Supplementary Table S2: List of somatic mutations identified in the cohort of 35 metaplastic breast cancers and list of primers used for validation with Sanger sequencing of selected mutations.

Sample name	Gene	Mutation	Effect	Chromo-some	Position	Reference allele	Alternate allele	Mutant allele fraction	Depth	Mutation Taster	FATHMM	CHASM	Provean	Cancer Gene Census	Kandoth et al 127 significantly mutated genes	Lawrence et al Cancer5000-S genes	Haplo-insufficient	LOH	Pathogenicity	Probability of mutation being clonal	Lower bound of 95% confidence interval for cancer cell fraction	Upper bound of 95% confidence interval for cancer cell fraction	Cancer cell fraction	Clonal	Validated using Sanger sequencing	Forward primer for Sanger sequencing	Reverse primer for Sanger sequencing
META31	*MMEL1*	p.Val141Ile	missense_variant	1	2541142	C	T	32.00%	25	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4224	46.20%	100.00%	97%	Subclonal			
META31	*PRDM16*	p.Asp36Asp	synonymous_variant	1	3102759	C	T	31.43%	35	.	.	.		true	.	.			.	0.4396	51.33%	100.00%	95%	Subclonal			
META31	*CEP104*	p.Gly392Gly	synonymous_variant	1	3753200	C	T	7.59%	79	.	.	.		.	.	.			.	0.0000	10.32%	46.65%	23%	Subclonal			
META31	*ENO1*	p.Arg50Arg	synonymous_variant	1	8931981	C	A	5.15%	97	.	.	.		.	.	.			.	0.0000	6.35%	34.25%	16%	Subclonal			
META31	*SPEN*	p.Asn870fs	frameshift_variant	1	16255339	GA	G	16.79%	131	A	.	.		.	.	true			Likely pathogenic	0.0001	33.84%	72.39%	51%	Subclonal			
META31	*HSPG2*	p.Arg92His	missense_variant	1	22217157	C	T	36.96%	92	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7019	75.58%	100.00%	100%	Clonal			
META31	*ZBTB40*	p.Lys803dup	disruptive_inframe_insertion	1	22838560	C	CAAG	17.78%	45	P	.	.	Neutral	.	.	.			Likely passenger	0.0414	27.68%	90.42%	54%	Subclonal			
META31	*ARID1A*	p.Pro1349fs	frameshift_variant	1	27100330	AC	A	22.22%	99	A	.	.		true	true	true			Likely pathogenic	0.0464	45.26%	92.34%	67%	Subclonal			
META31	*ZMYM4*	p.Ser18fs	frameshift_variant	1	35790967	C	CA	20.00%	40	A	.	.		.	.	.			Indeterminate	0.0954	31.16%	94.77%	60%	Subclonal			
META31	*NRD1*	p.Thr207Ala	missense_variant	1	52305909	T	C	39.34%	61	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6828	72.70%	100.00%	100%	Clonal			
META31	*TMEM59*	p.Asp174Asp	synonymous_variant	1	54509067	G	A	20.00%	30	.	.	.		.	.	.			.	0.1263	28.05%	95.88%	60%	Subclonal			
META31	*C1orf87*	p.Gly129Arg	missense_variant	1	60506761	C	T	18.18%	44	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0495	28.32%	91.44%	55%	Subclonal			
META31	*USP33*	p.Arg277*	stop_gained	1	78194379	G	A	33.78%	74	A	.	.		.	.	.			Indeterminate	0.5890	67.47%	100.00%	100%	Clonal			
META31	*SH3GLB1*	p.Leu179Leu	synonymous_variant	1	87190055	A	T	20.83%	24	.	.	.		.	.	.			.	0.1652	27.00%	96.85%	63%	Subclonal			
META31	*PKN2*	p.Arg917fs	frameshift_variant	1	89298831	A	AT	22.50%	40	D	.	.		.	.	.			Indeterminate	0.1627	36.32%	96.86%	68%	Subclonal			
META31	*NBPF6*	p.Pro648Pro	synonymous_variant	1	109010269	G	A	6.33%	79	.	.	.		.	.	.			.	0.0000	7.97%	41.73%	19%	Subclonal			
META31	*KCNA10*	p.Ala370Val	missense_variant	1	111060301	G	A	5.95%	84	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.42%	39.35%	18%	Subclonal			
META31	*KCNA10*	p.Val88Ala	missense_variant	1	111061147	A	G	9.33%	75	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.53%	54.02%	28%	Subclonal			
META31	*NOTCH2*	p.Asp1481Asp	synonymous_variant	1	120467996	A	G	3.48%	374	.	.	.		true	.	.			.	0.0006	24.20%	69.85%	42%	Subclonal			
META31	*PDE4DIP*	p.Ala347Thr	missense_variant	1	144921990	C	T	3.63%	689	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.0000	19.33%	42.01%	29%	Subclonal			
META31	*TXNIP*	p.Tyr279Tyr	synonymous_variant	1	145440637	T	C	7.33%	150	.	.	.		.	.	.			.	0.0027	24.60%	75.55%	44%	Subclonal			
META31	*CA14*	c.863-2A>G	splice_acceptor_variant	1	150236191	A	G	16.81%	357	D	.	.		.	.	.			Indeterminate	0.6593	76.21%	100.00%	100%	Clonal			
META31	*FLG*	p.Gly387Cys	missense_variant	1	152286203	C	A	10.78%	306	N	PASSENGER/OTHER	Passenger		.	.	true			Likely passenger	0.0144	46.38%	87.92%	65%	Subclonal			
META31	*NUP210L*	p.Thr864Ala	missense_variant	1	154034115	T	C	5.68%	88	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0053	14.61%	74.89%	34%	Subclonal			
META31	*UBAP2L*	p.Pro875Pro	synonymous_variant	1	154233414	G	A	5.94%	101	.	.	.		.	.	.			.	0.0037	16.36%	73.59%	36%	Subclonal			
META31	*CLK2*	p.Arg45Cys	missense_variant	1	155240636	G	A	7.89%	152	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0053	27.19%	79.23%	48%	Subclonal			
META31	*RUSC1*	p.Leu771Gln	missense_variant	1	155296821	T	A	10.23%	88	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1151	32.40%	95.60%	62%	Subclonal			
META31	*IGSF8*	p.Cys544Tyr	missense_variant	1	160062167	C	T	15.52%	58	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3987	45.47%	100.00%	93%	Subclonal			
META31	*CD84*	p.Arg84Trp	missense_variant	1	160535332	G	A	10.00%	230	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0138	40.24%	86.59%	60%	Subclonal			
META31	*SH2D1B*	p.Ser105Ile	missense_variant	1	162368762	C	A	5.69%	123	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0009	16.49%	67.38%	34%	Subclonal			
META31	*F5*	p.Thr206Thr	synonymous_variant	1	169528503	C	T	12.10%	124	.	.	.		.	.	.			.	0.1937	44.07%	97.46%	73%	Subclonal			
META31	*SELL*	p.Thr121Thr	synonymous_variant	1	169677706	A	G	12.11%	190	.	.	.		.	.	.			.	0.1434	48.73%	96.61%	73%	Subclonal			
META31	*METTL11B*	p.Ala56Ala	synonymous_variant	1	170129672	T	G	3.60%	222	.	.	.		.	.	.			.	0.0000	10.68%	41.32%	22%	Subclonal			
META31	*TNN*	p.Thr994Thr	synonymous_variant	1	175096158	G	A	14.17%	127	.	.	.		.	.	.			.	0.3589	53.04%	98.85%	85%	Subclonal			
META31	*RNASEL*	p.Ser591Ile	missense_variant	1	182551188	C	A	5.70%	228	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	19.85%	56.76%	34%	Subclonal			
META31	*RNASEL*	p.Pro242Thr	missense_variant	1	182555218	G	T	20.88%	91	N	CANCER	Passenger		.	.	.			Likely passenger	0.6381	67.85%	100.00%	100%	Clonal			
META31	*LAMC1*	p.Val503Ile	missense_variant	1	183085981	G	A	5.51%	127	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0006	15.98%	65.34%	33%	Subclonal			
META31	*ARPC5*	p.Gln59His	missense_variant	1	183602265	C	A	8.00%	125	D	.	Passenger		.	.	.			Indeterminate	0.0128	26.20%	83.38%	48%	Subclonal			
META31	*ZBTB41*	p.Gly627Gly	synonymous_variant	1	197144244	A	G	20.83%	120	.	.	.		.	.	.			.	0.6748	72.42%	100.00%	100%	Clonal			
META31	*CSRP1*	p.Gly78Gly	synonymous_variant	1	201459351	G	A	23.21%	56	.	.	.		.	.	.			.	0.6319	63.26%	100.00%	100%	Clonal			
META31	*IPO9*	p.His475Tyr	missense_variant	1	201828077	C	T	17.24%	58	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.4654	50.44%	100.00%	100%	Subclonal			
META31	*LGR6*	p.Arg844His	missense_variant	1	202287962	G	A	12.86%	70	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2765	39.67%	98.33%	77%	Subclonal			
META31	*FMOD*	p.Arg274Trp	missense_variant	1	203316579	G	A	14.63%	123	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3936	54.39%	100.00%	88%	Subclonal			
META31	*CR1*	p.Asp2254Val	missense_variant	1	207790019	A	T	7.82%	371	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	32.63%	65.75%	47%	Subclonal			
META31	*PLXNA2*	p.Pro1822Pro	synonymous_variant	1	208201477	T	C	7.41%	81	.	.	.		.	.	.			.	0.0284	20.51%	87.29%	45%	Subclonal			
META31	*USH2A*	p.Ser1741Tyr	missense_variant	1	216256874	G	T	5.43%	184	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	17.57%	57.97%	33%	Subclonal			
META31	*MIA3*	p.Ala87Val	missense_variant	1	222794627	C	T	11.96%	92	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2101	39.90%	97.66%	72%	Subclonal			
META31	*URB2*	p.Ser558Asn	missense_variant	1	229772033	G	A	8.99%	89	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0617	27.50%	92.53%	54%	Subclonal			
META31	*URB2*	p.Arg567Gln	missense_variant	1	229772060	G	A	9.30%	129	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0367	32.15%	90.04%	56%	Subclonal			
META31	*EXOC8*	p.Ala308Thr	missense_variant	1	231472570	C	T	19.08%	131	D	.	Passenger		.	.	.			Indeterminate	0.6425	69.73%	100.00%	100%	Clonal			
META31	*PCNXL2*	p.Lys619fs	frameshift_variant	1	233388512	CT	C	13.24%	136	A	.	.		.	.	.			Indeterminate	0.2792	50.07%	98.37%	80%	Subclonal			
META31	*LYST*	p.Asp2130Gly	missense_variant	1	235922764	T	C	14.17%	120	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3579	52.23%	98.84%	85%	Subclonal			
META31	*EDARADD*	p.Leu185Phe	missense_variant	1	236645854	C	T	6.10%	82	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0102	15.72%	79.44%	37%	Subclonal			
META31	*CHRM3*	p.Lys567fs	frameshift_variant	1	240072443	CA	C	15.13%	119	D	.	.		.	.	.			Indeterminate	0.4273	55.77%	100.00%	91%	Subclonal			
META31	*FH*	p.Thr277Thr	synonymous_variant	1	241669376	A	G	8.74%	103	.	.	.		true	.	.			.	0.0401	27.76%	90.14%	53%	Subclonal			
META31	*CHML*	p.Thr373Ala	missense_variant	1	241797952	T	C	5.67%	141	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0004	17.18%	64.49%	34%	Subclonal			
META31	*WDR64*	p.His748Arg	missense_variant	1	241934982	A	G	7.04%	71	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0309	18.21%	87.58%	42%	Subclonal			
META31	*HNRNPU*	p.Ala588Val	missense_variant	1	245019908	G	A	9.77%	174	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0259	36.85%	88.80%	59%	Subclonal			
META31	*OR2M2*	p.Ser21Arg	missense_variant	1	248343348	A	C	6.10%	328	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	23.52%	55.07%	37%	Subclonal			
META31	*OR14C36*	p.Phe105fs	frameshift_variant	1	248512383	GT	G	11.76%	85	D	.	.		.	.	.			Indeterminate	0.2042	38.15%	97.58%	71%	Subclonal			
META31	*TEX261*	p.Ala116fs	frameshift_variant	2	71216905	C	CA	22.22%	45	D	.	.		.	.	.			Indeterminate	0.1417	37.13%	96.41%	67%	Subclonal			
META31	*NAT8B*	p.Ala50fs	frameshift_variant	2	73928284	GC	G	14.29%	49	.	.	.		.	.	.			Indeterminate	0.0074	21.14%	79.66%	43%	Subclonal			
META31	*MTHFD2*	p.Met207Val	missense_variant	2	74437125	A	G	50.00%	12	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5856	50.40%	100.00%	100%	Clonal			
META31	*HK2*	p.Tyr461Cys	missense_variant	2	75107508	A	G	20.00%	35	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1102	29.73%	95.36%	60%	Subclonal			
META31	*LIPT1*	p.Lys123fs	frameshift_variant	2	99778780	CA	C	18.07%	83	D	.	.		.	.	.			Indeterminate	0.0073	33.59%	82.92%	55%	Subclonal			
META31	*POTEI*	p.Arg95Gly	missense_variant	2	131266526	T	C	6.11%	262	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	11.02%	28.78%	18%	Subclonal			
META31	*LRP1B*	p.Pro4538Pro	synonymous_variant	2	140992400	C	T	21.74%	23	.	.	.		.	.	.			.	0.1882	28.03%	97.28%	66%	Subclonal			
META31	*SCN3A*	p.Ser1753Gly	missense_variant	2	165947406	T	C	5.85%	171	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.24%	30.98%	18%	Subclonal			
META31	*LRP2*	p.Ser4075Ser	synonymous_variant	2	170011040	T	C	7.35%	68	.	.	.		.	.	.			.	0.0000	9.32%	48.13%	22%	Subclonal			
META31	*TTN*	p.Ala20265Asp	missense_variant	2	179455658	G	T	22.84%	197	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0076	52.43%	87.56%	69%	Subclonal			
META31	*CCDC141*	p.Asp904Asp	synonymous_variant	2	179730506	G	A	3.24%	185	.	.	.		.	.	.			.	0.0000	4.10%	20.32%	10%	Subclonal			
META31	*CWC22*	p.Lys505Asn	missense_variant	2	180819705	T	A	11.63%	43	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0033	15.11%	73.37%	35%	Subclonal			
META31	*ICA1L*	p.Ala412Val	missense_variant	2	203653561	G	A	29.03%	31	N	.	Passenger		.	.	.			Likely passenger	0.3680	45.16%	98.88%	88%	Subclonal			
META31	*RAPH1*	p.Pro765fs	frameshift_variant	2	204305618	TG	T	22.73%	22	D	.	.		.	.	.			Indeterminate	0.2125	29.11%	97.64%	69%	Subclonal			
META31	*CRYGC*	p.Ala159fs	frameshift_variant	2	208992976	G	GC	32.39%	71	D	.	.		.	.	.			Indeterminate	0.5370	64.37%	100.00%	98%	Clonal			
META31	*VIL1*	p.Arg184Arg	synonymous_variant	2	219293045	T	C	26.47%	34	.	.	.		.	.	.			.	0.2964	41.99%	98.46%	80%	Subclonal			
META31	*RNF25*	p.Pro375Pro	synonymous_variant	2	219528935	A	G	22.06%	68	.	.	.		.	.	.			.	0.0863	41.25%	94.63%	67%	Subclonal			
META31	*MFF*	p.Thr23Thr	synonymous_variant	2	228195372	T	A	10.17%	59	.	.	.		.	.	.			.	0.0002	14.06%	61.41%	31%	Subclonal			
META31	*KCNJ13*	p.Arg305Pro	missense_variant	2	233633070	C	G	15.69%	102	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0003	29.43%	71.94%	47%	Subclonal			
META31	*TRPM8*	p.Arg119Cys	missense_variant	2	234847648	C	T	26.19%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2826	44.49%	98.37%	79%	Subclonal			
META31	*ITPR1*	p.Tyr1340Cys	missense_variant	3	4735208	A	G	11.41%	184	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	22.43%	50.32%	34%	Subclonal			
META31	*TOP2B*	p.Glu103Gly	missense_variant	3	25685193	T	C	5.93%	135	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.75%	33.52%	18%	Subclonal			
META31	*SETD2*	p.Arg2122Trp	missense_variant	3	47098910	G	A	27.59%	58	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.3287	51.87%	98.68%	83%	Subclonal			
META31	*RBM6*	p.Lys834fs	frameshift_variant	3	50099449	GA	G	14.04%	57	A	.	.		.	.	.			Indeterminate	0.0033	21.67%	75.92%	42%	Subclonal			
META31	*DOCK3*	p.Ala1842Thr	missense_variant	3	51417579	G	A	32.50%	40	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4806	55.44%	100.00%	98%	Subclonal			
META31	*KBTBD8*	p.Ala237fs	frameshift_variant	3	67054094	A	AT	16.88%	77	A	.	.		.	.	.			Indeterminate	0.0047	30.21%	80.24%	51%	Subclonal			
META31	*OR5H2*	p.Asn94fs	frameshift_variant	3	98002007	CA	C	11.98%	167	D	.	.		.	.	.			Indeterminate	0.0000	23.35%	53.20%	36%	Subclonal			
META31	*IMPG2*	p.Glu1239Gly	missense_variant	3	100945823	T	C	15.63%	32	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0427	20.47%	90.04%	47%	Subclonal			
META31	*DBR1*	p.Pro350Pro	synonymous_variant	3	137881316	A	G	18.52%	27	.	.	.		.	.	.			.	0.1059	24.20%	95.09%	56%	Subclonal			
META31	*TRIM42*	p.Cys196Cys	synonymous_variant	3	140401550	C	T	17.54%	57	.	.	.		.	.	.			.	0.0208	29.25%	86.86%	53%	Subclonal			
META31	*SKIL*	p.Met32fs	frameshift_variant	3	170078206	GA	G	14.12%	85	A	.	.		.	.	.			Indeterminate	0.0003	24.55%	69.25%	43%	Subclonal			
META31	*TBL1XR1*	p.Phe322Leu	missense_variant	3	176756184	A	G	19.64%	56	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.0510	33.77%	91.94%	59%	Subclonal			
META31	*ATP11B*	p.Tyr884fs	frameshift_variant	3	182602673	AT	A	20.88%	91	A	.	.		.	.	.			Indeterminate	0.0283	41.17%	89.90%	63%	Subclonal			
META31	*BDH1*	p.Arg44Gln	missense_variant	3	197260385	C	T	8.93%	56	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	11.44%	57.76%	27%	Subclonal			
META31	*ZNF721*	p.Leu22Leu	synonymous_variant	4	438190	C	T	21.43%	56	.	.	.		.	.	.			.	0.0923	37.79%	94.79%	65%	Subclonal			
META31	*TADA2B*	p.Arg312Arg	synonymous_variant	4	7056454	G	A	13.54%	96	.	.	.		.	.	.			.	0.0001	24.02%	65.41%	41%	Subclonal			
META31	*RELL1*	p.Pro262Pro	synonymous_variant	4	37633040	A	G	19.18%	146	.	.	.		.	.	.			.	0.0009	40.63%	78.99%	58%	Subclonal			
META31	*FIP1L1*	p.Ile195Met	missense_variant	4	54257255	A	G	11.11%	126	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0000	19.92%	53.26%	34%	Subclonal			
META31	*TMPRSS11A*	p.Glu49fs	frameshift_variant	4	68810345	C	CT	17.86%	56	A	.	.		.	.	.			Indeterminate	0.0251	29.80%	87.93%	54%	Subclonal			
META31	*UGT2B10*	p.Asn201fs	frameshift_variant	4	69885464	AT	A	14.41%	118	.	.	.		.	.	.			Indeterminate	0.0000	27.31%	65.58%	43%	Subclonal			
META31	*USO1*	p.Phe203fs	frameshift_variant	4	76703899	AT	A	22.03%	59	A	.	.		.	.	.			Indeterminate	0.1034	39.71%	95.30%	67%	Subclonal			
META31	*FRAS1*	p.Ser3908Asn	missense_variant	4	79461962	G	A	22.22%	99	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0464	45.26%	92.34%	67%	Subclonal			
META31	*KLHL8*	p.Met493Ile	missense_variant	4	88091289	C	A	14.71%	68	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0020	24.35%	75.00%	44%	Subclonal			
META31	*SMARCAD1*	p.Asn347fs	frameshift_variant	4	95173909	TA	T	29.27%	41	A	.	.		.	.	.			Indeterminate	0.3874	50.12%	98.96%	88%	Subclonal			
META31	*SMARCAD1*	c.1482-2A>G	splice_acceptor_variant	4	95191877	A	G	19.61%	51	D	.	.		.	.	.			Indeterminate	0.0600	32.79%	92.68%	59%	Subclonal			
META31	*SMARCAD1*	p.His786Arg	missense_variant	4	95200134	A	G	21.05%	38	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1272	32.75%	95.96%	64%	Subclonal			
META31	*TSPAN5*	p.His5His	synonymous_variant	4	99579363	G	A	6.10%	82	.	.	.		.	.	.			.	0.0000	7.62%	40.27%	18%	Subclonal			
META31	*TET2*	p.Asn811Asn	synonymous_variant	4	106157532	T	C	21.43%	42	.	.	.		true	true	true			.	0.1263	34.66%	95.96%	65%	Subclonal			
META31	*TET2*	p.Gly1861Arg	missense_variant	4	106197248	G	A	32.35%	34	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.4602	52.35%	100.00%	98%	Subclonal			
META31	*NUDT6*	p.Ala188Ala	synonymous_variant	4	123814370	C	T	20.00%	65	.	.	.		.	.	.			.	0.0430	36.01%	91.27%	60%	Subclonal			
META31	*OTUD4*	p.Ser922Ser	synonymous_variant	4	146058966	G	A	4.25%	212	.	.	.		.	.	.			.	0.0000	6.32%	23.28%	13%	Subclonal			
META31	*OTUD4*	p.Thr909Ile	missense_variant	4	146059006	G	A	10.73%	177	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	20.61%	48.32%	32%	Subclonal			
META31	*OTUD4*	p.His897His	synonymous_variant	4	146059041	A	G	9.23%	130	.	.	.		.	.	.			.	0.0000	15.76%	46.16%	28%	Subclonal			
META31	*FAT1*	p.Met1688Ile	missense_variant	4	187542676	C	A	4.12%	170	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0000	5.62%	24.44%	12%	Subclonal			
META31	*SLC12A7*	p.Val157Met	missense_variant	5	1089117	C	T	20.83%	24	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1652	27.00%	96.85%	63%	Subclonal			
META31	*DHX29*	p.Ala1280Val	missense_variant	5	54557317	G	A	7.61%	92	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	10.94%	44.48%	23%	Subclonal			
META31	*CCDC125*	p.Lys353fs	frameshift_variant	5	68588054	CT	C	23.89%	113	A	.	.		.	.	.			Indeterminate	0.0811	50.69%	94.75%	72%	Subclonal			
META31	*ARSB*	p.Arg327*	stop_gained	5	78181570	G	A	14.29%	70	A	.	.		.	.	.			Indeterminate	0.0013	23.62%	73.05%	43%	Subclonal			
META31	*CMYA5*	p.Ser2190Thr	missense_variant	5	79031157	G	C	26.54%	162	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1667	60.79%	97.19%	80%	Subclonal			
META31	*MSH3*	p.Lys383fs	frameshift_variant	5	79970914	CA	C	18.07%	83	A	.	.		.	.	.			Indeterminate	0.0073	33.59%	82.92%	55%	Subclonal			
META31	*POLR3G*	p.Gly8Gly	synonymous_variant	5	89781408	A	G	13.33%	75	.	.	.		.	.	.			.	0.0004	22.01%	68.54%	40%	Subclonal			
META31	*CEP120*	p.Gln300Gln	synonymous_variant	5	122726942	C	T	9.09%	55	.	.	.		.	.	.			.	0.0001	11.66%	58.73%	27%	Subclonal			
META31	*ISOC1*	p.Val156Ile	missense_variant	5	128440914	G	A	14.49%	69	D	.	Passenger		.	.	.			Indeterminate	0.0016	24.00%	74.01%	44%	Subclonal			
META31	*TRPC7*	p.Thr241Thr	synonymous_variant	5	135692353	G	A	50.00%	12	.	.	.		.	.	.			.	0.5856	50.40%	100.00%	100%	Clonal			
META31	*HARS*	p.Arg137Gln	missense_variant	5	140058699	C	T	11.32%	106	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.50%	56.17%	34%	Subclonal			
META31	*PCDHB2*	p.Arg550Cys	missense_variant	5	140476022	C	T	16.00%	50	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0155	24.84%	84.56%	48%	Subclonal			
META31	*PCDHB14*	p.Ser698Ser	synonymous_variant	5	140605171	G	A	9.38%	64	.	.	.		.	.	.			.	0.0000	12.91%	56.91%	28%	Subclonal			
META31	*HMGXB3*	p.Lys659Glu	missense_variant	5	149412158	A	G	5.36%	112	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.12%	33.32%	16%	Subclonal			
META31	*GLRA1*	p.Arg413*	stop_gained	5	151202371	G	A	15.69%	51	D	.	.		.	.	.			Indeterminate	0.0126	24.33%	83.30%	47%	Subclonal			
META31	*RANBP17*	p.Ile231Ile	synonymous_variant	5	170338071	T	C	22.00%	50	.	.	.		true	.	.			.	0.1227	37.84%	95.90%	66%	Subclonal			
META31	*NSD1*	p.Arg2084Arg	synonymous_variant	5	176715920	G	A	10.42%	48	.	.	.		true	true	true	TRUE		.	0.0009	13.46%	66.56%	31%	Subclonal			
META31	*TRIM41*	p.Cys23Cys	synonymous_variant	5	180651068	C	T	17.86%	28	.	.	.		.	.	.			.	0.0898	23.37%	94.31%	54%	Subclonal			
META31	*KIF13A*	p.Thr517Ala	missense_variant	6	17826339	T	C	12.20%	82	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0001	20.05%	63.02%	37%	Subclonal			
META31	*NHLRC1*	p.Asp245Asn	missense_variant	6	18122105	C	T	15.38%	39	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0251	21.61%	86.85%	46%	Subclonal			
META31	*VARS2*	p.Leu613Leu	synonymous_variant	6	30889715	A	G	6.58%	76	.	.	.		.	.	.			.	0.0000	8.28%	43.31%	20%	Subclonal			
META31	*C6orf10*	p.Ala298Thr	missense_variant	6	32261558	C	T	8.57%	175	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	15.43%	40.77%	26%	Subclonal			
META31	*B3GALT4*	p.Arg201fs	frameshift_variant	6	33245793	GGA	G	22.22%	36	D	.	.		.	.	.			Indeterminate	0.1648	34.47%	96.89%	67%	Subclonal			
META31	*ITPR3*	p.Ala2253Thr	missense_variant	6	33657077	G	A	38.24%	68	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6821	72.98%	100.00%	100%	Clonal			
META31	*BRPF3*	p.Arg925Arg	synonymous_variant	6	36181949	C	T	8.47%	59	.	.	.		.	.	.			.	0.0000	10.84%	55.00%	26%	Subclonal			
META31	*MDN1*	p.Arg3935Cys	missense_variant	6	90394621	G	A	33.33%	21	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4305	44.83%	100.00%	100%	Subclonal			
META31	*PPIL6*	p.Arg77fs	frameshift_variant	6	109757308	CT	C	11.36%	88	A	.	.		.	.	.			Indeterminate	0.0000	18.60%	58.95%	34%	Subclonal			
META31	*LAMA4*	p.Val99Val	synonymous_variant	6	112537569	C	A	20.00%	30	.	.	.		.	.	.			.	0.1263	28.05%	95.88%	60%	Subclonal			
META31	*FAM26E*	p.Thr27Ala	missense_variant	6	116832938	A	G	18.92%	74	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0183	34.64%	87.07%	57%	Subclonal			
META31	*ECHDC1*	p.Phe305Phe	synonymous_variant	6	127611023	A	G	5.05%	99	.	.	.		.	.	.			.	0.0000	6.22%	33.58%	15%	Subclonal			
META31	*ARID1B*	p.Pro735fs	frameshift_variant	6	157405953	C	CG	14.04%	57	A	.	.		.	.	.			Indeterminate	0.0033	21.67%	75.92%	42%	Subclonal			
META31	*SDK1*	p.Thr729Thr	synonymous_variant	7	4050653	C	T	42.11%	19	.	.	.		.	.	.			.	0.5456	53.60%	100.00%	100%	Clonal			
META31	*CBX3*	p.Lys14fs	frameshift_variant	7	26245998	GA	G	33.33%	39	A	.	.		.	.	.			Indeterminate	0.4991	56.37%	100.00%	100%	Clonal			
META31	*CREB5*	p.Gly364fs	frameshift_variant	7	28848863	AG	A	16.28%	43	A	.	.		.	.	.			Indeterminate	0.0270	24.19%	87.62%	49%	Subclonal			
META31	*PCLO*	p.Glu1875Gly	missense_variant	7	82584645	T	C	17.03%	182	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	36.55%	69.48%	51%	Subclonal			
META31	*TRRAP*	p.Arg2858Trp	missense_variant	7	98576486	C	T	23.64%	55	D	CANCER	Driver		true	.	.			Likely pathogenic	0.1669	42.54%	96.99%	71%	Subclonal			
META31	*STAG3*	p.Leu837Leu	synonymous_variant	7	99799911	A	G	16.25%	80	.	.	.		.	.	.			.	0.0025	29.04%	77.54%	49%	Subclonal			
META31	*SRRT*	p.Ile618Thr	missense_variant	7	100484699	T	C	30.93%	97	D	.	Passenger		.	.	.			Indeterminate	0.5002	65.73%	100.00%	93%	Clonal			
META31	*MUC17*	p.Asp2748Asp	synonymous_variant	7	100682941	T	C	12.25%	253	.	.	.		.	.	true			.	0.0000	26.02%	50.47%	37%	Subclonal			
META31	*PUS7*	p.Asp646Glu	missense_variant	7	105098285	A	T	29.52%	105	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4241	63.65%	100.00%	89%	Subclonal			
META31	*CDHR3*	p.Leu595Leu	synonymous_variant	7	105660950	T	C	4.97%	181	.	PASSENGER/OTHER	.		.	.	.			.	0.0000	7.50%	27.23%	15%	Subclonal			
META31	*LAMB1*	p.Asp1617Gly	missense_variant	7	107569546	T	C	13.33%	150	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	26.12%	59.00%	40%	Subclonal			
META31	*UBN2*	p.Ala1059Val	missense_variant	7	138968827	C	T	20.73%	82	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0345	39.89%	90.62%	63%	Subclonal			
META31	*LUC7L2*	p.Glu253fs	frameshift_variant	7	139094364	AAG	A	30.00%	20	.	.	.		.	.	.			Indeterminate	0.3649	39.11%	98.86%	91%	Subclonal			
META31	*DENND2A*	p.Gly647Ser	missense_variant	7	140257963	C	T	34.62%	26	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4778	50.81%	100.00%	100%	Subclonal			
META31	*CNTNAP2*	p.Pro163Ser	missense_variant	7	146741083	C	T	7.14%	84	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.67%	43.98%	22%	Subclonal			
META31	*ZNF282*	p.Arg125Cys	missense_variant	7	148895632	C	T	12.82%	39	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0090	16.72%	79.51%	39%	Subclonal			
META31	*ACTR3B*	p.Thr162Thr	synonymous_variant	7	152513619	G	A	3.85%	130	.	.	.		.	.	.			.	0.0000	4.59%	25.73%	12%	Subclonal			
META31	*UBE3C*	p.Ala188Val	missense_variant	7	156971488	C	T	31.25%	32	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4274	49.47%	100.00%	94%	Subclonal			
META31	*FBXO25*	p.Leu176Pro	missense_variant	8	401320	T	C	31.25%	32	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0855	35.65%	93.53%	63%	Subclonal			
META31	*PCM1*	p.Met826Thr	missense_variant	8	17820623	T	C	23.08%	26	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.0172	21.93%	83.83%	47%	Subclonal			
META31	*PCM1*	p.Pro1936Pro	synonymous_variant	8	17872316	T	G	15.00%	60	.	.	.		true	.	.		TRUE	.	0.0000	15.97%	52.35%	30%	Subclonal			
META31	*ADAM7*	p.Leu594fs	frameshift_variant	8	24350674	AT	A	28.00%	25	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0649	28.33%	91.83%	57%	Subclonal			
META31	*UNC5D*	p.Asp413Asp	synonymous_variant	8	35579849	C	T	28.07%	57	.	.	.		.	.	.		TRUE	.	0.0048	36.03%	81.96%	57%	Subclonal			
META31	*WHSC1L1*	p.Ala620Val	missense_variant	8	38173557	G	A	11.80%	161	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.3242	52.28%	98.67%	83%	Subclonal			
META31	*ST18*	p.Asp165Asp	synonymous_variant	8	53084926	G	A	8.48%	165	.	.	.		.	.	.			.	0.1418	40.40%	96.49%	68%	Subclonal			
META31	*RP1*	p.Tyr199Tyr	synonymous_variant	8	55534123	C	T	8.97%	156	.	.	.		.	.	.			.	0.1925	42.56%	97.45%	72%	Subclonal			
META31	*EYA1*	p.Ile366Val	missense_variant	8	72156882	T	C	15.56%	45	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.4981	47.16%	100.00%	100%	Clonal			
META31	*PEX2*	p.Asp275Asp	synonymous_variant	8	77895590	G	A	7.48%	214	.	.	.		.	.	.			.	0.0416	36.92%	91.10%	60%	Subclonal			
META31	*RMDN1*	p.Leu278Arg	missense_variant	8	87487110	A	C	4.90%	204	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0010	21.21%	69.91%	39%	Subclonal			
META31	*RIPK2*	p.Arg375Arg	synonymous_variant	8	90801550	A	G	6.79%	162	.	.	.		.	.	.			.	0.0377	30.40%	90.03%	54%	Subclonal			
META31	*NCALD*	p.Asp111Asp	synonymous_variant	8	102731525	G	A	6.52%	276	.	.	.		.	.	.			.	0.0043	33.02%	80.10%	52%	Subclonal			
META31	*PKHD1L1*	p.Val2811Ile	missense_variant	8	110478824	G	A	8.16%	245	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0669	42.40%	93.63%	65%	Subclonal			
META31	*ZHX2*	p.Ser753Ser	synonymous_variant	8	123966009	C	T	13.97%	136	.	.	.		.	.	.			.	0.5815	63.83%	100.00%	100%	Clonal			
META31	*NSMCE2*	p.Thr168Thr	synonymous_variant	8	126369546	C	A	7.69%	143	.	.	.		.	.	.			.	0.0980	34.38%	94.98%	62%	Subclonal			
META31	*PHF20L1*	p.Arg8Cys	missense_variant	8	133790096	C	T	3.57%	252	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	14.82%	52.79%	29%	Subclonal			
META31	*CBWD1*	p.Tyr161Tyr	synonymous_variant	9	163985	A	G	5.11%	137	.	.	.		.	.	.			.	0.0000	7.14%	30.22%	15%	Subclonal			
META31	*ANKRD18B*	p.Met821Val	missense_variant	9	33566406	A	G	15.46%	97	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0004	28.55%	71.90%	47%	Subclonal			
META31	*KIF24*	p.Ile188Asn	missense_variant	9	34310782	A	T	6.40%	125	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	9.48%	36.11%	19%	Subclonal			
META31	*GRHPR*	p.Ser260Ser	synonymous_variant	9	37432050	T	C	21.21%	33	.	.	.		.	.	.			.	0.1460	31.44%	96.46%	64%	Subclonal			
META31	*TMEM2*	p.Ala47Val	missense_variant	9	74365150	G	A	11.11%	63	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0002	16.26%	63.64%	34%	Subclonal			
META31	*C9orf47*	p.Ser197_Phe198insLys	inframe_insertion	9	91606885	G	GAAA	23.33%	30	P	.	.	Deleterious	.	.	.			Indeterminate	0.2103	34.31%	97.62%	70%	Subclonal			
META31	*NANS*	p.Arg198Trp	missense_variant	9	100840618	C	T	23.81%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1999	39.63%	97.50%	72%	Subclonal			
META31	*NR4A3*	p.Pro134Leu	missense_variant	9	102590692	C	T	22.58%	31	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.1877	33.32%	97.29%	68%	Subclonal			
META31	*TMEFF1*	p.Asn358fs	frameshift_variant	9	103338807	CA	C	15.07%	73	D	.	.		.	.	.			Indeterminate	0.0018	25.66%	75.02%	45%	Subclonal			
META31	*OR13D1*	p.His342Tyr	missense_variant	9	107457726	C	T	12.00%	50	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0019	16.70%	71.44%	36%	Subclonal			
META31	*AKAP2*	p.Ala492Thr	missense_variant	9	112899724	G	A	9.80%	51	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0004	12.63%	62.96%	30%	Subclonal			
META31	*LARP4B*	p.Thr163fs	frameshift_variant	10	890938	GT	G	15.15%	66	A	.	.		.	.	.			Indeterminate	0.0032	25.13%	77.04%	46%	Subclonal			
META31	*USP6NL*	p.Leu598Ile	missense_variant	10	11505186	G	T	20.31%	64	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0504	36.57%	92.06%	61%	Subclonal			
META31	*CUL2*	p.Leu84fs	frameshift_variant	10	35351915	CA	C	17.02%	47	A	.	.		.	.	.			Indeterminate	0.0284	26.47%	88.19%	51%	Subclonal			
META31	*ERCC6*	p.Arg945Gln	missense_variant	10	50680512	C	T	26.67%	45	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.2978	46.43%	98.48%	81%	Subclonal			
META31	*EGR2*	p.Arg293Trp	missense_variant	10	64573521	G	A	55.56%	9	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6130	47.53%	100.00%	100%	Clonal			
META31	*C10orf35*	p.Arg49Cys	missense_variant	10	71392594	C	T	20.69%	29	D	.	Passenger		.	.	.			Indeterminate	0.1456	28.96%	96.43%	62%	Subclonal			
META31	*CDH23*	p.Arg3341Arg	synonymous_variant	10	73574993	C	T	7.89%	76	.	.	.		.	.	.			.	0.0000	10.76%	48.40%	24%	Subclonal			
META31	*TNKS2*	p.Phe1035fs	frameshift_variant	10	93619225	CT	C	26.56%	64	A	.	.		.	.	.			Indeterminate	0.2779	50.94%	98.34%	80%	Subclonal			
META31	*ADD3*	p.Lys701fs	frameshift_variant	10	111893349	CA	C	15.18%	112	D	.	.		.	.	.			Indeterminate	0.0001	28.85%	68.91%	46%	Subclonal			
META31	*TRUB1*	p.Asn271Ile	missense_variant	10	116734900	A	T	4.51%	133	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	5.92%	28.16%	14%	Subclonal			
META31	*PDZD8*	p.Thr982Met	missense_variant	10	119043299	G	A	8.29%	193	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.15%	38.89%	25%	Subclonal			
META31	*OR52B2*	p.Arg153Arg	synonymous_variant	11	6191100	G	T	23.08%	39	.	.	.		.	.	.			.	0.1828	37.19%	97.23%	70%	Subclonal			
META31	*FAR1*	p.Arg508Gln	missense_variant	11	13750296	G	A	14.68%	109	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	27.46%	67.57%	44%	Subclonal			
META31	*KIF18A*	p.Met672Val	missense_variant	11	28058146	T	C	13.04%	46	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0051	18.22%	76.81%	39%	Subclonal			
META31	*SLC39A13*	p.Pro2Pro	synonymous_variant	11	47431651	T	C	17.65%	34	.	.	.		.	.	.			.	0.0661	24.83%	92.81%	53%	Subclonal			
META31	*DDB1*	p.Val1028Ala	missense_variant	11	61070083	A	G	20.00%	90	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0178	38.93%	87.65%	60%	Subclonal			
META31	*KAT5*	p.Trp278Arg	missense_variant	11	65482107	T	C	17.33%	75	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0070	31.06%	82.10%	52%	Subclonal			
META31	*CCDC87*	p.Lys85Arg	missense_variant	11	66360233	T	C	29.17%	24	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3586	41.04%	98.83%	88%	Subclonal			
