	0.00%	448	259	0.98	0.9068	0.7526	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76807661	p.Arg150Asp	missense_variant	A	C	11.52%	0.00%	512	284	0.79	0.4708	0.6167	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76807223	p.Asp141Trp	missense_variant	G	A	12.89%	0.00%	414	244	0.91	0.8174	0.6811	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76838530	p.Glu74P	stop_gained	C	A	12.84%	0.00%	287	175	0.86	0.7724	0.6188	Clonal	Likely Pathogenic	A	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76838816	p.Val84Val	synonymous_variant	A	C	12.20%	0.00%	338	297	0.84	0.7195	0.6171	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76839248	p.Asp65Met	missense_variant	A	C	12.20%	0.00%	338	297	0.84	0.7195	0.6171	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76840067	p.Gly227Gly	synonymous_variant	T	C	11.06%	0.00%	189	127	0.76	0.6032	0.5012	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76853080	p.Arg73Gln	missense_variant	C	T	15.72%	0.00%	407	269	1.00	0.9393	0.7971	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	ATRX	X	76853080	p.Arg73Leu	missense_variant	C	T	15.72%	0.00%	407	269	1.00	0.9393	0.7971	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BAP1	3	52437189	p.Glu25Asp	missense_variant	A	C	15.22%	0.00%	381	135	1.00	0.9278	0.7720	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BAP1	3	52440379	p.Asp222Asp	missense_variant	C	T	18.25%	0.00%	274	121	1.00	0.9324	0.8002	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BAP1	3	52443767	p.Asp21Trp	missense_variant	A	T	15.29%	0.00%	457	186	0.94	0.8629	0.6838	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCL2L1	20	30030976	p.Ala81Val	missense_variant	G	A	11.89%	0.00%	295	123	0.82	0.6787	0.5887	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCL2L1	20	31107063	p.Arg153Trp	missense_variant	T	C	9.20%	0.54%	320	186	0.63	0.3747	0.4436	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39114443	p.Pro126Cys	missense_variant	G	A	17.75%	0.00%	400	221	1.00	0.9419	0.8099	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39113563	p.Arg158Gln	missense_variant	G	A	18.80%	0.00%	468	234	1.00	0.8651	0.6848	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39922203	p.Trp130Trp	synonymous_variant	G	A	4.83%	0.00%	352	123	0.73	0.3000	0.2049	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39924292	p.Ser17Trp	missense_variant	G	A	18.19%	0.00%	416	237	0.99	0.8840	0.7698	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39934335	p.Ile8Ile	synonymous_variant	G	A	10.64%	0.73%	451	137	0.73	0.3218	0.5631	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BCOR	X	39934448	p.Ala86Val	missense_variant	A	C	13.86%	0.00%	267	190	0.95	0.8676	0.6735	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BRCA1	17	11877871	p.Asp182Trp	missense_variant	G	A	18.61%	0.00%	335	169	0.91	0.8472	0.6723	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	BRCA2	13	32910880	p.Glu79P	stop_gained	G	T	14.81%	0.00%	378	237	1.00	0.9173	0.7633	Clonal	Likely Pathogenic	A	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	BRCA2	13	32912524	p.Trp153Met	missense_variant	G	A	12.89%	0.00%	424	262	0.99	0.9264	0.7867	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	BRCA2	13	32915000	p.Val219Gln	missense_variant	G	A	12.80%	0.00%	456	270	0.87	0.7530	0.6749	Clonal	Passenger	N	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	BRCA2	13	32972375	p.Arg239Gln	missense_variant	G	A	13.80%	0.56%	297	182	0.95	0.8688	0.6840	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CARD11	10	26655004	p.Arg293Gln	missense_variant	G	A	17.33%	0.00%	324	250	1.00	0.9329	0.8059	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	CARD11	10	2924121	p.Ser129Gln	missense_variant	G	C	20.00%	0.00%	420	150	1.00	0.9508	0.8936	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CBL	11	119144579	p.Trp198Asp	missense_variant	A	G	14.21%	0.00%	183	164	0.98	0.8660	0.6883	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	CBLB	3	10542095	p.Asp41Asp	synonymous_variant	G	A	16.27%	0.00%	401	210	0.99	0.8593	0.6868	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CBLB	3	10543032	p.Ile42Cys	missense_variant	G	A	10.41%	0.00%	394	277	0.72	0.2360	0.5301	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CND3	6	41908228	p.Arg49Gln	missense_variant	C	T	13.49%	0.00%	482	174	0.93	0.8604	0.7207	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CDC73	1	193119484	p.Val219Gln	missense_variant	T	C	4.89%	0.00%	434	184	0.99	0.9262	0.8192	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CDH1	16	6884234	p.Val132Asp	missense_variant	T	C	16.87%	0.00%	243	131	1.00	0.9319	0.8099	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CDK2	17	37657955	p.Arg82Trp	missense_variant	C	T	17.38%	0.00%	262	149	1.00	0.9389	0.8292	Clonal	Likely Pathogenic	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CDK2	17	37652446	p.Ile131Ile	synonymous_variant	C	T	16.85%	0.00%	404	221	1.00	0.9143	0.6778	Clonal	Passenger	N	CANCER	Passenger	TRUE	TRUE	TRUE
CCDS	CDK6	7	92349885	p.Phe164Phe	synonymous_variant	G	A	16.79%	0.42%	405	239	1.00	0.9481	0.8287	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CCDS	CDK8	13	26911717	p.Asp41Trp	missense_variant	C	T	12.60%	0.00%	373	269	0.87	0.7698	0.6492	Clonal	Passenger	D	PASS				

CC26	IC2F1	7	50688187	p.Cys644Cys	synonymous_variant	C	T	16.36%	0.00%	483	227	1.00	0.9512	0.8347	Clonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	INPFA	2	99189373	p.Leu877Ile	missense_variant	C	A	4.86%	0.00%	482	186	0.31	0.0000	0.2038	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	INSR	19	7117112	p.Lys1388Asn	missense_variant	C	A	14.67%	0.00%	461	149	1.00	0.9290	0.7830	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	INSR	19	7117241	p.Gln434Glu	missense_variant	C	A	4.48%	0.00%	393	243	0.00	0.0000	0.2038	Subclonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	IRF4	6	393179	p.Gly592Gly	synonymous_variant	C	T	13.22%	0.00%	174	48	0.91	0.8242	0.5820	Clonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	IRF4	6	4026028	p.Asn370Thr	missense_variant	C	A	12.66%	0.00%	474	227	0.87	0.7651	0.6748	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	IR51	2	22769914	p.Asn174Ile	missense_variant	C	A	4.40%	0.00%	470	192	0.00	0.0000	0.1423	Subclonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	IR51	2	22769930	p.Asn202Val	missense_variant	G	A	12.28%	0.61%	501	165	0.85	0.7134	0.6849	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	IR51	2	22769933	p.Trp184Ile	stop_gained	C	T	10.74% <th>0.00%<th>477</th><th>101</th><th>0.07</th><th>0.0060<td>0.6227</td><td>Clonal</td><td>Passenger</td><td>D</td><td>PASSSENGER/OTHER</td><td>Passenger</td><td>TRUE</td><td>TRUE</td><td>TRUE</td></th></th>	0.00% <th>477</th> <th>101</th> <th>0.07</th> <th>0.0060<td>0.6227</td><td>Clonal</td><td>Passenger</td><td>D</td><td>PASSSENGER/OTHER</td><td>Passenger</td><td>TRUE</td><td>TRUE</td><td>TRUE</td></th>	477	101	0.07	0.0060 <td>0.6227</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	0.6227	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	IR52	13	11043632	p.Asp1225Asn	missense_variant	C	T <td>12.85%</td> <td>0.00%</td> <td>166</td> <td>70</td> <td>0.87</td> <td>0.7847</td> <td>0.6575</td> <td>Clonal</td> <td>Passenger</td> <td>N</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	12.85%	0.00%	166	70	0.87	0.7847	0.6575	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	IR52	13	11043649	p.Leu1225Gln	missense_variant	C	T <td>17.00%</td> <td>0.00%</td> <td>190</td> <td>29</td> <td>1.00</td> <td>0.8902</td> <td>0.6948</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	17.00%	0.00%	190	29	1.00	0.8902	0.6948	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	IR52	13	11043650	p.Leu1225Gln	missense_variant	C	T <td>10.17%</td> <td>0.00%</td> <td>452</td> <td>308</td> <td>0.79</td> <td>0.0060</td> <td>0.5207</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	10.17%	0.00%	452	308	0.79	0.0060	0.5207	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KDR	4	5595209	p.Trp1152Thr	synonymous_variant	C	T <td>12.46%</td> <td>0.00%</td> <td>305</td> <td>171</td> <td>0.86</td> <td>0.7607</td> <td>0.6210</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	12.46%	0.00%	305	171	0.86	0.7607	0.6210	Clonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KDR	4	5595243	p.Lys887Asn	missense_variant	C	A <td>16.89%</td> <td>0.00%</td> <td>223</td> <td>161</td> <td>1.00</td> <td>0.9261</td> <td>0.7922</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Driver</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	16.89%	0.00%	223	161	1.00	0.9261	0.7922	Clonal	Likely Pathogenic	D	CANCER	Driver	TRUE	TRUE	TRUE
CC26	KDR	4	5595249	p.Arg838Ser	missense_variant	C	T <td>13.84%</td> <td>0.00%</td> <td>150</td> <td>94</td> <td>0.94</td> <td>0.8460</td> <td>0.6262</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.84%	0.00%	150	94	0.94	0.8460	0.6262	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KDR	4	5597201	p.Ala521Ala	synonymous_variant	C	T <td>13.33%</td> <td>0.00%</td> <td>390</td> <td>198</td> <td>0.92</td> <td>0.8454</td> <td>0.6918</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.33%	0.00%	390	198	0.92	0.8454	0.6918	Clonal	Passenger	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KDR	4	5597397	p.Asn476Thr	missense_variant	C	T <td>12.41%</td> <td>0.00%</td> <td>262</td> <td>145</td> <td>0.89</td> <td>0.7582</td> <td>0.6101</td> <td>Clonal</td> <td>Passenger</td> <td>N</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	12.41%	0.00%	262	145	0.89	0.7582	0.6101	Clonal	Passenger	N	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KIT	4	6959462	p.Arg376Thr	missense_variant	G	A <td>11.54%</td> <td>0.00%</td> <td>386</td> <td>197</td> <td>0.77</td> <td>0.8485</td> <td>0.5714</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	11.54%	0.00%	386	197	0.77	0.8485	0.5714	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KIT	4	55575630	p.Glu388Lys	missense_variant	C	A <td>8.73%</td> <td>0.00%</td> <td>438</td> <td>280</td> <td>0.60</td> <td>0.0058</td> <td>0.4416</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	8.73%	0.00%	438	280	0.60	0.0058	0.4416	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KIT	4	55575713	p.Lys456Asn	missense_variant	G	T <td>14.62%</td> <td>0.00%</td> <td>263</td> <td>138</td> <td>1.00</td> <td>0.8844</td> <td>0.6922</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.62%	0.00%	263	138	1.00	0.8844	0.6922	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11633365	p.Pro617Val	missense_variant	C	T <td>3.48%</td> <td>0.00%</td> <td>289</td> <td>212</td> <td>0.24</td> <td>0.0000</td> <td>0.1983</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	3.48%	0.00%	289	212	0.24	0.0000	0.1983	