META31	*DNAJB13*	p.Gly62Gly	synonymous_variant	11	73670552	C	A	18.18%	33	.	.	.		.	.	.			.	0.0786	25.57%	93.72%	55%	Subclonal			
META31	*MYO7A*	p.Gly229Asp	missense_variant	11	76868001	G	A	12.31%	65	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0005	18.91%	67.40%	37%	Subclonal			
META31	*RAB30*	p.Tyr89Cys	missense_variant	11	82698724	T	C	11.29%	62	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0003	16.52%	64.59%	34%	Subclonal			
META31	*SLC36A4*	p.Gly58Asp	missense_variant	11	92918863	C	T	15.56%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0179	23.09%	85.02%	47%	Subclonal			
META31	*KIAA1731*	p.Ile943Val	missense_variant	11	93430905	A	G	21.62%	74	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0640	41.07%	93.39%	65%	Subclonal			
META31	*PANX1*	p.Ala78Val	missense_variant	11	93886708	C	T	8.20%	61	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	10.45%	53.32%	25%	Subclonal			
META31	*ZPR1*	p.Thr381Thr	synonymous_variant	11	116652910	C	A	50.00%	12	.	.	.		.	.	.			.	0.5856	50.40%	100.00%	100%	Clonal			
META31	*TMPRSS13*	p.Pro465Ser	missense_variant	11	117774805	G	A	41.67%	12	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4807	42.78%	100.00%	100%	Clonal			
META31	*TECTA*	p.Ser376Ser	synonymous_variant	11	120989352	C	A	6.10%	82	.	.	.		.	.	.			.	0.0000	7.62%	40.27%	18%	Subclonal			
META31	*HSPA8*	p.Asp327Gly	missense_variant	11	122930321	T	C	16.33%	49	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0191	25.36%	85.79%	49%	Subclonal			
META31	*OR8G2*	p.Pro92fs	frameshift_variant	11	124095668	AC	A	11.84%	228	.	.	.		.	.	.			Indeterminate	0.0000	24.47%	49.89%	36%	Subclonal			
META31	*BICD1*	p.Ser499Gly	missense_variant	12	32480884	A	G	18.52%	81	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0106	34.45%	84.67%	56%	Subclonal			
META31	*YARS2*	p.Thr277Ala	missense_variant	12	32906970	T	C	23.08%	65	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1258	43.16%	96.07%	70%	Subclonal			
META31	*PUS7L*	p.Arg290Gly	missense_variant	12	44148181	T	C	4.32%	139	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	5.60%	26.95%	13%	Subclonal			
META31	*KIF5A*	p.Lys829del	disruptive_inframe_deletion	12	57972069	CAGA	C	15.79%	95	D	.	.	Deleterious	.	.	.			Indeterminate	0.0006	29.19%	73.33%	48%	Subclonal			
META31	*NAV3*	p.Gly33Trp	missense_variant	12	78225338	G	T	20.66%	121	N	PASSENGER/OTHER	Passenger		.	true	.			Likely passenger	0.0093	43.03%	86.01%	62%	Subclonal			
META31	*CEP290*	p.Asn2290fs	frameshift_variant	12	88449443	AT	A	28.95%	38	A	.	.		.	.	.			Indeterminate	0.3742	48.31%	98.91%	87%	Subclonal			
META31	*FGD6*	p.Leu1283Leu	synonymous_variant	12	95485486	A	G	18.52%	27	.	.	.		.	.	.			.	0.1059	24.20%	95.09%	56%	Subclonal			
META31	*CCDC38*	p.Lys458Lys	synonymous_variant	12	96266143	C	T	7.14%	112	.	.	.		.	.	.			.	0.0000	10.67%	40.18%	22%	Subclonal			
META31	*SVOP*	p.Leu241Phe	missense_variant	12	109332620	G	A	3.85%	260	.	.	Passenger		.	.	.			Indeterminate	0.0000	5.91%	20.46%	12%	Subclonal			
META31	*UBE3B*	p.Glu1053Lys	missense_variant	12	109972537	G	A	12.50%	56	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0014	18.38%	70.91%	38%	Subclonal			
META31	*TBX5*	c.362+1G>A	splice_donor_variant	12	114837317	C	T	10.64%	94	D	.	.		.	.	.	TRUE		Likely pathogenic	0.0000	17.36%	55.39%	32%	Subclonal			
META31	*CIT*	p.Ser1330Ser	synonymous_variant	12	120156517	G	A	20.25%	79	.	.	.		.	.	.			.	0.0300	38.38%	89.84%	61%	Subclonal			
META31	*TCTN2*	p.Leu241fs	frameshift_variant	12	124171533	T	TC	40.00%	130	A	.	.		.	.	.			Indeterminate	0.7784	83.63%	100.00%	100%	Clonal			
META31	*C1QTNF9B*	p.Tyr253His	missense_variant	13	24465673	A	G	4.14%	145	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	5.34%	25.86%	12%	Subclonal			

META31	C1QTNF9	p.Tyr253His	missense_variant	13	24895661	T	C	10.96%	73	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	16.74%	60.48%	33%	Subclonal			
META31	RNF6	p.Ser313Leu	missense_variant	13	26789081	G	A	3.70%	135	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	4.39%	24.78%	11%	Subclonal			
META31	USPL1	p.Tyr45Cys	missense_variant	13	31195935	A	G	18.48%	92	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0062	35.39%	82.74%	56%	Subclonal			
META31	GPALPP1	p.Asp83Asp	synonymous_variant	13	45580364	C	T	22.48%	129	.	.	.		.	.	.			.	0.0270	48.21%	90.60%	68%	Subclonal			
META31	POU4F1	p.Asn405Asp	missense_variant	13	79175597	T	C	14.71%	34	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0282	19.26%	87.29%	44%	Subclonal			
META31	DOCK9	p.Leu1413Ser	missense_variant	13	99489758	A	G	17.14%	105	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0011	33.16%	76.48%	52%	Subclonal			
META31	DOCK9	p.Thr1336fs	frameshift_variant	13	99502311	T	TA	14.29%	35	A	.	.		.	.	.			Indeterminate	0.0227	18.69%	85.80%	43%	Subclonal			
META31	ERCC5	p.Ala1143Val	missense_variant	13	103528120	C	T	24.32%	37	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.2262	39.03%	97.83%	73%	Subclonal			
META31	MYO16	p.Thr820Ser	missense_variant	13	109661261	C	G	16.67%	30	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0629	21.85%	92.41%	50%	Subclonal			
META31	MYH6	p.Ala1887Val	missense_variant	14	23852435	G	A	26.67%	30	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3027	40.44%	98.51%	81%	Subclonal			
META31	IPO4	p.Glu816Gly	missense_variant	14	24652023	T	C	5.00%	120	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	6.58%	31.15%	15%	Subclonal			
META31	VCPKMT	p.Thr116Ile	missense_variant	14	50582817	G	A	7.07%	99	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	10.11%	41.46%	21%	Subclonal			
META31	SOCS4	p.Val14Val	synonymous_variant	14	55509801	A	G	22.37%	76	.	.	.		.	.	.			.	0.0816	43.11%	94.47%	68%	Subclonal			
META31	KTN1	p.Lys270Asn	missense_variant	14	56084830	A	C	34.38%	64	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.5880	66.29%	100.00%	100%	Clonal			
META31	L3HYPDH	p.Leu202Leu	synonymous_variant	14	59945974	G	A	26.15%	65	.	.	.		.	.	.			.	0.2576	50.21%	98.17%	79%	Subclonal			
META31	NEK9	p.Val78Leu	missense_variant	14	75590914	C	G	70.83%	24	D	PASSENGER/OTHER	Driver		.	.	.		TRUE	Likely pathogenic	0.7053	75.46%	100.00%	100%	Clonal			
META31	NRDE2	p.Arg148His	missense_variant	14	90778852	C	T	30.36%	56	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0155	39.67%	86.75%	61%	Subclonal			
META31	BTBD7	p.Arg599Arg	synonymous_variant	14	93717954	G	A	34.78%	69	.	.	.		.	.	.		TRUE	.	0.0524	49.16%	92.42%	70%	Subclonal			
META31	CLMN	p.Leu495fs	frameshift_variant	14	95670201	C	CA	32.14%	28	A	.	.		.	.	.		TRUE	Likely pathogenic	0.1230	35.52%	95.07%	65%	Subclonal			
META31	ATG2B	p.Val1817Ala	missense_variant	14	96758412	A	G	18.42%	38	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0004	18.26%	67.20%	37%	Subclonal			
META31	TECPR2	p.Thr1047Ala	missense_variant	14	102916029	A	G	16.13%	31	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0005	14.06%	65.69%	33%	Subclonal			
META31	TRMT61A	p.Arg123His	missense_variant	14	103998955	G	A	44.44%	27	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4679	52.73%	100.00%	90%	Subclonal			
META31	OR4M2	p.Leu25Pro	missense_variant	15	22368649	T	C	6.55%	290	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.29%	29.74%	20%	Subclonal			
META31	CYFIP1	p.Gln886Arg	missense_variant	15	22980159	A	G	26.19%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2826	44.49%	98.37%	79%	Subclonal			
META31	GABRB3	p.Ser354Leu	missense_variant	15	26806098	G	A	14.44%	90	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0003	25.67%	69.51%	44%	Subclonal			
META31	HERC2	p.Arg3023Arg	synonymous_variant	15	28424127	C	A	25.58%	43	.	.	.		.	.	.			.	0.2600	43.59%	98.18%	77%	Subclonal			
META31	HERC2	p.Val1030Ala	missense_variant	15	28493844	A	G	18.18%	44	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0495	28.32%	91.44%	55%	Subclonal			
META31	LEO1	p.Gly120Asp	missense_variant	15	52258401	C	T	4.23%	189	N	.	Passenger		.	.	.			Likely passenger	0.0000	6.10%	24.03%	13%	Subclonal			
META31	UNC13C	p.Arg782*	stop_gained	15	54307444	C	T	25.81%	31	A	.	.		.	.	.			Indeterminate	0.2782	39.36%	98.33%	78%	Subclonal			
META31	HERC1	p.Cys2525Arg	missense_variant	15	63966814	A	G	32.93%	82	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5719	67.41%	100.00%	99%	Clonal			
META31	HERC1	p.Arg2330Cys	missense_variant	15	63970126	G	A	20.41%	147	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0030	43.87%	82.93%	62%	Subclonal			
META31	TLE3	p.Gly216Asp	missense_variant	15	70352936	C	T	6.06%	99	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.13%	37.56%	18%	Subclonal			
META31	TBC1D2B	p.Glu666Glu	synonymous_variant	15	78305437	C	T	17.07%	41	.	.	.		.	.	.			.	0.0398	25.39%	90.01%	52%	Subclonal			
META31	ACSBG1	p.Ala472Val	missense_variant	15	78471961	G	A	30.00%	20	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3649	39.11%	98.86%	91%	Subclonal			
META31	CHRNA3	p.Leu347Phe	missense_variant	15	78893943	C	G	24.32%	37	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2262	39.03%	97.83%	73%	Subclonal			
META31	WDR73	p.Pro351Pro	synonymous_variant	15	85186785	G	T	20.00%	35	.	.	.		.	.	.			.	0.1102	29.73%	95.36%	60%	Subclonal			
META31	TELO2	p.Thr455Met	missense_variant	16	1551666	C	T	44.44%	18	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5672	54.84%	100.00%	100%	Clonal			
META31	ABCC1	p.Val1248Gly	missense_variant	16	16219692	T	G	27.78%	18	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3175	34.01%	98.60%	84%	Subclonal			
META31	SALL1	p.Pro33Leu	missense_variant	16	51176035	G	A	36.78%	87	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.6904	74.56%	100.00%	100%	Clonal			
META31	RBL2	p.Glu648Gly	missense_variant	16	53501049	A	G	11.46%	96	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	19.28%	58.02%	35%	Subclonal			
META31	KIAA0513	p.Thr276Thr	synonymous_variant	16	85112535	C	T	7.81%	64	.	.	.		.	.	.			.	0.0000	9.96%	50.96%	24%	Subclonal			
META31	TRPV3	p.Arg733Arg	synonymous_variant	17	3419752	G	T	39.58%	48	.	.	.		.	.	.			.	0.6506	69.04%	100.00%	100%	Clonal			
META31	DHX33	p.Val191Val	synonymous_variant	17	5365744	G	A	47.06%	51	.	.	.		.	.	.			.	0.6698	77.61%	100.00%	100%	Clonal			
META31	NLRP1	p.Leu513Arg	missense_variant	17	5462478	A	C	14.08%	71	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0010	23.28%	72.10%	43%	Subclonal			
META31	PER1	p.Gly229Asp	missense_variant	17	8052947	C	T	37.84%	37	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.5843	62.09%	100.00%	100%	Clonal			
META31	SCO1	p.Gly138fs	frameshift_variant	17	10596229	TC	T	17.86%	56	A	.	.		.	.	.			Indeterminate	0.0251	29.80%	87.93%	54%	Subclonal			
META31	TLCD1	p.Met156Val	missense_variant	17	27051806	T	C	21.92%	73	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0735	41.62%	93.98%	66%	Subclonal			
META31	NSRP1	p.Lys86fs	frameshift_variant	17	28505166	GA	G	17.19%	64	A	.	.		.	.	.			Indeterminate	0.0120	29.42%	84.11%	52%	Subclonal			
META31	KRT40	p.Glu266Glu	synonymous_variant	17	39137293	T	C	20.35%	113	.	.	.		.	.	.			.	0.0098	41.68%	85.89%	61%	Subclonal			
META31	C17orf53	p.Ala486Val	missense_variant	17	42231928	C	T	11.32%	53	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0009	15.71%	67.78%	34%	Subclonal			
META31	COL1A1	p.Gly842Asp	missense_variant	17	48267396	C	T	53.33%	30	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.7393	73.25%	100.00%	100%	Clonal			
META31	CACNA1G	p.Arg198His	missense_variant	17	48649245	G	A	12.28%	57	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0011	18.06%	69.78%	37%	Subclonal			
META31	CYB561	p.Arg157His	missense_variant	17	61512540	C	T	12.50%	40	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0071	16.28%	77.93%	38%	Subclonal			
META31	HID1	p.Glu511Glu	synonymous_variant	17	72951990	C	T	33.33%	27	.	.	.		.	.	.			.	0.4574	49.65%	100.00%	100%	Subclonal			
META31	MFSD11	p.Tyr323fs	frameshift_variant	17	74771166	C	CT	15.73%	89	A	.	.		.	.	.			Indeterminate	0.0009	28.58%	74.10%	47%	Subclonal			
META31	BIRC5	p.Cys107Cys	synonymous_variant	17	76212775	C	T	11.43%	70	.	.	.		.	.	.			.	0.0001	17.49%	62.90%	35%	Subclonal			
META31	C1QTNF1	p.Val248Ala	missense_variant	17	77044067	T	C	34.62%	26	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4778	50.81%	100.00%	100%	Subclonal			
META31	ALYREF	p.Asp157Gly	missense_variant	17	79847126	T	C	20.00%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0821	32.38%	94.13%	60%	Subclonal			
META31	SMCHD1	p.Ala1305Ala	synonymous_variant	18	2747633	T	C	24.62%	65	.	.	.		.	.	.			.	0.4989	58.16%	100.00%	99%	Clonal			
META31	MYOM1	p.Leu736Leu	synonymous_variant	18	3135546	A	C	12.50%	120	.	.	.		.	.	.			.	0.0029	30.63%	78.24%	50%	Subclonal			
META31	ZBTB14	p.Ala422Val	missense_variant	18	5290942	G	A	6.67%	105	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.81%	52.29%	27%	Subclonal			
META31	SLC35G4	p.Pro216Ser	missense_variant	18	11610240	C	T	8.18%	110	.	.	.		.	.	.			Indeterminate	0.0000	17.19%	59.12%	33%	Subclonal			
META31	CTAGE1	p.Asn232Asn	synonymous_variant	18	19997079	A	G	15.00%	160	.	.	.		.	.	.			.	0.0086	40.92%	85.07%	60%	Subclonal			
META31	PSMA8	p.Glu22Gly	missense_variant	18	23713994	A	G	8.45%	71	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0013	15.55%	68.78%	34%	Subclonal			
META31	ELP2	p.Ala660Asp	missense_variant	18	33744460	C	A	14.91%	114	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0257	37.85%	88.97%	60%	Subclonal			
META31	EPG5	p.Ala1798Val	missense_variant	18	43462364	G	A	10.75%	93	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0022	23.55%	74.53%	43%	Subclonal			
META31	PLIN4	p.Ala1018Thr	missense_variant	19	4510878	C	T	17.50%	40	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0480	26.05%	91.12%	53%	Subclonal			
META31	PLIN5	p.Arg145Cys	missense_variant	19	4529172	G	A	28.57%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3653	49.18%	98.87%	86%	Subclonal			
META31	ZNF99	p.Tyr397His	missense_variant	19	22941522	A	G	3.60%	139	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	4.26%	24.06%	11%	Subclonal			
META31	ZNF585B	p.Lys725Glu	missense_variant	19	37676266	T	C	9.52%	63	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	13.12%	57.76%	29%	Subclonal			
META31	ZNF607	p.Cys563Cys	synonymous_variant	19	38189343	A	G	17.95%	39	.	.	.		.	.	.			.	0.0574	26.71%	92.14%	54%	Subclonal			
META31	CYP2A6	p.Gln242Arg	missense_variant	19	41352886	T	C	10.34%	58	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0002	14.30%	62.39%	31%	Subclonal			
META31	LIPE	p.Leu510fs	frameshift_variant	19	42912252	AAG	A	27.50%	40	A	.	.		.	.	.			Indeterminate	0.3285	46.37%	98.67%	83%	Subclonal			
META31	PSG6	p.Arg126Gln	missense_variant	19	43420327	C	T	5.31%	207	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	8.56%	27.50%	16%	Subclonal			
META31	PLAUR	p.Ser228Ser	synonymous_variant	19	44156447	G	T	34.72%	72	.	.	.		.	.	.			.	0.6133	68.65%	100.00%	100%	Clonal			
META31	PNMAL1	p.Lys248del	disruptive_inframe_deletion	19	46973546	GTTC	G	30.00%	50	P	.	.	Deleterious	.	.	.			Indeterminate	0.4220	54.59%	100.00%	91%	Subclonal			
META31	ZNF415	p.His480Tyr	missense_variant	19	53611860	G	A	7.65%	183	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.46%	37.04%	23%	Subclonal			
META31	MYADM	p.Thr153Ala	missense_variant	19	54377240	A	G	17.50%	40	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0480	26.05%	91.12%	53%	Subclonal			
META31	ZNF470	p.Arg633Cys	missense_variant	19	57089694	C	T	36.67%	30	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5337	56.48%	100.00%	100%	Clonal			
META31	PEG3	p.Ala519Thr	missense_variant	19	57328255	C	T	11.67%	120	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.96%	55.81%	35%	Subclonal			
META31	PDYN	p.Arg212Trp	missense_variant	20	1961100	G	A	17.60%	125	A	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1037	47.33%	95.49%	71%	Subclonal			
META31	ZNF343	p.Leu304Phe	missense_variant	20	2464820	G	A	10.34%	87	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0022	21.95%	73.84%	42%	Subclonal			
META31	GPCPD1	p.Asp193Asn	missense_variant	20	5559154	C	T	7.46%	67	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0008	12.78%	65.08%	30%	Subclonal			
META31	RIN2	p.Gln894Gln	synonymous_variant	20	19981427	G	A	6.72%	134	.	.	.		.	.	.			.	0.0000	14.02%	48.85%	27%	Subclonal			
META31	BPIFB2	p.Glu445Asp	missense_variant	20	31609605	G	T	14.86%	74	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0651	33.74%	93.08%	60%	Subclonal			
META31	MYH7B	p.Arg149His	missense_variant	20	33567585	G	A	28.57%	35	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5244	54.39%	100.00%	100%	Clonal			
META31	EPB41L1	p.Leu132Arg	missense_variant	20	34765926	T	G	14.58%	48	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1047	28.62%	95.12%	59%	Subclonal			
META31	CHD6	p.Glu1077Gly	missense_variant	20	40081473	T	C	5.93%	118	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.32%	46.71%	24%	Subclonal			
META31	CSE1L	p.Ser936Pro	missense_variant	20	47711480	T	C	11.11%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0363	19.28%	88.83%	45%	Subclonal			
META31	NRIP1	p.Pro793His	missense_variant	21	16338136	G	T	23.19%	69	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4482	55.82%	100.00%	93%	Subclonal			
META31	ADAMTS5	p.Glu689Glu	synonymous_variant	21	28302363	T	C	5.13%	156	.	.	.		.	.	.			.	0.0000	10.16%	38.86%	21%	Subclonal			
META31	RUNX1	p.Glu138Gly	missense_variant	21	36252949	T	C	14.81%	54	D	CANCER	Passenger		true	true	true	TRUE		Likely pathogenic	0.0988	30.45%	94.90%	60%	Subclonal			
META31	TTC3	p.Lys778fs	frameshift_variant	21	38524242	CA	C	25.38%	130	A	.	.		.	.	.			Indeterminate	0.6106	70.28%	100.00%	100%	Clonal			
META31	DYRK1A	p.Asn151fs	frameshift_variant	21	38853058	TA	T	17.65%	85	A	.	.		.	.	.	TRUE		Likely pathogenic	0.1568	43.45%	96.81%	71%	Subclonal			
META31	DSCAM	p.Pro47Pro	synonymous_variant	21	42080600	G	A	12.00%	50	.	.	.		.	.	.			.	0.0413	22.32%	89.91%	48%	Subclonal			
META31	PI4KA	p.Arg2028Trp	missense_variant	22	21064988	G	A	17.91%	134	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0004	36.80%	75.84%	54%	Subclonal			
META31	GNAZ	p.Thr183Met	missense_variant	22	23438430	C	T	8.00%	75	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	10.93%	48.99%	24%	Subclonal			
META31	C22orf42	p.Arg134Cys	missense_variant	22	32548054	G	A	29.41%	51	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4015	53.75%	100.00%	89%	Subclonal			
META31	EP300	p.Pro870Ser	missense_variant	22	41545993	C	T	26.23%	61	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.2657	49.58%	98.24%	79%	Subclonal	TRUE	TAGTCGTACCCCCACCCC	GCAGGAAGTGAAGGCTGC
META31	WNT7B	p.Ala144Ala	synonymous_variant	22	46327116	G	A	29.63%	27	.	.	.		.	.	.			.	0.3758	43.83%	98.91%	89%	Subclonal			
META31	MAPK12	p.Val241Ala	missense_variant	22	50694093	A	G	11.90%	42	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0043	15.47%	74.85%	36%	Subclonal			
META31	TLR8	p.Tyr968fs	frameshift_variant	X	12940000	C	CA	12.20%	82	D	.	.		.	.	.			Indeterminate	0.0001	20.05%	63.02%	37%	Subclonal			
META31	SH3KBP1	p.Leu155Pro	missense_variant	X	19713786	A	G	33.33%	93	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6013	69.89%	100.00%	100%	Clonal			
META31	RPGR	p.Ter1153Glnext*?	stop_lost	X	38144795	A	G	20.99%	81	N	.	.		.	.	.			Indeterminate	0.0403	40.38%	91.34%	63%	Subclonal			
META31	FTSJ1	p.Ala110Ala	synonymous_variant	X	48337473	G	A	31.58%	76	.	.	.		.	.	.			.	0.5119	63.80%	100.00%	95%	Clonal			
META31	RBM3	p.Ala82Ala	synonymous_variant	X	48434737	A	G	39.13%	23	D	.	.		.	.	.			.	0.5337	54.30%	100.00%	100%	Clonal			
META31	CDX4	p.Pro105Pro	synonymous_variant	X	72667404	C	T	24.00%	25	.	.	.		.	.	.			.	0.2366	33.03%	97.93%	72%	Subclonal			
META31	PCDH19	p.Asp124Tyr	missense_variant	X	99663226	C	A	30.77%	52	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4516	56.65%	100.00%	93%	Subclonal			
META31	CHRDL1	p.Phe281Phe	synonymous_variant	X	109931967	A	G	16.35%	104	.	.	.		.	.	.			.	0.0005	31.16%	73.91%	49%	Subclonal			
META31	DCX	p.Arg170*	stop_gained	X	110653362	G	A	33.64%	107	A	.	.		.	.	.			Indeterminate	0.6294	72.28%	100.00%	100%	Clonal			
META33	ATPIF1	p.Arg23Gln	missense_variant	1	28562762	G	A	60.00%	10	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8505	55.91%	100.00%	100%	Clonal			
META33	AGO1	p.Ile575fs	frameshift_variant	1	36379575	T	TTAACAAC	29.69%	64	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9046	72.44%	100.00%	100%	Clonal			
META33	POU3F1	p.Leu269Val	missense_variant	1	38511611	G	C	20.00%	25	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7393	36.78%	98.96%	100%	Clonal			
META33	GPA33	p.Asn93Lys	missense_variant	1	167038295	G	C	36.84%	19	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9196	56.45%	100.00%	100%	Clonal			
META33	GPA33	p.Asn78Lys	missense_variant	1	167038340	G	C	37.50%	16	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9098	52.75%	100.00%	100%	Clonal			
META33	CNOT11	p.Phe395Phe	synonymous_variant	2	101883288	C	T	14.29%	70	.	.	.		.	.	.			.	0.7060	44.65%	98.82%	86%	Clonal			
META33	SAP130	p.Pro158Leu	missense_variant	2	128774075	G	A	27.03%	37	D	.	Passenger		.	.	.			Indeterminate	0.8128	52.83%	100.00%	100%	Clonal			
META33	SESTD1	p.Ser426Asn	missense_variant	2	179988447	C	T	17.78%	90	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7494	53.53%	100.00%	89%	Clonal			
META33	ZC3H15	p.Gly167Val	missense_variant	2	187367280	G	T	27.45%	51	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9493	70.00%	100.00%	100%	Clonal			
META33	LRRN1	p.Val303Val	synonymous_variant	3	3887234	C	T	28.95%	38	.	.	.		.	.	.			.	0.9315	63.87%	100.00%	100%	Clonal			
META33	METTL6	p.Leu84Val	missense_variant	3	15466572	G	C	16.36%	55	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7664	47.02%	100.00%	98%	Clonal			
META33	HYAL1	p.Ala178Ser	missense_variant	3	50339856	C	A	30.77%	26	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8306	51.60%	100.00%	100%	Clonal			
META33	LRTM1	p.Gly202Trp	missense_variant	3	54958646	C	A	57.89%	38	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9446	81.91%	100.00%	100%	Clonal			
META33	SLC15A2	p.Val428Leu	missense_variant	3	121647343	G	T	18.89%	90	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7919	56.89%	100.00%	95%	Clonal			
META33	PTX3	p.Glu277Val	missense_variant	3	157160452	A	T	25.00%	52	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9033	64.81%	100.00%	100%	Clonal			
META33	CCDC158	p.Glu596Lys	missense_variant	4	77288491	C	T	9.59%	73	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5187	32.05%	97.45%	67%	Clonal			
META33	ARHGEF38	p.Lys576Lys	synonymous_variant	4	106588324	A	G	13.04%	92	.	.	.		.	.	.		TRUE	.	0.0592	30.25%	84.82%	52%	Subclonal			
META33	TMEM155	p.Thr124Asn	missense_variant	4	122681471	G	T	20.83%	24	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6714	33.32%	98.59%	84%	Clonal			
META33	CMYA5	p.Leu2448Leu	synonymous_variant	5	79031932	C	T	7.94%	63	.	.	.		.	.	.		TRUE	.	0.0076	13.62%	68.88%	32%	Subclonal			
META33	CEP120	p.Lys799Lys	synonymous_variant	5	122708428	T	C	63.89%	36	.	.	.		.	.	.		TRUE	.	0.8685	83.33%	100.00%	100%	Clonal			
META33	ATP10B	p.Leu1127Leu	synonymous_variant	5	160025960	G	A	61.54%	39	.	.	.		.	.	.		TRUE	.	0.9070	83.64%	100.00%	100%	Clonal			
META33	RNF5	p.Ala170Pro	missense_variant	6	32148068	G	C	31.20%	125	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9693	86.14%	100.00%	100%	Clonal			
META33	HOXA3	p.Ala392Val	missense_variant	7	27147691	G	A	50.00%	16	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9136	61.66%	100.00%	100%	Clonal			
META33	SRRT	p.Arg617Pro	missense_variant	7	100484696	G	C	7.35%	68	D	.	Passenger		.	.	.			Indeterminate	0.1585	19.03%	89.52%	44%	Subclonal			
META33	SLCO5A1	p.Ile657Ile	synonymous_variant	8	70591666	T	A	33.68%	95	.	.	.		.	.	.			.	0.9344	85.54%	100.00%	100%	Clonal			
META33	KIAA1161	p.Pro585Leu	missense_variant	9	34371188	G	A	27.78%	18	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8711	44.74%	100.00%	100%	Clonal			
META33	TRPM3	p.Arg1670Gly	missense_variant	9	73150985	G	C	37.25%	102	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9553	87.40%	100.00%	100%	Clonal			
META33	NAA35	p.Gly292Ala	missense_variant	9	88593294	G	C	41.07%	112	D	.	Passenger		.	.	.			Indeterminate	0.8777	89.93%	100.00%	100%	Clonal			
META33	CNTRL	p.Ala1627_Glu1634del	disruptive_inframe_deletion	9	123921243	GGAAGCTCTGAGACTGGGAGAGACT	G	23.33%	30	.	.	.	Deleterious	true	.	.		TRUE	Likely pathogenic	0.7370	41.97%	98.97%	94%	Clonal			
META33	ZEB1	p.Arg326*	stop_gained	10	31809236	C	T	23.53%	34	A	.	.		.	.	.			Indeterminate	0.8645	53.14%	100.00%	100%	Clonal			
META33	KCNMA1	p.Ala552Thr	missense_variant	10	78832950	C	T	31.25%	16	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8620	44.38%	100.00%	100%	Clonal			
META33	PNLIPRP2	p.Glu206Glu	synonymous_variant	10	118389494	G	A	33.33%	30	.	.	.		.	.	.			.	0.8626	58.24%	100.00%	100%	Clonal			
META33	OR52I1	p.Gly206Val	missense_variant	11	4615885	G	T	10.26%	156	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0179	31.79%	79.73%	51%	Subclonal			
META33	OR8J1	p.Leu55Ile	missense_variant	11	56127885	C	A	5.15%	97	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0083	13.21%	68.59%	31%	Subclonal			
META33	OR8D2	p.Pro129Ala	missense_variant	11	124189709	G	C	21.74%	23	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6901	34.28%	98.70%	87%	Clonal			
META33	ABCC9	p.Pro664Pro	synonymous_variant	12	22035727	G	C	33.78%	74	.	.	.		.	.	.			.	0.8336	83.07%	100.00%	100%	Clonal			
META33	OR4K17	p.Pro198Pro	synonymous_variant	14	20586159	C	G	5.66%	106	.	.	.		.	.	.			.	0.0093	15.55%	70.39%	34%	Subclonal			
META33	FANCM	p.Arg573Gln	missense_variant	14	45633698	G	A	45.95%	37	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8429	77.79%	100.00%	100%	Clonal			
META33	PELI2	p.Arg38Gln	missense_variant	14	56645088	G	A	34.78%	46	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9534	74.06%	100.00%	100%	Clonal			
META33	NRDE2	p.Thr243Ser	missense_variant	14	90770556	G	C	15.38%	52	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3798	31.57%	95.76%	62%	Subclonal			
META33	EML1	p.Ile518_Gln521delinsMet	disruptive_inframe_deletion	14	100380517	TTCCAGAACA	T	18.60%	43	D	.	.	Deleterious	.	.	.			Indeterminate	0.7999	48.11%	100.00%	100%	Clonal			
META33	PLA2G4F	p.Val359Gly	missense_variant	15	42439944	A	C	50.00%	14	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9319	56.90%	100.00%	100%	Clonal			
META33	TRPM7	p.Glu800Asp	missense_variant	15	50902039	T	A	51.61%	62	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9714	85.88%	100.00%	100%	Clonal			
META33	EFTUD1	p.Glu895*	stop_gained	15	82444112	C	A	12.99%	77	A	.	.		.	.	.			Indeterminate	0.7372	46.30%	98.99%	91%	Clonal			
META33	NCOR1	p.Ser1195Asn	missense_variant	17	15978934	C	T	30.00%	60	D	CANCER	Passenger		.	true	true		TRUE	Likely pathogenic	0.8768	67.00%	100.00%	100%	Clonal			
META33	UNC13D	p.Ala356Gly	missense_variant	17	73832988	G	C	24.00%	25	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9010	51.36%	100.00%	100%	Clonal			
META33	C19orf67	p.Trp265*	stop_gained	19	14193389	C	T	45.45%	33	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9562	72.51%	100.00%	100%	Clonal			
META33	UPF1	p.Ile466Ile	synonymous_variant	19	18965787	C	A	61.54%	13	.	.	.		.	.	.		TRUE	.	0.9222	62.53%	100.00%	100%	Clonal			
META33	DLGAP4	p.Gly213Ser	missense_variant	20	35060757	G	A	33.33%	18	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9084	51.47%	100.00%	100%	Clonal			
META33	BRWD1	p.Leu1612Leu	synonymous_variant	21	40571508	A	G	14.68%	109	.	.	.		.	.	.			.	0.8549	62.30%	100.00%	100%	Clonal			
META33	TNRC6B	p.Ser273Thr	missense_variant	22	40661051	T	A	18.18%	121	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7786	59.08%	100.00%	91%	Clonal			
META39	VPS13D	p.Leu4153Leu	synonymous_variant	1	12516179	G	A	75.76%	33	.	.	.		.	.	.		TRUE	.	0.9808	84.41%	100.00%	100%	Clonal			
META39	TAL1	p.Arg230His	missense_variant	1	47685699	C	T	62.50%	24	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.8138	76.77%	100.00%	100%	Clonal			
META39	MROH7	p.Val742Val	synonymous_variant	1	55145112	G	A	25.00%	24	.	.	.		.	.	.			.	0.8246	43.54%	100.00%	100%	Clonal			
META39	COL24A1	p.Arg635Leu	missense_variant	1	86515808	C	A	37.50%	120	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9550	87.42%	100.00%	100%	Clonal			
META39	TSHB	p.Ile78Met	missense_variant	1	115576665	C	G	43.43%	251	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9852	95.01%	100.00%	100%	Clonal	TRUE	TTATGCTCTCTTTTCTGTTCTTTCC	AGTCAGTATTGCACTTGCCACA
META39	TSHB	p.Tyr97*	stop_gained	1	115576722	T	A	45.42%	251	D	.	.		.	.	.			Indeterminate	0.9810	95.31%	100.00%	100%	Clonal	TRUE	AATATGCTCTGTCCCAGGATGT	ACTTCTGAGGTTTGGTACAGTAGTTTG
META39	SEC22B	p.Asn171Asn	synonymous_variant	1	145115754	C	T	8.76%	251	.	.	.		.	.	.			.	0.0000	26.68%	59.32%	41%	Subclonal			
META39	SEMA6C	p.Cys332Tyr	missense_variant	1	151109035	C	T	14.47%	228	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8579	66.33%	100.00%	96%	Clonal			
META39	SPRR3	p.Gly81Gly	synonymous_variant	1	152975739	T	C	5.94%	101	.	.	.		.	.	.			.	0.0549	18.07%	80.24%	39%	Subclonal			
META39	ITLN1	p.Leu176Leu	synonymous_variant	1	160850980	G	C	28.07%	57	.	.	.		.	.	.		TRUE	.	0.8950	66.39%	100.00%	100%	Clonal			
META39	IGFN1	p.Ile121Ile	synonymous_variant	1	201166441	C	T	83.33%	12	.	.	.		.	.	.		TRUE	.	0.4917	70.44%	100.00%	100%	Clonal			
META39	PIK3C2B	p.Asp1158Val	missense_variant	1	204408106	T	A	31.37%	51	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9104	69.04%	100.00%	100%	Clonal			
META39	TLR5	p.Ile402Ile	synonymous_variant	1	223285168	A	T	22.30%	148	.	.	.		.	.	.		TRUE	.	0.8955	70.39%	100.00%	100%	Clonal			
META39	CAPN9	p.Gly287Arg	missense_variant	1	230907829	G	A	42.86%	49	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9676	79.02%	100.00%	100%	Clonal			
META39	OR2AK2	p.Arg69Thr	missense_variant	1	248128839	G	C	18.78%	181	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7704	62.30%	98.94%	87%	Clonal			
META39	OR2L5	p.Arg262Arg	synonymous_variant	1	248186033	A	C	22.78%	316	.	.	.		.	.	.		TRUE	.	0.9361	80.65%	100.00%	100%	Clonal			
META39	EIF2B4	p.Leu443Val	missense_variant	2	27587690	A	C	41.94%	62	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9706	82.01%	100.00%	100%	Clonal			
META39	MTHFD2	p.Pro287Pro	synonymous_variant	2	74438965	C	T	52.73%	55	.	.	.		.	.	.			.	0.9212	85.53%	100.00%	100%	Clonal			
META39	INO80B	p.Leu161Arg	missense_variant	2	74683341	T	G	24.39%	41	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8479	53.45%	100.00%	100%	Clonal			
META39	BUB1	p.Glu87Lys	missense_variant	2	111430401	C	T	36.92%	65	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9541	79.10%	100.00%	100%	Clonal			
META39	DARS	p.Gln36Glu	missense_variant	2	136740985	G	C	41.67%	36	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9612	72.68%	100.00%	100%	Clonal			
META39	TTN	p.Leu25184Arg	missense_variant	2	179435308	A	C	32.95%	88	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9196	74.94%	100.00%	100%	Clonal			
META39	FZD7	p.Ile532Val	missense_variant	2	202900964	A	G	27.96%	93	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9253	78.37%	100.00%	100%	Clonal	TRUE	CTGGGAGCGCACCTGGCT	CTAAGTCTGTGGTAGAAGCGGCG
META39	LOC100652824	p.Ser914Thr	missense_variant	2	203055040	T	A	7.96%	113	.	.	Passenger		.	.	.			Indeterminate	0.0423	23.61%	80.25%	45%	Subclonal			
META39	RQCD1	p.Phe238Leu	missense_variant	2	219457104	C	A	14.74%	156	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7198	55.05%	98.64%	83%	Clonal			