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11834230	p.Ser252Ser	synonymous_variant	C	T <td>13.78%</td> <td>0.00%</td> <td>312</td> <td>238</td> <td>0.95</td> <td>0.8692</td> <td>0.6889</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.78%	0.00%	312	238	0.95	0.8692	0.6889	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11834235	p.Pro251Trp	missense_variant	T <th>G</th> <td>16.29%</td> <td>0.00%</td> <td>451</td> <td>245</td> <td>1.00</td> <td>0.9558</td> <td>0.8054</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	G	16.29%	0.00%	451	245	1.00	0.9558	0.8054	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11835250	p.Lys1255Asn	missense_variant	C	T <td>11.18%</td> <td>0.29%</td> <td>653</td> <td>343</td> <td>0.77</td> <td>0.2260</td> <td>0.6124</td> <td>Subclonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	11.18%	0.29%	653	343	0.77	0.2260	0.6124	Subclonal	Likely Pathogenic	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11836046	p.Asn1567Thr	missense_variant	G	A <td>5.00%</td> <td>0.00%</td> <td>300</td> <td>170</td> <td>0.34</td> <td>0.0000</td> <td>0.2056</td> <td>Subclonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	5.00%	0.00%	300	170	0.34	0.0000	0.2056	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2A	11	11836053	p.Glu1615Val	missense_variant	G	A <td>13.23%</td> <td>0.00%</td> <td>338</td> <td>215</td> <td>0.91</td> <td>0.8309</td> <td>0.6873</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.23%	0.00%	338	215	0.91	0.8309	0.6873	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2C	7	15184234	p.Arg697Gly	stop_gained	G	A <td>20.10%</td> <td>0.00%</td> <td>383</td> <td>219</td> <td>1.00</td> <td>0.9512</td> <td>0.8896</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	20.10%	0.00%	383	219	1.00	0.9512	0.8896	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2C	7	15184609	p.Asn430Val	missense_variant	C	A <td>13.85%</td> <td>0.00%</td> <td>403</td> <td>147</td> <td>0.94</td> <td>0.8687</td> <td>0.7108</td> <td>Clonal</td> <td>Passenger</td> <td>N</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.85%	0.00%	403	147	0.94	0.8687	0.7108	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2C	7	15185027	p.Asn430Val	missense_variant	C	A <td>13.85%</td> <td>0.00%</td> <td>398</td> <td>174</td> <td>0.94</td> <td>0.8687</td> <td>0.6838</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.85%	0.00%	398	174	0.94	0.8687	0.6838	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2C	7	15186837	p.Gln314Gln	synonymous_variant	C	T <td>12.07%</td> <td>0.00%</td> <td>290</td> <td>200</td> <td>0.83</td> <td>0.7121</td> <td>0.5849</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	12.07%	0.00%	290	200	0.83	0.7121	0.5849	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2D	12	48420778	p.Arg491Trp	missense_variant	C	A <td>10.11%</td> <td>0.00%</td> <td>455</td> <td>185</td> <td>0.69</td> <td>0.1053</td> <td>0.5220</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	10.11%	0.00%	455	185	0.69	0.1053	0.5220	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2D	12	48421028	p.Asn491Trp	missense_variant	C	T <td>10.10%</td> <td>0.00%</td> <td>452</td> <td>308</td> <td>0.79</td> <td>0.0060</td> <td>0.5207</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	10.10%	0.00%	452	308	0.79	0.0060	0.5207	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	KMT2D	12	48425643	p.Arg482Gln	missense_variant	C	T <td>14.15%</td> <td>0.00%</td> <td>318</td> <td>88</td> <td>0.97</td> <td>0.8873</td> <td>0.7076</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.15%	0.00%	318	88	0.97	0.8873	0.7076	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	LDHA	11	18424551	p.Arg222Tyr	missense_variant	T <th>C</th> <td>11.06%</td> <td>0.00%</td> <td>199</td> <td>119</td> <td>0.76</td> <td>0.6332</td> <td>0.5012</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	C	11.06%	0.00%	199	119	0.76	0.6332	0.5012	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	LMO1	2	6248504	p.Arg165Gln	synonymous_variant	C	T <td>11.82%</td> <td>0.00%</td> <td>407</td> <td>268</td> <td>0.80</td> <td>0.7760</td> <td>0.6070</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	11.82%	0.00%	407	268	0.80	0.7760	0.6070	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K	7	77824369	p.Pro704Leu	missense_variant	G	A <td>18.88%</td> <td>0.00%</td> <td>295</td> <td>143</td> <td>1.00</td> <td>0.9126</td> <td>0.8423</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	18.88%	0.00%	295	143	1.00	0.9126	0.8423	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K	7	78130910	p.Glu313Tyr	missense_variant	C	T <td>15.09%</td> <td>0.00%</td> <td>232</td> <td>170</td> <td>1.00</td> <td>0.9303</td> <td>0.7053</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	15.09%	0.00%	232	170	1.00	0.9303	0.7053	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K	7	78130912	p.Asn313Tyr	missense_variant	C	T <td>15.09%</td> <td>0.00%</td> <td>232</td> <td>170</td> <td>1.00</td> <td>0.9303</td> <td>0.7189</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	15.09%	0.00%	232	170	1.00	0.9303	0.7189	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K4	10	12024475	p.Arg316Gln	missense_variant	G	A <td>18.13%</td> <td>0.00%</td> <td>320</td> <td>227</td> <td>1.00</td> <td>0.9396</td> <td>0.8343</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	