META39	MKRN2	p.Pro360His	missense_variant	3	12623417	C	A	5.53%	235	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	21.24%	60.74%	37%	Subclonal			
META39	RTP3	p.Glu6Lys	missense_variant	3	46539568	G	A	51.52%	33	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8993	71.58%	100.00%	100%	Clonal			
META39	OR5H15	p.Gly161Val	missense_variant	3	97888025	G	T	40.37%	109	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9739	88.01%	100.00%	100%	Clonal			
META39	CPOX	p.Gln380fs	frameshift_variant	3	98304318	T	TG	39.13%	230	A	.	.		.	.	.			Indeterminate	0.9674	93.37%	100.00%	100%	Clonal			
META39	SLC9C1	p.Pro1070Arg	missense_variant	3	111887752	G	C	5.61%	107	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	11.73%	53.68%	26%	Subclonal			
META39	HCLS1	p.Met384Ile	missense_variant	3	121351267	C	A	32.86%	213	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3904	89.98%	100.00%	100%	Clonal			
META39	PIK3CA	p.Glu542Lys	missense_variant	3	178936082	G	A	37.65%	85	D	CANCER	Driver		true	true	true			Likely pathogenic	0.9589	83.48%	100.00%	100%	Clonal	TRUE	CTGTGAATCCAGAGGGGAAA	ACATGCTGAGATCAGCCAAA
META39	CLOCK	p.Arg82*	stop_gained	4	56344994	G	A	71.23%	73	A	.	.		.	.	.			Indeterminate	0.4270	92.45%	100.00%	100%	Clonal			
META39	NDST4	p.Ser673Ser	synonymous_variant	4	115767075	C	T	16.25%	80	.	.	.		.	.	.			.	0.7913	51.07%	100.00%	91%	Clonal			
META39	CDH9	p.Arg357*	stop_gained	5	26902769	G	A	52.44%	82	A	.	.		.	.	.			Indeterminate	0.9039	89.70%	100.00%	100%	Clonal			
META39	ARAP3	p.Ile927Met	missense_variant	5	141044508	G	C	91.67%	12	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9452	72.54%	100.00%	100%	Clonal			
META39	CSF1R	p.Arg727Lys	missense_variant	5	149437108	C	T	39.13%	23	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.8310	51.06%	100.00%	100%	Clonal			
META39	DOCK2	p.Ser608Tyr	missense_variant	5	169141195	C	A	16.36%	55	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6563	39.31%	98.18%	76%	Clonal			
META39	COL11A2	p.Gly1273Asp	missense_variant	6	33136766	C	T	57.35%	68	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7401	89.27%	100.00%	100%	Clonal			
META39	C6orf223	p.Pro225Pro	synonymous_variant	6	43970809	A	C	25.81%	31	.	.	.		.	.	.			.	0.8475	50.31%	100.00%	100%	Clonal			
META39	FILIP1	p.Thr822Thr	synonymous_variant	6	76023091	C	T	42.40%	125	.	.	.		.	.	.			.	0.9438	81.76%	100.00%	100%	Clonal			
META39	HBS1L	p.Arg668Pro	missense_variant	6	135287507	C	G	32.28%	127	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7895	84.24%	100.00%	100%	Clonal			
META39	BCLAF1	p.Arg283Gln	missense_variant	6	136599171	C	T	14.95%	107	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.4498	42.98%	96.19%	69%	Subclonal			
META39	GRID2IP	p.Asp1058Asn	missense_variant	7	6541728	C	T	37.50%	24	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8826	56.77%	100.00%	100%	Clonal			
META39	H2AFV	p.Ile119Thr	missense_variant	7	44874131	A	G	10.87%	46	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0687	17.03%	81.79%	39%	Subclonal			
META39	CDK14	p.Asp314Asp	synonymous_variant	7	90585127	C	T	24.43%	176	.	.	.		.	.	.			.	0.8650	82.70%	100.00%	100%	Clonal			
META39	CUL1	p.Tyr50Asp	missense_variant	7	148451075	T	G	42.31%	26	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9180	63.67%	100.00%	100%	Clonal	TRUE	GAATGCATTGGTAATGAAATATAAGAA	AACTGAGCTCCTCCAGGTGT
META39	GBX1	p.Ter364Serext*?	stop_lost	7	150845677	C	G	43.33%	30	N	.	.		.	.	.			Indeterminate	0.9276	67.64%	100.00%	100%	Clonal			
META39	LONRF1	p.Phe294Tyr	missense_variant	8	12598465	A	T	31.15%	122	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6135	61.34%	97.89%	82%	Clonal			
META39	LONRF1	p.Phe294Val	missense_variant	8	12598466	A	C	31.67%	120	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6617	62.35%	98.24%	83%	Clonal			
META39	PPP3CC	p.Arg51Gln	missense_variant	8	22332569	G	A	44.00%	50	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9120	71.26%	100.00%	100%	Clonal			
META39	CHMP7	p.Pro442Ser	missense_variant	8	23118074	C	T	86.67%	75	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8730	94.03%	100.00%	100%	Clonal			
META39	MYC	p.Gln52His	missense_variant	8	128750619	G	C	18.00%	100	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.9292	70.95%	100.00%	100%	Clonal	TRUE	TCACCAACAGGAACTATGACCTCGA	AGCAGAGCCCGGAGCGGC
META39	KLHL9	p.Leu54Leu	synonymous_variant	9	21334697	C	T	19.59%	97	.	.	.		.	.	.			.	0.4387	46.24%	96.09%	71%	Subclonal			
META39	ENTPD2	c.1029+2T>C	splice_donor_variant	9	139944734	A	G	8.93%	56	D	.	.		.	.	.			Indeterminate	0.0098	13.88%	69.40%	32%	Subclonal			
META39	ITIH2	p.Glu631Gly	missense_variant	10	7776989	A	G	47.50%	40	D	PASSENGER/OTHER	Driver		.	.	.		TRUE	Likely pathogenic	0.9094	71.30%	100.00%	100%	Clonal			
META39	SLC16A9	c.436+1G>A	splice_donor_variant	10	61423984	C	T	21.62%	37	D	.	.		.	.	.			Indeterminate	0.6858	39.18%	98.39%	78%	Clonal			
META39	HKDC1	p.Ala314Ala	synonymous_variant	10	71005901	C	T	22.22%	63	.	.	.		.	.	.			.	0.6992	48.18%	98.49%	81%	Clonal			
META39	ECD	p.Ser473Ser	synonymous_variant	10	74899168	G	C	60.00%	75	.	.	.		.	.	.			.	0.9707	90.11%	100.00%	100%	Clonal			
META39	SYNPO2L	p.Phe686Phe	synonymous_variant	10	75407352	G	A	22.22%	54	.	.	.		.	.	.			.	0.7030	46.05%	98.51%	81%	Clonal			
META39	OPN4	p.Arg179Cys	missense_variant	10	88418318	C	T	4.24%	165	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.4121	27.75%	95.59%	58%	Subclonal			
META39	SEC31B	p.Gly946Cys	missense_variant	10	102249894	C	A	42.86%	21	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8532	53.82%	100.00%	100%	Clonal			
META39	ATHL1	p.His657Asn	missense_variant	11	294427	C	A	33.93%	56	N	.	Passenger		.	.	.			Likely passenger	0.9017	69.02%	100.00%	100%	Clonal			
META39	OR8I2	p.Val135Ile	missense_variant	11	55861186	G	A	56.20%	137	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9840	93.59%	100.00%	100%	Clonal			
META39	SCGB1D4	p.Lys48Lys	synonymous_variant	11	62065042	T	C	30.94%	181	.	.	.		.	.	.			.	0.9407	81.26%	100.00%	100%	Clonal			
META39	FGF19	p.Thr204Thr	synonymous_variant	11	69514069	G	A	56.82%	44	.	.	.		.	.	.			.	0.9726	83.04%	100.00%	100%	Clonal			
META39	INTS4	p.Leu456Pro	missense_variant	11	77639392	A	G	22.58%	31	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.7136	38.44%	98.58%	82%	Clonal			
META39	APOC3	p.Val55Leu	missense_variant	11	116701596	G	C	66.67%	9	N	.	Passenger		.	.	.		TRUE	Likely passenger	0.8911	48.41%	100.00%	100%	Clonal			
META39	ADAMTS20	p.Ser1667*	stop_gained	12	43770452	G	C	20.79%	202	A	.	.		.	.	.			Indeterminate	0.9280	78.03%	100.00%	100%	Clonal			
META39	ADAMTS20	p.Trp1080Arg	missense_variant	12	43825158	A	G	47.53%	263	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2742	96.17%	100.00%	100%	Clonal			
META39	OR6C2	p.Leu217Val	missense_variant	12	55846646	T	G	27.09%	203	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7116	87.35%	100.00%	100%	Clonal			
META39	TMEM132D	p.Pro219Pro	synonymous_variant	12	130184666	C	A	36.00%	25	.	.	.		.	.	.			.	0.8740	55.86%	100.00%	100%	Clonal			
META39	RFC3	p.Gln117Lys	missense_variant	13	34399981	C	A	81.40%	43	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6316	89.41%	100.00%	100%	Clonal			
META39	ARHGEF40	c.4519-2A>C	splice_acceptor_variant	14	21556987	A	C	9.46%	74	D	.	.		.	.	.			Indeterminate	0.0703	21.32%	82.78%	44%	Subclonal			
META39	NOP9	p.Arg577Gln	missense_variant	14	24773781	G	A	59.26%	27	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8626	77.52%	100.00%	100%	Clonal			
META39	GCNT3	p.Leu276Leu	synonymous_variant	15	59911265	A	G	21.08%	166	.	.	.		.	.	.		TRUE	.	0.0001	40.44%	72.93%	55%	Subclonal			
META39	CHRNB4	p.Cys21Cys	synonymous_variant	15	78927922	G	A	81.13%	106	.	.	.		.	.	.		TRUE	.	0.9782	95.14%	100.00%	100%	Clonal			
META39	IL21R	p.Ala190Val	missense_variant	16	27454433	C	T	28.57%	49	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.8925	64.28%	100.00%	100%	Clonal			

META39	*PRR14*	p.Arg183fs	frameshift_variant	16	30665532	ACCTTGCCCTTCACCCCAGAG	A	17.97%	128	A	.	.		.	.	.			Indeterminate	0.7213	55.46%	98.65%	83%	Clonal			
META39	*GOT2*	p.Tyr246Tyr	synonymous_variant	16	58750682	G	A	21.05%	57	.	.	.		.	.	.		TRUE	.	0.0845	32.37%	86.31%	55%	Subclonal			
META39	*LCAT*	p.Trp275Ser	missense_variant	16	67974306	C	G	25.00%	28	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5062	32.45%	96.71%	66%	Clonal			
META39	*CDH1*	p.Gly278fs	frameshift_variant	16	68844240	T	TC	89.86%	69	A	.	.		true	true	true		TRUE	Likely pathogenic	0.5771	93.88%	100.00%	100%	Clonal			
META39	*TP53*	p.Cys275Arg	missense_variant	17	7577115	A	G	92.86%	28	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.8272	86.66%	100.00%	100%	Clonal	TRUE	CATAACTGCACCCTTGGTCTC	GGACCTGATTTCCTTACTGCC
META39	*DNAH9*	p.Phe2996Leu	missense_variant	17	11725892	C	G	48.42%	95	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9109	84.45%	100.00%	100%	Clonal			
META39	*TAOK1*	p.Val258Val	synonymous_variant	17	27818826	A	G	35.87%	92	.	.	.		.	.	.		TRUE	.	0.8588	68.05%	100.00%	94%	Clonal			
META39	*GREB1L*	p.Leu1165Met	missense_variant	18	19079791	C	A	61.22%	49	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9640	86.08%	100.00%	100%	Clonal			
META39	*DCC*	p.Ala865Glu	missense_variant	18	50918163	C	A	66.32%	95	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8240	93.16%	100.00%	100%	Clonal			
META39	*MUC16*	p.Ser8860Ser	synonymous_variant	19	9060866	A	C	24.77%	109	.	.	.		.	.	.			.	0.8081	61.86%	100.00%	90%	Clonal			
META39	*JAK3*	p.Pro986Ser	missense_variant	19	17942059	G	A	43.48%	23	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.9227	62.12%	100.00%	100%	Clonal			
META39	*ZNF180*	p.Thr460Ala	missense_variant	19	44981320	T	C	29.41%	85	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8953	68.58%	100.00%	100%	Clonal			
META39	*RBM38*	p.Pro129Ala	missense_variant	20	55967761	C	G	10.94%	64	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7193	37.82%	98.65%	83%	Clonal			
META39	*KRTAP15-1*	p.Ala34Thr	missense_variant	21	31812745	G	A	36.36%	44	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8976	67.81%	100.00%	100%	Clonal			
META39	*KRTAP15-1*	p.Ala34Gly	missense_variant	21	31812746	C	G	34.88%	43	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8924	65.48%	100.00%	100%	Clonal			
META39	*SEPT5*	p.Phe280Phe	synonymous_variant	22	19709370	C	T	57.69%	26	D	PASSENGER/OTHER	.		true	.	.		TRUE	.	0.9646	74.87%	100.00%	100%	Clonal			
META39	*SLC9A7*	p.Ile186Leu	missense_variant	X	46539160	T	G	48.08%	52	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9597	82.84%	100.00%	100%	Clonal			
META39	*FAM50A*	p.Lys216Lys	synonymous_variant	X	153677302	G	A	92.59%	27	.	.	.		.	.	.		TRUE	.	0.8495	86.17%	100.00%	100%	Clonal			
META40	*ABCA4*	p.Gly1441Gly	synonymous_variant	1	94496013	G	A	38.46%	39	.	.	.		.	.	.	TRUE		.	0.8183	61.98%	100.00%	100%	Clonal			
META40	*ABCA4*	p.Leu244Leu	synonymous_variant	1	94564388	G	A	24.56%	57	.	.	.		.	.	.	TRUE		.	0.3291	42.27%	96.02%	69%	Subclonal			
META40	*KCNH1*	p.Glu848Lys	missense_variant	1	210857051	C	T	27.78%	36	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0159	28.36%	79.64%	51%	Subclonal			
META40	*OR2T33*	p.Asp269Glu	missense_variant	1	248436310	G	T	40.51%	79	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1554	54.68%	92.61%	74%	Subclonal			
META40	*DYSF*	p.Pro1504Leu	missense_variant	2	71847723	C	T	26.53%	49	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0013	29.03%	72.88%	48%	Subclonal			
META40	*LRP1B*	p.Asp3747His	missense_variant	2	141116408	C	G	58.44%	77	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9340	80.52%	100.00%	100%	Clonal			
META40	*PDCD1*	p.Phe228Val	missense_variant	2	242793395	A	C	38.46%	13	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5469	30.78%	97.47%	70%	Clonal			
META40	*CHL1*	p.Asn113Asn	synonymous_variant	3	369991	T	C	72.12%	104	.	.	.		.	.	.	TRUE	TRUE	.	0.9807	94.08%	100.00%	100%	Clonal			
META40	*LSAMP*	p.Gly177Val	missense_variant	3	115571449	C	A	25.37%	67	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3436	45.80%	96.28%	72%	Subclonal			
META40	*CCDC39*	p.Leu806Leu	synonymous_variant	3	180334472	G	C	3.63%	193	.	.	.		.	.	.			.	0.0000	8.15%	34.66%	17%	Subclonal			
META40	*MUC4*	p.Asp3557Asn	missense_variant	3	195507782	C	T	18.10%	105	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2738	44.89%	95.24%	69%	Subclonal			
META40	*TBC1D9*	p.Leu430Leu	synonymous_variant	4	141590935	G	A	70.00%	10	.	.	.		.	.	.		TRUE	.	0.8593	55.12%	100.00%	100%	Clonal			
META40	*FREM3*	p.Leu646Val	missense_variant	4	144619893	G	C	7.06%	85	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	5.52%	25.99%	13%	Subclonal			
META40	*AFF4*	p.Lys741Arg	missense_variant	5	132232100	T	C	47.62%	63	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7188	64.00%	98.77%	87%	Clonal			
META40	*PSD2*	p.Asp362Asp	synonymous_variant	5	139197135	C	T	60.61%	33	.	.	.		.	.	.		TRUE	.	0.9047	71.20%	100.00%	100%	Clonal			
META40	*FAM114A2*	p.Leu460Leu	synonymous_variant	5	153374482	T	C	52.63%	38	.	.	.		.	.	.		TRUE	.	0.8423	64.55%	100.00%	96%	Clonal			
META40	*TRIM39*	p.Leu243Met	missense_variant	6	30303699	T	A	24.53%	53	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3452	41.39%	96.23%	69%	Subclonal			
META40	*PTCHD4*	p.Gly394Gly	synonymous_variant	6	47847398	G	T	66.67%	99	.	.	.		.	.	.		TRUE	.	0.9696	92.86%	100.00%	100%	Clonal			
META40	*RIMS1*	p.Arg211*	stop_gained	6	72889437	C	T	48.66%	187	A	.	.		.	.	.			Indeterminate	0.9652	93.99%	100.00%	100%	Clonal			
META40	*COX7A2*	p.Ala51Thr	missense_variant	6	75950945	C	T	47.92%	240	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9530	95.06%	100.00%	100%	Clonal			
META40	*UTRN*	p.Thr2307Ile	missense_variant	6	144872210	C	T	34.21%	76	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7981	65.76%	100.00%	96%	Clonal			
META40	*MTHFD1L*	p.Leu915Leu	synonymous_variant	6	151358148	A	G	36.09%	169	.	.	.		.	.	.			.	0.8872	78.75%	100.00%	100%	Clonal			
META40	*ADAM28*	p.Ile597Val	missense_variant	8	24199229	A	G	53.49%	43	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8601	67.40%	100.00%	97%	Clonal			
META40	*PRRC2B*	p.Ala1081Ala	synonymous_variant	9	134350759	T	C	50.00%	18	.	.	.		.	.	.		TRUE	.	0.7684	49.18%	100.00%	91%	Clonal			
META40	*USP47*	p.Asp1123His	missense_variant	11	11971454	G	C	6.90%	116	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.55%	36.24%	19%	Subclonal			
META40	*PDE3B*	p.His1064Asn	missense_variant	11	14891057	C	A	31.37%	153	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6929	68.11%	98.99%	88%	Clonal			
META40	*CATSPER1*	p.Leu738Leu	synonymous_variant	11	65784633	G	A	50.00%	10	.	.	.		.	.	.			.	0.7971	45.21%	100.00%	100%	Clonal			
META40	*CCDC84*	p.Gln201Gln	synonymous_variant	11	118882883	G	A	17.39%	46	.	.	.		.	.	.			.	0.0549	25.26%	85.04%	49%	Subclonal			
META40	*OR10G7*	p.Cys96Cys	synonymous_variant	11	123909421	G	A	25.00%	76	.	.	.		.	.	.			.	0.2796	46.28%	95.38%	70%	Subclonal			
META40	*NCAPD3*	p.Lys405Asn	missense_variant	11	134073941	C	G	41.67%	72	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8910	76.09%	100.00%	100%	Clonal			
META40	*LRMP*	p.Ala470Val	missense_variant	12	25260903	C	T	3.91%	128	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	6.09%	33.16%	15%	Subclonal			
META40	*DGKA*	p.Asp446His	missense_variant	12	56335867	G	C	64.10%	39	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9258	76.89%	100.00%	100%	Clonal			
META40	*ZFC3H1*	p.Arg508Lys	missense_variant	12	72036320	C	T	13.41%	82	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	13.47%	40.40%	24%	Subclonal			
META40	*ACSS3*	p.Gly78Val	missense_variant	12	81472132	G	T	81.25%	16	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8622	72.67%	100.00%	100%	Clonal			
META40	*GNPTAB*	p.Glu632Gln	missense_variant	12	102158801	C	G	63.24%	68	D	PASSENGER/OTHER	Passenger		.	.	true		TRUE	Likely pathogenic	0.9446	83.38%	100.00%	100%	Clonal			
META40	*HCAR3*	p.Arg111Leu	missense_variant	12	123200953	C	A	63.16%	19	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8823	63.65%	100.00%	100%	Clonal			
META40	*NBEA*	p.Thr2918Thr	synonymous_variant	13	36245041	T	G	86.00%	50	.	.	.		.	.	.		TRUE	.	0.6668	91.22%	100.00%	100%	Clonal			
META40	*SLTM*	p.Arg666fs	frameshift_variant	15	59182563	G	GCT	30.07%	143	A	.	.		.	.	.			Indeterminate	0.5899	64.40%	98.49%	85%	Clonal			
META40	*DIS3L*	c.2856+2T>C	splice_donor_variant	15	66625250	T	C	48.65%	74	D	.	.		.	.	.			Indeterminate	0.8250	82.95%	100.00%	100%	Clonal			
META40	*OR1A2*	p.Val81Met	missense_variant	17	3101053	G	A	70.00%	70	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8691	87.89%	100.00%	100%	Clonal			
META40	*DHRS7C*	p.Ala5Gly	missense_variant	17	9694588	G	C	63.16%	19	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8823	63.65%	100.00%	100%	Clonal			
META40	*MBD1*	p.Val572Val	synonymous_variant	18	47799194	C	A	45.45%	44	.	.	.		.	.	.			.	0.8712	72.43%	100.00%	100%	Clonal			
META40	*MBD1*	p.Pro519Pro	synonymous_variant	18	47799731	G	A	37.50%	32	.	.	.		.	.	.			.	0.7896	57.02%	100.00%	100%	Clonal			
META40	*SMARCA4*	p.Tyr1118Phe	missense_variant	19	11138597	A	T	43.12%	109	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.9105	83.04%	100.00%	100%	Clonal			
META40	*LDLR*	p.Asn247Lys	missense_variant	19	11217287	C	G	19.61%	51	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0965	30.63%	89.00%	55%	Subclonal			
META40	*IGFL1*	p.Val10Val	synonymous_variant	19	46733369	C	G	52.08%	48	.	.	.		.	.	.		TRUE	.	0.8438	67.11%	100.00%	95%	Clonal			
META40	*ZNF587*	p.Glu174Glu	synonymous_variant	19	58370302	G	A	14.29%	56	.	.	.		.	.	.		TRUE	.	0.0000	13.11%	46.43%	26%	Subclonal			
META40	*PI4KA*	p.Phe1139Phe	synonymous_variant	22	21098955	G	A	32.35%	34	.	.	.		.	.	.			.	0.7053	50.18%	100.00%	91%	Clonal			
META40	*FBLN1*	c.1972+1G>T	splice_donor_variant	22	45972989	G	T	50.00%	26	D	.	.		.	.	.	TRUE		Likely pathogenic	0.8528	66.90%	100.00%	100%	Clonal			
META40	*OFD1*	p.Lys980Asn	missense_variant	X	13786848	G	T	3.14%	255	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	4.07%	16.63%	9%	Subclonal			
META40	*PORCN*	p.Trp305Cys	missense_variant	X	48372982	G	C	56.52%	23	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8552	60.86%	100.00%	100%	Clonal	TRUE	AAATGGATTTGCATATCTCTTCTG	AAATGTTGTATGAATGTATGAAAGGG
META40	*KLHL4*	p.Gly677Val	missense_variant	X	86919868	G	T	40.38%	52	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8604	69.48%	100.00%	100%	Clonal			
META40	*BRS3*	p.Ser383Ile	missense_variant	X	135574482	G	T	29.27%	41	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6199	47.63%	98.63%	83%	Clonal			
META42	*UBR4*	p.Thr2331Thr	synonymous_variant	1	19478810	G	C	43.86%	57	.	.	.		.	.	.		TRUE	.	0.8118	62.58%	100.00%	89%	Clonal			
META42	*KPNA6*	p.Trp274*	stop_gained	1	32628036	G	A	63.77%	69	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9760	89.61%	100.00%	100%	Clonal			
META42	*SLC2A1*	p.Leu284Gln	missense_variant	1	43395280	A	T	55.56%	27	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.9325	72.78%	100.00%	100%	Clonal			
META42	*DPH2*	p.Ala472Thr	missense_variant	1	44438155	G	A	40.00%	20	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.8236	52.37%	100.00%	100%	Clonal			
META42	*AGBL4*	p.Asn89fs	frameshift_variant	1	50162993	CTTTCACAT	C	32.26%	62	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8221	62.14%	100.00%	97%	Clonal			
META42	*LRRC40*	p.Gln359Leu	missense_variant	1	70639183	T	A	38.46%	39	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8629	63.91%	100.00%	100%	Clonal			
META42	*ARHGAP29*	p.Glu795Gln	missense_variant	1	94645378	C	G	14.94%	154	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	30.24%	64.24%	45%	Subclonal			
META42	*GSTM1*	p.Asn151Asp	missense_variant	1	110232983	A	G	30.43%	23	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7274	42.29%	98.95%	92%	Clonal			
META42	*SPAG17*	p.Glu1325*	stop_gained	1	118566023	C	A	62.00%	50	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9688	85.65%	100.00%	100%	Clonal			
META42	*CRNN*	p.Gln142Arg	missense_variant	1	152383133	T	C	5.39%	167	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	11.12%	39.43%	22%	Subclonal			
META42	*SUCO*	p.Thr75Ser	missense_variant	1	172501835	A	T	37.70%	61	N	.	Passenger		.	.	.			Likely passenger	0.8863	76.88%	100.00%	100%	Clonal			
META42	*LGR6*	c.1070+2T>C	splice_donor_variant	1	202273760	T	C	32.26%	31	D	.	.		.	.	.			Indeterminate	0.8482	57.48%	100.00%	100%	Clonal			
META42	*USH2A*	p.Asp349Gly	missense_variant	1	216498744	T	C	31.82%	44	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8649	64.00%	100.00%	100%	Clonal			
META42	*CDC42BPA*	p.Pro261Thr	missense_variant	1	227335173	G	T	31.91%	47	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7986	57.16%	100.00%	96%	Clonal			
META42	*CEP170*	p.Leu962Phe	missense_variant	1	243328378	G	A	33.90%	59	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8466	64.25%	100.00%	100%	Clonal			
META42	*DCDC2C*	p.Gln261*	stop_gained	2	3815398	C	T	17.77%	197	.	.	.		.	.	.			Indeterminate	0.8832	72.09%	100.00%	100%	Clonal			
META42	*APOB*	p.Gly3996Ser	missense_variant	2	21227242	C	T	14.29%	42	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5696	32.02%	97.96%	72%	Clonal			
META42	*APOB*	p.Asp3739Gly	missense_variant	2	21228524	T	C	56.76%	148	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6284	94.77%	100.00%	100%	Clonal			
META42	*APOB*	p.Asp2293Glu	missense_variant	2	21232861	A	T	11.66%	163	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0626	37.69%	86.62%	59%	Subclonal			
META42	*PRKD3*	p.Glu487Lys	missense_variant	2	37501756	C	T	20.25%	79	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8600	63.91%	100.00%	100%	Clonal			
META42	*ANKRD36*	p.Ile906Val	missense_variant	2	97864356	A	G	8.57%	70	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0792	19.83%	84.83%	43%	Subclonal			
META42	*TTN*	p.Pro16840Ala	missense_variant	2	179476518	G	C	18.70%	230	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8214	68.94%	100.00%	94%	Clonal			
META42	*ITGA4*	p.Ile410Asn	missense_variant	2	182358127	T	A	8.62%	58	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1269	18.63%	88.09%	43%	Subclonal			
META42	*ANKAR*	p.Asn76Ile	missense_variant	2	190541443	A	T	51.70%	147	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6211	94.26%	100.00%	100%	Clonal			
META42	*PMS1*	p.Arg751Gly	missense_variant	2	190728863	A	G	21.45%	331	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.8689	86.70%	100.00%	100%	Clonal			
META42	*AOX1*	p.Asn954His	missense_variant	2	201515709	A	C	8.00%	100	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0995	24.47%	87.06%	48%	Subclonal			
META42	*CDK15*	p.Arg64Pro	missense_variant	2	202672284	G	C	33.88%	242	N	CANCER	Passenger		.	.	.			Likely passenger	0.9756	93.19%	100.00%	100%	Clonal			
META42	*FASTKD2*	p.Asn183Asp	missense_variant	2	207631964	A	G	28.95%	190	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9445	88.93%	100.00%	100%	Clonal			
META42	*CXCR2*	p.Ser193Thr	missense_variant	2	219000102	G	C	6.98%	86	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0106	16.05%	71.64%	35%	Subclonal			
META42	*ITPR1*	p.Ala879Ala	synonymous_variant	3	4716835	C	A	64.38%	73	.	.	.		.	.	.		TRUE	.	0.9775	90.28%	100.00%	100%	Clonal			
META42	*LRRC31*	p.Glu171*	stop_gained	3	169574637	C	A	47.86%	351	A	.	.		.	.	.		TRUE	Likely pathogenic	0.3266	97.44%	100.00%	100%	Clonal			
META42	*TNIK*	p.Glu1303Asp	missense_variant	3	170784066	C	A	26.40%	678	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2196	97.22%	100.00%	100%	Clonal			
META42	*SLC51A*	p.Thr310Asn	missense_variant	3	195959976	C	A	45.28%	53	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9575	80.52%	100.00%	100%	Clonal			
META42	*CPZ*	p.Ser626Ser	synonymous_variant	4	8621263	G	A	85.71%	14	.	.	.		.	.	.		TRUE	.	0.8761	73.90%	100.00%	100%	Clonal			
META42	*KLB*	p.Leu35Phe	missense_variant	4	39408674	G	T	21.57%	51	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7096	47.20%	98.87%	87%	Clonal			
META42	*POLR2B*	p.Ala843Thr	missense_variant	4	57889507	G	A	19.44%	36	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6285	36.88%	98.38%	78%	Clonal			
META42	*HSD17B13*	p.Ile15Leu	missense_variant	4	88243951	T	G	86.05%	43	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3762	90.03%	100.00%	100%	Clonal			
META42	*PPP3CA*	p.Asp234His	missense_variant	4	102015015	C	G	52.94%	51	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8628	81.68%	100.00%	100%	Clonal			
META42	*CDH9*	p.Arg683Gly	missense_variant	5	26881568	T	C	25.36%	138	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9026	78.38%	100.00%	100%	Clonal			
META42	*PARP8*	p.Thr693Ser	missense_variant	5	50123877	A	T	20.45%	44	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.3144	33.14%	94.83%	62%	Subclonal			
META42	*CMYA5*	p.His3622Gln	missense_variant	5	79041176	T	A	24.66%	73	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8163	60.15%	100.00%	99%	Clonal			
META42	*ARSK*	p.His135Pro	missense_variant	5	94903741	A	C	33.33%	51	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8792	68.86%	100.00%	100%	Clonal			
META42	*PCDHGB4*	p.Ala514Val	missense_variant	5	140768992	C	T	13.04%	46	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2424	24.27%	93.04%	52%	Subclonal			
META42	*FAT2*	p.Val1882Phe	missense_variant	5	150925044	C	A	10.34%	87	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0092	21.96%	73.88%	42%	Subclonal			
META42	*NUP153*	p.Lys1013Glu	missense_variant	6	17629486	T	C	23.68%	76	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7945	58.51%	100.00%	95%	Clonal			
META42	*EGFL8*	p.Ser39Ser	synonymous_variant	6	32134290	C	T	10.71%	56	.	.	.		.	.	.			.	0.2849	24.77%	94.11%	54%	Subclonal			
META42	*UBR2*	p.Asp1751His	missense_variant	6	42658894	G	C	28.45%	116	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8559	80.32%	100.00%	100%	Clonal			
META42	*EPB41L2*	p.Ala528Thr	missense_variant	6	131211512	C	T	72.22%	72	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6622	92.33%	100.00%	100%	Clonal			
META42	*DNAH11*	p.Gln3366Glu	missense_variant	7	21840824	C	G	7.25%	69	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	9.19%	47.51%	22%	Subclonal			
META42	*ABCA13*	p.Ala2481Ser	missense_variant	7	48318232	G	T	52.85%	246	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9736	96.08%	100.00%	100%	Clonal			
META42	*PTCD1*	p.Lys680Asn	missense_variant	7	99017653	C	A	5.56%	126	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0221	18.86%	76.43%	39%	Subclonal			
META42	*LRRC17*	p.Lys234Asn	missense_variant	7	102575062	G	T	45.45%	88	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5391	89.54%	100.00%	100%	Clonal			
META42	*RELN*	p.Ser2555Arg	missense_variant	7	103162472	A	T	7.89%	114	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.2194	29.20%	92.66%	55%	Subclonal			
META42	*TNPO3*	p.Val644Leu	missense_variant	7	128619168	C	G	17.53%	154	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8899	72.78%	100.00%	100%	Clonal			
META42	*SMO*	p.Pro560Ala	missense_variant	7	128850831	C	G	11.11%	72	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.6251	38.06%	98.39%	78%	Clonal			
META42	*SSPO*	p.Pro2171Thr	missense_variant	7	149492731	C	A	6.67%	90	.	.	Passenger		.	.	.			Indeterminate	0.0000	9.02%	41.20%	20%	Subclonal			
META42	*SULF1*	p.Ala315Gly	missense_variant	8	70513947	C	G	11.76%	85	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0316	25.87%	80.80%	47%	Subclonal			
META42	*PABPC1*	p.Gln534Pro	missense_variant	8	101718880	T	G	33.78%	74	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8858	75.81%	100.00%	100%	Clonal			
META42	*TOP1MT*	p.Thr472Ile	missense_variant	8	144398212	G	A	16.33%	49	N	CANCER	Passenger		.	.	.			Likely passenger	0.6613	39.94%	98.60%	82%	Clonal			
META42	*ZC3H3*	p.Ser318Ala	missense_variant	8	144620585	A	C	42.31%	104	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9646	88.90%	100.00%	100%	Clonal			
META42	*IFNA4*	p.Arg184Ser	missense_variant	9	21186979	T	A	30.46%	151	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8074	69.87%	100.00%	92%	Clonal			
META42	*COL15A1*	p.Phe152Phe	synonymous_variant	9	101748202	C	T	69.01%	71	.	.	.		.	.	.		TRUE	.	0.5726	91.75%	100.00%	100%	Clonal			
META42	*EHMT1*	p.Leu260Leu	synonymous_variant	9	140622938	A	T	30.56%	36	.	.	.		.	.	.	TRUE	TRUE	.	0.7557	50.33%	100.00%	92%	Clonal			
META42	*BMI1*	p.Ser324Phe	missense_variant	10	22618461	C	T	19.10%	89	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5634	48.33%	97.93%	77%	Clonal			
META42	*ITGB1*	p.Arg413Gly	missense_variant	10	33209205	T	C	54.43%	79	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9599	89.41%	100.00%	100%	Clonal			
META42	*TLL2*	p.Phe714Leu	missense_variant	10	98144396	G	C	34.21%	38	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8200	57.33%	100.00%	100%	Clonal			
META42	*SLC5A12*	p.Pro320Leu	missense_variant	11	26718792	G	A	34.18%	79	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8692	69.13%	100.00%	100%	Clonal			
META42	*DAGLA*	p.Arg91Cys	missense_variant	11	61488326	C	T	56.52%	23	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9365	70.26%	100.00%	100%	Clonal			
META42	*FIBP*	p.Leu256Leu	synonymous_variant	11	65652557	C	T	16.67%	48	.	.	.		.	.	.			.	0.4733	34.05%	97.07%	67%	Subclonal			
META42	*LRP5*	p.Pro1236Leu	missense_variant	11	68197112	C	T	11.90%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2002	20.66%	91.59%	48%	Subclonal	TRUE	GACCTCTGTTTGTCTTGTTTTGTCT	GGTACCTGTCCATCACCCC
META42	*OR6T1*	p.Thr75Thr	synonymous_variant	11	123814321	A	T	60.47%	43	.	.	.		.	.	.		TRUE	.	0.9389	77.92%	100.00%	100%	Clonal			
META42	*ARHGAP32*	p.Lys294Lys	synonymous_variant	11	128932214	T	C	61.82%	55	.	.	.		.	.	.		TRUE	.	0.9392	82.27%	100.00%	100%	Clonal			
META42	*LTBR*	p.Gly398Gly	synonymous_variant	12	6499989	G	A	12.80%	211	.	.	.		.	.	.			.	0.8796	70.36%	100.00%	100%	Clonal			
META42	*USP5*	p.Lys291*	stop_gained	12	6967594	A	T	19.57%	92	A	.	.		.	.	.			Indeterminate	0.9396	73.04%	100.00%	100%	Clonal			
META42	*PZP*	p.Val331Leu	missense_variant	12	9349027	C	G	43.31%	127	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6979	91.63%	100.00%	100%	Clonal			
META42	*CLEC1B*	p.Ala18Asp	missense_variant	12	10151647	G	T	10.89%	248	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1240	45.24%	90.77%	66%	Subclonal			
META42	*GSG1*	p.Gln127His	missense_variant	12	13242194	C	G	7.58%	66	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5451	28.02%	97.79%	68%	Clonal			
META42	*AEBP2*	c.1174+1_1174+4delGTAA	splice_donor_variant	12	19646920	CGTAA	C	46.28%	121	.	.	.		.	.	.			Indeterminate	0.3182	92.72%	100.00%	100%	Clonal			
META42	*SLCO1B7*	p.Pro107Leu	missense_variant	12	21174496	C	T	5.43%	184	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0728	26.57%	85.41%	49%	Subclonal			
META42	*CUX2*	p.Val317Val	synonymous_variant	12	111744817	G	A	60.87%	23	.	.	.		.	.	.		TRUE	.	0.9554	72.93%	100.00%	100%	Clonal			
META42	*SRRM4*	p.Lys171Asn	missense_variant	12	119559923	A	T	17.53%	97	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0102	33.51%	78.92%	53%	Subclonal			
META42	*RXFP2*	p.Leu603Leu	synonymous_variant	13	32371360	C	A	10.42%	48	.	.	.		.	.	.		TRUE	.	0.0039	13.47%	66.60%	31%	Subclonal			
META42	*BRCA2*	p.Cys3287Ser	missense_variant	13	32972510	G	C	13.33%	105	D	PASSENGER/OTHER	Passenger		true	true	.	TRUE	TRUE	Likely pathogenic	0.0001	24.10%	63.45%	40%	Subclonal			