18.13%	0.00%	320	227	1.00	0.9396	0.8343	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K1	5	56105091	p.Arg289Gln	missense_variant	G	A <td>17.61%</td> <td>0.79%</td> <td>443</td> <td>254</td> <td>1.00</td> <td>0.9434</td> <td>0.8882</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	17.61%	0.79%	443	254	1.00	0.9434	0.8882	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K1	5	56105494	p.Ser289Gln	missense_variant	G	A <td>17.61%</td> <td>0.79%</td> <td>443</td> <td>254</td> <td>1.00</td> <td>0.9434</td> <td>0.8882</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	17.61%	0.79%	443	254	1.00	0.9434	0.8882	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K6	10	30746491	p.Ser422Leu	missense_variant	C	T <td>15.84%</td> <td>0.00%</td> <td>358</td> <td>194</td> <td>1.00</td> <td>0.9332</td> <td>0.7800</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	15.84%	0.00%	358	194	1.00	0.9332	0.7800	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K1	22	22123563	p.Phe331Phe	synonymous_variant	C	A <td>14.72%</td> <td>0.48%</td> <td>428</td> <td>208</td> <td>1.00</td> <td>0.9184</td> <td>0.7681</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.72%	0.48%	428	208	1.00	0.9184	0.7681	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MAP3K1	22	22123570	p.Arg331Gln	missense_variant	C	A <td>14.78%</td> <td>0.00%</td> <td>344</td> <td>202</td> <td>1.00</td> <td>0.9200</td> <td>0.7436</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.78%	0.00%	344	202	1.00	0.9200	0.7436	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MEI2	X	70348158	p.Ile1074Ile	synonymous_variant	C	T <td>10.10%</td> <td>0.00%</td> <td>334</td> <td>160</td> <td>0.70</td> <td>0.2576</td> <td>0.5000</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	10.10%	0.00%	334	160	0.70	0.2576	0.5000	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MEI2	X	70449899	p.Arg1264His	missense_variant	C	A <td>15.97%</td> <td>0.00%</td> <td>357</td> <td>161</td> <td>1.00</td> <td>0.9378</td> <td>0.7884</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	15.97%	0.00%	357	161	1.00	0.9378	0.7884	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MEI2	X	70452290	p.Arg626Gln	missense_variant	C	T <td>17.07%</td> <td>0.00%</td> <td>411</td> <td>192</td> <td>1.00</td> <td>0.8349</td> <td>0.4816</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	17.07%	0.00%	411	192	1.00	0.8349	0.4816	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MEI	7	11634214	p.Arg359Gln	missense_variant	G	A <td>4.41%</td> <td>0.00%</td> <td>363</td> <td>204</td> <td>0.30</td> <td>0.0000</td> <td>0.1843</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	4.41%	0.00%	363	204	0.30	0.0000	0.1843	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MIF	3	70014016	p.Arg347Ile	stop_gained	C	T <td>14.07%</td> <td>0.00%</td> <td>263</td> <td>175</td> <td>0.97</td> <td>0.8764</td> <td>0.6810</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.07%	0.00%	263	175	0.97	0.8764	0.6810	Clonal	Likely Pathogenic	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MPL	1	43812465	p.Arg263Gln	missense_variant	C	A <td>7.88%</td> <td>0.00%</td> <td>369</td> <td>174</td> <td>0.94</td> <td>0.8056</td> <td>0.5793</td> <td>Subclonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	7.88%	0.00%	369	174	0.94	0.8056	0.5793	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MPL	1	43812374	p.Arg252Gln	missense_variant	C	A <td>13.23%</td> <td>0.00%</td> <td>461</td> <td>254</td> <td>0.91</td> <td>0.8377</td> <td>0.7032</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.23%	0.00%	461	254	0.91	0.8377	0.7032	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MPL	1	43818533	p.Arg252Gln	missense_variant	C	A <td>16.97%</td> <td>0.00%</td> <td>458</td> <td>262</td> <td>1.00</td> <td>0.9525</td> <td>0.8457</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	16.97%	0.00%	458	262	1.00	0.9525	0.8457	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MRE11A	11	94203941	p.Glu33Asp	missense_variant	C	A <td>13.38%</td> <td>0.00%</td> <td>299</td> <td>231</td> <td>0.92</td> <td>0.8441</td> <td>0.6848</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.38%	0.00%	299	231	0.92	0.8441	0.6848	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	MSH2	2	48026019	p.Lys299Lys	synonymous_variant	G	A <td>13.73%</td> <td>0.00%</td> <td>255</td> <td>203</td> <td>0.94</td> <td>0.8585</td> <td>0.6820</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.73%	0.00%	255	203	0.94	0.8585	0.6820	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MSH2	2	48026020	p.Arg299Lys	missense_variant	G	A <td>13.73%</td> <td>0.00%</td> <td>255</td> <td>203</td> <td>0.94</td> <td>0.8585</td> <td>0.6820</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.73%	0.00%	255	203	0.94	0.8585	0.6820	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MSH2	2	48033396	p.Glu334Ser	stop_gained	C	T <td>14.38%</td> <td>0.00%</td> <td>313</td> <td>214</td> <td>0.99</td> <td>0.8956</td> <td>0.7154</td> <td>Clonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.38%	0.00%	313	214	0.99	0.8956	0.7154	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	MTOR	1	11186276	p.Asn252Asn	synonymous_variant	C	T <td>14.86%</td> <td>0.76%</td> <td>315</td> <td>199</td> <td>1.00</td> <td>0.9306</td> <td>0.7255</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.86%	0.76%	315	199	1.00	0.9306	0.7255	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MTOR	1	11186683	p.Asn252Asn	synonymous_variant	C	T <td>13.00%</td> <td>0.00%</td> <td>318</td> <td>244</td> <td>0.98</td> <td>0.8262</td> <td>0.6813</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.00%	0.00%	318	244	0.98	0.8262	0.6813	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MTOR	1	11188825	p.Arg195Gln	missense_variant	C	A <td>3.80%</td> <td>0.00%</td> <td>342</td> <td>203</td> <td>0.26</td> <td>0.0000</td> <td>0.1496</td> <td>Subclonal</td> <td>Likely Pathogenic</td> <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	3.80%	0.00%	342	203	0.26	0.0000	0.1496	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE
CC26	MTOR	1	11256651	p.Glu1342Lys	missense_variant	C	A <td>16.11%</td> <td>0.00%</td> <td>298</td> <td>166</td> <td>1.00</td> <td>0.9332</td> <td>0.7444</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	16.11%	0.00%	298	166	1.00	0.9332	0.7444	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MTOR	1	11300388	p.Ser1342Lys	missense_variant	C	A <td>13.07%</td> <td>0.00%</td> <td>284</td> <td>162</td> <td>0.94</td> <td>0.8569</td> <td>0.6922</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.07%	0.00%	284	162	0.94	0.8569	0.6922	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	MYC	2	16085739	p.Asn305Asn	synonymous_variant	C	T <td>14.35%</td> <td>0.00%</td> <td>446</td> <td>235</td> <td>0.99</td> <td>0.9080</td> <td>0.7537</td> <td>Clonal</td> <td>Passenger</td> <td>N</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	14.35%	0.00%	446	235	0.99	0.9080	0.7537	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	NBN	8	80967639	p.Lys442Asn	missense_variant	C	A <td>16.67%</td> <td>0.00%</td> <td>351</td> <td>250</td> <td>1.00</td> <td>0.9335</td> <td>0.7798</td> <td>Clonal</td> <td>Passenger</td> <td>N</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	16.67%	0.00%	351	250	1.00	0.9335	0.7798	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	NCOA2	2	7100002	p.Arg165Gln	synonymous_variant	C	T <td>11.82%</td> <td>0.00%</td> <td>417</td> <td>268</td> <td>0.80</td> <td>0.7743</td> <td>0.6018</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	11.82%	0.00%	417	268	0.80	0.7743	0.6018	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	NCOA2	2	7100003	p.Arg165Gln	missense_variant	C	T <td>13.70%</td> <td>0.00%</td> <td>270</td> <td>141</td> <td>0.94</td> <td>0.8603</td> <td>0.6880</td> <td>Clonal</td> <td>Passenger</td> <td>D</td> <td>PASSSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td> <td>TRUE</td>	13.70%	0.00%	270	141	0.94	0.8603	0.6880	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE
CC26	NF1	17	29533315	p.Arg342Phe	stop_gained																	







CCSI	MYCN	2	16086051	p.Pro290Phe	synonymous_variant	G	A	24.91%	0.34%	554	295	1.0	0.7960	0.9152	Clonal	Passenger		TRUE	TRUE				
CCSI	MYO8	3	38180393	p.Ala81Ser	missense_variant	G	T	24.55%	0.00%	660	440	1.0	0.8100	0.9220	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	MYO8	3	38182897	p.Pro288Leu	synonymous_variant	C	T	20.98%	0.00%	367	207	1.00	0.9544	0.8055	Clonal	Passenger <td></td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>		PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NCOA2	7	17054403	p.Pro277Gln	missense_variant	C	T	19.01%	0.00%	277	160	1.00	0.8173	0.6218	Clonal	Passenger <td></td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>		PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NCOA2	8	71068262	p.Trp773Ile	missense_variant	G	A	19.54%	0.55%	302	182	0.97	0.8416	0.7415	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NF1	17	29509997	p.Gln291Val	missense_variant	A	T	19.48%	0.00%	267	178	0.97	0.8326	0.7262	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NF1	17	29509673	p.Asp292Glu	missense_variant	A	T	19.48%	0.00%	299	162	1.00	0.8202	0.7823	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NF1	17	29507072	p.Ala1349Thr	missense_variant	G	A	19.43%	0.00%	350	273	0.97	0.8454	0.7543	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NF1	17	29605074	p.Pro242Gln	missense_variant	G	T	7.44%	0.00%	339	192	0.37	0.0000	0.2480	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NF1	17	29617688	p.Ser271Trp	missense_variant	G	A	25.02%	0.00%	227	140	1.00	0.8899	0.8454	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>CANCER</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	CANCER	TRUE	TRUE		
CCSI	NF2	22	30047302	p.Arg282Cys	stop_gained	LOH	C	T	19.34%	1.78%	243	169	0.96	0.8212	0.7114	Clonal	Likely Pathogenic <td>A</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	A	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NF2	22	17809804	p.Gln210Cys	missense_variant	TRUE	C	T	4.92%	0.00%	305	186	0.24	0.0000	0.1444	Subclonal	Likely Pathogenic <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NFKB1	4	19302128	p.Trp435Asp	synonymous_variant	G	A	15.34%	0.00%	239	142	1.00	0.7468	0.5989	Clonal	Passenger <td></td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>		PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NFKB1	4	10353324	p.Pro798Ser	missense_variant	C	T <td>12.85%</td> <td>0.00%</td> <td>249</td> <td>144</td> <td>0.64</td> <td>0.0372</td> <td>0.2463</td> <td>Subclonal</td> <td>Passenger</td>	12.85%	0.00%	249	144	0.64	0.0372	0.2463	Subclonal	Passenger	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NFKB2	