META42	*NBEA*	c.972+1G>T	splice_donor_variant	13	35624533	G	T	30.65%	124	D	.	.		.	.	.		TRUE	Likely pathogenic	0.8106	68.12%	100.00%	93%	Clonal			
META42	*MZT1*	p.Ser62Ser	synonymous_variant	13	73293129	C	G	57.14%	133	.	.	.		.	.	.		TRUE	.	0.8502	92.96%	100.00%	100%	Clonal			
META42	*NPAS3*	p.Thr272Ser	missense_variant	14	34204500	A	T	44.44%	18	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.7968	45.88%	98.96%	90%	Clonal			
META42	*C14orf159*	p.Glu324Glu	synonymous_variant	14	91655291	G	A	38.10%	21	.	.	.		.	.	.			.	0.8800	55.99%	100.00%	100%	Clonal			
META42	*TRIP11*	p.Glu185Gln	missense_variant	14	92487935	C	G	13.89%	72	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.1652	30.66%	90.95%	56%	Subclonal			
META42	*TJP1*	p.Ser1276Tyr	missense_variant	15	30010720	G	T	18.84%	69	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7675	52.49%	100.00%	95%	Clonal			
META42	*TRPM1*	p.Ala1062Thr	missense_variant	15	31321589	C	T	14.29%	49	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5619	34.11%	97.90%	72%	Clonal			
META42	*GANC*	p.Ala906Asp	missense_variant	15	42644309	C	A	20.83%	24	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4617	27.01%	96.86%	63%	Subclonal			
META42	*MNS1*	p.Ile245Val	missense_variant	15	56736006	T	C	38.89%	72	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9042	74.69%	100.00%	100%	Clonal			
META42	*CSPG4*	p.Arg450Trp	missense_variant	15	75982058	T	A	12.20%	41	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2237	21.17%	92.38%	49%	Subclonal			
META42	*ZNF710*	p.Thr514Ile	missense_variant	15	90616385	C	T	28.89%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8432	59.87%	100.00%	100%	Clonal			
META42	*HERPUD1*	p.Thr163Ser	missense_variant	16	56973204	A	T	41.27%	189	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.9748	93.20%	100.00%	100%	Clonal			
META42	*CNOT1*	p.Ala1596fs	frameshift_variant	16	58575418	GC	G	15.83%	120	A	.	.		.	.	.			Indeterminate	0.6127	50.88%	98.30%	79%	Clonal			
META42	*CDH16*	p.Ile490_Asp494del	disruptive_inframe_deletion	16	66946209	GTGTCTCCCCTCTCAA	G	25.64%	39	.	.	.	Deleterious	.	.	.			Indeterminate	0.7899	51.28%	100.00%	100%	Clonal			
META42	*DPEP2*	p.Leu375*	stop_gained	16	68021837	A	T	20.24%	84	A	.	.		.	.	.			Indeterminate	0.6493	50.92%	98.52%	81%	Clonal			
META42	*CA5A*	p.Asp198Glu	missense_variant	16	87935542	G	T	16.22%	74	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0157	28.38%	78.73%	49%	Subclonal			
META42	*TP53*	p.Cys176Phe	missense_variant	17	7578403	C	A	74.07%	27	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.6859	82.30%	100.00%	100%	Clonal	TRUE	CTGGGCAACCAGCCCTGT	TGTTCACTTGTGCCCTGACTT
META42	*FKBP10*	p.Leu218Met	missense_variant	17	39974704	C	A	72.73%	22	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9570	77.69%	100.00%	100%	Clonal			
META42	*CALCOCO2*	p.Ile452Ile	synonymous_variant	17	46940310	C	A	76.00%	50	.	.	.		.	.	.		TRUE	.	0.9321	89.54%	100.00%	100%	Clonal			
META42	*EME1*	p.Gly207Val	missense_variant	17	48453189	G	T	20.31%	64	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1879	36.59%	92.09%	61%	Subclonal			
META42	*STXBP4*	p.Val440Val	synonymous_variant	17	53156061	A	G	62.75%	51	.	.	.		.	.	.		TRUE	.	0.9709	86.17%	100.00%	100%	Clonal			
META42	*KCTD2*	p.Val189Leu	missense_variant	17	73055629	G	C	52.94%	17	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8867	65.02%	100.00%	100%	Clonal			
META42	*DNAH17*	p.Ala2970Ala	synonymous_variant	17	76462767	G	A	15.00%	40	.	.	.		.	.	.		TRUE	.	0.6042	33.26%	98.22%	75%	Clonal			
META42	*SMCHD1*	p.Arg1669Gln	missense_variant	18	2771570	G	A	64.52%	93	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9799	92.21%	100.00%	100%	Clonal			
META42	*DSC1*	p.Ala748Ser	missense_variant	18	28711802	C	A	27.08%	48	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8273	57.89%	100.00%	100%	Clonal			
META42	*TPGS2*	p.Met109Ile	missense_variant	18	34385392	C	T	11.38%	123	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1111	34.26%	88.97%	57%	Subclonal			
META42	*ZNF560*	p.Arg694*	stop_gained	19	9577543	G	A	36.70%	109	D	.	.		.	.	.			Indeterminate	0.9140	77.47%	100.00%	100%	Clonal			
META42	*LRRC25*	p.Ala252Ala	synonymous_variant	19	18507018	G	C	52.94%	34	.	.	.		.	.	.			.	0.9544	77.82%	100.00%	100%	Clonal			
META42	*C19orf60*	p.Ser199Cys	missense_variant	19	18702980	C	G	46.15%	26	N	.	Passenger		.	.	.			Likely passenger	0.9435	68.25%	100.00%	100%	Clonal			
META42	*ZNF493*	p.Pro544Arg	missense_variant	19	21607092	C	G	23.42%	111	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8064	63.35%	100.00%	94%	Clonal			
META42	*ZNF461*	p.Leu218Leu	synonymous_variant	19	37130593	A	G	39.87%	158	.	.	.		.	.	.		TRUE	.	0.6881	90.06%	100.00%	100%	Clonal			
META42	*KLK8*	p.Gln97His	missense_variant	19	51503754	C	G	13.19%	91	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6350	44.58%	98.45%	79%	Clonal			
META42	*HAS1*	p.Gln234Glu	missense_variant	19	52222461	G	C	41.86%	43	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8994	78.04%	100.00%	100%	Clonal			
META42	*PPP6R1*	p.Pro281Pro	synonymous_variant	19	55753536	C	T	9.21%	76	.	.	.		.	.	.			.	0.2871	26.92%	94.23%	55%	Subclonal			
META42	*COL20A1*	p.Val626Gly	missense_variant	20	61943845	T	G	83.33%	6	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8587	51.12%	100.00%	100%	Clonal			
META42	*CCDC116*	p.Arg544His	missense_variant	22	21991148	G	A	70.37%	27	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9639	80.22%	100.00%	100%	Clonal			
META42	*APOBEC3B*	p.Asp339Asp	synonymous_variant	22	39387630	T	C	26.67%	30	.	.	.		.	.	.		TRUE	.	0.7854	48.09%	100.00%	100%	Clonal			
META42	*CDKL5*	p.Ile958Ile	synonymous_variant	X	18668606	C	A	46.88%	32	.	.	.		.	.	.		TRUE	.	0.8521	58.74%	100.00%	95%	Clonal			
META42	*ALG13*	p.Gln776*	stop_gained	X	110971491	C	T	48.94%	47	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8925	67.32%	100.00%	99%	Clonal			
META52	*NPPA*	c.124-1G>T	splice_acceptor_variant	1	11907497	C	A	29.41%	17	D	.	.		.	.	.		TRUE	Likely pathogenic	0.5338	28.70%	97.12%	66%	Clonal			
META52	*USP48*	p.Arg267His	missense_variant	1	22074739	C	T	56.52%	23	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8927	66.09%	100.00%	100%	Clonal			
META52	*PIGM*	p.Ser289Ser	synonymous_variant	1	160000663	G	C	51.75%	114	.	.	.		.	.	.			.	0.9642	91.97%	100.00%	100%	Clonal			
META52	*CACNA1E*	p.Gln2198Lys	missense_variant	1	181767620	C	A	6.98%	86	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0010	13.48%	60.69%	30%	Subclonal			
META52	*TEDDM1*	p.Asp189Glu	missense_variant	1	182369054	G	C	48.89%	45	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9646	80.56%	100.00%	100%	Clonal			
META52	*CFH*	p.Pro923Ala	missense_variant	1	196706775	C	G	15.56%	45	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5256	31.95%	97.11%	66%	Clonal			
META52	*NVL*	p.Ala400Gly	missense_variant	1	224482095	G	C	16.13%	31	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7647	36.48%	98.95%	100%	Clonal			
META52	*SNAP47*	p.Gly281Gly	synonymous_variant	1	227946906	G	T	22.11%	95	.	.	.		.	.	.			.	0.9002	71.92%	100.00%	100%	Clonal			
META52	*CAD*	p.Gly1255Asp	missense_variant	2	27457531	G	A	20.59%	34	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7339	39.94%	98.80%	87%	Clonal			
META52	*SULT6B1*	p.Met68Ile	missense_variant	2	37410652	C	T	20.51%	39	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5036	34.14%	96.85%	67%	Clonal			
META52	*DNAH6*	p.Leu1776Ile	missense_variant	2	84880690	C	A	28.89%	90	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9092	73.44%	100.00%	100%	Clonal			
META52	*CCDC148*	p.Arg488fs	frameshift_variant	2	159035416	CG	C	13.16%	114	A	.	.		.	.	.		TRUE	Likely pathogenic	0.7065	48.96%	98.64%	82%	Clonal			
META52	*ABCB11*	p.Val1024fs	frameshift_variant	2	169789018	CACTCAGTACA	C	68.09%	94	A	.	.		.	.	.		TRUE	Likely pathogenic	0.5357	93.96%	100.00%	100%	Clonal			
META52	*UNC80*	p.Glu1212fs	frameshift_variant	2	210714345	C	CT	41.43%	70	A	.	.		.	.	.			Indeterminate	0.9574	82.57%	100.00%	100%	Clonal			
META52	*SGPP2*	p.Leu227Leu	synonymous_variant	2	223423098	C	G	36.17%	47	.	.	.		.	.	.			.	0.9173	71.66%	100.00%	100%	Clonal			
META52	*PARP9*	p.Lys266Glu	missense_variant	3	122274327	T	C	8.13%	123	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0002	18.64%	60.37%	35%	Subclonal			
META52	*IGSF10*	p.Gly2429Gly	synonymous_variant	3	151155062	G	A	3.94%	127	.	.	.		.	.	.			.	0.0000	6.88%	37.22%	17%	Subclonal			
META52	*RNF168*	p.Ala128_Glu130del	inframe_deletion	3	196214437	GCTCTGCCGC	G	14.94%	87	D	.	.	Deleterious	.	.	.			Indeterminate	0.3197	37.48%	94.36%	63%	Subclonal			
META52	*FGFBP1*	p.Pro201Gln	missense_variant	4	15937654	G	T	31.11%	45	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8406	57.47%	100.00%	100%	Clonal			
META52	*FGFBP1*	p.Asn119Lys	missense_variant	4	15937899	A	T	73.81%	42	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9103	87.44%	100.00%	100%	Clonal			
META52	*KIT*	p.Glu198Gly	missense_variant	4	55564705	A	G	27.50%	40	N	CANCER	Passenger		true	true	true			Likely passenger	0.7690	48.86%	98.98%	89%	Clonal			
META52	*MROH2B*	p.Thr38Asn	missense_variant	5	41067298	G	T	38.10%	42	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8917	66.60%	100.00%	100%	Clonal			
META52	*TMCO6*	p.Arg424Trp	missense_variant	5	140024209	C	T	94.19%	86	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9751	95.28%	100.00%	100%	Clonal			
META52	*PCDH1*	p.Ala313Val	missense_variant	5	141244958	G	A	82.14%	28	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9692	83.62%	100.00%	100%	Clonal			
META52	*GPRIN1*	p.Arg890Arg	synonymous_variant	5	176024166	C	A	30.43%	23	.	.	.		.	.	.			.	0.8974	52.55%	100.00%	100%	Clonal			
META52	*NSD1*	p.Lys1964Asn	missense_variant	5	176707835	G	T	14.10%	78	D	PASSENGER/OTHER	Passenger		true	true	true	TRUE		Likely pathogenic	0.6079	41.04%	97.91%	74%	Clonal			
META52	*CUL7*	p.Ser288Arg	missense_variant	6	43019472	T	G	43.14%	102	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9521	89.23%	100.00%	100%	Clonal			
META52	*PLG*	p.Glu660Glu	synonymous_variant	6	161160202	G	A	29.55%	44	.	.	.		.	.	.		TRUE	.	0.8149	54.29%	100.00%	96%	Clonal			
META52	*COL1A2*	p.Pro771Pro	synonymous_variant	7	94050338	C	T	13.56%	59	.	.	.		.	.	.	TRUE		.	0.7196	40.59%	98.72%	85%	Clonal			
META52	*CFTR*	p.Ser1037Leu	missense_variant	7	117250694	C	T	60.61%	66	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5416	90.29%	100.00%	100%	Clonal			
META52	*CHRM2*	p.Gly167Ala	missense_variant	7	136700112	G	C	21.74%	69	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7964	54.29%	100.00%	92%	Clonal			
META52	*TRPV5*	p.Pro453Ala	missense_variant	7	142612146	G	C	57.78%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9116	84.45%	100.00%	100%	Clonal			
META52	*SLC18A1*	p.Leu73Leu	synonymous_variant	8	20036901	G	A	42.86%	14	.	.	.		.	.	.		TRUE	.	0.7793	42.07%	100.00%	96%	Clonal			
META52	*MMP16*	p.Tyr52*	stop_gained	8	89209512	G	T	14.29%	35	A	.	.		.	.	.			Indeterminate	0.7716	36.80%	98.98%	100%	Clonal			
META52	*RAD54B*	p.Ser240Ala	missense_variant	8	95419730	A	C	32.61%	138	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9287	89.17%	100.00%	100%	Clonal			
META52	*SPAG1*	p.Ala815Ala	synonymous_variant	8	101252795	T	C	13.33%	75	.	.	.		.	.	.			.	0.7882	48.04%	100.00%	97%	Clonal			
META52	*UBR5*	p.Asp752Asn	missense_variant	8	103324371	C	T	34.62%	52	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.9113	77.52%	100.00%	100%	Clonal			
META52	*EIF3E*	p.Val404Glu	missense_variant	8	109215300	A	T	61.15%	139	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.4026	95.26%	100.00%	100%	Clonal			
META52	*HHLA1*	p.Ala451Ala	synonymous_variant	8	133083703	T	G	16.67%	30	.	.	.		.	.	.			.	0.8123	39.55%	100.00%	100%	Clonal			
META52	*DOCK8*	p.Gln1044His	missense_variant	9	399157	G	T	10.71%	56	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5633	30.06%	97.51%	67%	Clonal			
META52	*SMARCA2*	p.Lys493del	inframe_deletion	9	2058414	CAGA	C	11.90%	210	D	.	.	Deleterious	.	.	.			Indeterminate	0.4916	50.52%	96.93%	74%	Subclonal			
META52	*HAUS6*	p.Thr643Thr	synonymous_variant	9	19058836	G	T	71.71%	152	.	.	.		.	.	.			.	0.2421	96.31%	100.00%	100%	Clonal			
META52	*TESK1*	p.Arg536Trp	missense_variant	9	35609464	C	T	20.00%	40	N	CANCER	Passenger		.	.	.			Likely passenger	0.7240	41.30%	98.74%	85%	Clonal			
META52	*ALDH1A1*	p.Pro172Arg	missense_variant	9	75540518	G	C	46.00%	50	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9669	80.55%	100.00%	100%	Clonal			
META52	*FOXB2*	p.Lys267Thr	missense_variant	9	79635370	A	C	40.00%	20	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9206	57.49%	100.00%	100%	Clonal			

META52	RMI1	p.Glu504fs	frameshift_variant	9	86617409	AG	A	49.07%	108	D	.	.		.	.	.			Indeterminate	0.9753	90.78%	100.00%	100%	Clonal			
META52	RABGAP1	p.Arg316*	stop_gained	9	125758342	A	T	40.74%	54	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8166	62.05%	100.00%	92%	Clonal			
META52	SLC35G1	p.Gln307His	missense_variant	10	95661070	A	T	27.50%	40	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7690	48.86%	98.98%	89%	Clonal			
META52	NOC3L	p.Val559Val	synonymous_variant	10	96100221	G	A	58.82%	34	.	.	.		.	.	.		TRUE	.	0.9690	79.34%	100.00%	100%	Clonal			
META52	MGEA5	p.Phe703fs	frameshift_variant	10	103552661	GAA	G	52.78%	36	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9087	70.92%	100.00%	100%	Clonal			
META52	NRAP	p.Pro1117Arg	missense_variant	10	115372141	G	C	34.04%	47	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9514	72.35%	100.00%	100%	Clonal			
META52	VAX1	p.Gly297Gly	synonymous_variant	10	118893633	A	C	33.33%	15	.	.	.		.	.	.			.	0.8543	43.39%	100.00%	100%	Clonal			
META52	DBX1	p.Gln337Glu	missense_variant	11	20177783	G	C	3.85%	130	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	5.03%	27.71%	12%	Subclonal			
META52	OR4C3	p.Arg163Ser	missense_variant	11	48346981	G	T	20.59%	68	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7588	51.09%	98.94%	87%	Clonal			
META52	OR5F1	p.His176Pro	missense_variant	11	55761575	T	G	38.89%	36	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7646	53.31%	98.94%	87%	Clonal			
META52	OR5T3	p.Ser220Thr	missense_variant	11	56020333	T	A	51.89%	106	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9454	84.75%	100.00%	100%	Clonal			
META52	OR5R1	p.Leu157Leu	synonymous_variant	11	56185238	G	T	55.26%	38	.	.	.		.	.	.			.	0.9147	74.09%	100.00%	100%	Clonal			
META52	SERPING1	p.Ala461Pro	missense_variant	11	57381932	G	C	59.09%	22	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8922	67.33%	100.00%	100%	Clonal			
META52	ZBTB3	p.Met79Ile	missense_variant	11	62521050	C	T	26.09%	23	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7175	37.12%	98.67%	85%	Clonal			
META52	FAT3	p.Ser2244Ile	missense_variant	11	92532910	G	T	38.24%	102	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9249	80.68%	100.00%	100%	Clonal			
META52	AMOTL1	p.Leu529Gln	missense_variant	11	94564645	T	A	18.88%	143	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6328	55.60%	98.13%	80%	Clonal			
META52	TMPRSS13	p.Leu175Leu	synonymous_variant	11	117787916	G	A	90.91%	11	.	.	.		.	.	.		TRUE	.	0.9780	70.14%	100.00%	100%	Clonal			
META52	ZNF705A	p.Lys163Lys	synonymous_variant	12	8329765	A	G	91.22%	205	.	.	.		.	.	.		TRUE	.	0.9916	97.79%	100.00%	100%	Clonal			
META52	PTHLH	p.Lys134Lys	synonymous_variant	12	28116403	C	T	51.85%	54	.	.	.		.	.	.			.	0.9601	84.54%	100.00%	100%	Clonal			
META52	LRRK2	p.Val1903Glu	missense_variant	12	40722213	T	A	36.96%	46	D	PASSENGER/OTHER	Driver		.	true	.			Likely pathogenic	0.8923	66.80%	100.00%	100%	Clonal			
META52	OTOGL	c.1132+2T>A	splice_donor_variant	12	80645581	T	A	5.88%	85	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0003	10.53%	54.91%	25%	Subclonal			
META52	CCER1	p.Ser366*	stop_gained	12	91347423	G	C	47.32%	112	D	.	.		.	.	.		TRUE	Likely pathogenic	0.9777	90.51%	100.00%	100%	Clonal			
META52	SLC25A3	p.Leu342Phe	missense_variant	12	98995241	C	T	93.10%	29	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9846	87.01%	100.00%	100%	Clonal			
META52	SLITRK1	p.Asn76Ile	missense_variant	13	84455416	T	A	21.24%	113	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7977	60.09%	100.00%	90%	Clonal			
META52	RYR3	p.Gly4222Ala	missense_variant	15	34130846	G	C	88.89%	9	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9266	61.19%	100.00%	100%	Clonal			
META52	CILP	p.Arg1157*	stop_gained	15	65489155	G	A	90.91%	11	D	.	.		.	.	.		TRUE	Likely pathogenic	0.9780	70.14%	100.00%	100%	Clonal			
META52	CACNA1H	p.Ala2175Ala	synonymous_variant	16	1270457	C	T	50.00%	18	.	.	.		.	.	.		TRUE	.	0.9433	63.39%	100.00%	100%	Clonal			
META52	NKD1	p.Glu299Ala	missense_variant	16	50667175	A	C	36.17%	47	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6741	52.57%	98.38%	81%	Clonal	TRUE	ATTAAATGTCTGTTGAATTGGTTCC	CTGGAGCTCTGAGACCTTGG
META52	SLC25A11	p.His292fs	frameshift_variant	17	4841106	TG	T	66.67%	15	D	.	.		.	.	.		TRUE	Likely pathogenic	0.8807	64.73%	100.00%	100%	Clonal			
META52	GPS2	p.Leu77Phe	missense_variant	17	7217696	C	A	10.42%	48	N	PASSENGER/OTHER	Passenger		.	.	true		TRUE	Likely passenger	0.0000	9.90%	49.45%	23%	Subclonal			
META52	TP53	p.Arg342fs	frameshift_variant	17	7574002	CG	C	88.89%	18	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9820	79.06%	100.00%	100%	Clonal	TRUE	GGGGAGTAGGGCCAGGAA	ACTGTGTATATACTTACTTCTCCCCC
META52	GAS2L2	p.Glu230Val	missense_variant	17	34076175	T	A	92.86%	14	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9807	75.84%	100.00%	100%	Clonal			
META52	RDM1	p.Phe194fs	frameshift_variant	17	34249649	GTCTTCCTTTTCATAAGGAA	G	29.23%	65	A	.	.		.	.	.		TRUE	Likely pathogenic	0.1525	43.47%	90.95%	66%	Subclonal			
META52	GPR179	p.Gln1157Arg	missense_variant	17	36485982	T	C	15.79%	57	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	18.79%	61.11%	35%	Subclonal			
META52	DSG1	p.Ile194Thr	missense_variant	18	28911727	T	C	49.15%	59	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.8799	82.25%	100.00%	100%	Clonal			
META52	NOL4	p.Lys464Glu	missense_variant	18	31537328	T	C	83.33%	12	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9214	62.88%	100.00%	100%	Clonal			
META52	NPHS1	p.Glu1116Asp	missense_variant	19	36322237	C	A	41.11%	90	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9645	87.12%	100.00%	100%	Clonal			
META52	SIPA1L3	p.Glu540*	stop_gained	19	38579444	G	T	22.41%	58	A	.	.		.	.	.			Indeterminate	0.8632	59.33%	100.00%	100%	Clonal			
META52	RYR1	p.Val3156Ile	missense_variant	19	39003117	G	A	60.00%	35	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.5856	82.42%	100.00%	100%	Clonal			
META52	LGALS4	p.Thr187Ile	missense_variant	19	39294172	G	A	58.06%	62	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5111	88.87%	100.00%	100%	Clonal			
META52	PLA2G4C	p.Lys383Lys	synonymous_variant	19	48565393	C	T	42.11%	19	.	.	.		.	.	.			.	0.8727	54.82%	100.00%	100%	Clonal			
META52	KLK15	p.Arg130His	missense_variant	19	51330226	C	T	38.46%	13	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8272	42.30%	100.00%	100%	Clonal			
META52	ZNF677	p.Ala467fs	frameshift_variant	19	53740567	ACGTTTGATAAAG	A	12.20%	41	.	.	.		.	.	.			Indeterminate	0.0605	17.11%	81.37%	40%	Subclonal			
META52	LILRA3	p.Asp253Asp	synonymous_variant	19	54802682	G	A	45.00%	20	.	.	.		.	.	.			.	0.8931	58.88%	100.00%	100%	Clonal			
META52	MKKS	p.Thr392Ala	missense_variant	20	10388362	T	C	71.43%	21	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9484	76.63%	100.00%	100%	Clonal			
META52	UPB1	p.Phe127Leu	missense_variant	22	24906733	C	G	28.57%	49	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8018	54.22%	100.00%	93%	Clonal			
META52	UPK3A	p.Thr245Ser	missense_variant	22	45691469	A	T	31.94%	72	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8798	66.61%	100.00%	100%	Clonal			
META52	BCOR	p.Arg761Trp	missense_variant	X	39932318	G	A	32.86%	140	N	PASSENGER/OTHER	Passenger		true	.	true			Likely passenger	0.8020	84.55%	100.00%	100%	Clonal			
META52	NXF3	p.Cys286fs	frameshift_variant	X	102337217	A	AC	95.10%	102	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8297	96.15%	100.00%	100%	Clonal			
META52	FAM199X	p.Glu369fs	frameshift_variant	X	103434396	AGAGGT	A	5.19%	135	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0178	18.14%	73.96%	38%	Subclonal			
META52	COL4A6	p.Gly1220Val	missense_variant	X	107412808	C	A	41.18%	17	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9180	54.73%	100.00%	100%	Clonal			
META55	NASP	p.Pro345Pro	synonymous_variant	1	46073618	A	G	10.53%	57	.	.	.		.	.	.			.	0.0092	17.08%	73.81%	37%	Subclonal			
META55	ASH1L	p.Thr2156Ile	missense_variant	1	155340640	G	A	38.46%	91	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.8578	87.13%	100.00%	100%	Clonal			
META55	CCDC181	p.Asp222Gly	missense_variant	1	169391004	T	C	9.35%	139	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1722	35.74%	93.46%	61%	Subclonal			
META55	SLC15A2	p.Pro341Ser	missense_variant	3	121643216	C	T	5.95%	84	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.76%	45.97%	21%	Subclonal			
META55	PDS5A	p.His72Tyr	missense_variant	4	39929709	G	A	69.32%	88	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4569	93.39%	100.00%	100%	Clonal			
META55	PDS5A	p.Leu71Phe	missense_variant	4	39929710	C	G	69.66%	89	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4475	93.50%	100.00%	100%	Clonal			
META55	PPARGC1B	p.Arg180Cys	missense_variant	5	149210402	C	T	20.27%	74	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3471	43.94%	96.84%	71%	Subclonal			
META55	COL21A1	p.Ser261*	stop_gained	6	56035785	G	C	24.17%	120	A	.	.		.	.	.		TRUE	Likely pathogenic	0.5972	59.95%	98.77%	85%	Clonal			
META55	KLHL38	p.Leu370Leu	synonymous_variant	8	124664057	C	A	4.63%	108	.	.	.		.	.	.			.	0.4257	27.48%	97.72%	67%	Subclonal			
META55	EEF1D	p.Ala402Ala	synonymous_variant	8	144668908	G	A	12.17%	115	.	.	.		.	.	.			.	0.9200	69.18%	100.00%	100%	Clonal			
META55	OPTN	p.Glu227Lys	missense_variant	10	13160940	G	A	27.63%	76	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8801	74.37%	100.00%	100%	Clonal			
META55	CD5	p.Arg36Lys	missense_variant	11	60885659	G	A	20.00%	40	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4233	35.80%	97.58%	70%	Subclonal			
META55	ASB2	p.Arg248Pro	missense_variant	14	94417482	C	G	32.26%	31	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.7551	54.63%	100.00%	100%	Clonal			
META55	TP53	p.Arg342fs	frameshift_variant	17	7574002	CG	C	60.00%	15	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9327	64.34%	100.00%	100%	Clonal	TRUE	GGGGAGTAGGGCCAGGAA	ACTGTGTATATACTTACTTCTCCCCC
META55	KLHL26	p.Val80Ile	missense_variant	19	18775225	G	A	20.00%	50	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6417	46.83%	98.99%	90%	Clonal			
META55	CEP89	p.Tyr157Tyr	synonymous_variant	19	33444542	G	A	17.61%	352	.	.	.		true	.	.			.	0.2673	62.71%	96.26%	80%	Subclonal			
META57	AMIGO1	p.Val333Val	synonymous_variant	1	110050536	G	A	22.64%	53	.	.	.		.	.	.			.	0.7861	56.91%	100.00%	100%	Clonal			
META57	ITIH3	p.Arg309Arg	synonymous_variant	3	52833789	A	G	25.00%	28	.	.	.		.	.	.			.	0.7728	48.26%	100.00%	100%	Clonal			
META57	WNT5A	p.Ala31Pro	missense_variant	3	55514862	C	G	20.83%	72	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7767	58.37%	100.00%	100%	Clonal			
META57	PIK3CA	p.His1047Arg	missense_variant	3	178952085	A	G	23.33%	60	D	CANCER	Driver		true	true	true			Likely pathogenic	0.8081	60.71%	100.00%	100%	Clonal	TRUE	ATCTCTTCATAAATCTTTTCTCAAT	ACAGTGCAGTGTGGAATCCA
META57	TMPRSS11F	p.Gly437Ser	missense_variant	4	68919635	C	T	12.20%	41	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3862	25.86%	96.82%	61%	Subclonal			
META57	MCTP1	p.Leu655Val	missense_variant	5	94208917	G	C	24.44%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8005	57.26%	100.00%	100%	Clonal			
META57	APC	p.Phe1838fs	frameshift_variant	5	112176801	GT	G	20.90%	67	D	.	.		true	true	true	TRUE		Likely pathogenic	0.7719	57.26%	100.00%	100%	Clonal	TRUE	GTTTTCTCAGACAACAAAGATTCAAA	ATCATCATCAAAATCTAGAGAACTCAA
META57	OR2Y1	p.Leu304Leu	synonymous_variant	5	180166147	T	C	6.40%	125	.	.	.		.	.	.			.	0.0003	16.12%	60.26%	32%	Subclonal			
META57	IGF2R	p.Trp611*	stop_gained	6	160466843	G	A	7.32%	82	A	.	.		.	.	.			Indeterminate	0.0136	16.82%	74.63%	37%	Subclonal			
META57	SDK1	p.Asn1256Asn	synonymous_variant	7	4153851	C	T	48.48%	33	.	.	.		.	.	.			.	0.4915	77.69%	100.00%	100%	Clonal			
META57	ANGPT2	p.Gln207Gln	synonymous_variant	8	6378877	C	T	20.00%	80	.	.	.		.	.	.			.	0.7633	58.03%	100.00%	100%	Clonal			
META57	FAM135B	p.Ser919Ser	synonymous_variant	8	139163961	G	T	21.52%	79	.	.	.		.	.	.			.	0.8004	61.64%	100.00%	100%	Clonal			
META57	SIRT1	p.Asn342Asp	missense_variant	10	69666628	A	G	10.87%	46	D	PASSENGER/OTHER	Driver		.	.	.		TRUE	Likely pathogenic	0.1293	18.82%	87.70%	44%	Subclonal			
META57	OR52K2	p.Ser245Phe	missense_variant	11	4471303	C	T	9.52%	168	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0033	29.39%	74.21%	48%	Subclonal			
META57	OR52K2	p.Ala249Ser	missense_variant	11	4471314	G	T	30.46%	174	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6331	87.24%	100.00%	100%	Clonal			
META57	GRIA4	p.Leu167Leu	synonymous_variant	11	105732763	C	G	15.49%	71	.	.	.		.	.	.		TRUE	.	0.3098	35.10%	94.49%	62%	Subclonal			
META57	SLC2A3	p.Leu160Leu	synonymous_variant	12	8083873	G	A	6.67%	75	.	.	.		.	.	.			.	0.0117	14.28%	72.73%	33%	Subclonal			
META57	CCDC33	p.Gln724*	stop_gained	15	74628296	C	T	22.03%	59	D	.	.		.	.	.			Indeterminate	0.7847	57.61%	100.00%	100%	Clonal			
META57	TOP3A	p.Val82Ile	missense_variant	17	18211735	C	T	12.50%	40	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.2627	21.62%	93.03%	50%	Subclonal			
META57	MADCAM1	p.Pro246Gln	missense_variant	19	501738	C	A	21.74%	23	P	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7017	38.38%	100.00%	100%	Clonal			
META57	ZNF878	p.Cys512fs	frameshift_variant	19	12154681	C	CA	16.44%	73	D	.	.		.	.	.			Indeterminate	0.6058	46.20%	98.65%	82%	Clonal			
META57	PROSER3	p.Ala172Thr	missense_variant	19	36253228	G	A	32.93%	82	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9194	80.08%	100.00%	100%	Clonal			
META57	ZNF280A	p.Lys430Asn	missense_variant	22	22868665	T	A	21.78%	101	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8269	66.36%	100.00%	100%	Clonal			
META57	CRYBB2	p.Ser3Ser	synonymous_variant	22	25617405	A	G	30.77%	26	.	.	.		.	.	.			.	0.8515	55.23%	100.00%	100%	Clonal			
META57	WNK3	p.Lys439Asn	missense_variant	X	54324689	T	A	25.29%	87	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8579	71.12%	100.00%	100%	Clonal			
META57	STAG2	p.Tyr1142fs	frameshift_variant	X	123224565	A	AGT	20.35%	113	A	.	.		true	true	true			Likely pathogenic	0.8015	64.47%	100.00%	100%	Clonal			
META61	MUC7	p.Gln200Pro	missense_variant	4	71347060	A	C	5.71%	105	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4007	28.51%	97.15%	64%	Subclonal			
META61	GZMK	p.Ser43Pro	missense_variant	5	54320550	T	C	22.73%	22	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8398	47.79%	100.00%	100%	Clonal			
META61	PIK3R1	p.Leu193fs	frameshift_variant	5	67575503	C	CT	10.75%	93	A	.	.		true	true	true	TRUE		Likely pathogenic	0.7722	53.22%	100.00%	100%	Clonal			
META61	PIK3R1	p.Phe456_Gln457dup	disruptive_inframe_insertion	5	67589598	C	CTCAGTT	7.46%	134	P	.	.	Deleterious	true	true	true	TRUE		Likely pathogenic	0.5985	42.92%	98.68%	83%	Clonal	TRUE	ATCTTTCTAGGATCAAGTTGTCAAAGA	CTCACCTGGGATGTGCGG
META61	COBL	p.Pro1148Pro	synonymous_variant	7	51095520	C	T	22.00%	50	.	.	.		.	.	.			.	0.8924	66.75%	100.00%	100%	Clonal			
META61	AKAP9	p.Ile3486Val	missense_variant	7	91726957	A	G	16.00%	100	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.9288	70.61%	100.00%	100%	Clonal			
META61	AGTPBP1	p.Val237Val	synonymous_variant	9	88287478	T	C	4.17%	120	.	.	.		.	.	.			.	0.1643	19.83%	92.00%	46%	Subclonal			
META61	TEX10	p.Ile389Met	missense_variant	9	103102622	A	C	8.96%	201	N	.	Passenger		.	.	.			Likely passenger	0.7515	58.47%	100.00%	100%	Clonal			
META61	CACNA1B	p.Ala1297Ala	synonymous_variant	9	140948381	C	T	3.62%	138	.	.	.		.	.	.			.	0.0762	17.25%	86.19%	40%	Subclonal			
META61	CMKLR1	p.Arg151His	missense_variant	12	108686288	C	T	13.33%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8027	46.28%	100.00%	100%	Clonal			
META61	SCEL	p.Thr243Asn	missense_variant	13	78167684	C	A	13.89%	36	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7960	42.65%	100.00%	100%	Clonal			
META61	SNX1	p.Phe190Leu	missense_variant	15	64418337	T	A	6.85%	73	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5360	30.26%	98.29%	76%	Clonal			
META61	SPAG7	p.Gly89Gly	synonymous_variant	17	4863589	G	C	15.15%	33	.	.	.		.	.	.			.	0.8158	43.75%	100.00%	100%	Clonal			
META61	CREB3L3	p.Trp46*	stop_gained	19	4155006	G	A	11.63%	43	A	.	.		.	.	.			Indeterminate	0.7460	40.12%	100.00%	100%	Clonal			
META61	CDKL5	p.Arg248Trp	missense_variant	X	18606261	C	T	3.55%	169	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0392	18.08%	81.51%	40%	Subclonal			
MP1	NKAIN1	p.Leu64Leu	synonymous_variant	1	31660899	G	A	24.54%	216	.	.	.		.	.	.			.	0.8367	72.72%	100.00%	95%	Clonal			
MP1	SPOCD1	p.Ala642Gly	missense_variant	1	32264146	G	C	13.49%	608	N	CANCER	Passenger		.	.	.			Likely passenger	0.0003	53.29%	79.88%	66%	Subclonal			
MP1	ERMAP	p.Leu18Val	missense_variant	1	43296171	C	G	18.45%	851	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	61.68%	81.96%	72%	Subclonal			
MP1	IPO13	p.Gly953Arg	missense_variant	1	44433319	G	C	40.47%	771	D	.	Passenger		.	.	.			Indeterminate	0.0000	97.49%	100.00%	100%	Clonal			
MP1	MROH7	p.Gln36Pro	missense_variant	1	55118706	A	C	36.52%	408	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9607	88.19%	100.00%	100%	Clonal			
MP1	RPRD2	p.Ile857Ile	synonymous_variant	1	150443995	C	A	15.67%	849	.	.	.		.	.	.		TRUE	.	0.0112	64.93%	88.83%	77%	Subclonal			
MP1	HRNR	p.His2149His	synonymous_variant	1	152187658	G	A	3.68%	680	.	.	.		.	.	.		TRUE	.	0.0000	16.77%	36.54%	25%	Subclonal			
MP1	CD84	p.Ile343Thr	missense_variant	1	160518056	A	G	14.32%	803	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.4072	70.52%	97.16%	84%	Subclonal			
MP1	ATF6	p.Cys467fs	frameshift_variant	1	161821590	TTGTCAGCCCC	T	7.23%	692	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	32.07%	54.88%	43%	Subclonal			
MP1	F5	p.Met1909Ile	missense_variant	1	169494136	C	T	11.54%	260	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1457	47.85%	92.08%	68%	Subclonal			
MP1	C1orf112	p.Ile167Met	missense_variant	1	169775167	C	G	3.30%	546	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	11.89%	29.85%	19%	Subclonal			
MP1	RGS16	p.Glu138Lys	missense_variant	1	182569624	C	T	43.11%	283	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4645	94.78%	100.00%	100%	Clonal			
MP1	HMCN1	p.Pro4788Thr	missense_variant	1	186114630	C	A	5.51%	508	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	14.42%	30.04%	21%	Subclonal			
MP1	GREM2	p.Lys66Asn	missense_variant	1	240656578	C	G	16.09%	814	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8493	79.56%	100.00%	95%	Clonal			
MP1	TTC31	p.Gly371Ala	missense_variant	2	74719523	G	C	27.84%	783	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9611	91.04%	100.00%	100%	Clonal			
MP1	DNAH6	p.Ile710fs	frameshift_variant	2	84806703	TC	T	24.13%	630	A	.	.		.	.	.			Indeterminate	0.8315	80.50%	100.00%	94%	Clonal			
MP1	ANKRD23	p.Leu126Leu	synonymous_variant	2	97506574	G	A	27.72%	505	.	.	.		.	.	.			.	0.9493	87.91%	100.00%	100%	Clonal			