10	10413695	p.Trp777Thr	synonymous_variant	C	T	7.05%	0.48%	454	209	0.35	0.0000	0.2459	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NKX2-1	14	38697200	p.Ser168Ser	synonymous_variant	G	A	20.96%	0.00%	242	100	1.00	0.8731	0.7119	Clonal	Passenger <td></td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>		PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13949034	p.Gln219Ser	missense_variant	G	A	9.21%	0.00%	76	39	0.46	0.0713	0.2225	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13950090	p.Asp219Ser	missense_variant	C	T	8.74%	0.30%	232	136	0.29	0.0000	0.1981	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13959136	p.Ser229Gln	missense_variant	G	T	18.55%	0.00%	512	310	0.52	0.7788	0.7540	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13959229	p.His184Tyr	missense_variant	G	A	0.36%	0.00%	682	393	0.32	0.0000	0.2321	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13959744	p.Ser186Tyr	missense_variant	G	A	9.95%	0.38%	530	312	0.71	0.0659	0.5398	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH1	9	13960120	p.Gly1280Asp	missense_variant	C	T	5.88%	0.31%	612	327	0.29	0.0000	0.2078	Subclonal	Likely Pathogenic <td>D</td> <td>PASSENGER/OTHER</td> <td>Driver</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Driver	TRUE	TRUE		
CCSI	NOTCH1	9	13961334	p.Ala343Tyr	missense_variant	LOH	G	T	18.50%	0.00%	489	382	0.64	0.8128	0.7838	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH2	1	12045817	p.Arg400Cys	stop_gained	TRUE	G	A	23.34%	0.81%	287	123	1.00	0.9235	0.8343	Clonal	Likely Pathogenic <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH2	1	12046166	p.Arg193His	missense_variant	G	T	17.81%	1.41%	219	142	0.88	0.7111	0.6456	Clonal	Likely Pathogenic <td>D</td> <td>CANCER</td> <td>Driver</td> <td>TRUE</td> <td>TRUE</td>	D	CANCER	Driver	TRUE	TRUE		
CCSI	NOTCH2	1	12046207	p.Ile189Met	missense_variant	G	T	21.74%	0.30%	345	184	0.30	0.9165	0.8181	Clonal	Likely Pathogenic <td>D</td> <td>CANCER</td> <td>Driver</td> <td>TRUE</td> <td>TRUE</td>	D	CANCER	Driver	TRUE	TRUE		
CCSI	NOTCH2	1	12046436	p.Arg127Gln	missense_variant	G	A	20.15%	0.00%	273	159	1.00	0.8651	0.7520	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12046913	p.Ala133Cys	missense_variant	G	A	19.27%	0.00%	327	209	0.96	0.8336	0.7421	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12049771	p.Asp136Gln	missense_variant	G	A	8.98%	0.00%	227	135	0.63	0.0000	0.1228	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12049622	p.Arg75Tyr	missense_variant	G	T	18.32%	0.00%	191	140	0.91	0.7511	0.6488	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12049778	p.Ala92Val	missense_variant	G	A	18.28%	0.00%	219	96	0.91	0.7485	0.6823	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12051208	p.Ala82Met	missense_variant	G	A	15.88%	0.00%	279	162	0.98	0.8467	0.7278	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH2	1	12051233	p.Gln33Tyr	missense_variant	G	T	15.28%	0.00%	216	134	0.76	0.3441	0.5441	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15278999	p.Ala177Ser	missense_variant	C	T	19.70%	1.54%	467	259	0.98	0.8717	0.7903	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15280000	p.Ser177Ser	missense_variant	C	T	20.28%	0.00%	401	260	1.00	0.8669	0.7990	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15284964	p.Gly156Ile	missense_variant	C	T	23.81%	0.00%	481	300	1.00	0.9269	0.8914	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15285030	p.Ala159Ile	missense_variant	C	T	23.02%	0.00%	291	165	1.00	0.9229	0.8310	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15285163	p.Asp140Tyr	missense_variant	C	T	7.15%	0.80%	324	194	0.60	0.0000	0.2448	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15285172	p.Asp148Asp	synonymous_variant	G	A	17.52%	0.00%	411	258	0.87	0.8359	0.6938	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	NOTCH3	19	15296390	p.Pro68Ala	synonymous_variant	LOH	G	T	21.16%	0.44%	320	229	1.00	0.9195	0.8296	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH3	19	15296984	p.Asp173Val	splice_region_variant	synonymous_variant	LOH	G	A	9.82%	0.27%	470	392	0.49	0.0000	0.3742	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE
CCSI	NOTCH3	19	32163302	p.Ala177Val	missense_variant	LOH	G	A	34.45%	0.00%	119	107	1.00	0.8641	0.8296	Clonal	Likely Pathogenic <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	CANCER	Passenger	TRUE	TRUE	
CCSI	NOTCH4	6	32166303	p.Leu151Pro	missense_variant	LOH	G	A	29.07%	0.00%	258	208	1.00	0.9369	0.8499	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH4	6	32166714	p.Ala154Met	missense_variant	LOH	G	A	27.02%	0.00%	113	89	0.60	0.3461	0.4978	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH4	6	32185787	p.Ala53Asp	synonymous_variant	LOH	G	A	22.74%	0.00%	321	259	0.90	0.9739	0.7221	Clonal	Passenger <td>N</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	N	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NOTCH4	6	32190340	p.Gln133Cys	synonymous_variant	LOH	G	A	22.15%	0.00%	299	241	0.88	0.6941	0.6938	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE	
CCSI	NTRK1	1	14663363	p.Pro37Tyr	missense_variant	LOH	G	A	19.68%	0.00%	113	89	0.60	0.7911	0.6920	Clonal	Likely Pathogenic <td>D</td> <td>CANCER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	CANCER	Passenger	TRUE	TRUE	
CCSI	NTRK1	1	14684465	p.Ser252Ser	synonymous_variant	T <td>C</td> <td>21.89%</td> <td>0.00%</td> <td>402</td> <td>214</td> <td>1.00</td> <td>0.9261</td> <td>0.8376</td> <td>Clonal</td> <td>Passenger</td>	C	21.89%	0.00%	402	214	1.00	0.9261	0.8376	Clonal	Passenger	D	CANCER	Passenger	TRUE	TRUE		
CCSI	NTRK2	1	8707008	p.Gln64Asp	missense_variant	A <td>G</td> <td>26.81%</td> <td>0.00%</td> <td>186</td> <td>88</td> <td>1.00</td> <td>0.8975</td> <td>0.8265</td> <td>Clonal</td> <td>Likely Pathogenic</td>	G	26.81%	0.00%	186	88	1.00	0.8975	0.8265	Clonal	Likely Pathogenic	D	CANCER	Driver	TRUE	TRUE		
CCSI	NTRK2	1	8808665	p.Asp116Met	missense_variant	A <td>G</td> <td>8.58%</td> <td>0.00%</td> <td>292</td> <td>175</td> <td>0.42</td> <td>0.0000</td> <td>0.2895</td> <td>Subclonal</td> <td>Passenger</td>	G	8.58%	0.00%	292	175	0.42	0.0000	0.2895	Subclonal	Passenger	D	CANCER	Driver	TRUE	TRUE		
CCSI	PKnox1	20	8520309	p.Ser61Pro	missense_variant	A <td>G</td> <td>22.31%</td> <td>0.00%</td> <td>209</td> <td>118</td> <td>1.00</td> <td>0.8933</td> <td>0.7993</td> <td>Clonal</td> <td>Likely Pathogenic</td>	G	22.31%	0.00%	209	118	1.00	0.8933	0.7993	Clonal	Likely Pathogenic	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PKnox1	20	8568988	p.Ser61Pro	missense_variant	A <td>G</td> <td>22.31%</td> <td>0.00%</td> <td>209</td> <td>118</td> <td>1.00</td> <td>0.8933</td> <td>0.7993</td> <td>Clonal</td> <td>Likely Pathogenic</td>	G	22.31%	0.00%	209	118	1.00	0.8933	0.7993	Clonal	Likely Pathogenic	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PKnox1	20	8561383	p.Ser133Ser	synonymous_variant	G	A	15.84%	0.55%	303	155	0.75	0.3634	0.5976	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PALB2	16	23646582	p.Gln37Tyr	missense_variant	C	A	5.67%	0.00%	141	60	0.28	0.0000	0.1408	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PALB2	16	23646582	p.Ser148Ser	missense_variant	C	T	19.48%	0.00%	257	153	0.97	0.8207	0.7215	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PALB2	16	23647187	p.Asp224Asp	synonymous_variant	C	T	19.48%	0.00%	257	153	0.97	0.8207	0.7215	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Arg24Pro	synonymous_variant	G	A	21.29%	1.00%	155	92	1.00	0.8586	0.7120	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Ala22Met	missense_variant	G	A	16.37%	0.00%	123	69	0.63	0.0000	0.1489	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Ala22Met	missense_variant	G	A	16.37%	0.00%	123	69	0.63	0.0000	0.1489	Subclonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00	0.8787	0.7696	Clonal	Passenger <td>D</td> <td>PASSENGER/OTHER</td> <td>Passenger</td> <td>TRUE</td> <td>TRUE</td>	D	PASSENGER/OTHER	Passenger	TRUE	TRUE		
CCSI	PARK2	6	16220934	p.Asp24Tyr	missense_variant	G	A	20.33%	0.52%	300	192	1.00											

CC31	SNHG	1	17356577	p.Thc8Thr	synonymous_variant	G	T	15.82%	0.94%	397	212	0.78	0.2289	0.6108	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SETD2	3	47125634	p.Arg197His	missense_variant	C	T	4.23%	0.00%	189	119	0.21	0.0000	0.1033	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SETD2	3	47188224	p.Arg1482Gln	missense_variant	C	T	9.38%	0.00%	256	205	0.47	0.0001	0.3122	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SETD2	3	47188228	p.Arg1482Gln	stop_gain	G	A	1.00%	0.00%	132	132	0.62	0.0000	0.6403	Clonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	SF3B1	2	18828792	p.Glu1061Glu	synonymous_variant	C	T	17.88%	0.38%	380	267	0.89	0.1726	0.7066	Clonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SF3B1	2	18828793	p.Glu809Asp	missense_variant	C	A	5.26%	0.35%	437	289	0.26	0.0000	0.1708	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SF3B1	2	18828794	p.Glu809Asp	missense_variant	C	A	22.03%	0.00%	454	246	1.00	0.0001	0.8413	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SHQ1	3	72866403	p.Arg27His	missense_variant	C	T	22.22%	0.00%	306	171	1.00	0.9175	0.8180	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMAD2	18	45395764	p.Pro124Ser	missense_variant	C	T	17.00%	0.75%	229	133	0.89	0.1705	0.6540	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMAD2	18	45395765	p.Ser115Ser	synonymous_variant	C	A	5.21%	0.00%	211	119	0.25	0.0000	0.1417	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SMAD3	15	67457653	p.Arg159Asn	missense_variant	G	A	19.27%	0.00%	654	398	0.96	0.8550	0.8016	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMAD3	15	67473723	p.Arg230Gln	missense_variant	G	A	9.92%	0.00%	484	300	0.47	0.0000	0.3038	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMAD4	19	48584504	p.Arg270Val	missense_variant	T	T	7.67%	0.00%	194	108	0.36	0.0001	0.2038	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11094934	p.Pro31Leu	missense_variant	G	T	25.75%	0.00%	299	219	1.00	0.8697	0.8758	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11094964	p.Ser49Ile	missense_variant	G	T	9.73%	0.00%	298	227	0.48	0.0000	0.3098	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11095043	p.Met70Ile	missense_variant	C	A	19.70%	0.30%	401	288	0.98	0.8676	0.7779	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11095893	p.Glu128Asp	missense_variant	G	T	19.86%	0.30%	521	329	0.99	0.8929	0.8157	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11103597	p.Arg90Iyr	missense_variant	G	T	7.74%	0.00%	452	275	0.38	0.0000	0.2739	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11144146	p.Arg124Ile	missense_variant	C	T	23.92%	0.63%	430	319	1.00	0.9414	0.8881	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11144517	