MP1	TTN	p.Glu28192Lys	missense_variant	2	179426285	C	T	21.95%	788	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2610	74.19%	96.12%	85%	Subclonal			
MP1	TTN	p.Arg18343Trp	missense_variant	2	179467102	T	A	27.84%	776	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9609	90.99%	100.00%	100%	Clonal			
MP1	EPHA4	p.Pro787Thr	missense_variant	2	222298999	G	T	25.13%	191	D	CANCER	Driver		.	.	.			Likely pathogenic	0.8534	72.95%	100.00%	98%	Clonal			
MP1	ATG7	p.Ile229Val	missense_variant	3	11372820	A	G	18.38%	370	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0190	56.96%	87.58%	72%	Subclonal			
MP1	DCBLD2	p.Asn418Lys	missense_variant	3	98531285	A	T	6.59%	440	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	17.50%	35.73%	26%	Subclonal			
MP1	MORC1	p.Gly106Arg	missense_variant	3	108818312	C	T	12.44%	193	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0001	32.61%	68.93%	48%	Subclonal			
MP1	HCLS1	p.Thr225Thr	synonymous_variant	3	121354598	C	G	22.61%	115	.	.	.		.	.	.			.	0.7230	60.10%	100.00%	88%	Clonal			
MP1	CHST2	p.Val133Val	synonymous_variant	3	142840057	C	T	14.29%	693	.	.	.		.	.	.			.	0.8847	79.45%	100.00%	98%	Clonal			
MP1	ZIC4	p.Lys181Asn	missense_variant	3	147113934	C	A	18.34%	894	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5717	92.57%	100.00%	100%	Clonal			
MP1	CPB1	p.Phe28Cys	missense_variant	3	148545800	T	G	13.55%	760	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8197	76.57%	100.00%	93%	Clonal			
MP1	MME	p.Arg385*	stop_gained	3	154860084	C	T	12.13%	701	A	.	.		.	.	.			Indeterminate	0.0093	57.92%	86.40%	71%	Subclonal			
MP1	PLCH1	p.Val441Val	synonymous_variant	3	155267579	C	T	15.82%	354	.	.	.		.	.	.			.	0.8067	71.12%	100.00%	93%	Clonal			
MP1	ZBBX	p.Gly350Gly	synonymous_variant	3	167035319	A	T	13.38%	755	.	.	.		.	.	.			.	0.9242	83.09%	100.00%	100%	Clonal			
MP1	WHSC1	p.Asp1123His	missense_variant	4	1962873	G	C	37.86%	280	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.9577	87.19%	100.00%	100%	Clonal			
MP1	KIAA0232	p.Ser1114Phe	missense_variant	4	6865450	C	T	33.65%	422	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.9157	83.19%	100.00%	97%	Clonal			
MP1	REST	p.Asp1066Asp	synonymous_variant	4	57798222	T	C	21.40%	458	.	.	.		.	.	.			.	0.3531	69.06%	96.66%	83%	Subclonal			
MP1	ENPEP	p.Ser68*	stop_gained	4	111397773	C	G	24.94%	453	A	.	.		.	.	.			Indeterminate	0.8818	80.62%	100.00%	97%	Clonal			
MP1	CLPTM1L	p.Thr345Thr	synonymous_variant	5	1330440	C	T	22.24%	751	.	.	.		.	.	.			.	0.9533	89.08%	100.00%	100%	Clonal			
MP1	PIK3R1	p.Ser652fs	frameshift_variant	5	67592135	AGCAGTAAACAGGGCTGCTAT	A	8.16%	637	.	.	.		true	true	true	TRUE		Likely pathogenic	0.0000	23.96%	40.58%	32%	Subclonal			
MP1	PCSK1	p.Arg740Gly	missense_variant	5	95728749	G	C	24.20%	653	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8380	80.99%	100.00%	94%	Clonal			
MP1	PPARGC1B	p.Ser994Leu	missense_variant	5	149227030	C	T	27.29%	722	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9563	89.54%	100.00%	100%	Clonal			
MP1	ITK	p.Glu597Lys	missense_variant	5	156676015	G	A	28.40%	81	D	CANCER	Passenger		true	.	.		TRUE	Likely pathogenic	0.6691	55.88%	98.43%	82%	Clonal			
MP1	CPEB4	p.Ala518Val	missense_variant	5	173376969	C	T	37.80%	291	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9585	87.41%	100.00%	100%	Clonal			
MP1	CCHCR1	p.Gln261Glu	missense_variant	6	31122293	G	C	26.14%	853	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9444	88.18%	100.00%	100%	Clonal			
MP1	CYP21A2	p.Leu246Leu	synonymous_variant	6	31975054	G	C	8.57%	70	.	.	.		.	.	.		TRUE	.	0.0000	11.21%	50.06%	25%	Subclonal			
MP1	VEGFA	p.Arg350Gly	missense_variant	6	43748554	C	G	23.87%	243	D	.	Passenger		.	.	.			Indeterminate	0.8063	72.05%	100.00%	93%	Clonal			
MP1	MRPL14	p.Arg37Gln	missense_variant	6	44081908	C	T	26.13%	620	D	.	Passenger		.	.	.			Indeterminate	0.9336	86.09%	100.00%	100%	Clonal			
MP1	PHIP	p.Tyr1063*	stop_gained	6	79679568	G	C	22.39%	67	A	.	.		.	.	.			Indeterminate	0.7038	52.17%	98.93%	87%	Clonal			
MP1	HTR1E	p.Thr135Met	missense_variant	6	87725456	C	T	26.75%	673	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9479	88.05%	100.00%	100%	Clonal			
MP1	L3MBTL3	p.Ser31Arg	missense_variant	6	130363937	T	A	21.83%	701	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.2781	73.12%	96.20%	85%	Subclonal			
MP1	BCLAF1	p.Gly278Glu	missense_variant	6	136599186	C	T	13.70%	387	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0000	40.86%	67.54%	53%	Subclonal			
MP1	THBS2	p.Asp1142_Tyr1145del	disruptive_inframe_deletion	6	169620369	GTAGGTTTGGTCA	G	15.76%	330	D	.	.	Deleterious	.	.	.			Indeterminate	0.0004	47.08%	77.66%	61%	Subclonal			
MP1	NOD1	p.Arg27Arg	synonymous_variant	7	30496457	C	A	21.18%	727	.	.	.		.	.	.			.	0.1063	70.98%	93.87%	82%	Subclonal			
MP1	AKAP9	p.Gln2368Gln	synonymous_variant	7	91708551	G	A	23.85%	629	.	.	.		true	.	.			.	0.8008	79.58%	100.00%	93%	Clonal			
MP1	NAT16	p.Asp291Tyr	missense_variant	7	100815599	C	A	4.75%	295	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	10.60%	29.88%	18%	Subclonal			
MP1	KIAA1549	p.Ala1496fs	frameshift_variant	7	138555958	ACGGGAGGTGC	A	25.10%	785	A	.	.		true	.	.			Likely pathogenic	0.9054	84.90%	100.00%	98%	Clonal			
MP1	TAS2R38	p.Arg8Cys	missense_variant	7	141673468	G	A	33.91%	522	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0364	94.35%	100.00%	100%	Clonal			
MP1	KMT2C	p.Leu736Leu	synonymous_variant	7	151945313	A	G	13.16%	38	.	.	.		true	true	true		TRUE	.	0.0346	16.42%	78.11%	38%	Subclonal			
MP1	CSMD1	p.Cys873Cys	synonymous_variant	8	3245179	G	A	24.48%	723	.	.	.		.	.	.			.	0.8635	82.50%	100.00%	95%	Clonal			
MP1	HR	p.Arg940Gln	missense_variant	8	21977644	C	T	34.49%	748	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0002	96.12%	100.00%	100%	Clonal			
MP1	SDCBP	p.Thr219Ile	missense_variant	8	59492259	C	T	22.79%	136	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7345	62.65%	100.00%	89%	Clonal			
MP1	TMEM67	p.Ala123Ala	synonymous_variant	8	94770767	C	T	25.53%	760	.	.	.		.	.	.			.	0.9230	85.91%	100.00%	99%	Clonal			
MP1	CPQ	p.His104Asn	missense_variant	8	97797435	C	A	26.92%	520	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9418	86.56%	100.00%	100%	Clonal			
MP1	SCRIB	p.Leu186Met	missense_variant	8	144895492	G	T	28.24%	262	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9294	83.15%	100.00%	100%	Clonal			
MP1	DOCK8	p.Arg2033Cys	missense_variant	9	463545	C	T	17.79%	551	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6077	71.80%	98.47%	87%	Clonal			
MP1	IFNA10	p.Ser176Ser	synonymous_variant	9	21206569	C	A	11.11%	72	.	.	.		.	.	.			.	0.1977	27.71%	92.35%	54%	Subclonal			
MP1	FBXO10	p.Glu146*	stop_gained	9	37541330	C	A	23.91%	757	A	.	.		.	.	.			Indeterminate	0.8014	80.95%	100.00%	93%	Clonal			
MP1	TRPM6	p.Val183Val	synonymous_variant	9	77449034	C	A	25.89%	448	.	.	.		.	.	.			.	0.9154	83.07%	100.00%	100%	Clonal			
MP1	CENPP	p.Gly109Glu	missense_variant	9	95099859	G	A	22.88%	354	D	.	Passenger		.	.	.			Indeterminate	0.7117	72.30%	98.97%	89%	Clonal			
MP1	TTC16	p.Leu124Ser	missense_variant	9	130479996	T	C	39.18%	319	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9598	89.71%	100.00%	100%	Clonal			
MP1	TUBB8	p.Arg276Gln	missense_variant	10	93505	C	T	11.11%	45	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3198	23.27%	95.18%	54%	Subclonal			
MP1	ARMC3	p.Lys74Asn	missense_variant	10	23244791	G	T	3.96%	404	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.09%	24.16%	15%	Subclonal			
MP1	PALD1	p.Tyr428Asp	missense_variant	10	72297621	T	G	21.43%	154	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6241	60.01%	98.51%	83%	Clonal			
MP1	STAMBPL1	p.Asp360Tyr	missense_variant	10	90681076	G	T	12.01%	783	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	38.08%	55.82%	47%	Subclonal			
MP1	PPP1R3C	p.Asp274Tyr	missense_variant	10	93389818	C	A	27.90%	663	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9577	90.10%	100.00%	100%	Clonal			
MP1	ENTPD1	p.Gln354*	stop_gained	10	97607413	C	T	22.28%	561	A	.	.		.	.	.			Indeterminate	0.5089	73.46%	97.90%	87%	Clonal			
MP1	SH3PXD2A	p.Ser741Ser	synonymous_variant	10	105362668	G	A	26.18%	802	.	.	.		.	.	.			.	0.9434	87.92%	100.00%	100%	Clonal			
MP1	SORCS1	p.Thr804Thr	synonymous_variant	10	108412203	C	G	26.63%	413	.	.	.		.	.	.			.	0.9284	84.13%	100.00%	100%	Clonal			
MP1	IKZF5	p.Leu19Gln	missense_variant	10	124758086	A	T	25.63%	679	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9228	85.41%	100.00%	100%	Clonal			
MP1	B4GALNT4	p.Gly552Val	missense_variant	11	376778	G	T	31.15%	61	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8691	68.22%	100.00%	100%	Clonal			
MP1	MUC6	p.Ala1471Thr	missense_variant	11	1018390	C	T	9.09%	77	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0033	17.13%	68.00%	35%	Subclonal			
MP1	DENND5A	p.Ser433Ala	missense_variant	11	9202472	A	C	23.89%	540	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8096	78.71%	100.00%	93%	Clonal			
MP1	ELP4	p.Lys23Lys	synonymous_variant	11	31531400	G	A	27.43%	638	.	.	.		.	.	.			.	0.9540	89.04%	100.00%	100%	Clonal			
MP1	SPTBN2	p.Ala1545Ala	synonymous_variant	11	66460876	C	T	23.47%	524	.	.	.		.	.	.		TRUE	.	0.7615	77.15%	100.00%	91%	Clonal			
MP1	MAML2	p.Ala5Gly	missense_variant	11	96075046	G	C	36.32%	603	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.9683	90.36%	100.00%	100%	Clonal			
MP1	AGAP2	p.Thr1126Thr	synonymous_variant	12	58120536	C	G	25.49%	204	.	.	.		.	.	.		TRUE	.	0.8679	74.57%	100.00%	99%	Clonal			
MP1	HECTD4	p.Arg3718Gly	missense_variant	12	112613580	T	C	24.60%	313	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8531	76.53%	100.00%	96%	Clonal			
MP1	BRCA2	p.Glu2226fs	frameshift_variant	13	32915166	CAG	C	20.17%	585	A	.	.		true	true	.	TRUE		Likely pathogenic	0.0429	66.11%	91.31%	78%	Subclonal			
MP1	TGM1	p.Glu558Gln	missense_variant	14	24724433	C	G	29.29%	553	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9471	90.92%	100.00%	100%	Clonal			
MP1	ADCY4	p.Ser499Ile	missense_variant	14	24798295	C	A	23.81%	462	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8043	77.34%	100.00%	93%	Clonal			
MP1	GPR137C	p.Thr227Thr	synonymous_variant	14	53067023	A	T	23.79%	290	.	.	.		.	.	.			.	0.8040	73.48%	100.00%	93%	Clonal			
MP1	ADCK1	p.Asp275Gly	missense_variant	14	78374228	A	G	35.28%	326	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9420	84.48%	100.00%	100%	Clonal			
MP1	ZC3H14	p.Ser330Ile	missense_variant	14	89041164	G	T	36.87%	377	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.9609	88.14%	100.00%	100%	Clonal			
MP1	SLC25A29	p.Cys234Phe	missense_variant	14	100758831	C	A	35.43%	398	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9499	86.25%	100.00%	100%	Clonal			
MP1	TRPM1	p.Ser1400*	stop_gained	15	31294755	G	C	5.30%	641	D	.	.		.	.	.			Indeterminate	0.0000	14.34%	27.97%	21%	Subclonal			
MP1	IVD	p.Ala217_Val219del	inframe_deletion	15	40703840	CTGGCTGCTG	C	13.42%	596	D	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.0000	42.01%	63.32%	52%	Subclonal			
MP1	TTBK2	p.Gly98Cys	missense_variant	15	43122276	C	A	8.79%	182	D	PASSENGER/OTHER	Driver		.	.	.		TRUE	Likely pathogenic	0.0000	20.92%	53.24%	34%	Subclonal			
MP1	NEO1	p.Leu916Phe	missense_variant	15	73562686	G	C	20.05%	434	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1047	63.89%	92.82%	78%	Subclonal			
MP1	STRA6	p.Gln74His	missense_variant	15	74494504	C	G	29.01%	293	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9380	85.49%	100.00%	100%	Clonal			
MP1	CCDC33	p.Leu338Phe	missense_variant	15	74573131	C	T	23.76%	181	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7934	68.65%	100.00%	92%	Clonal			
MP1	AP3B2	p.Lys1033Asn	missense_variant	15	83328653	T	G	26.91%	405	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9322	84.55%	100.00%	100%	Clonal			
MP1	CACNA1H	p.Glu2210Gln	missense_variant	16	1270560	G	C	27.17%	173	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3763	60.39%	96.02%	79%	Subclonal			
MP1	NLRC3	p.Gly519Ser	missense_variant	16	3613383	C	T	21.49%	335	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4891	67.20%	97.69%	84%	Subclonal			
MP1	SULT1A2	p.Leu215Leu	synonymous_variant	16	28603714	C	T	6.94%	72	.	.	.		.	.	.			.	0.0007	11.45%	58.88%	27%	Subclonal			
MP1	CDH5	p.Gly167Trp	missense_variant	16	66421000	G	T	24.74%	190	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8392	71.87%	100.00%	96%	Clonal			
MP1	NECAB2	p.Asp329Tyr	missense_variant	16	84034351	G	T	4.20%	286	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.99%	27.50%	16%	Subclonal			
MP1	ZFPM1	p.Gly850Arg	missense_variant	16	88600914	G	C	28.57%	175	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9134	79.32%	100.00%	100%	Clonal			
MP1	GEMIN4	p.Phe159Val	missense_variant	17	650808	A	C	36.62%	669	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9718	91.37%	100.00%	100%	Clonal			
MP1	TP53	p.Arg110Pro	missense_variant	17	7579358	C	G	31.69%	344	N	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.8103	77.16%	100.00%	92%	Clonal			
MP1	SARM1	p.Glu433Glu	synonymous_variant	17	26711860	G	A	5.31%	414	.	.	.		.	.	.		TRUE	.	0.0000	13.26%	30.32%	21%	Subclonal			
MP1	TBC1D3B	p.Ser484Tyr	missense_variant	17	34797685	G	T	25.00%	48	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7653	52.79%	100.00%	97%	Clonal			
MP1	DDX52	p.Pro230Pro	synonymous_variant	17	35990117	G	A	21.03%	271	.	.	.		.	.	.		TRUE	.	0.4650	63.99%	97.46%	82%	Subclonal			
MP1	KRT39	p.Ala214Ala	synonymous_variant	17	39119945	G	C	28.18%	582	.	.	.		.	.	.		TRUE	.	0.9553	89.66%	100.00%	100%	Clonal			
MP1	WNK4	p.Pro1042Ala	missense_variant	17	40947744	C	G	2.48%	686	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	5.48%	14.83%	10%	Subclonal			
MP1	PNPO	p.Leu22Val	missense_variant	17	46019105	C	G	29.29%	751	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9382	92.72%	100.00%	100%	Clonal			
MP1	KPNA2	p.Ala364Val	missense_variant	17	66040114	C	T	18.29%	82	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7233	52.72%	100.00%	89%	Clonal			
MP1	CD300E	p.Glu39Asp	missense_variant	17	72613528	C	G	12.30%	691	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	48.69%	72.70%	60%	Subclonal			
MP1	TNRC6C	p.Asn356Lys	missense_variant	17	76046211	T	A	18.49%	687	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7285	76.30%	100.00%	90%	Clonal			
MP1	DNAH17	p.Leu927Leu	synonymous_variant	17	76533459	C	T	18.08%	813	.	.	.		.	.	.			.	0.0104	93.55%	100.00%	100%	Clonal			
MP1	OSBPL1A	p.Ile716fs	frameshift_variant	18	21752396	G	GAT	21.03%	561	A	.	.		.	.	.			Indeterminate	0.1764	69.01%	94.74%	82%	Subclonal			
MP1	CXXC1	p.Arg439Gly	missense_variant	18	47810374	G	C	24.62%	719	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8740	82.92%	100.00%	96%	Clonal			
MP1	EEF2	p.Ala515Ala	synonymous_variant	19	3979866	A	C	33.07%	127	.	.	.		.	.	.		TRUE	.	0.8992	81.89%	100.00%	100%	Clonal			
MP1	VAV1	p.Asp476His	missense_variant	19	6832129	G	C	14.24%	288	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0880	51.70%	90.58%	70%	Subclonal			
MP1	CD320	p.Asp144Tyr	missense_variant	19	8368811	C	A	22.71%	665	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9514	89.14%	100.00%	100%	Clonal			
MP1	ZNF763	p.Ala391Thr	missense_variant	19	12089901	G	A	41.83%	416	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9746	96.72%	100.00%	100%	Clonal			
MP1	NOTCH3	p.Arg2234fs	frameshift_variant	19	15271721	TGGGAACCCGCAGGAAGC	T	22.88%	590	.	.	.		.	.	.			Indeterminate	0.9486	88.57%	100.00%	100%	Clonal			
MP1	CHERP	p.Asp166Asn	missense_variant	19	16643848	C	T	20.69%	759	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9267	85.17%	100.00%	100%	Clonal			
MP1	NCAN	p.Trp817Leu	missense_variant	19	19338879	G	T	20.61%	456	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9037	80.85%	100.00%	100%	Clonal			
MP1	ETV2	p.Val308Leu	missense_variant	19	36135647	G	C	25.89%	479	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9179	83.56%	100.00%	100%	Clonal			

MP1	SYT3	p.Glu191Gln	missense_variant	19	51135646	C	G	25.00%	484	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8866	81.29%	100.00%	97%	Clonal
MP1	BRSK1	p.Pro362Ala	missense_variant	19	55814734	C	G	19.05%	378	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0458	59.44%	90.05%	74%	Subclonal
MP1	DEFB125	c.59-1G>A	splice_acceptor_variant	20	76645	G	A	28.91%	256	D	.	.		.	.	.			Indeterminate	0.9329	84.06%	100.00%	100%	Clonal
MP1	SLC32A1	p.Lys164Asn	missense_variant	20	37356196	G	T	25.17%	735	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9072	84.68%	100.00%	98%	Clonal
MP1	MAFB	p.Cys298Trp	missense_variant	20	39316597	G	C	22.57%	421	D	.	Passenger		true	.	.			Likely pathogenic	0.6427	72.55%	98.65%	88%	Clonal
MP1	ADNP	p.Asp1070Asn	missense_variant	20	49508043	C	T	27.47%	768	D	.	Passenger		.	.	true			Likely pathogenic	0.9593	90.27%	100.00%	100%	Clonal
MP1	ADNP	p.Glu888Gln	missense_variant	20	49508589	C	G	26.21%	782	N	.	Passenger		.	.	true			Likely passenger	0.9433	87.82%	100.00%	100%	Clonal
MP1	ADNP	p.Trp796*	stop_gained	20	49508863	C	T	25.45%	605	D	.	.		.	.	true			Likely pathogenic	0.9129	84.18%	100.00%	99%	Clonal
MP1	ADNP	p.Glu787Lys	missense_variant	20	49508892	C	T	25.13%	577	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.8981	82.98%	100.00%	98%	Clonal
MP1	ADNP	p.Glu785Lys	missense_variant	20	49508898	C	T	25.35%	568	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.9069	83.44%	100.00%	99%	Clonal
MP1	ADNP	p.Glu747Lys	missense_variant	20	49509012	C	T	29.30%	669	D	.	Passenger		.	.	true			Likely pathogenic	0.9432	92.10%	100.00%	100%	Clonal
MP1	GATA5	p.Ser306Ser	synonymous_variant	20	61040516	G	A	28.88%	232	.	.	.		.	.	.			.	0.9288	83.01%	100.00%	100%	Clonal
MP1	ATP5J	c.18-2A>G	splice_acceptor_variant	21	27102114	T	C	26.15%	65	D	.	.		.	.	.			Indeterminate	0.8118	60.33%	100.00%	100%	Clonal
MP1	COL18A1	p.Trp202_Pro208del	disruptive_inframe_deletion	21	46876042	AGGCCCTGGGCACCACTCACGG	A	9.39%	852	.	.	.	Deleterious	.	.	.			Indeterminate	0.0000	29.11%	44.42%	37%	Subclonal
MP1	BCR	p.Arg592Gln	missense_variant	22	23610617	G	A	27.46%	193	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.9058	78.36%	100.00%	100%	Clonal
MP1	MYO18B	p.Leu1560Leu	synonymous_variant	22	26294283	T	C	11.36%	317	.	.	.		.	.	.			.	0.0000	31.89%	59.13%	44%	Subclonal
MP1	CHEK2	p.Trp93Ser	missense_variant	22	29130432	C	G	25.80%	566	D	CANCER	Passenger		true	true	.			Likely pathogenic	0.9216	84.59%	100.00%	100%	Clonal
MP1	SYN3	p.Asp24Gly	missense_variant	22	33402577	T	C	23.40%	329	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7723	73.39%	100.00%	91%	Clonal
MP1	POLR3H	p.Phe2Phe	synonymous_variant	22	41940100	G	A	26.20%	832	.	.	.		.	.	.			.	0.9449	88.17%	100.00%	100%	Clonal
MP1	TCEANC	p.Arg328Thr	missense_variant	X	13681520	G	C	33.99%	612	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0075	95.14%	100.00%	100%	Clonal
MP1	MAGEB10	p.Arg15Arg	synonymous_variant	X	27839468	C	T	17.33%	427	.	.	.		.	.	.			.	0.5568	67.99%	98.14%	85%	Clonal
MP1	DMD	p.His512His	synonymous_variant	X	32613940	G	A	25.16%	763	.	.	.		.	.	.			.	0.6092	93.35%	100.00%	100%	Clonal
MP1	KDM6A	p.Arg571fs	frameshift_variant	X	44922693	AC	A	20.38%	1457	A	.	.		true	true	true			Likely pathogenic	0.9366	88.26%	100.00%	100%	Clonal
MP1	ZNF41	p.Glu234*	stop_gained	X	47308469	C	A	23.71%	523	D	.	.		.	.	.			Indeterminate	0.9401	89.10%	100.00%	100%	Clonal
MP1	USP27X	p.Arg131Trp	missense_variant	X	49645301	C	T	10.65%	845	.	.	Passenger		.	.	.			Indeterminate	0.0000	42.26%	62.68%	52%	Subclonal
MP1	MAGED2	p.Ala115Ala	synonymous_variant	X	54836454	T	A	11.05%	552	.	.	.		.	.	.			.	0.0000	42.07%	67.71%	54%	Subclonal
MP1	MED12	p.Leu366Leu	synonymous_variant	X	70341661	C	T	4.92%	244	.	.	.		true	.	true			.	0.0000	10.57%	32.19%	19%	Subclonal
MP1	MED12	p.Gln415Lys	missense_variant	X	70342191	C	A	3.03%	628	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.0000	7.09%	17.73%	12%	Subclonal
MP1	GLRA4	p.Arg93Trp	missense_variant	X	102979223	G	A	7.64%	157	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	16.82%	49.67%	30%	Subclonal
MP1	IRS4	p.Gln158His	missense_variant	X	107979101	C	G	15.37%	501	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	48.06%	72.64%	60%	Subclonal
MP1	DCAF12L2	p.Arg337His	missense_variant	X	125298898	C	T	31.91%	702	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2304	94.58%	100.00%	100%	Clonal
MP1	ZFP92	p.Pro319Arg	missense_variant	X	152686791	C	G	18.70%	460	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0101	59.39%	87.08%	73%	Subclonal
MP1	TMLHE	p.Arg407Ser	missense_variant	X	154721241	T	A	17.02%	47	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.4348	33.71%	96.89%	66%	Subclonal
MP11	MEGF6	p.Leu1511fs	frameshift_variant	1	3407502	TCGGGGAG	T	19.71%	695	D	.	.		.	.	.			Indeterminate	0.0248	93.03%	100.00%	100%	Clonal
MP11	CCDC27	p.Glu516Gly	missense_variant	1	3683813	A	G	2.81%	640	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	15.78%	39.50%	26%	Subclonal
MP11	PER3	p.Lys158Asn	missense_variant	1	7848188	G	C	11.39%	825	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7871	81.33%	100.00%	100%	Clonal
MP11	PER3	p.Gln598His	missense_variant	1	7880537	A	T	37.71%	822	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0104	98.24%	100.00%	100%	Clonal
MP11	ENO1	p.Asp266Tyr	missense_variant	1	8925413	C	A	8.70%	713	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1561	61.59%	96.36%	79%	Subclonal
MP11	C1orf167	p.Leu843Leu	synonymous_variant	1	11839015	C	G	22.26%	283	.	.	.		.	.	.			.	0.9435	90.86%	100.00%	100%	Clonal
MP11	RSC1A1	p.Leu429Leu	synonymous_variant	1	15987650	A	G	7.09%	663	.	.	.		.	.	.			.	0.0043	48.33%	83.93%	64%	Subclonal
MP11	PLEKHM2	p.Leu723Val	missense_variant	1	16056383	C	G	3.47%	346	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	17.74%	53.67%	32%	Subclonal
MP11	DDOST	p.Arg25Arg	synonymous_variant	1	20987822	G	T	21.04%	808	.	.	.		.	.	.			.	0.0007	94.82%	100.00%	100%	Clonal
MP11	ZBTB40	p.Ala1220Ala	synonymous_variant	1	22852829	G	T	15.94%	715	.	.	.		.	.	.			.	0.8605	87.03%	100.00%	100%	Clonal
MP11	HTR1D	p.Pro325Ser	missense_variant	1	23519740	G	A	24.33%	826	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5944	96.31%	100.00%	100%	Clonal
MP11	MATN1	p.Leu64Leu	synonymous_variant	1	31194501	C	T	14.83%	762	.	.	.		.	.	.			.	0.8385	88.60%	100.00%	100%	Clonal
MP11	ZMYM4	p.Gly1372Gly	synonymous_variant	1	35881122	C	T	3.46%	722	.	.	.		.	.	.			.	0.0000	18.56%	40.44%	28%	Subclonal
MP11	NCDN	p.Tyr39Ser	missense_variant	1	36024790	A	C	5.16%	523	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	28.41%	59.40%	42%	Subclonal
MP11	TIE1	p.Arg382Gln	missense_variant	1	43774759	G	A	19.59%	439	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4792	91.24%	100.00%	100%	Clonal
MP11	C1orf228	p.Ser410Thr	missense_variant	1	45190981	G	C	21.40%	799	N	.	Passenger		.	.	.			Likely passenger	0.7308	95.71%	100.00%	100%	Clonal
MP11	MKNK1	p.Pro386Leu	missense_variant	1	47025921	G	A	20.67%	450	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7520	92.31%	100.00%	100%	Clonal
MP11	DMRTB1	p.Arg31Cys	missense_variant	1	53925217	C	T	23.25%	628	D	.	Passenger		.	.	.			Indeterminate	0.9498	95.44%	100.00%	100%	Clonal
MP11	C1orf177	p.Arg370Gln	missense_variant	1	55282720	G	A	8.90%	674	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0256	55.94%	90.44%	72%	Subclonal
MP11	PCSK9	p.Arg682Arg	synonymous_variant	1	55529224	G	A	6.34%	347	.	.	.		.	.	.			.	0.0013	33.72%	75.59%	51%	Subclonal
MP11	PCSK9	p.His683Asn	missense_variant	1	55529225	C	A	6.41%	343	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0017	34.13%	76.45%	52%	Subclonal
MP11	SLC16A4	p.Leu160Val	missense_variant	1	110923652	G	C	3.14%	605	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	13.85%	33.88%	22%	Subclonal
MP11	HIPK1	p.Gly734Gly	synonymous_variant	1	114506107	C	G	4.62%	585	.	.	.		.	.	.		TRUE	.	0.0000	22.14%	46.51%	33%	Subclonal
MP11	RPRD2	p.Tyr1167Cys	missense_variant	1	150444924	A	G	3.48%	861	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.32%	39.38%	28%	Subclonal
MP11	FLG2	p.Ser1087Thr	missense_variant	1	152327003	A	T	6.38%	643	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	37.81%	68.53%	52%	Subclonal
MP11	KCNN3	p.Ala357Gly	missense_variant	1	154744829	G	C	5.04%	456	D	.	Passenger		.	.	.			Indeterminate	0.0000	26.93%	59.78%	41%	Subclonal
MP11	FLAD1	p.Val380Val	synonymous_variant	1	154962058	G	A	3.36%	327	.	.	.		.	.	.			.	0.0000	14.89%	47.38%	27%	Subclonal
MP11	SPTA1	p.Gln2195Glu	missense_variant	1	158587344	G	C	3.62%	525	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	23.07%	55.81%	36%	Subclonal
MP11	SPTA1	p.Phe1719Phe	synonymous_variant	1	158607855	G	A	21.31%	427	.	.	.		.	.	.			.	0.9336	93.62%	100.00%	100%	Clonal
MP11	IGSF9	p.Leu113Met	missense_variant	1	159907539	G	T	6.31%	602	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0096	46.26%	85.51%	64%	Subclonal
MP11	ATP1A4	p.Met822Val	missense_variant	1	160146034	A	G	4.69%	768	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	33.88%	64.27%	47%	Subclonal
MP11	PPOX	p.Arg113Ser	missense_variant	1	161137785	G	T	14.29%	378	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5998	85.36%	100.00%	100%	Clonal
MP11	ADCY10	p.Arg983Gln	missense_variant	1	167814860	C	T	3.59%	753	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	22.05%	46.46%	33%	Subclonal
MP11	SLC9C2	p.Phe258Phe	synonymous_variant	1	173551014	A	G	3.05%	787	.	.	.		.	.	.			.	0.0000	18.22%	40.38%	28%	Subclonal
MP11	ABL2	p.Glu551Asp	missense_variant	1	179079589	C	G	4.27%	703	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0000	26.84%	54.26%	39%	Subclonal
MP11	CACNA1E	p.Glu880Gly	missense_variant	1	181701861	A	G	4.05%	765	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	25.58%	51.24%	37%	Subclonal
MP11	C1orf106	p.Arg84Pro	missense_variant	1	200867482	G	C	5.61%	535	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	35.48%	71.21%	51%	Subclonal
MP11	IRF6	p.Glu264_Glu272del	inframe_deletion	1	209964083	GCTCCAGGCTGACGGGACCAAAGAGCTC	G	11.55%	1134	.	.	.	Deleterious	.	.	.	TRUE		Likely pathogenic	0.8314	84.93%	100.00%	100%	Clonal
MP11	KCNH1	p.Tyr526Cys	missense_variant	1	210977394	T	C	4.71%	700	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	30.21%	58.97%	43%	Subclonal
MP11	USH2A	p.Gly1301Arg	missense_variant	1	216371837	C	G	5.82%	498	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0004	36.66%	74.35%	53%	Subclonal
MP11	EPHX1	p.Trp227Ser	missense_variant	1	226027005	G	C	6.10%	426	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0029	37.71%	79.33%	55%	Subclonal
MP11	PSEN2	p.Gly363Gly	synonymous_variant	1	227081724	C	G	5.04%	556	.	.	.		.	.	.			.	0.0000	31.40%	64.76%	46%	Subclonal
MP11	GUK1	p.Arg169Trp	missense_variant	1	228335367	C	T	27.38%	252	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6717	92.61%	100.00%	100%	Clonal
MP11	OBSCN	p.Tyr8270*	stop_gained	1	228560418	C	G	6.64%	648	A	.	.		.	.	.			Indeterminate	0.0011	44.61%	79.62%	60%	Subclonal
MP11	FMN2	p.Ser614Pro	missense_variant	1	240341278	T	C	2.90%	758	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	26.67%	60.85%	41%	Subclonal
MP11	FMN2	p.Leu711Pro	missense_variant	1	240370244	T	C	8.08%	866	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8098	81.96%	100.00%	100%	Clonal
MP11	OR6F1	p.Arg261Leu	missense_variant	1	247875276	C	A	2.80%	892	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	26.38%	57.33%	39%	Subclonal
MP11	OR2M4	p.Ser264Ser	synonymous_variant	1	248403022	T	G	3.55%	816	.	.	.		.	.	.			.	0.0001	34.56%	70.74%	50%	Subclonal
MP11	APOB	p.Thr1590Thr	synonymous_variant	2	21234970	G	C	3.07%	781	.	.	.		.	.	.			.	0.0000	16.28%	36.14%	25%	Subclonal
MP11	KCNK3	p.Ser286Leu	missense_variant	2	26951108	C	T	11.19%	420	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5305	67.22%	100.00%	90%	Clonal
MP11	KHK	p.Ile101Met	missense_variant	2	27317438	C	G	8.45%	722	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0056	53.15%	85.97%	68%	Subclonal
MP11	ZNF513	p.His434Asp	missense_variant	2	27600738	G	C	10.80%	824	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.3980	70.86%	98.71%	87%	Subclonal
MP11	GPN1	p.Ala113Pro	missense_variant	2	27854750	G	C	4.89%	675	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	27.85%	54.38%	40%	Subclonal
MP11	NLRC4	p.Arg141Arg	synonymous_variant	2	32476510	C	T	2.96%	710	.	.	.		.	.	.			.	0.0000	15.23%	35.73%	24%	Subclonal
MP11	KCNK12	p.Leu313Val	missense_variant	2	47748402	G	C	14.11%	475	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.7833	85.34%	100.00%	100%	Clonal
MP11	PEX13	p.Gln352Glu	missense_variant	2	61275747	C	G	14.63%	834	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3260	91.29%	100.00%	100%	Clonal
MP11	CNNM4	p.Arg670Pro	missense_variant	2	97474358	G	C	3.21%	530	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.83%	40.56%	26%	Subclonal
MP11	GALNT13	p.Lys377Gln	missense_variant	2	155158075	A	C	3.77%	345	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.74%	57.08%	34%	Subclonal
MP11	BAZ2B	p.Ala127Ala	synonymous_variant	2	160304874	T	G	3.33%	421	.	.	.		.	.	.			.	0.0000	17.67%	49.51%	30%	Subclonal
MP11	COBLL1	c.1195-2A>T	splice_acceptor_variant	2	165561617	T	A	2.92%	342	D	.	.		.	.	.			Indeterminate	0.0000	14.13%	47.62%	27%	Subclonal
MP11	TTN	p.Ile25662Thr	missense_variant	2	179433874	A	G	4.37%	823	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	25.20%	47.97%	35%	Subclonal
MP11	ALS2CR11	p.Glu1139Glu	synonymous_variant	2	202357647	T	C	24.70%	842	.	.	.		.	.	.		TRUE	.	0.9692	96.99%	100.00%	100%	Clonal
MP11	ALS2CR11	p.Cys231Tyr	missense_variant	2	202438993	C	T	4.38%	639	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	24.18%	50.11%	35%	Subclonal
MP11	CPS1	p.Gly1254Arg	missense_variant	2	211523398	G	C	3.04%	493	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	18.26%	49.52%	31%	Subclonal
MP11	WNT6	p.Leu233Leu	synonymous_variant	2	219738168	G	A	5.25%	305	.	.	.		.	.	.			.	0.0127	32.44%	83.17%	53%	Subclonal
MP11	SGPP2	p.Gly286Ala	missense_variant	2	223423274	G	C	14.76%	867	D	.	Passenger		.	.	.			Indeterminate	0.0193	93.09%	100.00%	100%	Clonal
MP11	MROH2A	p.Glu1462Lys	missense_variant	2	234737614	G	A	4.06%	665	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	22.21%	46.75%	33%	Subclonal
MP11	NEU4	p.Arg255Gly	missense_variant	2	242757643	C	G	4.68%	470	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	18.45%	41.99%	28%	Subclonal
MP11	CCDC174	p.Pro155Pro	synonymous_variant	3	14703194	C	G	27.81%	791	D	.	.		.	.	.			.	0.9701	97.09%	100.00%	100%	Clonal
MP11	SLC22A14	p.Ser574Tyr	missense_variant	3	38358003	C	A	3.23%	402	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.05%	38.13%	23%	Subclonal
MP11	LRRC2	p.Leu371Ile	missense_variant	3	46560509	G	T	25.04%	667	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8505	95.85%	100.00%	100%	Clonal
MP11	COL7A1	p.Gly2304Arg	missense_variant	3	48609962	C	T	5.85%	325	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	22.51%	53.95%	36%	Subclonal
MP11	DENND6A	p.Gln247Glu	missense_variant	3	57644868	G	C	3.14%	636	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	14.04%	33.58%	22%	Subclonal
MP11	ESYT3	p.Lys702Lys	synonymous_variant	3	138191570	G	A	9.69%	877	.	.	.		.	.	.			.	0.8045	81.90%	100.00%	100%	Clonal
MP11	AADACL2	p.Thr46Thr	synonymous_variant	3	151451961	G	T	2.56%	664	.	.	.		.	.	.			.	0.0000	17.34%	44.53%	28%	Subclonal
MP11	SMC4	c.2606-2A>G	splice_acceptor_variant	3	160146539	A	G	14.94%	549	D	.	.		.	.	.			Indeterminate	0.5364	88.51%	100.00%	100%	Clonal
MP11	SLITRK3	p.Glu325Lys	missense_variant	3	164907646	C	T	4.67%	792	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	30.47%	57.42%	42%	Subclonal
MP11	AHSG	p.Arg340Cys	missense_variant	3	186338633	C	T	5.68%	845	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0970	55.91%	94.69%	74%	Subclonal
MP11	RFC4	p.Ala353Gly	missense_variant	3	186507792	G	C	2.93%	921	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	26.03%	54.87%	38%	Subclonal
MP11	RTP2	p.Asp146His	missense_variant	3	187416528	C	G	11.23%	855	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1212	90.81%	100.00%	100%	Clonal
MP11	PIGG	p.Ala567Thr	missense_variant	4	517332	G	A	11.61%	689	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0032	56.88%	85.98%	71%	Subclonal
MP11	RASL11B	p.Val26Gly	missense_variant	4	53728751	T	G	8.75%	526	N	CANCER	Passenger		.	.	.			Likely passenger	0.2312	59.48%	97.41%	79%	Subclonal
MP11	ALB	p.Ala388Ala	synonymous_variant	4	74280857	A	G	4.66%	429	.	.	.		.	.	.			.	0.0000	27.18%	63.92%	42%	Subclonal
MP11	GPRIN3	p.Asn85Asn	synonymous_variant	4	90171007	A	G	4.27%	844	.	.	.		.	.	.			.	0.0000	27.65%	52.65%	39%	Subclonal
MP11	MMRN1	p.Tyr1130Tyr	synonymous_variant	4	90874272	T	C	9.77%	778	.	.	.		.	.	.			.	0.4705	70.54%	100.00%	89%	Subclonal
MP11	EGF	p.Val428Val	synonymous_variant	4	110883113	G	A	3.42%	673	.	.	.		.	.	.			.	0.0000	20.32%	45.63%	31%	Subclonal
MP11	SLC7A11	p.Lys105*	stop_gained	4	139157570	T	A	4.81%	686	A	.	.		.	.	.			Indeterminate	0.0000	27.37%	53.52%	39%	Subclonal
MP11	FAM198B	p.Arg74Arg	synonymous_variant	4	159092306	G	A	4.13%	848	.	.	.		.	.	.			.	0.0000	23.62%	45.49%	33%	Subclonal
MP11	TENM3	p.Gln234_Val240del	disruptive_inframe_deletion	4	183522261	CGTCCAGCTGCAGGACAGCTGG	C	9.38%	725	.	.	.	Deleterious	.	.	.			Indeterminate	0.0596	59.86%	93.41%	76%	Subclonal
MP11	ADCY2	p.Asp222Gly	missense_variant	5	7626374	A	G	10.62%	725	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8285	84.25%	100.00%	100%	Clonal
MP11	DROSHA	p.Ser1101Tyr	missense_variant	5	31423011	G	T	7.42%	445	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0449	47.96%	91.20%	67%	Subclonal
MP11	EGFLAM	p.Phe641_Pro643del	inframe_deletion	5	38427218	ACATTTCGGC	A	10.32%	1047	D	.	.	Deleterious	.	.	.			Indeterminate	0.6242	76.93%	100.00%	94%	Clonal
MP11	C5orf34	p.Glu523Ala	missense_variant	5	43492329	T	G	3.58%	837	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	22.42%	45.59%	33%	Subclonal
MP11	MAP1B	p.Gly491Gly	synonymous_variant	5	71490655	G	A	25.80%	810	.	.	.		.	.	.			.	0.9126	96.69%	100.00%	100%	Clonal
MP11	PCDHA6	p.Ala720Ala	synonymous_variant	5	140209836	G	A	11.40%	719	.	.	.		.	.	.		TRUE	.	0.5782	73.70%	100.00%	92%	Clonal
MP11	PCDHB4	p.Ser473Arg	missense_variant	5	140502997	A	C	4.22%	166	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0015	16.38%	67.70%	34%	Subclonal
MP11	GABRP	p.Arg293Arg	synonymous_variant	5	170236618	C	T	5.31%	358	.	.	.		.	.	.		TRUE	.	0.0001	27.26%	65.32%	43%	Subclonal
MP11	STK10	p.Arg636Gln	missense_variant	5	171509412	C	T	5.03%	576	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	28.08%	57.21%	41%	Subclonal
MP11	NSD1	p.Asn1933His	missense_variant	5	176707740	A	C	27.02%	692	D	PASSENGER/OTHER	Passenger		true	true	true	TRUE	TRUE	Likely pathogenic	0.9610	96.47%	100.00%	100%	Clonal
MP11	C6orf62	p.Ter230fs	frameshift_variant	6	24706360	GTACTC	G	10.14%	1164	P	.	.		.	.	.			Indeterminate	0.5697	76.45%	100.00%	92%	Clonal
MP11	SCGN	p.Leu137Leu	synonymous_variant	6	25670244	C	G	4.28%	725	.	.	.		.	.	.			.	0.0000	27.06%	54.05%	39%	Subclonal
MP11	OR2J2	p.Phe104Ile	missense_variant	6	29141722	T	A	6.45%	248	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0452	36.04%	89.95%	59%	Subclonal
MP11	GPANK1	p.Arg277Gln	missense_variant	6	31630284	C	T	10.02%	838	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1505	65.49%	96.38%	81%	Subclonal
MP11	HLA-DQB2	p.Glu220Asp	missense_variant	6	32725647	T	A	6.52%	598	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	38.38%	70.59%	53%	Subclonal
MP11	UHRF1BP1	p.Glu114Glu	synonymous_variant	6	34801997	A	G	4.26%	751	.	.	.		.	.	.			.	0.0000	24.07%	47.65%	34%	Subclonal
MP11	FANCE	p.Arg62Cys	missense_variant	6	35420506	C	T	38.75%	80	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.2831	86.60%	100.00%	100%	Clonal
MP11	TNFRSF21	p.Thr161Ala	missense_variant	6	47253947	T	C	15.20%	875	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0643	92.44%	100.00%	100%	Clonal
MP11	DST	p.Ala960Val	missense_variant	6	56501437	G	A	20.78%	770	.	CANCER	Passenger		.	.	.			Likely pathogenic	0.9523	95.81%	100.00%	100%	Clonal
MP11	GJA10	p.Glu127Lys	missense_variant	6	90604566	G	A	25.46%	487	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8055	95.46%	100.00%	100%	Clonal
MP11	CEP57L1	p.Met275Val	missense_variant	6	109480472	A	G	14.50%	745	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5063	90.24%	100.00%	100%	Clonal
MP11	RAET1E	p.Val71Val	synonymous_variant	6	150211154	G	T	4.00%	400	.	.	.		.	.	.		TRUE	.	0.0000	17.12%	44.83%	28%	Subclonal
MP11	EZR	p.Ile260Val	missense_variant	6	159197457	T	C	3.53%	425	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.0000	14.80%	40.17%	25%	Subclonal
MP11	PACRG	p.Met203Val	missense_variant	6	163510434	A	G	6.29%	556	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	31.85%	60.65%	45%	Subclonal
MP11	RPS6KA2	p.Leu531Pro	missense_variant	6	166843954	A	G	5.14%	311	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	22.20%	57.56%	36%	Subclonal
MP11	INTS1	p.Leu959Leu	synonymous_variant	7	1526360	C	T	40.92%	325	.	.	.		.	.	.		TRUE	.	0.1882	96.18%	100.00%	100%	Clonal
MP11	CARD11	p.Asn781Lys	missense_variant	7	2959173	G	T	28.31%	724	D	PASSENGER/OTHER	Passenger		true	.	true		TRUE	Likely pathogenic	0.5298	96.45%	100.00%	100%	Clonal
MP11	OSBPL3	p.Val547Leu	missense_variant	7	24874212	C	G	22.87%	870	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9346	96.48%	100.00%	100%	Clonal
MP11	AVL9	p.Ala477Ala	synonymous_variant	7	32612891	A	G	10.26%	819	.	.	.		.	.	.			.	0.2210	67.02%	97.40%	83%	Subclonal
MP11	GPR141	p.Ile296Met	missense_variant	7	37780883	T	G	5.26%	437	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	28.13%	62.36%	43%	Subclonal
MP11	ZMIZ2	p.Pro714Ala	missense_variant	7	44805076	C	G	25.27%	364	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9132	92.96%	100.00%	100%	Clonal
MP11	ABCA13	p.Leu3667His	missense_variant	7	48411961	T	A	23.23%	637	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9496	95.49%	100.00%	100%	Clonal
MP11	VSTM2A	p.Ala81Ala	synonymous_variant	7	54612478	G	T	4.73%	169	.	.	.		.	.	.			.	0.0033	19.28%	72.58%	38%	Subclonal
MP11	MLXIPL	p.Gly555Gly	synonymous_variant	7	73011201	C	T	18.22%	214	.	.	.		.	.	.			.	0.7174	82.17%	100.00%	100%	Clonal
MP11	ABCB4	p.Val439Ala	missense_variant	7	87072675	A	G	3.36%	446	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	18.19%	49.23%	31%	Subclonal
MP11	MUC12	p.Glu3963Lys	missense_variant	7	100645731	G	A	8.33%	96	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2406	33.62%	97.34%	67%	Subclonal
MP11	MUC17	p.Glu3573Glu	synonymous_variant	7	100685416	A	G	4.98%	703	.	.	.		.	.	true			.	0.0000	28.63%	54.85%	40%	Subclonal
MP11	SH2B2	p.Tyr470Cys	missense_variant	7	101960943	A	G	4.33%	554	.	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	23.22%	50.95%	35%	Subclonal
MP11	LRRN3	p.Tyr244Tyr	synonymous_variant	7	110763560	C	T	3.09%	842	.	.	.		.	.	.			.	0.0000	16.61%	35.78%	25%	Subclonal
MP11	LRRN3	p.Thr610Thr	synonymous_variant	7	110764658	C	T	3.48%	805	.	.	.		.	.	.			.	0.0000	19.08%	39.78%	28%	Subclonal
MP11	FLNC	p.Gly1890Gly	synonymous_variant	7	128491510	G	A	4.63%	540	.	.	.		.	.	.			.	0.0000	25.07%	54.02%	37%	Subclonal
MP11	ZC3HAV1	p.Gln278*	stop_gained	7	138764855	G	A	15.86%	870	A	.	.		.	.	.			Indeterminate	0.4802	91.60%	100.00%	100%	Clonal
MP11	TAS2R40	p.Ala290Ala	synonymous_variant	7	142920041	C	T	5.87%	766	.	.	.		.	.	.			.	0.0000	35.24%	62.34%	47%	Subclonal
MP11	FAM131B	p.Ala244Ser	missense_variant	7	143053996	C	A	6.57%	654	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	39.28%	70.16%	53%	Subclonal
MP11	PRKDC	p.Leu1796Phe	missense_variant	8	48777299	G	A	20.71%	280	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8447	88.54%	100.00%	100%	Clonal
MP11	RGS22	p.Glu414Gln	missense_variant	8	101075756	C	G	3.93%	814	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	33.35%	65.93%	48%	Subclonal
MP11	PABPC1	p.Thr319Ile	missense_variant	8	101724606	G	A	3.53%	283	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0054	23.05%	76.30%	43%	Subclonal
MP11	CSMD3	p.Asp2335Glu	missense_variant	8	113348895	A	T	3.90%	794	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	32.97%	65.83%	47%	Subclonal
MP11	FER1L6	p.Asp1378His	missense_variant	8	125088478	G	C	13.76%	814	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6952	93.19%	100.00%	100%	Clonal
MP11	DENND3	p.Asn972Asp	missense_variant	8	142199154	A	G	4.25%	776	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	24.14%	47.31%	34%	Subclonal
MP11	FOXH1	p.Cys4Cys	synonymous_variant	8	145701128	G	A	8.57%	280	.	.	.		.	.	.			.	0.1189	46.58%	94.95%	69%	Subclonal
MP11	IL33	p.Lys180Asn	missense_variant	9	6254481	G	C	2.60%	693	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	19.48%	48.67%	31%	Subclonal
MP11	FAM189A2	p.Leu407Val	missense_variant	9	72006586	C	G	5.90%	610	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	38.53%	72.76%	54%	Subclonal
MP11	AUH	p.Arg226Gly	missense_variant	9	93983254	G	C	4.24%	283	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0003	21.83%	65.49%	39%	Subclonal
MP11	AKNA	p.Pro75Arg	missense_variant	9	117143390	G	C	22.24%	661	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9024	95.27%	100.00%	100%	Clonal
MP11	MAN1B1	p.Leu507Leu	synonymous_variant	9	140001216	C	G	13.76%	218	.	.	.		.	.	.		TRUE	.	0.1090	49.37%	93.56%	70%	Subclonal
MP11	NSMF	p.Arg248Arg	synonymous_variant	9	140349726	C	G	14.60%	363	.	.	.		.	.	.		TRUE	.	0.0811	57.14%	93.10%	74%	Subclonal
MP11	PTPLA	p.Gly132Gly	synonymous_variant	10	17645646	T	C	10.23%	430	.	.	.		.	.	.			.	0.3337	61.48%	98.32%	83%	Subclonal
MP11	GDF2	p.Cys393Ser	missense_variant	10	48413690	C	G	30.82%	691	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0386	97.34%	100.00%	100%	Clonal
MP11	ANKRD1	p.Pro288Ser	missense_variant	10	92672721	G	A	15.43%	810	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7250	90.35%	100.00%	100%	Clonal
MP11	HTRA1	p.Glu277Gln	missense_variant	10	124266258	G	C	6.83%	878	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0089	53.42%	87.10%	69%	Subclonal
MP11	TEX36	p.Phe18Ile	missense_variant	10	127350546	A	T	5.85%	496	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	28.58%	58.10%	41%	Subclonal
MP11	AP2A2	p.Ser99Ser	synonymous_variant	11	972079	T	G	15.53%	206	.	.	.		.	.	.		TRUE	.	0.5858	65.34%	100.00%	94%	Clonal
MP11	CDKN1C	p.Pro140Gln	missense_variant	11	2906301	G	T	7.32%	82	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0383	20.48%	87.22%	45%	Subclonal
MP11	OR52N5	p.Gly208Gly	synonymous_variant	11	5799241	A	G	3.01%	732	.	.	.		.	.	.			.	0.0000	15.63%	35.94%	24%	Subclonal
MP11	MRVI1	p.Pro230Ser	missense_variant	11	10649537	G	A	23.65%	241	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9406	89.69%	100.00%	100%	Clonal
MP11	MICALCL	p.Arg162Gly	missense_variant	11	12315462	A	G	3.44%	726	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	18.45%	40.21%	28%	Subclonal
MP11	OTOG	p.Thr417Pro	missense_variant	11	17580708	A	C	4.78%	314	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	23.18%	62.00%	39%	Subclonal
MP11	SAAL1	p.His180Arg	missense_variant	11	18111772	T	C	3.13%	638	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	16.04%	38.25%	25%	Subclonal
MP11	OSBP	p.Glu125Gln	missense_variant	11	59378052	C	G	4.91%	835	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	32.58%	59.42%	45%	Subclonal
MP11	KCNK7	p.Ala52Pro	missense_variant	11	65363090	C	G	4.84%	310	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	20.51%	54.96%	34%	Subclonal
MP11	SART1	p.Leu294Leu	synonymous_variant	11	65733590	G	C	3.43%	525	.	.	.		.	.	.			.	0.0000	15.02%	37.45%	24%	Subclonal
MP11	TCIRG1	p.Trp752*	stop_gained	11	67817972	G	A	4.52%	177	A	.	.		.	.	.			Indeterminate	0.0002	16.06%	60.86%	32%	Subclonal
MP11	INPPL1	p.Thr213Ala	missense_variant	11	71940252	A	G	3.42%	730	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.70%	44.97%	31%	Subclonal
MP11	CLPB	p.Arg417*	stop_gained	11	72013356	G	A	16.89%	598	A	.	.		.	.	.			Indeterminate	0.1754	91.99%	100.00%	100%	Clonal
MP11	PDE2A	p.Asn674Lys	missense_variant	11	72292424	G	C	3.48%	230	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0002	15.81%	60.45%	32%	Subclonal
MP11	MYO7A	p.Asp1960Glu	missense_variant	11	76919498	C	A	4.55%	550	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	27.69%	59.69%	41%	Subclonal
MP11	TENM4	p.Thr1324Ala	missense_variant	11	78423611	T	C	4.50%	777	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	29.12%	55.84%	41%	Subclonal
MP11	PICALM	p.Tyr44*	stop_gained	11	85742652	G	C	20.92%	411	A	.	.		true	.	.			Likely pathogenic	0.9470	92.67%	100.00%	100%	Clonal
MP11	FAT3	p.Ile2723Val	missense_variant	11	92534346	A	G	5.15%	854	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	34.58%	61.71%	47%	Subclonal
MP11	GUCY1A2	p.Gln541His	missense_variant	11	106680788	T	G	4.94%	385	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	25.29%	60.78%	40%	Subclonal
MP11	FDXACB1	p.Lys547Asn	missense_variant	11	111745880	C	G	22.48%	832	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9090	96.24%	100.00%	100%	Clonal
MP11	DSCAML1	p.Ser84Arg	missense_variant	11	117651500	G	C	2.81%	392	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.31%	39.55%	23%	Subclonal
MP11	ARCN1	p.Ser244Ala	missense_variant	11	118455271	T	G	17.02%	429	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5368	87.86%	100.00%	100%	Clonal
MP11	PDZD3	p.Gly456Glu	missense_variant	11	119059793	G	A	14.91%	738	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8337	88.51%	100.00%	100%	Clonal
MP11	ITFG2	p.Glu362Gln	missense_variant	12	2932953	G	C	7.43%	350	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0133	40.97%	85.35%	60%	Subclonal
MP11	CLEC6A	p.Ser17Thr	missense_variant	12	8610511	T	A	3.23%	310	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	13.87%	46.67%	26%	Subclonal
MP11	ABCC9	p.Leu835Leu	synonymous_variant	12	22012522	A	G	3.95%	583	.	.	.		.	.	.		TRUE	.	0.0000	20.93%	46.80%	32%	Subclonal
MP11	KIAA1551	p.Lys1365fs	frameshift_variant	12	32137980	TGAAACTCAAATCA	T	12.50%	680	A	.	.		.	.	.			Indeterminate	0.8344	84.23%	100.00%	100%	Clonal
MP11	COL2A1	p.Gly822Ala	missense_variant	12	48374750	C	G	9.68%	155	D	PASSENGER/OTHER	Passenger		true	.	.	TRUE		Likely pathogenic	0.4573	51.15%	98.96%	88%	Subclonal
MP11	SDR9C7	p.Ser312Cys	missense_variant	12	57317625	T	A	4.74%	211	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0001	18.05%	59.74%	34%	Subclonal
MP11	LGR5	p.Lys675Asn	missense_variant	12	71977815	A	C	5.22%	785	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	30.84%	56.17%	42%	Subclonal
MP11	LUM	p.Leu329Val	missense_variant	12	91497974	G	C	6.96%	503	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0006	40.32%	76.51%	56%	Subclonal
MP11	EEA1	p.Cys1361Ser	missense_variant	12	93170651	C	G	6.22%	756	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	37.56%	65.57%	50%	Subclonal
MP11	SLC8B1	p.Asn498Asn	synonymous_variant	12	113742189	G	A	4.34%	369	.	.	.		.	.	.		TRUE	.	0.0000	21.30%	55.51%	35%	Subclonal
MP11	TMEM132D	p.Val179Leu	missense_variant	12	130184788	C	A	7.04%	795	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	38.22%	63.55%	50%	Subclonal
MP11	IFT88	p.Ser525Thr	missense_variant	13	21212630	T	A	3.45%	435	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	16.54%	44.86%	28%	Subclonal
MP11	SACS	p.Arg3875His	missense_variant	13	23906391	C	T	4.99%	742	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.97%	54.48%	40%	Subclonal
MP11	NUFIP1	p.Ser372Ser	synonymous_variant	13	45523879	T	C	5.08%	177	.	.	.		.	.	.			.	0.0046	21.52%	75.08%	41%	Subclonal
MP11	OLFM4	p.Ile212Ser	missense_variant	13	53617304	T	G	4.35%	620	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	32.94%	68.91%	48%	Subclonal
MP11	SLITRK5	p.Thr148Ser	missense_variant	13	88328086	C	G	6.85%	832	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0975	58.50%	94.82%	76%	Subclonal
MP11	KDELC1	p.Gly36Gly	synonymous_variant	13	103450913	T	C	3.83%	392	.	.	.		.	.	.			.	0.0004	25.47%	68.41%	42%	Subclonal
MP11	OR11G2	p.Gly49Ala	missense_variant	14	20665640	G	C	27.95%	644	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8241	96.81%	100.00%	100%	Clonal
MP11	PARP2	p.Gly429Ala	missense_variant	14	20824766	G	C	5.01%	559	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	27.74%	57.27%	40%	Subclonal
MP11	OR10G2	p.Ser222Ser	synonymous_variant	14	22102333	G	C	4.95%	303	.	.	.		.	.	.			.	0.0001	24.06%	64.23%	40%	Subclonal
MP11	LRP10	p.Arg51Gly	missense_variant	14	23342591	C	G	26.41%	814	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9463	96.92%	100.00%	100%	Clonal
MP11	FANCM	p.Glu167Lys	missense_variant	14	45605733	G	A	29.04%	785	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9668	97.22%	100.00%	100%	Clonal
MP11	MIS18BP1	p.Ser175*	stop_gained	14	45715966	G	C	5.26%	285	A	.	.		.	.	.			Indeterminate	0.0000	22.37%	59.74%	37%	Subclonal
MP11	ADAM21	p.Ser26Ser	synonymous_variant	14	70924294	C	T	3.83%	287	.	.	.		.	.	.			.	0.0000	17.05%	53.91%	31%	Subclonal
MP11	ATP10A	p.Asp1486Glu	missense_variant	15	25924530	G	T	16.54%	659	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0642	92.23%	100.00%	100%	Clonal
MP11	DISP2	p.Pro745His	missense_variant	15	40660547	C	A	22.88%	319	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6851	90.36%	100.00%	100%	Clonal
MP11	SLTM	p.Val558Gly	missense_variant	15	59185539	A	C	30.54%	704	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9257	97.20%	100.00%	100%	Clonal
MP11	RBPMS2	p.Ala181Gly	missense_variant	15	65040643	G	C	4.71%	170	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0004	16.73%	63.31%	33%	Subclonal

MP11	ACAN	p.Glu1997Glu	synonymous_variant	15	89401807	G	A	9.98%	611	.	.	.		.	.	.		TRUE	.	0.2116	62.87%	97.21%	81%	Subclonal			
MP11	ABHD2	p.Pro38Arg	missense_variant	15	89659671	C	G	8.40%	762	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0036	53.13%	85.02%	68%	Subclonal			
MP11	SV2B	p.Arg229Gly	missense_variant	15	91795651	C	G	5.89%	475	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	32.77%	67.33%	48%	Subclonal			
MP11	LRRK1	p.Ala1040Ala	synonymous_variant	15	101586342	G	A	5.25%	628	.	.	.		.	.	.		TRUE	.	0.0000	30.00%	58.44%	42%	Subclonal			
MP11	AXIN1	p.Ser359Arg	missense_variant	16	360012	G	C	18.15%	259	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.7690	77.17%	100.00%	100%	Clonal			
MP11	PRSS21	p.Asp182Glu	missense_variant	16	2868966	T	G	7.28%	206	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0099	31.23%	81.76%	52%	Subclonal			
MP11	CORO7	p.Thr207Ser	missense_variant	16	4438629	T	A	13.18%	296	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5787	66.95%	100.00%	93%	Clonal			
MP11	UBN1	p.Lys447Met	missense_variant	16	4920545	A	T	15.64%	569	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8342	84.08%	100.00%	100%	Clonal			
MP11	GTF3C1	p.Glu377Lys	missense_variant	16	27519974	C	T	24.64%	211	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9404	89.20%	100.00%	100%	Clonal			
MP11	QPRT	p.Leu6Gln	missense_variant	16	29705988	T	A	25.24%	733	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9652	96.58%	100.00%	100%	Clonal			
MP11	ABCC11	p.Arg135His	missense_variant	16	48258332	C	T	5.86%	614	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	34.03%	64.28%	47%	Subclonal			
MP11	THAP11	p.Glu272Val	missense_variant	16	67877272	A	T	3.55%	901	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	22.46%	44.68%	32%	Subclonal			
MP11	SLC12A4	p.Thr351Arg	missense_variant	16	67985812	G	C	3.02%	496	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	16.29%	44.28%	27%	Subclonal			
MP11	HYDIN	p.Tyr5036Asn	missense_variant	16	70841743	A	T	9.83%	814	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4858	71.36%	100.00%	89%	Subclonal			
MP11	CDH13	p.Val539Met	missense_variant	16	83712002	G	A	5.70%	579	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	36.66%	71.25%	52%	Subclonal			
MP11	SLC38A8	p.Val284Ile	missense_variant	16	84050848	C	T	13.02%	599	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8320	84.72%	100.00%	100%	Clonal			
MP11	TP53	p.Cys229fs	frameshift_variant	17	7577593	TAC	T	34.53%	472	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.2255	96.72%	100.00%	100%	Clonal			
MP11	MYH3	p.Cys793Arg	missense_variant	17	10543699	A	G	17.71%	830	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5875	91.73%	100.00%	100%	Clonal			
MP11	DNAH9	p.Ile2857Thr	missense_variant	17	11711198	T	C	5.24%	191	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0005	20.01%	65.85%	37%	Subclonal			
MP11	UTP6	p.Asp269His	missense_variant	17	30207754	C	G	3.71%	458	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	16.08%	41.03%	26%	Subclonal			
MP11	CCL2	p.Ile43Ile	synonymous_variant	17	32583293	C	A	4.11%	657	.	.	.		.	.	.		TRUE	.	0.0000	19.63%	41.41%	29%	Subclonal			
MP11	MMP28	p.Arg122Gly	missense_variant	17	34105907	G	C	4.38%	821	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	22.09%	42.08%	31%	Subclonal			
MP11	SOCS7	p.Gln271Glu	missense_variant	17	36517616	C	G	6.66%	646	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	34.79%	62.18%	47%	Subclonal			
MP11	STAC2	p.Gly335Gly	synonymous_variant	17	37369374	G	A	7.99%	413	.	.	.		.	.	.		TRUE	.	0.0009	40.25%	77.50%	57%	Subclonal			
MP11	STAC2	p.Gly335Ala	missense_variant	17	37369375	C	G	7.35%	408	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0002	36.37%	72.51%	52%	Subclonal			
MP11	KRTAP4-11	p.Arg51Arg	synonymous_variant	17	39274415	C	T	10.26%	234	.	.	.		.	.	.		TRUE	.	0.1792	48.89%	96.49%	73%	Subclonal			
MP11	KRTAP4-2	p.Val122Glu	missense_variant	17	39334052	A	T	9.16%	415	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0123	47.30%	86.56%	65%	Subclonal			
MP11	LEPREL4	p.Asp263His	missense_variant	17	39967115	C	G	4.36%	344	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.41%	49.59%	31%	Subclonal			
MP11	EME1	p.Ser411Thr	missense_variant	17	48456548	G	C	4.52%	775	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	25.94%	49.77%	37%	Subclonal			
MP11	MRC2	p.Asn69Ser	missense_variant	17	60741996	A	G	3.47%	864	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	21.71%	44.14%	32%	Subclonal			
MP11	SMURF2	p.Leu456Leu	synonymous_variant	17	62553789	G	C	4.06%	763	.	.	.		.	.	.		TRUE	.	0.0000	25.66%	51.39%	37%	Subclonal			
MP11	MFSD11	c.152+2T>C	splice_donor_variant	17	74735077	T	C	9.32%	783	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0005	52.49%	81.43%	66%	Subclonal			
MP11	TMC8	p.Leu170Ile	missense_variant	17	76128928	C	A	8.55%	503	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0010	44.94%	79.68%	61%	Subclonal			
MP11	PPP1R27	p.Val72Met	missense_variant	17	79792506	C	T	8.68%	668	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	40.73%	66.81%	53%	Subclonal			
MP11	WDR7	p.Thr1076Arg	missense_variant	18	54483298	C	G	5.86%	307	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	26.09%	63.81%	42%	Subclonal			
MP11	SALL3	p.Val1272Phe	missense_variant	18	76757233	G	T	17.88%	537	N	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Likely passenger	0.7486	88.76%	100.00%	100%	Clonal			
MP11	LRG1	p.Pro180Ala	missense_variant	19	4538458	G	C	35.98%	667	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8896	97.51%	100.00%	100%	Clonal			
MP11	SPC24	p.Arg28Pro	missense_variant	19	11266370	C	G	16.06%	523	N	.	Passenger		.	.	.			Likely passenger	0.7135	88.01%	100.00%	100%	Clonal			
MP11	RFX1	p.Gln263Leu	missense_variant	19	14090305	T	A	19.00%	221	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7328	83.85%	100.00%	100%	Clonal			
MP11	ZNF682	p.Asp8Asp	synonymous_variant	19	20135165	A	G	17.37%	501	.	.	.		.	.	.			.	0.2706	89.74%	100.00%	100%	Clonal			
MP11	ZNF536	p.Lys404Asn	missense_variant	19	30935681	G	T	3.91%	512	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.12%	47.67%	32%	Subclonal			
MP11	WDR87	p.Gln272Glu	missense_variant	19	38385529	G	C	14.88%	551	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8326	85.86%	100.00%	100%	Clonal			
MP11	CAPN12	p.Thr378Ser	missense_variant	19	39228025	G	C	15.21%	776	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7914	89.58%	100.00%	100%	Clonal			
MP11	FBXO27	p.Gln207Leu	missense_variant	19	39517598	T	A	6.96%	632	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	41.78%	74.01%	56%	Subclonal			
MP11	SPTBN4	p.Arg504Arg	synonymous_variant	19	41009884	C	A	12.30%	764	.	.	.		.	.	.			.	0.7404	79.39%	100.00%	99%	Clonal			
MP11	PHLDB3	p.Pro500Pro	synonymous_variant	19	43983731	T	G	15.79%	57	.	.	.		.	.	.			.	0.6226	52.97%	100.00%	100%	Clonal			
MP11	DMPK	p.Leu630Leu	synonymous_variant	19	46273824	C	T	22.91%	755	D	.	.		.	.	.	TRUE		.	0.9579	96.37%	100.00%	100%	Clonal			
MP11	PRR12	p.Glu1712Gln	missense_variant	19	50119113	G	C	4.46%	717	D	.	Passenger		.	.	.			Indeterminate	0.0000	25.22%	49.89%	36%	Subclonal			
MP11	PTOV1	p.Gln267Gln	synonymous_variant	19	50361036	G	A	11.59%	716	.	.	.		.	.	.			.	0.6190	74.81%	100.00%	94%	Clonal			
MP11	TBC1D17	p.Gly149Cys	missense_variant	19	50384650	G	T	9.57%	470	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1755	57.89%	96.60%	77%	Subclonal			
MP11	ZNF579	p.Ser187Ser	synonymous_variant	19	56090445	G	A	4.00%	200	.	.	.		.	.	.			.	0.0003	16.20%	61.67%	32%	Subclonal			
MP11	ZNF256	p.Ile339Ile	synonymous_variant	19	58453159	A	G	5.43%	571	.	.	.		.	.	.			.	0.0000	30.66%	60.96%	44%	Subclonal			
MP11	ZNF837	p.Arg257Gln	missense_variant	19	58879930	C	T	3.48%	574	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	17.88%	42.53%	28%	Subclonal			
MP11	ZNF132	p.Lys218Lys	synonymous_variant	19	58946157	C	T	2.59%	771	.	.	.		.	.	.			.	0.0000	13.16%	31.64%	21%	Subclonal			
MP11	PDYN	p.Arg212Gln	missense_variant	20	1961099	C	T	10.59%	793	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0220	60.68%	90.87%	75%	Subclonal			
MP11	LZTS3	p.Asp493His	missense_variant	20	3145507	C	G	7.25%	262	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0030	32.83%	77.71%	51%	Subclonal			
MP11	LZTS3	p.Ser492Thr	missense_variant	20	3145509	C	G	7.25%	262	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0030	32.83%	77.71%	51%	Subclonal			
MP11	SLX4IP	p.Gln379Glu	missense_variant	20	10603935	C	G	4.80%	646	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	23.60%	47.19%	34%	Subclonal			
MP11	SEL1L2	p.Ala519Pro	missense_variant	20	13830890	C	G	4.24%	495	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.31%	44.83%	30%	Subclonal			
MP11	ITCH	p.Asp774Gly	missense_variant	20	33077175	A	G	15.34%	515	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8125	82.13%	100.00%	100%	Clonal			
MP11	ADNP	c.-5-1G>C	splice_acceptor_variant	20	49520539	C	G	3.29%	700	.	.	.		.	.	true			Likely pathogenic	0.0000	19.50%	43.86%	30%	Subclonal			
MP11	LAMA5	p.Arg2258Pro	missense_variant	20	60894838	C	G	5.40%	278	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0051	29.57%	78.45%	49%	Subclonal			
MP11	ZBTB46	p.Leu353Leu	synonymous_variant	20	62407194	G	T	4.67%	493	.	.	.		.	.	.			.	0.0000	28.01%	62.22%	42%	Subclonal			
MP11	MYT1	p.Thr119Thr	synonymous_variant	20	62837113	G	C	5.77%	797	.	.	.		.	.	.			.	0.0000	39.09%	68.68%	52%	Subclonal			
MP11	ADAMTS5	p.Ala202Gly	missense_variant	21	28338106	G	C	4.84%	620	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	30.51%	61.51%	44%	Subclonal			
MP11	CCT8	p.Asp548Asn	missense_variant	21	30428801	C	T	3.29%	669	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.35%	44.29%	30%	Subclonal			
MP11	KRTAP10-10	p.Met6Ile	missense_variant	21	46057352	G	T	15.77%	336	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6442	72.11%	100.00%	96%	Clonal			
MP11	TRMT2A	p.Ala553Pro	missense_variant	22	20100307	C	G	6.59%	455	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0004	37.20%	74.35%	53%	Subclonal			
MP11	KREMEN1	p.Pro32Ser	missense_variant	22	29469212	C	T	23.81%	42	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8325	62.44%	100.00%	100%	Clonal			
MP11	GAS2L1	p.Val158Met	missense_variant	22	29704567	G	A	7.72%	661	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0009	47.35%	80.38%	62%	Subclonal			
MP11	PISD	p.Leu217Leu	synonymous_variant	22	32017073	G	C	12.12%	520	.	.	.		.	.	.			.	0.6830	74.65%	100.00%	98%	Clonal			
MP11	APOBEC3B	p.Leu216Leu	synonymous_variant	22	39385538	T	C	3.09%	517	.	.	.		.	.	.			.	0.0000	15.05%	39.67%	25%	Subclonal			
MP11	APOBEC3F	p.Gly141Gly	synonymous_variant	22	39441197	G	A	3.14%	350	.	.	.		.	.	.			.	0.0000	13.87%	44.28%	25%	Subclonal			
MP11	MCHR1	p.Gly176Gly	synonymous_variant	22	41077191	G	C	3.26%	859	.	.	.		.	.	.			.	0.0000	15.53%	32.62%	23%	Subclonal			
MP11	MBTPS2	p.Thr97Met	missense_variant	X	21863354	C	T	3.73%	750	D	.	Passenger		.	.	.			Indeterminate	0.0000	20.49%	42.71%	30%	Subclonal			
MP11	CHDC2	p.Arg424Gly	missense_variant	X	36162687	A	G	11.51%	617	N	.	Passenger		.	.	.			Likely passenger	0.5975	72.96%	100.00%	93%	Clonal			
MP11	USP9X	p.Gly1923Ala	missense_variant	X	41075588	G	C	4.57%	831	D	PASSENGER/OTHER	Passenger		.	true	.			Likely pathogenic	0.0000	26.58%	49.76%	37%	Subclonal			
MP11	PPP1R3F	p.Arg498Cys	missense_variant	X	49142644	C	T	15.87%	378	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5125	86.62%	100.00%	100%	Clonal			
MP11	MAGED1	p.Asn631Ser	missense_variant	X	51641275	A	G	5.88%	680	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	39.06%	71.39%	53%	Subclonal			
MP11	RIBC1	p.Gln43Arg	missense_variant	X	53454961	A	G	4.46%	650	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	27.94%	57.04%	41%	Subclonal			
MP11	IL2RG	p.Asn254Ser	missense_variant	X	70328542	T	C	3.28%	580	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	14.44%	35.36%	23%	Subclonal			
MP11	KCNE1L	p.Cys72Ser	missense_variant	X	108868036	A	T	10.92%	586	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0993	60.72%	94.96%	77%	Subclonal			
MP11	ZFP92	p.Thr8Thr	synonymous_variant	X	152683804	G	C	17.93%	368	.	.	.		.	.	.		TRUE	.	0.3972	87.81%	100.00%	100%	Clonal			
MP11	F8	p.Leu1201Leu	synonymous_variant	X	154158462	T	C	4.05%	666	.	.	.		.	.	.			.	0.0000	25.01%	52.52%	37%	Subclonal			
MP11	F8	p.Leu548Val	missense_variant	X	154185342	G	C	4.49%	758	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.86%	55.86%	41%	Subclonal			
MP15	CNKSR1	p.Leu16Leu	synonymous_variant	1	26504086	G	A	5.73%	558	.	.	.		.	.	.		TRUE	.	0.0000	23.36%	46.05%	33%	Subclonal			
MP15	PCSK9	p.Gly263Ser	missense_variant	1	55518452	G	A	15.28%	144	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8542	71.44%	100.00%	100%	Clonal			
MP15	DNAJC6	p.Ter971Tyrext*?	stop_lost	1	65878708	A	T	27.07%	569	N	.	.		.	.	.			Indeterminate	0.9718	96.14%	100.00%	100%	Clonal			
MP15	ELTD1	p.Ser262Ala	missense_variant	1	79402073	A	C	7.87%	356	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0342	42.60%	86.29%	62%	Subclonal			
MP15	GLMN	p.Met372Ile	missense_variant	1	92732281	C	T	24.24%	66	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9399	72.15%	100.00%	100%	Clonal			
MP15	ARHGAP29	p.Tyr868His	missense_variant	1	94643602	A	G	10.78%	640	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8009	73.95%	100.00%	95%	Clonal			