p.Pro128Ser	synonymous_variant	C	T	5.33%	0.43%	729	466	0.27	0.0000	0.1907	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11150223	p.Arg142Asn	synonymous_variant	C	A	16.14%	0.33%	502	304	0.80	0.2423	0.6486	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SMARCA4	19	11176648	p.Arg161Tyr	synonymous_variant	A	A	16.77%	0.00%	488	284	0.83	0.4333	0.3692	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SMARCB1	22	24167350	p.Arg132Thr	missense_variant	G	A	5.00%	0.00%	360	205	0.25	0.0000	0.1034	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMD	7	12862972	p.Gly4Asp	missense_variant	G	A	3.18%	0.00%	377	223	0.16	0.0000	0.0692	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMD	7	12865131	p.Arg65His	missense_variant	G	A	17.80%	0.67%	472	299	0.88	0.8702	0.7165	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SMD	7	12865203	p.Pro68Ile	frameshift_variant	AC	A	18.32%	0.27%	644	375	0.91	0.7372	0.7618	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SRC	20	3012635	p.Arg27Thr	missense_variant	C	A	30.28%	0.30%	109	81	1.00	0.7723	0.8168	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SRC	20	3014503	p.Leu101Leu	synonymous_variant	C	C	6.26%	0.00%	231	268	0.31	0.0000	0.2108	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	SRC	20	3022235	p.Gly130Asn	missense_variant	A	A	18.29%	0.00%	525	309	0.91	0.7475	0.7464	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SRC	20	3031742	p.Trp246Met	missense_variant	C	T	19.80%	0.27%	607	373	0.99	0.8024	0.8188	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	STAT3	X	12318602	p.Arg37Gln	missense_variant	G	A	18.83%	0.85%	377	234	0.93	0.8045	0.7386	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	STAT3	X	12319005	p.Arg42Thr	missense_variant	G	A	7.24%	0.00%	373	242	0.36	0.0000	0.2444	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	STK11	19	1237052	p.Gln24Ile	missense_variant	C	T	20.13%	0.00%	254	228	0.86	0.9153	0.8378	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	STK11	19	1221971	p.Lys256Asn	missense_variant	G	T	19.76%	0.00%	582	412	0.98	0.8836	0.8106	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	STK11	19	1223054	p.Arg331Trp	missense_variant	C	T	20.28%	0.00%	688	468	1.00	0.9127	0.8400	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SYK	9	9363453	p.Arg142Gln	missense_variant	C	T	20.28%	0.00%	688	468	1.00	0.9127	0.8400	Clonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	SYK	9	9363888	p.Asn408Asn	synonymous_variant	C	T	17.30%	0.47%	310	213	0.86	0.6101	0.6759	Clonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	TBK1	12	64860749	p.Arg142Cys	missense_variant	C	T	18.88%	0.42%	359	237	0.91	0.7630	0.7170	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TBK1	12	64869203	p.Arg142Cys	missense_variant	C	T	22.76%	0.00%	430	259	1.00	0.9384	0.8480	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TBK1	12	6489098	p.Gln33Gln	synonymous_variant	A	A	19.19%	0.48%	370	209	0.95	0.8301	0.7499	Clonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	TBK1	12	64891510	p.Arg681Ser	missense_variant	A	G	19.38%	0.00%	280	195	0.96	0.8312	0.7915	Clonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9261934	p.Glu169Asp	missense_variant	A	G	7.67%	0.00%	374	229	0.36	0.0000	0.2424	Subclonal	Likely Pathogenic	D	CANCER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	92718816	p.Arg171	stop_gain	C	T	5.67%	0.00%	194	79	0.28	0.0000	0.1545	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	92718904	p.Glu169Lys	missense_variant	A	G	7.66%	0.00%	225	133	0.37	0.0000	0.2224	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9272014	p.Ser49Phe	missense_variant	A	G	4.82%	0.00%	242	141	0.24	0.0000	0.2424	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9272111	p.Val79Ile	missense_variant	C	T	7.01%	0.49%	613	408	0.35	0.0000	0.2654	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9272180	p.His74Ser	missense_variant	A	A	16.63%	0.36%	403	290	0.83	0.4150	0.6662	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9272181	p.Trp41Ile	missense_variant	C	T	22.76%	0.00%	430	259	1.00	0.9384	0.8480	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9272993	p.Gly33Gln	synonymous_variant	G	A	5.46%	0.00%	313	360	0.27	0.0000	0.1837	Subclonal	Passenger	D			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273195	p.Arg28Ser	missense_variant	C	T	21.00%	0.00%	321	207	1.00	0.9085	0.8055	Clonal	Passenger	N	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273317	p.Met69Phe	missense_variant	A	A	4.82%	0.00%	253	141	0.24	0.0000	0.1336	Subclonal	Passenger	D	PASSSENGER/OTHER	Passenger	TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273383	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114	0.76	0.4476	0.5068	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273402	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114	0.76	0.4476	0.5068	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273403	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114	0.76	0.4476	0.5068	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273404	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114	0.76	0.4476	0.5068	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273405	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114	0.76	0.4476	0.5068	Subclonal	Passenger	A			TRUE	TRUE	TRUE	TRUE
CC31	TEK	9	9273406	p.Arg50P	stop_gain	C	T	15.23%	1.73%	111	114												