MP15	HIST2H2AB	p.Ser17Trp	missense_variant	1	149859417	G	C	22.96%	832	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8996	96.97%	100.00%	100%	Clonal			
MP15	TCHH	p.Glu1568*	stop_gained	1	152080991	C	A	5.08%	846	D	.	.		.	.	.			Indeterminate	0.0000	36.84%	66.13%	50%	Subclonal			
MP15	TCHH	p.Glu1561Lys	missense_variant	1	152081012	C	T	5.11%	841	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	37.07%	66.53%	50%	Subclonal			
MP15	SLC9C2	p.Leu60fs	frameshift_variant	1	173569300	GAGAA	G	20.54%	667	A	.	.		.	.	.			Indeterminate	0.9784	95.37%	100.00%	100%	Clonal			
MP15	DHX9	p.Tyr554*	stop_gained	1	182841576	T	G	24.83%	439	A	.	.		.	.	.			Indeterminate	0.7284	95.08%	100.00%	100%	Clonal			
MP15	KIF14	p.Cys1312Arg	missense_variant	1	200534334	A	G	18.05%	615	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9425	93.72%	100.00%	100%	Clonal			
MP15	CACNA1S	p.Tyr299*	stop_gained	1	201058389	G	C	6.82%	674	A	.	.		.	.	.			Indeterminate	0.0311	50.21%	87.60%	67%	Subclonal			
MP15	LEMD1	p.Ala118Thr	missense_variant	1	205350980	C	T	24.93%	369	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7730	94.22%	100.00%	100%	Clonal			
MP15	HNRNPU	p.Lys489Glu	missense_variant	1	245021342	T	C	13.85%	491	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9507	90.17%	100.00%	100%	Clonal			
MP15	PXDN	p.Asp1085Tyr	missense_variant	2	1652299	C	A	10.41%	874	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7484	74.33%	100.00%	92%	Clonal			
MP15	NTSR2	p.Leu311Val	missense_variant	2	11800227	G	C	19.72%	776	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8863	95.24%	100.00%	100%	Clonal			
MP15	KCNK3	p.Asn267Asn	synonymous_variant	2	26951052	C	T	5.42%	683	.	.	.		.	.	.			.	0.0000	34.45%	64.67%	48%	Subclonal			
MP15	TET3	p.Glu1599Glu	synonymous_variant	2	74328712	G	A	19.81%	535	.	.	.		.	.	.			.	0.9753	94.05%	100.00%	100%	Clonal			
MP15	MAP3K19	p.Ala1175Ala	synonymous_variant	2	135738786	A	T	11.46%	672	.	.	.		.	.	.		TRUE	.	0.0009	53.52%	81.66%	67%	Subclonal			
MP15	LRP2	p.Leu1439Leu	synonymous_variant	2	170094790	A	T	39.29%	196	.	.	.		.	.	.		TRUE	.	0.9251	93.38%	100.00%	100%	Clonal			
MP15	TTN	p.Thr18843Arg	missense_variant	2	179463992	G	C	27.80%	241	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9581	91.94%	100.00%	100%	Clonal			
MP15	AAMP	p.Arg391His	missense_variant	2	219129800	C	T	33.08%	399	N	CANCER	Passenger		.	.	.			Likely passenger	0.2974	96.11%	100.00%	100%	Clonal			
MP15	ZFAND2B	p.Leu210Leu	synonymous_variant	2	220073333	C	T	9.98%	661	.	.	.		.	.	.			.	0.2289	61.52%	95.50%	78%	Subclonal			
MP15	KCNJ13	p.His297fs	frameshift_variant	2	233633081	AGATGCAAAACAGT	A	19.29%	1161	.	.	.		.	.	.			Indeterminate	0.0002	96.03%	100.00%	100%	Clonal			
MP15	DNAH1	p.Ser1490Leu	missense_variant	3	52393993	C	T	9.96%	251	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0153	39.42%	82.69%	58%	Subclonal			
MP15	DNAH1	p.His3044Tyr	missense_variant	3	52422309	C	T	12.73%	715	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0211	60.60%	89.05%	74%	Subclonal			
MP15	VGLL3	p.Pro37Arg	missense_variant	3	87039784	G	C	10.76%	158	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8042	62.66%	100.00%	100%	Clonal			
MP15	COL6A6	c.5092-1G>C	splice_acceptor_variant	3	130360495	G	C	48.28%	58	D	.	.		.	.	.			Indeterminate	0.3116	86.66%	100.00%	100%	Clonal			
MP15	EPHB1	p.Gln715His	missense_variant	3	134920330	G	C	17.53%	713	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8914	94.17%	100.00%	100%	Clonal			
MP15	DZIP1L	p.Asp134Asp	synonymous_variant	3	137822412	G	A	26.17%	703	.	.	.		.	.	.			.	0.1508	97.07%	100.00%	100%	Clonal			
MP15	ABCF3	p.Ile298Leu	missense_variant	3	183906604	A	C	6.80%	853	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7724	71.16%	100.00%	94%	Clonal			
MP15	OPA1	p.Gln352Gln	synonymous_variant	3	193355761	G	A	4.69%	512	.	.	.		.	.	.	TRUE		.	0.1272	43.39%	92.08%	65%	Subclonal			
MP15	ATP13A3	p.Arg634His	missense_variant	3	194158138	C	T	60.86%	815	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1220	99.02%	100.00%	100%	Clonal			
MP15	LRRC66	p.Met591Ile	missense_variant	4	52861415	C	A	21.79%	615	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6404	91.57%	100.00%	100%	Clonal			
MP15	KDR	p.Asp1052Asn	missense_variant	4	55956161	C	T	13.60%	375	D	CANCER	Driver		true	.	.		TRUE	Likely pathogenic	0.3536	60.60%	96.91%	79%	Subclonal			
MP15	SHROOM3	p.Gln1919Arg	missense_variant	4	77700095	A	G	29.97%	377	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8545	95.21%	100.00%	100%	Clonal			
MP15	UNC5C	p.Cys594Phe	missense_variant	4	96127900	C	A	9.68%	248	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1410	44.53%	92.55%	66%	Subclonal			
MP15	SGMS2	p.Leu149Leu	synonymous_variant	4	108817154	C	T	11.81%	237	.	.	.		.	.	.		TRUE	.	0.5295	55.68%	98.28%	81%	Clonal			
MP15	SCOC	p.Val5Ile	missense_variant	4	141294703	G	A	19.91%	633	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.1740	92.15%	100.00%	100%	Clonal			
MP15	PRMT9	p.Glu433Lys	missense_variant	4	148578976	C	T	9.33%	343	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0367	45.21%	87.07%	64%	Subclonal			
MP15	FAT1	p.Ser1566Phe	missense_variant	4	187549421	G	A	5.21%	595	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0000	28.45%	56.69%	41%	Subclonal			
MP15	ICE1	p.Ser422*	stop_gained	5	5460712	C	G	30.75%	517	A	.	.		.	.	.			Indeterminate	0.5641	96.52%	100.00%	100%	Clonal			
MP15	MTMR12	p.Val203Ile	missense_variant	5	32263325	C	T	11.03%	435	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6292	64.87%	98.85%	86%	Clonal			
MP15	SLC45A2	p.Cys428_Leu430del	disruptive_inframe_deletion	5	33947344	AACAGGCTGC	A	20.94%	702	D	.	.	Deleterious	.	.	.			Indeterminate	0.4978	94.79%	100.00%	100%	Clonal			
MP15	PIK3R1	c.1746-2A>C	splice_acceptor_variant	5	67591246	A	C	14.80%	500	D	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.5779	68.95%	98.59%	86%	Clonal			
MP15	MEGF10	p.Cys615Tyr	missense_variant	5	126770382	G	A	29.11%	749	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8278	97.27%	100.00%	100%	Clonal			
MP15	PCDHAC1	p.Arg111Arg	synonymous_variant	5	140306810	G	T	4.09%	783	.	.	.		.	.	.			.	0.0000	28.14%	55.68%	40%	Subclonal			
MP15	PCDHB6	p.Leu214Leu	synonymous_variant	5	140530480	G	A	13.04%	790	.	.	.		.	.	.			.	0.7874	89.26%	100.00%	100%	Clonal			
MP15	HDAC3	p.Ala372Ala	synonymous_variant	5	141004876	T	A	27.71%	462	.	.	.		.	.	.			.	0.6141	95.80%	100.00%	100%	Clonal			
MP15	GABRG2	p.Gln438Glu	missense_variant	5	161580138	C	G	10.80%	213	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0798	42.14%	89.70%	63%	Subclonal			
MP15	TRIM10	p.Val178Met	missense_variant	6	30126400	C	T	34.72%	553	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7435	97.34%	100.00%	100%	Clonal			
MP15	SCUBE3	p.Glu662Lys	missense_variant	6	35211445	G	A	6.71%	641	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0014	43.85%	78.23%	59%	Subclonal			
MP15	BTBD9	p.Ala253Ala	synonymous_variant	6	38560407	G	A	3.46%	433	.	.	.		.	.	.			.	0.0000	18.22%	49.28%	31%	Subclonal			
MP15	DAAM2	p.Asp659Val	missense_variant	6	39855284	A	T	9.32%	740	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4216	65.04%	97.62%	82%	Subclonal			
MP15	TDRD6	p.Glu1542Gln	missense_variant	6	46660489	G	C	31.98%	763	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6520	97.92%	100.00%	100%	Clonal			
MP15	DOPEY1	p.Val1905Glu	missense_variant	6	83858486	T	A	45.83%	72	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7930	87.08%	100.00%	100%	Clonal			
MP15	BEND3	p.Gly637Val	missense_variant	6	107390485	C	A	7.06%	836	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2029	59.17%	94.98%	76%	Subclonal			
MP15	PDSS2	p.Leu159Leu	synonymous_variant	6	107595386	G	T	6.60%	515	.	.	.		.	.	true			.	0.2036	51.08%	94.60%	71%	Subclonal			
MP15	TBC1D32	c.1231+1G>A	splice_donor_variant	6	121615715	C	T	4.92%	366	D	.	.		.	.	.			Indeterminate	0.0198	33.54%	81.91%	53%	Subclonal			
MP15	BCLAF1	p.Arg69Pro	missense_variant	6	136599813	C	G	9.31%	838	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.8478	86.61%	100.00%	100%	Clonal			
MP15	AP5Z1	p.His105Asp	missense_variant	7	4821332	C	G	10.44%	833	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8813	80.14%	100.00%	100%	Clonal			
MP15	CROT	p.Trp142_Pro143delinsCys	disruptive_inframe_deletion	7	86990806	GGCC	G	24.15%	907	P	.	.	Deleterious	.	.	.			Indeterminate	0.9754	96.99%	100.00%	100%	Clonal			
MP15	RELN	p.Cys2491Phe	missense_variant	7	103163856	C	A	25.17%	147	D	PASSENGER/OTHER	Driver		.	.	.	TRUE		Likely pathogenic	0.9618	85.55%	100.00%	100%	Clonal			
MP15	CNTNAP2	c.3715+1G>A	splice_donor_variant	7	148080981	G	A	27.17%	92	D	.	.		.	.	.			Indeterminate	0.9488	81.11%	100.00%	100%	Clonal			
MP15	PCM1	p.Glu1579Asp	missense_variant	8	17851038	A	C	7.65%	523	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.0030	43.92%	79.75%	60%	Subclonal			
MP15	BMP1	p.Leu505Leu	synonymous_variant	8	22052308	C	G	27.13%	682	.	.	.		.	.	.			.	0.9715	96.74%	100.00%	100%	Clonal			
MP15	CHD7	p.Gln555*	stop_gained	8	61655654	C	T	27.44%	164	A	.	.		.	.	.	TRUE		Likely pathogenic	0.8613	85.86%	100.00%	100%	Clonal			
MP15	CLVS1	c.455+1G>A	splice_donor_variant	8	62212842	G	A	26.55%	113	D	.	.		.	.	.			Indeterminate	0.8790	80.13%	100.00%	100%	Clonal			
MP15	PKHD1L1	p.Asn2948Ser	missense_variant	8	110488822	A	G	4.91%	754	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5468	59.26%	98.47%	83%	Clonal			
MP15	PLEC	p.Ser3350Thr	missense_variant	8	144994352	A	T	41.60%	815	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2833	98.54%	100.00%	100%	Clonal			
MP15	FOCAD	p.Arg499Thr	missense_variant	9	20819835	G	C	8.70%	161	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6965	52.42%	100.00%	94%	Clonal			
MP15	AGTPBP1	p.Thr571Thr	synonymous_variant	9	88248035	A	G	32.59%	316	.	.	.		.	.	.			.	0.4930	95.08%	100.00%	100%	Clonal			
MP15	MURC	p.Leu171Leu	synonymous_variant	9	103348151	G	A	52.12%	424	.	.	.		.	.	.		TRUE	.	0.0375	98.02%	100.00%	100%	Clonal			
MP15	SPTAN1	p.Leu552Leu	synonymous_variant	9	131344976	T	C	8.08%	396	.	.	.		.	.	.		TRUE	.	0.0012	39.05%	75.91%	55%	Subclonal			
MP15	PRKCQ	p.Tyr545Cys	missense_variant	10	6498649	T	C	3.33%	150	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0001	9.53%	51.12%	23%	Subclonal			
MP15	ZNF438	p.Arg617Gly	missense_variant	10	31137485	G	C	5.29%	208	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0003	20.01%	62.49%	36%	Subclonal			
MP15	CCAR1	p.Gln97His	missense_variant	10	70497646	G	C	6.91%	463	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0174	43.16%	84.06%	61%	Subclonal			
MP15	COL13A1	p.Leu75Gln	missense_variant	10	71562403	T	A	22.83%	530	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9776	94.96%	100.00%	100%	Clonal			
MP15	LCOR	p.Leu33Arg	missense_variant	10	98708912	T	G	13.43%	603	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.7466	73.45%	100.00%	92%	Clonal			
MP15	PDCD11	p.Glu788Asp	missense_variant	10	105181191	G	C	49.28%	483	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1824	98.05%	100.00%	100%	Clonal			
MP15	MUC6	p.Phe1843Ser	missense_variant	11	1017273	A	G	5.71%	245	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0033	26.51%	72.78%	45%	Subclonal			
MP15	LRRC55	p.Arg88Gly	missense_variant	11	56949629	C	G	8.11%	826	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0005	49.94%	79.17%	64%	Subclonal			
MP15	CD6	p.Gly219Gly	synonymous_variant	11	60776193	C	T	31.30%	837	.	.	.		.	.	.			.	0.0504	97.92%	100.00%	100%	Clonal			
MP15	SLC22A11	p.Phe511Val	missense_variant	11	64337272	T	G	28.13%	576	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9473	96.37%	100.00%	100%	Clonal			
MP15	RASGRP2	p.Arg290Arg	synonymous_variant	11	64504450	C	T	4.72%	805	.	.	.		.	.	.			.	0.0000	26.58%	49.74%	37%	Subclonal			
MP15	MAP4K2	p.Arg677Cys	missense_variant	11	64559444	G	A	15.84%	562	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8836	87.46%	100.00%	100%	Clonal			
MP15	CLCF1	p.Leu133Leu	synonymous_variant	11	67132888	G	A	7.32%	287	.	.	.		.	.	.			.	0.0300	37.44%	84.64%	57%	Subclonal			
MP15	FAT3	p.Ile2233Thr	missense_variant	11	92532877	T	C	27.40%	551	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9667	96.12%	100.00%	100%	Clonal			
MP15	ARHGAP20	c.1416-1G>T	splice_acceptor_variant	11	110454462	C	A	11.52%	191	D	.	.		.	.	.			Indeterminate	0.6937	57.85%	100.00%	90%	Clonal			
MP15	FDXACB1	p.Gln601His	missense_variant	11	111745718	C	G	6.38%	752	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	37.47%	64.97%	50%	Subclonal			
MP15	SIK3	p.Met1258Ile	missense_variant	11	116718226	C	A	12.11%	322	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7707	67.62%	100.00%	95%	Clonal			
MP15	COPS7A	p.Glu4Ala	missense_variant	12	6833833	A	C	14.60%	226	D	.	Passenger		.	.	.			Indeterminate	0.8595	73.26%	100.00%	100%	Clonal			
MP15	TAS2R8	p.Val52Phe	missense_variant	12	10959426	C	A	29.40%	398	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8978	95.29%	100.00%	100%	Clonal			
MP15	OR10A7	p.Ile289Val	missense_variant	12	55615673	A	G	29.96%	691	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6301	97.21%	100.00%	100%	Clonal			
MP15	IFT81	p.Thr25Thr	synonymous_variant	12	110565260	G	A	7.18%	348	.	.	.		.	.	.			.	0.0099	38.05%	80.78%	56%	Subclonal			
MP15	LOC100128554	n.498-26_498-2delGGTCTCACAGGAGTCTGCACCCGCA	splice_acceptor_variant	12	126942576	GGGTCTCACAGGAGTCTGCACCCGCA	G	17.15%	344	.	.	.		.	.	.		TRUE	Likely pathogenic	0.8471	75.48%	100.00%	100%	Clonal			
MP15	VWA8	p.Asp1831His	missense_variant	13	42144722	C	G	3.16%	507	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	10.94%	29.01%	18%	Subclonal			
MP15	RB1	p.Glu837*	stop_gained	13	49047515	G	T	34.18%	196	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9733	91.73%	100.00%	100%	Clonal			
MP15	POTEG	p.Lys26Lys	synonymous_variant	14	19553494	G	A	11.90%	42	.	.	.		.	.	.			.	0.5707	31.98%	98.50%	81%	Clonal			
MP15	AP5M1	p.Trp198*	stop_gained	14	57741481	G	A	35.67%	541	A	.	.		.	.	.			Indeterminate	0.6834	97.38%	100.00%	100%	Clonal			
MP15	MAP3K9	p.Met307Lys	missense_variant	14	71227800	A	T	9.67%	362	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0524	47.58%	88.80%	66%	Subclonal			
MP15	HSP90AA1	p.Gln526*	stop_gained	14	102550258	G	A	58.82%	187	A	.	.		true	.	.		TRUE	Likely pathogenic	0.2411	96.25%	100.00%	100%	Clonal			
MP15	PAK6	p.Asp544His	missense_variant	15	40565764	G	C	7.69%	767	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0002	46.57%	76.22%	60%	Subclonal			
MP15	GANC	p.Leu272Pro	missense_variant	15	42602573	T	C	12.40%	379	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8038	71.03%	100.00%	97%	Clonal			
MP15	CHRNA3	p.Met455Ile	missense_variant	15	78893619	C	G	12.89%	543	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8597	77.35%	100.00%	100%	Clonal			
MP15	CPEB1	c.191-1G>T	splice_acceptor_variant	15	83240283	C	A	9.34%	514	D	.	.		.	.	.			Indeterminate	0.1403	55.22%	93.38%	73%	Subclonal			
MP15	PRR35	p.Pro262Ala	missense_variant	16	614078	C	G	13.82%	463	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8984	83.61%	100.00%	100%	Clonal			
MP15	RNPS1	p.Asp33Asn	missense_variant	16	2314307	C	T	6.74%	727	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0006	44.89%	77.22%	60%	Subclonal			
MP15	PRM1	p.Arg41Arg	synonymous_variant	16	11374882	G	A	9.15%	831	.	.	.		true	.	.	TRUE		.	0.0183	57.21%	87.90%	72%	Subclonal			
MP15	BFAR	p.Pro265fs	frameshift_variant	16	14755759	CA	C	27.54%	276	A	.	.		.	.	.			Indeterminate	0.9621	92.73%	100.00%	100%	Clonal			
MP15	TMC5	p.Leu762Leu	synonymous_variant	16	19492710	G	T	7.74%	439	.	.	.		.	.	.			.	0.0106	43.35%	82.66%	61%	Subclonal			
MP15	GGA2	p.Ala537Ala	synonymous_variant	16	23481326	A	G	26.58%	395	.	.	.		.	.	.			.	0.9733	94.40%	100.00%	100%	Clonal			
MP15	TP53	p.Gly112fs	frameshift_variant	17	7579351	GC	G	43.54%	735	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.0006	98.19%	100.00%	100%	Clonal			
MP15	MPO	p.Ala585Ala	synonymous_variant	17	56350146	A	T	48.50%	468	.	.	.		.	.	true			.	0.2367	98.05%	100.00%	100%	Clonal			
MP15	TRIM47	p.Gln383His	missense_variant	17	73872034	C	G	4.60%	805	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	29.14%	54.89%	41%	Subclonal			
MP15	RPTOR	p.Arg485Gly	missense_variant	17	78831644	C	G	7.60%	684	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0177	51.14%	86.25%	67%	Subclonal			
MP15	MRO	p.Val48Ile	missense_variant	18	48333220	C	T	35.73%	361	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5628	96.02%	100.00%	100%	Clonal			
MP15	ATP9B	p.Val987Met	missense_variant	18	77119409	G	A	2.99%	501	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.84%	37.73%	23%	Subclonal			
MP15	PRSS57	p.Ser218Cys	missense_variant	19	685915	G	C	4.62%	325	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	21.65%	58.03%	36%	Subclonal			
MP15	ABCA7	p.Thr748Pro	missense_variant	19	1047626	A	C	25.92%	382	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9755	94.04%	100.00%	100%	Clonal			
MP15	PTPRS	p.Glu415Asp	missense_variant	19	5244237	C	G	11.05%	851	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5504	70.65%	98.48%	86%	Clonal			
MP15	SAMD1	p.Thr275Thr	synonymous_variant	19	14199986	G	A	12.72%	723	.	.	.		.	.	.			.	0.8652	79.33%	100.00%	100%	Clonal			
MP15	RYR1	c.6664-1G>C	splice_acceptor_variant	19	38987048	G	C	9.70%	567	D	.	.		.	.	.	TRUE		Likely pathogenic	0.5969	65.53%	98.70%	86%	Clonal			
MP15	HNRNPL	p.Asp390His	missense_variant	19	39330801	C	G	2.69%	483	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.51%	39.68%	24%	Subclonal			
MP15	EXOSC5	p.Phe223fs	frameshift_variant	19	41892579	A	AACGGAAG	19.54%	1274	D	.	.		.	.	.			Indeterminate	0.6555	97.00%	100.00%	100%	Clonal			
MP15	ATP1A3	p.Pro532Thr	missense_variant	19	42482833	G	T	3.39%	709	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.71%	43.57%	30%	Subclonal			
MP15	GSK3A	p.Ala51Pro	missense_variant	19	42746467	C	G	22.94%	109	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9521	80.37%	100.00%	100%	Clonal			
MP15	PPP2R1A	p.Ala242Ala	synonymous_variant	19	52716282	C	T	34.60%	841	.	.	.		true	true	true		TRUE	.	0.9867	97.92%	100.00%	100%	Clonal			
MP15	ZNF578	p.Leu75Phe	missense_variant	19	53013859	G	C	15.38%	52	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6435	42.33%	98.89%	90%	Clonal			
MP15	LILRB3	p.Ser591Pro	missense_variant	19	54721090	A	G	4.90%	143	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0141	18.50%	75.49%	38%	Subclonal			
MP15	ZNF544	p.Gly582Val	missense_variant	19	58773717	G	T	9.20%	402	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1867	52.35%	94.27%	72%	Subclonal			
MP15	DEFB126	p.Ala62Ala	synonymous_variant	20	126183	T	C	19.10%	754	.	.	.		.	.	.			.	0.3561	92.33%	100.00%	100%	Clonal			
MP15	REM1	p.Leu108Pro	missense_variant	20	30064571	T	C	13.07%	199	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7978	65.57%	100.00%	100%	Clonal			
MP15	HCK	p.Ser509Thr	missense_variant	20	30689267	G	C	10.86%	746	D	CANCER	Driver		.	.	.			Likely pathogenic	0.5095	68.40%	98.23%	85%	Clonal			
MP15	ACOT8	p.Glu276Lys	missense_variant	20	44472181	C	T	27.55%	766	D	.	Passenger		.	.	.			Indeterminate	0.9620	97.13%	100.00%	100%	Clonal			
MP15	KCNQ2	p.Val733Val	synonymous_variant	20	62038417	C	T	28.77%	219	.	.	.		.	.	.	TRUE		.	0.9431	91.63%	100.00%	100%	Clonal			
MP15	COL6A1	p.His181Gln	missense_variant	21	47406554	C	G	31.83%	487	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.2784	96.52%	100.00%	100%	Clonal			
MP15	TANGO2	p.Asp79Glu	missense_variant	22	20030935	C	G	4.09%	635	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	21.52%	45.95%	32%	Subclonal			
MP15	SCARF2	p.Ala298Ala	synonymous_variant	22	20785156	G	A	12.66%	561	.	.	.		.	.	.			.	0.8460	76.54%	100.00%	99%	Clonal			
MP15	SMTN	p.Gly863Ala	missense_variant	22	31494826	G	C	5.33%	319	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0189	32.58%	81.46%	52%	Subclonal			
MP15	XPNPEP3	p.Gly92Gly	synonymous_variant	22	41277868	G	C	8.83%	566	.	.	.		.	.	.			.	0.6379	65.36%	98.89%	87%	Clonal			
MP15	XPNPEP3	p.Ser159Asn	missense_variant	22	41278068	G	A	7.12%	829	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0318	54.16%	88.51%	70%	Subclonal			
MP15	TUBGCP6	p.Ala680Ala	synonymous_variant	22	50662965	T	C	24.11%	788	.	.	.		.	.	.			.	0.9747	96.42%	100.00%	100%	Clonal			
MP15	CDKL5	p.His32Pro	missense_variant	X	18528970	A	C	32.52%	489	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.7011	96.88%	100.00%	100%	Clonal			
MP15	PHEX	p.Phe351Ile	missense_variant	X	22117241	T	A	3.60%	806	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	21.75%	44.73%	32%	Subclonal			
MP15	KLHL15	p.Gly418Ala	missense_variant	X	24006600	C	G	32.11%	766	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6719	97.96%	100.00%	100%	Clonal			
MP15	HDAC6	p.Thr1016Asn	missense_variant	X	48681856	C	A	2.58%	854	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	12.91%	29.81%	20%	Subclonal			
MP15	HDAC6	p.Thr1016Thr	synonymous_variant	X	48681857	C	G	2.47%	850	.	.	.		.	.	.			.	0.0000	12.21%	28.85%	19%	Subclonal			
MP15	TAF1	p.Leu784Phe	missense_variant	X	70607176	G	C	7.50%	560	D	CANCER	Passenger		.	true	.			Likely pathogenic	0.0012	43.35%	77.69%	59%	Subclonal			
MP15	LPAR4	p.Thr79Ala	missense_variant	X	78010601	A	G	7.35%	721	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	43.88%	73.83%	58%	Subclonal			

MP15	TGIF2LX	p.His134His	synonymous_variant	X	89177486	C	T	31.30%	460	.	.	.		.	.	.	.	.			.	0.4804	96.25%	100.00%	100%	Clonal
MP15	AMOT	p.Gln436Gln	synonymous_variant	X	112058670	C	T	8.77%	718	.	.	.		.	.	.	.	.			.	0.0126	53.68%	86.13%	69%	Subclonal
MP15	MAMLD1	p.Ile161fs	frameshift_variant	X	149638397	CA	C	31.27%	614	A	.	.		.	.	.	.	.			Indeterminate	0.2369	97.14%	100.00%	100%	Clonal
MP17	CASZ1	p.Arg1335Arg	synonymous_variant	1	10703232	G	A	33.92%	743	.	.	.		.	.	.	.	.			.	0.3298	94.77%	100.00%	100%	Clonal
MP17	MRPS15	p.Pro192Arg	missense_variant	1	36921849	G	C	11.79%	653	D	.	Passenger		.	.	.	.	.			Indeterminate	0.0000	33.35%	50.96%	42%	Subclonal
MP17	C1orf177	p.Val268Val	synonymous_variant	1	55279528	A	G	3.20%	281	.	.	.		.	.	.	.	.			.	0.0000	5.53%	20.73%	11%	Subclonal
MP17	HMCN1	p.Thr5501Ile	missense_variant	1	186157102	C	T	29.45%	849	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9152	90.45%	100.00%	100%	Clonal
MP17	PRKD3	p.Glu703*	stop_gained	2	37486764	C	A	3.86%	726	A	.	.		.	.	.	.	.			Indeterminate	0.0000	9.05%	19.09%	14%	Subclonal
MP17	PRKCE	p.Val73fs	frameshift_variant	2	45879452	CGATGTGTGCAACGGACGCAA	C	12.76%	854	A	.	.		.	.	.	.	.			Indeterminate	0.0000	37.43%	53.41%	45%	Subclonal
MP17	SLC1A4	p.Val282Leu	missense_variant	2	65243617	G	T	17.81%	539	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	52.11%	75.02%	63%	Subclonal
MP17	ST6GAL2	p.Pro164Pro	synonymous_variant	2	107459942	C	T	35.73%	764	.	.	.		.	.	.	.	.			.	0.0057	95.86%	100.00%	100%	Clonal
MP17	NEB	p.Ile8053Phe	missense_variant	2	152355874	T	A	5.29%	397	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	11.92%	27.76%	19%	Subclonal
MP17	PIK3CA	p.His1047Arg	missense_variant	3	178952085	A	G	29.37%	790	D	CANCER	Driver		true	true	true	true	true			Likely pathogenic	0.9094	89.94%	100.00%	100%	Clonal
MP17	RBM47	p.Glu200Glu	synonymous_variant	4	40440311	C	T	27.95%	891	.	.	.		.	.	.	.	.			.	0.8560	87.48%	100.00%	99%	Clonal
MP17	ZGRF1	p.Leu1308Leu	synonymous_variant	4	113506876	G	A	9.86%	213	.	.	.		.	.	.	.	.			.	0.0000	22.77%	51.40%	35%	Subclonal
MP17	FAT4	p.Ile1219Ile	synonymous_variant	4	126241223	A	T	30.74%	823	.	.	.		.	.	.	.	.			.	0.9271	92.29%	100.00%	100%	Clonal
MP17	FAT4	p.Asp4023Asn	missense_variant	4	126389828	G	A	26.28%	799	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6438	82.16%	100.00%	93%	Clonal
MP17	PCDHB2	p.Gln496Gln	synonymous_variant	5	140475862	G	A	12.68%	71	.	.	.		.	.	.	.	.			.	0.0093	23.88%	78.72%	45%	Subclonal
MP17	SOX30	p.Val462Ala	missense_variant	5	157073647	A	G	25.88%	255	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6262	72.86%	100.00%	92%	Clonal
MP17	RGL2	p.Arg424Trp	missense_variant	6	33262762	G	A	19.55%	133	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0971	48.16%	93.45%	69%	Subclonal
MP17	RSPH9	p.Thr219Lys	missense_variant	6	43634191	C	A	29.73%	481	N	.	Passenger		.	.	.	.	.			Likely passenger	0.8878	87.31%	100.00%	100%	Clonal
MP17	MUC17	p.Glu862Asp	missense_variant	7	100677283	A	C	2.92%	240	N	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely passenger	0.0000	4.57%	20.46%	10%	Subclonal
MP17	EPHB6	p.Gln771Lys	missense_variant	7	142566754	C	A	5.67%	194	D	CANCER	Driver		.	true	.	true	.		TRUE	Likely pathogenic	0.0000	10.94%	34.57%	20%	Subclonal
MP17	ESYT2	p.Arg256*	stop_gained	7	158581071	G	A	42.09%	278	A	.	.		.	.	.	.	.		TRUE	Likely pathogenic	0.0010	93.83%	100.00%	100%	Clonal
MP17	CORO2A	p.Asp95Tyr	missense_variant	9	100899889	C	A	4.60%	413	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	7.09%	17.60%	12%	Subclonal
MP17	ABO	p.Ala342Ala	synonymous_variant	9	136131089	C	T	14.42%	638	.	.	.		.	.	.	.	.		TRUE	.	0.0000	41.78%	61.16%	51%	Subclonal
MP17	ELMOD1	p.Gly111Val	missense_variant	11	107506403	G	T	8.03%	585	D	.	Passenger		.	.	.	.	.			Indeterminate	0.0000	21.15%	36.88%	29%	Subclonal
MP17	NCAM1	p.Arg346Gln	missense_variant	11	113085211	G	A	9.76%	246	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	23.14%	49.63%	35%	Subclonal
MP17	PHLDB1	p.Thr616Asn	missense_variant	11	118501943	C	A	31.60%	655	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9117	92.13%	100.00%	100%	Clonal
MP17	KMT2D	p.Gln809fs	frameshift_variant	12	49445040	TG	T	32.89%	1493	A	.	.		true	true	true	true	true		TRUE	Likely pathogenic	0.0782	96.58%	100.00%	100%	Clonal
MP17	TUBA1B	p.Tyr408Phe	missense_variant	12	49521874	T	A	18.75%	144	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0484	46.45%	90.56%	67%	Subclonal
MP17	ALDH1L2	p.Arg16Gly	missense_variant	12	105478169	G	C	18.55%	124	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0626	44.58%	91.39%	66%	Subclonal
MP17	MIPEP	p.Gln439fs	frameshift_variant	13	24413811	G	GA	25.00%	632	A	.	.		.	.	.	.	.			Indeterminate	0.3800	76.76%	98.36%	89%	Subclonal
MP17	ACOT1	p.Pro151Pro	synonymous_variant	14	74004578	G	C	10.71%	336	.	.	.		.	.	.	.	.			.	0.0000	27.35%	50.93%	38%	Subclonal
MP17	SERPINA10	p.Lys46Lys	synonymous_variant	14	94756793	C	T	16.46%	656	.	.	.		.	.	.	.	.			.	0.0000	48.56%	68.76%	58%	Subclonal
MP17	SRCAP	p.Ala1017Ala	synonymous_variant	16	30732097	G	A	25.85%	797	.	.	.		.	.	.	.	.			.	0.5443	80.77%	100.00%	92%	Clonal
MP17	GPR114	p.Leu66Leu	synonymous_variant	16	57597058	C	T	14.23%	787	.	.	.		.	.	.	.	.			.	0.0000	42.01%	59.36%	51%	Subclonal
MP17	CDH8	p.Ser767*	stop_gained	16	61687612	G	T	25.07%	754	D	.	.		.	.	.	.	.			Indeterminate	0.3451	77.95%	98.18%	89%	Subclonal
MP17	EDC4	p.Gly1209Asp	missense_variant	16	67916765	G	A	27.46%	590	D	.	Passenger		.	.	.	.	.			Indeterminate	0.7977	83.72%	100.00%	98%	Clonal
MP17	ZFHX3	p.Ala66Ala	synonymous_variant	16	72993847	C	T	27.47%	830	.	.	.		.	.	true	.	true			.	0.8144	85.86%	100.00%	98%	Clonal
MP17	TP53	c.673-1G>A	splice_acceptor_variant	17	7577609	C	T	14.43%	395	D	.	.		true	true	true	true	true	TRUE		Likely pathogenic	0.0000	39.65%	64.30%	51%	Subclonal
MP17	TP53	p.Val173Leu	missense_variant	17	7578413	C	A	26.74%	778	D	CANCER	Driver		true	true	true	true	true	TRUE		Likely pathogenic	0.7246	83.38%	100.00%	95%	Clonal
MP17	BCAS3	p.Thr782Thr	synonymous_variant	17	59155864	A	T	5.86%	751	.	.	.		.	.	.	.	.			.	0.0000	15.11%	27.11%	21%	Subclonal
MP17	PIEZO2	p.Glu2283Asp	missense_variant	18	10696074	C	G	15.98%	438	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	45.14%	69.52%	57%	Subclonal
MP17	NOTCH3	p.Tyr2244fs	frameshift_variant	19	15271708	TA	T	29.81%	624	D	.	.		.	.	.	.	.			Indeterminate	0.9057	89.25%	100.00%	100%	Clonal
MP17	FCGBP	p.Asp5159Asn	missense_variant	19	40360933	C	T	3.81%	577	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	8.45%	19.79%	14%	Subclonal
MP17	PSG6	p.Leu203Gln	missense_variant	19	43414830	A	T	37.10%	62	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7855	74.23%	100.00%	100%	Clonal
MP17	NLRP8	p.Val571Met	missense_variant	19	56467135	G	A	29.26%	680	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8981	88.81%	100.00%	100%	Clonal
MP17	GNAS	p.Arg844Cys	missense_variant	20	57484420	C	T	28.37%	839	D	CANCER	Passenger		true	.	.	.	.	TRUE		Likely pathogenic	0.8771	88.18%	100.00%	100%	Clonal
MP17	NCAM2	p.Pro622Ser	missense_variant	21	22841072	C	T	22.47%	356	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.1041	65.00%	94.84%	80%	Subclonal
MP17	GNAZ	p.Ile213Ile	synonymous_variant	22	23438521	C	T	17.52%	685	.	.	.		.	.	.	.	.			.	0.0000	52.24%	72.49%	62%	Subclonal
MP17	CDKL5	p.Arg840Cys	missense_variant	X	18646512	C	T	4.16%	817	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.0000	10.13%	19.95%	15%	Subclonal
MP17	DMD	c.9361+2_9361+3insT	splice_donor_variant	X	31241161	T	TA	35.15%	754	.	.	.		.	.	.	.	.			Indeterminate	0.0284	95.48%	100.00%	100%	Clonal
MP18	KLHL17	p.Ala258Val	missense_variant	1	897796	C	T	3.25%	770	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	7.91%	17.58%	12%	Subclonal
MP18	PTCHD2	p.Ala493fs	frameshift_variant	1	11575448	TGCCAG	T	8.31%	421	A	.	.		.	.	.	.	.			Indeterminate	0.0000	22.41%	42.58%	32%	Subclonal
MP18	NBPF1	p.Asp679Glu	missense_variant	1	16902844	G	T	8.11%	111	.	.	Passenger		.	.	true	.	true			Likely pathogenic	0.0000	16.07%	55.32%	31%	Subclonal
MP18	NBPF1	p.Arg646Gln	missense_variant	1	16902944	C	T	31.82%	22	.	.	Passenger		.	.	true	.	true			Likely pathogenic	0.4799	48.40%	100.00%	100%	Clonal
MP18	HP1BP3	p.Met153Leu	missense_variant	1	21099997	T	A	23.70%	346	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.3945	73.15%	100.00%	90%	Subclonal
MP18	ZNF436	p.Glu88Gly	missense_variant	1	23689612	T	C	8.80%	761	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	26.06%	41.40%	33%	Subclonal
MP18	GRIK3	p.Ile67Phe	missense_variant	1	37356614	T	A	3.13%	735	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	7.39%	17.17%	12%	Subclonal
MP18	WDR63	p.Ser383Asn	missense_variant	1	85560213	G	A	4.01%	424	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	9.09%	23.55%	15%	Subclonal
MP18	HRNR	p.Gly717Arg	missense_variant	1	152191956	C	T	10.53%	209	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0003	33.39%	73.49%	50%	Subclonal
MP18	CRNN	p.Thr313Ile	missense_variant	1	152382620	G	A	9.49%	801	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	36.17%	55.71%	45%	Subclonal
MP18	DCST1	p.Ala651Val	missense_variant	1	155023175	C	T	13.46%	312	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0032	48.05%	84.33%	65%	Subclonal
MP18	CCT3	p.Met59Ile	missense_variant	1	156304534	C	T	8.24%	607	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	29.73%	50.81%	39%	Subclonal
MP18	CD1C	p.Asp291Asp	synonymous_variant	1	158262648	C	T	4.69%	384	.	.	.		.	.	.	.	.			.	0.0000	16.86%	41.75%	27%	Subclonal
MP18	TMCC2	p.Lys162Gln	missense_variant	1	205210909	A	C	9.27%	572	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	33.82%	56.70%	44%	Subclonal
MP18	PARP1	p.Val818Phe	missense_variant	1	226553708	C	A	4.14%	435	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	12.16%	30.44%	20%	Subclonal
MP18	OBSCN	p.Arg7879Cys	missense_variant	1	228559243	C	T	23.30%	382	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7827	85.06%	100.00%	100%	Clonal
MP18	DISC1	p.Cys239Cys	synonymous_variant	1	231830221	C	T	10.86%	810	.	.	.		.	.	.	.	.			.	0.0000	42.19%	62.79%	52%	Subclonal
MP18	OR13G1	p.Leu247Phe	missense_variant	1	247835605	G	A	9.34%	257	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0012	36.39%	77.84%	54%	Subclonal
MP18	NTSR2	p.Leu356Val	missense_variant	2	11798772	G	C	14.07%	263	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	38.94%	70.84%	53%	Subclonal
MP18	GKN1	p.Gln109Gln	synonymous_variant	2	69206083	A	G	17.74%	372	.	.	.		.	.	.	.	.			.	0.0005	53.37%	82.82%	67%	Subclonal
MP18	ZAP70	p.Pro91Ala	missense_variant	2	98340770	C	G	5.20%	654	N	CANCER	Passenger		.	.	.	.	.			Likely passenger	0.0000	13.69%	26.77%	20%	Subclonal
MP18	MFSD9	p.Leu124Leu	synonymous_variant	2	103343359	G	C	7.36%	231	.	.	.		.	.	.	.	.			.	0.0000	17.18%	43.03%	28%	Subclonal
MP18	ALS2	p.Thr387Arg	missense_variant	2	202622436	G	C	22.71%	207	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.3153	65.52%	98.76%	86%	Subclonal
MP18	SP110	p.Lys432Glu	missense_variant	2	231048342	T	C	6.40%	469	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	16.63%	33.64%	24%	Subclonal
MP18	ALPPL2	p.Tyr418Cys	missense_variant	2	233274111	A	G	5.84%	137	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	10.99%	41.65%	22%	Subclonal
MP18	RBM44	p.Pro215Gln	missense_variant	2	238726203	C	A	12.44%	217	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	32.52%	65.93%	47%	Subclonal
MP18	CAND2	p.Pro648Pro	synonymous_variant	3	12858375	C	A	6.51%	553	.	.	.		.	.	.	.	.			.	0.0000	17.46%	33.23%	25%	Subclonal
MP18	ILDR1	p.Arg360Arg	synonymous_variant	3	121712518	T	G	33.84%	263	.	.	.		.	.	.	.	.			.	0.5783	89.57%	100.00%	100%	Clonal
MP18	MSL2	p.Pro57Arg	missense_variant	3	135871553	G	C	5.76%	451	D	.	Passenger		.	.	.	.	.			Indeterminate	0.0000	14.53%	31.05%	22%	Subclonal
MP18	SERPINI2	p.Asp152Tyr	missense_variant	3	167184897	C	A	4.45%	382	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	12.98%	33.12%	21%	Subclonal
MP18	TRA2B	p.Arg47Ser	missense_variant	3	185644418	T	A	8.76%	137	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0005	24.02%	69.95%	42%	Subclonal
MP18	ZFYVE28	p.Glu193Asp	missense_variant	4	2339166	C	G	6.98%	301	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	17.05%	39.09%	26%	Subclonal
MP18	LAP3	p.Thr363Thr	synonymous_variant	4	17600090	T	A	4.96%	242	.	.	.		.	.	.	.	.			.	0.0000	10.39%	31.65%	19%	Subclonal
MP18	NIPAL1	p.Cys321Phe	missense_variant	4	48037918	G	T	3.83%	392	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	8.35%	23.09%	15%	Subclonal
MP18	SEC24D	p.Thr285Thr	synonymous_variant	4	119727056	G	C	3.41%	352	.	.	.		.	.	.	.	.			.	0.0000	7.02%	21.77%	13%	Subclonal
MP18	DNAJC21	p.Glu236Lys	missense_variant	5	34937698	G	A	32.14%	112	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7093	78.44%	100.00%	100%	Clonal
MP18	ANKRD55	p.Glu601Gln	missense_variant	5	55396054	C	G	9.27%	248	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	23.29%	50.88%	35%	Subclonal
MP18	ANKHD1	p.Pro1870Ala	missense_variant	5	139908139	C	G	18.48%	644	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.0000	43.28%	60.03%	52%	Subclonal
MP18	ZSCAN23	p.Glu184Asp	missense_variant	6	28403241	C	A	3.70%	433	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	8.19%	21.95%	14%	Subclonal
MP18	HLA-B	p.Glu176Ala	missense_variant	6	31324036	T	G	13.51%	37	N	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely passenger	0.0701	22.14%	93.55%	51%	Subclonal
MP18	HLA-B	p.Glu176Lys	missense_variant	6	31324037	C	T	13.16%	38	N	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely passenger	0.0611	21.56%	92.80%	50%	Subclonal
MP18	NOTCH4	p.Pro382Pro	synonymous_variant	6	32188195	T	C	13.21%	492	.	.	.		.	.	.	.	.			.	0.0000	39.35%	62.09%	50%	Subclonal
MP18	TSPO2	p.Ser55Ser	synonymous_variant	6	41010889	T	G	24.74%	380	.	.	.		.	.	.	.	.			.	0.5301	77.10%	100.00%	94%	Clonal
MP18	DOPEY1	p.Gly2265Val	missense_variant	6	83869538	G	T	22.88%	319	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.2903	69.88%	98.63%	87%	Subclonal
MP18	MDN1	p.Gln4932Glu	missense_variant	6	90368556	G	C	28.72%	470	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8226	88.12%	100.00%	100%	Clonal
MP18	ZUFSP	p.Gly232Ser	missense_variant	6	116980064	C	T	24.86%	366	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.5443	77.16%	100.00%	94%	Clonal
MP18	ARG1	p.Gly106Gly	synonymous_variant	6	131900414	C	T	32.65%	49	.	.	.		.	.	true	.	true			.	0.5996	65.90%	100.00%	100%	Clonal
MP18	SLC35D3	p.Leu91Leu	synonymous_variant	6	137243839	C	T	20.49%	327	.	.	.		.	.	.	.	.			.	0.0495	62.01%	94.22%	78%	Subclonal
MP18	KIAA1244	p.Val1889Ile	missense_variant	6	138655648	G	A	7.63%	629	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	21.50%	37.39%	29%	Subclonal
MP18	SUN1	p.Val338Ala	missense_variant	7	892549	T	C	19.13%	115	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.1176	48.65%	96.28%	73%	Subclonal
MP18	ABCA13	p.Thr4150Ile	missense_variant	7	48452170	C	T	32.58%	178	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7499	84.63%	100.00%	100%	Clonal
MP18	ZNF479	p.His86Arg	missense_variant	7	57193730	T	C	12.00%	50	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0234	21.09%	86.91%	46%	Subclonal
MP18	PVRIG	p.Val181Phe	missense_variant	7	99818241	G	T	10.58%	737	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	32.03%	48.89%	40%	Subclonal
MP18	DLC1	p.Lys1179Glu	missense_variant	8	12950326	T	C	51.33%	113	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.2057	89.03%	100.00%	100%	Clonal
MP18	CCAR2	p.Gly51Val	missense_variant	8	22464121	G	T	9.36%	299	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	17.85%	36.44%	26%	Subclonal
MP18	CLVS1	p.Tyr136Tyr	synonymous_variant	8	62212794	C	T	30.45%	220	.	.	.		.	.	.	.	.			.	0.7716	84.09%	100.00%	100%	Clonal
MP18	MMP16	p.Pro314Leu	missense_variant	8	89128878	G	A	5.88%	238	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	16.52%	45.70%	28%	Subclonal
MP18	UBR5	p.Ile374Leu	missense_variant	8	103341606	T	G	3.05%	590	D	PASSENGER/OTHER	Passenger		true	.	.	.	.			Likely pathogenic	0.0000	8.81%	22.41%	15%	Subclonal
MP18	COL22A1	p.Val175Val	synonymous_variant	8	139890126	C	T	9.66%	787	.	.	.		.	.	.	.	.			.	0.0002	52.40%	80.53%	66%	Subclonal
MP18	DGAT1	p.Val192Ala	missense_variant	8	145542025	A	G	7.68%	469	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	37.55%	70.50%	52%	Subclonal
MP18	IFT74	p.Gln440His	missense_variant	9	27048259	G	C	11.90%	336	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	33.17%	59.52%	45%	Subclonal
MP18	ANXA1	p.Thr169Thr	synonymous_variant	9	75777729	C	T	36.76%	389	.	.	.		.	.	.	.	.		TRUE	.	0.8428	86.64%	100.00%	100%	Clonal
MP18	PTCH1	p.Asp293Ala	missense_variant	9	98242739	T	G	3.72%	215	D	CANCER	Passenger		true	.	.	.	.	TRUE	TRUE	Likely pathogenic	0.0000	6.77%	26.72%	14%	Subclonal
MP18	C9orf152	p.Ser238*	stop_gained	9	112963235	G	C	5.30%	264	N	.	.		.	.	.	.	.		TRUE	Likely pathogenic	0.0000	11.62%	32.56%	20%	Subclonal
MP18	KLF6	p.Ser151Ser	synonymous_variant	10	3824056	A	G	33.88%	800	.	.	.		true	.	.	.	.	TRUE		.	0.0013	97.18%	100.00%	100%	Clonal
MP18	UPF2	p.Asp76His	missense_variant	10	12077197	C	G	18.26%	745	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	58.88%	79.92%	69%	Subclonal
MP18	ZNF518A	p.Lys350Asn	missense_variant	10	97917129	A	T	7.04%	199	.	.	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	11.36%	31.57%	20%	Subclonal
MP18	AKIP1	p.Val182Ile	missense_variant	11	8940938	G	A	17.65%	340	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0009	52.49%	83.22%	67%	Subclonal
MP18	ZP1	p.Val221Val	synonymous_variant	11	60637354	G	C	8.92%	706	.	.	.		.	.	.	.	.			.	0.0000	26.20%	42.24%	34%	Subclonal
MP18	VPS37C	p.Pro183Leu	missense_variant	11	60899812	G	A	3.62%	304	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	7.24%	23.67%	14%	Subclonal
MP18	WDR74	p.Arg374Pro	missense_variant	11	62600461	C	G	14.49%	428	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	31.53%	50.22%	40%	Subclonal
MP18	DSCAML1	p.Gly2082Cys	missense_variant	11	117299142	C	A	13.71%	649	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	42.29%	62.44%	52%	Subclonal
MP18	CD3E	p.Ser55Pro	missense_variant	11	118183392	T	C	31.95%	626	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.4181	93.68%	100.00%	100%	Clonal
MP18	BCL9L	p.Phe1499Leu	missense_variant	11	118769127	G	T	28.87%	381	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8044	86.70%	100.00%	100%	Clonal
MP18	ROBO4	p.Arg285Lys	missense_variant	11	124765535	C	T	13.21%	583	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	40.11%	60.97%	50%	Subclonal
MP18	SHMT2	p.His504Tyr	missense_variant	12	57628139	C	T	38.21%	403	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.8819	89.08%	100.00%	100%	Clonal
MP18	UHRF1BP1L	p.Ala194Gly	missense_variant	12	100491231	G	C	22.75%	189	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.3266	64.78%	98.81%	86%	Subclonal
MP18	DNAH10	p.Arg2487Cys	missense_variant	12	124358132	C	T	11.95%	544	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	35.48%	56.24%	45%	Subclonal
MP18	RIMBP2	p.Gly827Arg	missense_variant	12	130898843	C	T	6.84%	351	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	21.77%	47.35%	33%	Subclonal
MP18	DLGAP5	p.Asn236Lys	missense_variant	14	55646413	G	C	5.59%	179	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	8.13%	27.42%	16%	Subclonal
MP18	CYFIP1	p.Ala823Pro	missense_variant	15	22969241	G	C	23.48%	626	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.2806	76.51%	98.61%	89%	Subclonal
MP18	TJP1	p.Arg1097fs	frameshift_variant	15	30011250	GTCTGGCC	G	25.65%	616	A	.	.		.	.	.	.	.			Indeterminate	0.6644	83.30%	100.00%	97%	Clonal
MP18	EPB42	p.Ser671Leu	missense_variant	15	43489654	G	A	10.37%	376	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	21.01%	38.29%	29%	Subclonal
MP18	MAP1A	p.Ala728Asp	missense_variant	15	43815854	C	A	29.06%	265	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.1078	66.31%	95.65%	81%	Subclonal
MP18	ALPK3	p.Asp1439Val	missense_variant	15	85401679	A	T	5.80%	138	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	7.89%	30.33%	16%	Subclonal
MP18	SPSB3	p.Val222Met	missense_variant	16	1827805	C	T	14.35%	432	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	42.60%	67.74%	54%	Subclonal
MP18	SYT17	p.Leu61Met	missense_variant	16	19184899	C	A	13.33%	390	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0007	49.00%	81.37%	64%	Subclonal
MP18	CRISPLD2	p.Arg216Arg	synonymous_variant	16	84888374	G	C	5.53%	217	.	.	.		.	.	.	.	.		TRUE	.	0.0000	11.67%	35.25%	21%	Subclonal
MP18	TP53	p.Ile195Phe	missense_variant	17	7578266	T	A	39.94%	333	D	CANCER	Driver		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.8858	89.78%	100.00%	100%	Clonal
MP18	TMEM101	p.Gly197Gly	synonymous_variant	17	42089479	G	T	14.73%	421	.	.	.		.	.	.	.	.		TRUE	.	0.0000	43.76%	69.48%	56%	Subclonal
MP18	SLC4A1	p.Gly609Ala	missense_variant	17	42332639	C	G	10.00%	230	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0001	31.97%	69.35%	48%	Subclonal
MP18	NPEPPS	p.Gly322Asp	missense_variant	17	45663749	G	A	5.00%	140	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	11.37%	47.27%	24%	Subclonal
MP18	CDK5RAP3	p.Glu276Glu	synonymous_variant	17	46053334	A	G	5.06%	613	.	.	.		.	.	.	.	.		TRUE	.	0.0000	16.69%	33.53%	24%	Subclonal
MP18	C17orf80	p.Ala319Pro	missense_variant	17	71232576	G	C	8.07%	731	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	42.37%	69.33%	55%	Subclonal
MP18	MRPS7	p.Leu110His	missense_variant	17	73258938	T	A	10.20%	716	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	38.76%	60.06%	49%	Subclonal
MP18	SOCS3	p.Cys193*	stop_gained	17	76354598	A	T	5.14%	486	D	.	.		.	.	.	.	.		TRUE	Likely pathogenic	0.0000	16.33%	35.42%	25%	Subclonal
MP18	LAMA1	p.His1833His	synonymous_variant	18	6985397	G	A	33.80%	426	.	.	.		.	.	.	.	.			.	0.0992	95.07%	100.00%	100%	Clonal
MP18	ONECUT3	p.Ser478Ser	synonymous_variant	19	1775393	C	T	17.81%	73	.	.	.		.	.	.	.	.		TRUE	.	0.1153	40.02%	96.06%	68%	Subclonal
MP18	KLF16	p.His201Gln	missense_variant	19	1854614	G	T	46.95%	328	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.7831	96.11%	100.00%	100%	Clonal
MP18	WDR87	p.Ser2560Arg	missense_variant	19	38376631	G	T	3.18%	503	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	7.03%	18.88%	12%	Subclonal
MP18	KCNA7	p.Arg227Arg	synonymous_variant	19	49574010	G	T	2.80%	750	.	.	.		.	.	.	.	.			.	0.0000	6.41%	15.66%	11%	Subclonal
MP18	ZNF83	p.Phe108Val	missense_variant	19	53117496	A	C	3.42%	292	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	8.51%	29.17%	16%	Subclonal
MP18	NLRP12	p.Val902Val	synonymous_variant	19	54304534	C	A	6.25%	448	.	.	.		.	.	.	.	.			.	0.0000	20.41%	42.11%	30%	Subclonal
MP18	NLRP11	p.Leu12Leu	synonymous_variant	19	56329505	C	G	7.00%	200	.	.	.		.	.	.	.	.			.	0.0000	19.81%	54.22%	34%	Subclonal
MP18	ZNF814	p.Leu815Val	missense_variant	19	58384315	G	C	4.30%	256	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	8.71%	28.07%	16%	Subclonal
MP18	SDCBP2	p.His230Gln	missense_variant	20	1293023	G	C	2.87%	766	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	6.69%	15.87%	11%	Subclonal
MP18	ACSS2	p.Ile93Thr	missense_variant	20	33470696	T	C	3.95%	405	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	8.81%	23.52%	15%	Subclonal
MP18	LAMA5	p.Asn327His	missense_variant	20	60922062	T	G	8.37%	203	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	19.64%	48.87%	32%	Subclonal
MP18	PDE9A	p.Ile83Met	missense_variant	21	44119108	C	G	4.38%	320	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	9.47%	26.87%	17%	Subclonal
MP18	TOP3B	p.Arg414Ile	missense_variant	22	22317229	C	A	4.63%	367	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	10.55%	27.19%	18%	Subclonal
MP18	TOP3B	p.Arg414Arg	synonymous_variant	22	22317230	T	G	4.74%	359	.	.	.		.	.	.	.	.			.	0.0000	10.83%	27.80%	18%	Subclonal
MP18	PITPNB	p.Met76Ile	missense_variant	22	28293856	C	G	12.75%	455	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	37.41%	60.73%	48%	Subclonal
MP18	PRR14L	p.Ser458Cys	missense_variant	22	32112452	G	C	7.27%	729	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	26.34%	44.55%	35%	Subclonal
MP18	APOBEC3B	p.Leu35Leu	synonymous_variant	22	39380165	C	T	29.50%	261	.	.	.		.	.	.	.	.			.	0.1827	89.61%	100.00%	100%	Clonal
MP18	TUBGCP6	p.Pro278Leu	missense_variant	22	50678705	G	A	5.10%	353	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	15.13%	37.49%	24%	Subclonal
MP18	KDM6A	p.Ile1022fs	frameshift_variant	X	44937717	G	GT	40.13%	800	A	.	.		true	true	true	true	true			Likely pathogenic	0.0000	97.44%	100.00%	100%	Clonal
MP18	GSPT2	p.Asp90Asn	missense_variant	X	51486990	G	A	6.12%	392	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	15.25%	33.50%	23%	Subclonal
MP19	TTC34	p.Arg149Trp	missense_variant	1	2702459	G	A	26.55%	177	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8253	83.58%	100.00%	100%	Clonal
MP19	ARID1A	p.Thr2105Ile	missense_variant	1	27106703	C	T	22.22%	495	D	PASSENGER/OTHER	Passenger		true	true	true	true	true			Likely pathogenic	0.9243	87.17%	100.00%	100%	Clonal
MP19	MAP7D1	p.Ser41Leu	missense_variant	1	36636647	C	T	13.38%	568	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.3012	65.23%	96.74%	81%	Subclonal
MP19	TAL1	p.Thr163Asn	missense_variant	1	47689729	G	T	4.67%	150	N	PASSENGER/OTHER	Passenger		true	.	.	.	.			Likely passenger	0.0001	13.55%	56.13%	28%	Subclonal
MP19	BEND5	p.Ser134Ser	synonymous_variant	1	49224915	G	A	4.06%	813	.	.	.		.	.	.	.	.			.	0.0000	17.17%	33.83%	25%	Subclonal
MP19	ZFYVE9	p.Ser314Asn	missense_variant	1	52704030	G	A	6.49%	231	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0001	23.76%	62.94%	39%	Subclonal
MP19	ZYG11A	p.Cys123Trp	missense_variant	1	53322782	C	G	13.13%	160	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.5096	52.00%	98.31%	80%	Clonal
MP19	PKN2	p.Ile341Ile	synonymous_variant	1	89250359	C	A	18.52%	297	.	.	.		.	.	.	.	.			.	0.8854	79.81%	100.00%	100%	Clonal
MP19	LRRC39	p.Glu68Val	missense_variant	1	100626038	T	A	26.34%	224	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8875	79.66%	100.00%	100%	Clonal
MP19	ASH1L	p.Ala7Asp	missense_variant	1	155491291	G	T	13.66%	432	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.4554	64.56%	98.00%	83%	Subclonal
MP19	OLFML2B	p.Arg91Lys	missense_variant	1	161989875	C	T	5.15%	874	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	23.05%	40.95%	31%	Subclonal
MP19	SELP	p.Arg359Ser	missense_variant	1	169580800	T	A	12.79%	258	N	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely passenger	0.3860	55.54%	97.40%	78%	Subclonal
MP19	ACBD3	p.Ala114Ser	missense_variant	1	226353648	C	A	34.75%	400	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7612	96.37%	100.00%	100%	Clonal
MP19	KIF26B	p.Leu607Leu	synonymous_variant	1	245772735	C	T	14.58%	583	.	.	.		.	.	.	.	.			.	0.9074	85.56%	100.00%	100%	Clonal
MP19	CYP1B1	p.Ile327Ile	synonymous_variant	2	38301551	G	A	21.09%	773	.	.	.		.	.	.	.	.			.	0.9327	88.19%	100.00%	100%	Clonal
MP19	PSD4	p.Gly522Glu	missense_variant	2	113943769	G	A	8.16%	343	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0001	34.24%	69.70%	50%	Subclonal
MP19	THSD7B	p.Gly1004Glu	missense_variant	2	138208559	G	A	6.82%	132	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0087	21.76%	74.99%	41%	Subclonal
MP19	GAD1	p.Asn20Ser	missense_variant	2	171675160	A	G	19.89%	709	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8628	90.83%	100.00%	100%	Clonal
MP19	STAT4	p.Lys590Glu	missense_variant	2	191898300	T	C	20.94%	468	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7987	89.24%	100.00%	100%	Clonal
MP19	SGOL2	p.Phe1184Leu	missense_variant	2	201438619	T	C	18.27%	301	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8819	79.30%	100.00%	100%	Clonal
MP19	ALS2CR11	p.Thr372Met	missense_variant	2	202410313	G	A	52.00%	225	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7862	96.18%	100.00%	100%	Clonal
MP19	ADAM23	p.Cys573Ser	missense_variant	2	207437899	T	A	41.82%	275	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.8249	95.98%	100.00%	100%	Clonal
MP19	SLC11A1	p.Glu123Asp	missense_variant	2	219249965	G	C	7.69%	845	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	42.54%	68.07%	54%	Subclonal
MP19	SP140	p.Glu164Gln	missense_variant	2	231106202	G	C	42.94%	177	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7918	94.09%	100.00%	100%	Clonal
MP19	D2HGDH	p.Ile147Ile	synonymous_variant	2	242681940	C	T	18.91%	534	.	.	.		.	.	.	.	.			.	0.5148	90.27%	100.00%	100%	Clonal
MP19	C3orf20	p.Trp51Ser	missense_variant	3	14724372	G	C	5.41%	628	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	19.30%	37.47%	27%	Subclonal
MP19	SCAP	p.Pro813Ser	missense_variant	3	47459634	G	A	21.59%	301	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.8923	81.05%	100.00%	100%	Clonal
MP19	FLNB	p.Pro610Pro	synonymous_variant	3	58092489	C	A	52.21%	385	.	.	.		.	.	.	.	.		TRUE	.	0.1624	97.50%	100.00%	100%	Clonal
MP19	GOLGB1	p.Glu2608Gly	missense_variant	3	121410388	T	C	46.09%	358	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7466	97.09%	100.00%	100%	Clonal
MP19	PARP14	p.Glu604Asp	missense_variant	3	122419213	G	T	20.99%	362	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8487	87.08%	100.00%	100%	Clonal
MP19	IFT122	p.Tyr345Cys	missense_variant	3	129195222	A	G	12.05%	556	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8848	80.35%	100.00%	100%	Clonal
MP19	H1FOO	p.Ile332Met	missense_variant	3	129270138	C	G	2.99%	536	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	16.31%	43.00%	27%	Subclonal
MP19	ACAD11	p.Pro346Thr	missense_variant	3	132347218	G	T	36.97%	165	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6398	92.80%	100.00%	100%	Clonal
MP19	GOLIM4	p.Glu173Asp	missense_variant	3	167759261	C	G	43.48%	184	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.3785	94.67%	100.00%	100%	Clonal
MP19	SPATA16	p.Asp392Asn	missense_variant	3	172643190	C	T	29.08%	282	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.6635	93.94%	100.00%	100%	Clonal
MP19	LPHN3	p.Ile1072Ile	synonymous_variant	4	62894597	C	T	20.11%	189	.	.	.		.	.	.	.	.			.	0.8130	81.37%	100.00%	100%	Clonal
MP19	AFF1	p.Ser278Cys	missense_variant	4	87968520	C	G	39.81%	844	D	PASSENGER/OTHER	Passenger		true	.	.	.	.			Likely pathogenic	0.9851	98.11%	100.00%	100%	Clonal
MP19	KIAA1109	p.Glu4083Lys	missense_variant	4	123260458	G	A	9.65%	342	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	34.85%	66.77%	49%	Subclonal
MP19	PCDH18	p.Cys98Tyr	missense_variant	4	138452950	C	T	35.69%	367	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9407	95.19%	100.00%	100%	Clonal
MP19	WWC2	p.Leu446Val	missense_variant	4	184182112	C	G	8.25%	291	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	28.03%	60.36%	42%	Subclonal
MP19	ADCY2	p.Val695Leu	missense_variant	5	7757688	G	T	26.65%	349	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7781	94.28%	100.00%	100%	Clonal
MP19	CDC20B	p.Gly367Val	missense_variant	5	54420746	C	A	27.84%	255	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.4217	88.80%	100.00%	100%	Clonal
MP19	FAM159B	p.Ala80Thr	missense_variant	5	63991380	G	A	10.53%	209	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0043	35.38%	77.81%	53%	Subclonal
MP19	WDR41	p.Asn282Asn	synonymous_variant	5	76736674	A	G	4.41%	136	.	.	.		.	.	.	.	.		TRUE	.	0.0000	10.06%	46.67%	22%	Subclonal
MP19	TCERG1	p.His336Gln	missense_variant	5	145843229	C	A	6.84%	541	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	24.94%	46.68%	35%	Subclonal
MP19	FOXF2	p.Ser341Thr	missense_variant	6	1391204	G	C	6.29%	350	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	25.03%	56.25%	38%	Subclonal
MP19	MRPL2	p.Leu6Val	missense_variant	6	43027104	G	C	31.99%	816	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7640	97.76%	100.00%	100%	Clonal
MP19	SLC29A1	p.Ala174Thr	missense_variant	6	44198149	G	A	11.98%	601	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.4957	67.39%	98.29%	85%	Subclonal
MP19	DDX43	p.Gln287His	missense_variant	6	74116140	G	C	33.27%	499	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6591	96.68%	100.00%	100%	Clonal
MP19	FUT9	p.Asp78Val	missense_variant	6	96651264	A	T	4.48%	424	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	20.02%	48.30%	32%	Subclonal
MP19	WASF1	p.Gln309*	stop_gained	6	110423388	G	A	12.78%	180	A	.	.		.	.	.	.	.			Indeterminate	0.6774	58.71%	100.00%	90%	Clonal
MP19	NHSL1	p.Glu844Gln	missense_variant	6	138752964	C	G	55.27%	807	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.5085	98.91%	100.00%	100%	Clonal
MP19	TMEM242	p.Ala69Ser	missense_variant	6	157739936	C	A	3.09%	583	N	.	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	9.45%	24.00%	16%	Subclonal
MP19	CHN2	p.Pro437Pro	synonymous_variant	7	29546938	T	G	33.52%	179	.	.	.		.	.	.	.	.			.	0.8971	89.76%	100.00%	100%	Clonal
MP19	NOD1	p.Leu384Ile	missense_variant	7	30491883	G	T	29.60%	554	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9237	95.99%	100.00%	100%	Clonal
MP19	PCLO	p.Thr1669Ala	missense_variant	7	82585264	T	C	4.00%	600	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	21.36%	47.02%	32%	Subclonal
MP19	C7orf43	p.Thr43Thr	synonymous_variant	7	99755994	A	G	10.46%	497	.	.	.		.	.	.	.	.			.	0.5407	64.30%	98.54%	85%	Clonal
MP19	MEPCE	p.Leu197Leu	synonymous_variant	7	100028232	G	C	11.20%	857	.	.	.		.	.	.	.	.			.	0.6862	73.81%	100.00%	90%	Clonal
MP19	MUC17	p.Ser2216Arg	missense_variant	7	100681345	T	G	5.61%	196	N	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely passenger	0.1378	31.50%	92.11%	57%	Subclonal
MP19	RELN	p.Met1956Leu	missense_variant	7	103194210	T	A	23.00%	413	N	PASSENGER/OTHER	Passenger		.	.	.	.	.	TRUE		Likely passenger	0.2353	90.72%	100.00%	100%	Clonal
MP19	MEST	p.Ser45Phe	missense_variant	7	130135316	C	T	9.54%	650	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7895	73.27%	100.00%	96%	Clonal
MP19	DCTN6	p.Tyr95Tyr	synonymous_variant	8	30036925	T	C	44.29%	70	.	.	.		.	.	.	.	.		TRUE	.	0.9488	83.96%	100.00%	100%	Clonal
MP19	PREX2	p.Tyr1558Tyr	synonymous_variant	8	69129920	C	T	7.60%	566	.	.	.		.	.	.	.	.		TRUE	.	0.0000	34.11%	60.77%	46%	Subclonal
MP19	PLEC	p.Thr64Thr	synonymous_variant	8	145024683	G	C	4.50%	866	.	.	.		.	.	.	.	.			.	0.0000	29.57%	54.86%	41%	Subclonal
MP19	CDKN2A	p.His83Tyr	missense_variant	9	21971111	G	A	61.15%	399	D	CANCER	Driver		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.8531	98.09%	100.00%	100%	Clonal
MP19	DNAJB5	p.Arg277Gln	missense_variant	9	34996538	G	A	51.47%	713	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.9720	98.27%	100.00%	100%	Clonal
MP19	SVEP1	p.Val1096Leu	missense_variant	9	113228181	C	G	47.53%	223	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.6239	95.34%	100.00%	100%	Clonal
MP19	DNAJC1	p.Arg340Ile	missense_variant	10	22094988	C	A	16.44%	219	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8598	75.26%	100.00%	100%	Clonal
MP19	GPR158	p.Pro958Thr	missense_variant	10	25887427	C	A	19.41%	304	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8954	82.24%	100.00%	100%	Clonal
MP19	TTC18	p.Glu1101Asp	missense_variant	10	75013796	C	A	9.02%	122	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0002	20.45%	62.46%	37%	Subclonal
MP19	CHST15	p.Leu122Phe	missense_variant	10	125805363	C	G	20.70%	343	N	.	Passenger		.	.	.	.	.			Likely passenger	0.8809	80.15%	100.00%	100%	Clonal
MP19	OR51T1	p.Pro158Thr	missense_variant	11	4903520	C	A	12.94%	425	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.2807	60.69%	96.39%	79%	Subclonal

MP19	ZNF143	p.Val482Phe	missense_variant	11	9534063	G	T	62.26%	159	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7903	95.69%	100.00%	100%	Clonal
MP19	CTNND1	p.Ala493Ala	synonymous_variant	11	57571151	A	T	23.55%	293	.	.	.		.	.	.		TRUE		0.9026	84.71%	100.00%	100%	Clonal
MP19	GAL3ST3	p.Arg121Arg	synonymous_variant	11	65810911	C	A	42.38%	564	.	.	.		.	.	.			.	0.9509	97.56%	100.00%	100%	Clonal
MP19	CTSF	p.His414His	synonymous_variant	11	66332108	G	A	24.07%	216	.	.	.		.	.	.			.	0.8895	82.26%	100.00%	100%	Clonal
MP19	PCF11	p.Glu580Lys	missense_variant	11	82877677	G	A	33.46%	257	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8499	92.47%	100.00%	100%	Clonal
MP19	DYNC2H1	p.Asp1304Asn	missense_variant	11	103027282	G	A	8.65%	208	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0002	27.73%	66.88%	44%	Subclonal
MP19	PRDM10	p.Gln908Glu	missense_variant	11	129784730	G	C	6.53%	796	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	25.01%	42.53%	33%	Subclonal
MP19	KCNA1	p.Gly6Gly	synonymous_variant	12	5020562	G	A	43.54%	356	.	.	.		.	.	.			.	0.3634	96.83%	100.00%	100%	Clonal
MP19	TAS2R46	p.His120Arg	missense_variant	12	11214535	T	C	5.95%	84	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0249	15.48%	78.56%	36%	Subclonal
MP19	KCNJ8	p.Gly333Val	missense_variant	12	21918934	C	A	14.89%	282	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6983	66.38%	100.00%	91%	Clonal
MP19	HOXC10	p.Glu248Val	missense_variant	12	54379786	A	T	41.50%	347	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9692	96.16%	100.00%	100%	Clonal
MP19	FAM19A2	p.Cys69Trp	missense_variant	12	62148705	G	C	19.71%	137	D	.	Passenger		.	.	.			Indeterminate	0.7798	66.03%	100.00%	100%	Clonal
MP19	OAS2	p.Gln14His	missense_variant	12	113416455	G	C	53.61%	416	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3917	97.87%	100.00%	100%	Clonal
MP19	ELF1	p.Tyr592Asp	missense_variant	13	41507647	A	C	45.31%	320	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8026	96.38%	100.00%	100%	Clonal
MP19	ZC3H13	p.Lys1058Glu	missense_variant	13	46543507	T	C	5.35%	467	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.09%	39.02%	27%	Subclonal
MP19	METTL3	p.Glu226Asp	missense_variant	14	21971361	C	G	16.42%	743	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9191	88.48%	100.00%	100%	Clonal
MP19	PPP1R3E	p.Arg179Pro	missense_variant	14	23770949	C	G	60.00%	35	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3824	83.09%	100.00%	100%	Clonal
MP19	ARHGAP5	p.Glu555*	stop_gained	14	32561538	G	T	14.43%	201	A	.	.		.	.	.			Indeterminate	0.6469	60.43%	100.00%	88%	Clonal
MP19	SLC8A3	p.Thr460Thr	synonymous_variant	14	70633760	G	T	6.86%	758	.	.	.		.	.	.			.	0.0000	31.52%	53.54%	42%	Subclonal
MP19	SIPA1L1	p.Ser992Ile	missense_variant	14	72139210	G	T	4.99%	802	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	21.92%	40.38%	30%	Subclonal
MP19	FAM161B	p.Leu102Leu	synonymous_variant	14	74413246	C	G	11.70%	359	.	.	.		.	.	.			.	0.1004	52.84%	92.25%	71%	Subclonal
MP19	SERPINA1	p.Trp218Ser	missense_variant	14	94847472	C	G	17.89%	123	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6851	58.83%	100.00%	91%	Clonal
MP19	DYNC1H1	p.Asp3725Asn	missense_variant	14	102505152	G	A	34.08%	672	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1659	97.51%	100.00%	100%	Clonal
MP19	SPTBN5	p.Lys3649Lys	synonymous_variant	15	42142132	T	C	30.30%	429	.	.	.		.	.	.			.	0.0236	94.10%	100.00%	100%	Clonal
MP19	PCSK6	p.Ala494Pro	missense_variant	15	101922346	C	G	4.63%	670	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	29.30%	58.47%	42%	Subclonal
MP19	OR4F15	p.Tyr35*	stop_gained	15	102358494	C	A	57.01%	649	D	.	.		.	.	.			Indeterminate	0.3549	98.72%	100.00%	100%	Clonal
MP19	PRR25	p.Thr4Asn	missense_variant	16	855453	C	A	10.31%	223	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0695	41.94%	89.49%	63%	Subclonal
MP19	MAPK8IP3	p.Leu532Leu	synonymous_variant	16	1812411	C	T	9.71%	350	.	.	.		.	.	.			.	0.0040	42.30%	80.14%	59%	Subclonal
MP19	ANKS3	p.Glu373Gln	missense_variant	16	4751437	C	G	8.07%	161	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0162	28.69%	80.18%	49%	Subclonal
MP19	ITPRIPL2	p.Ala210Asp	missense_variant	16	19126412	C	A	7.17%	711	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	32.95%	56.08%	44%	Subclonal
MP19	CCDC113	p.Asp73Gly	missense_variant	16	58286747	A	G	7.25%	138	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0006	19.89%	64.66%	37%	Subclonal
MP19	C16orf74	p.Ala76Val	missense_variant	16	85741618	G	A	14.97%	374	N	.	Passenger		.	.	.			Likely passenger	0.8628	77.33%	100.00%	100%	Clonal
MP19	NEURL4	p.Tyr467_Val470 del	inframe_deletion	17	7228748	CCACCACACC ATA	C	15.53%	818	D	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.0000	53.33%	73.62%	63%	Subclonal
MP19	TP53	p.Thr123fs	frameshift_variant	17	7579321	C	CA	49.18%	488	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9851	97.57%	100.00%	100%	Clonal
MP19	MYH8	p.Asp1624Ala	missense_variant	17	10298541	T	G	48.30%	176	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8106	94.69%	100.00%	100%	Clonal
MP19	SHMT1	p.Val33Phe	missense_variant	17	18257131	C	A	16.30%	227	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.5223	60.32%	98.39%	83%	Clonal
MP19	SLFN5	p.Ala46Ser	missense_variant	17	33585845	G	T	12.44%	402	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0020	48.09%	80.88%	63%	Subclonal
MP19	PGAP3	p.Ala18Ala	synonymous_variant	17	37844214	C	T	66.06%	165	.	.	.		true	.	true		TRUE	.	0.5018	96.16%	100.00%	100%	Clonal
MP19	KRT38	p.Gln235*	stop_gained	17	39595484	G	A	12.23%	458	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0004	47.96%	78.47%	62%	Subclonal
MP19	HDAC5	p.Pro932Pro	synonymous_variant	17	42157801	G	A	3.90%	616	.	.	.		.	.	.		TRUE	.	0.0000	12.90%	28.64%	20%	Subclonal
MP19	C17orf82	p.Asn103Lys	missense_variant	17	59489645	C	G	7.31%	834	P	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0050	51.58%	83.77%	66%	Subclonal
MP19	SCN4A	c.1101-2A>G	splice_acceptor_variant	17	62043605	T	C	5.69%	422	D	.	.		.	.	.			Indeterminate	0.0000	26.82%	58.44%	40%	Subclonal
MP19	TNRC6C	p.Gly301Val	missense_variant	17	76046045	G	T	15.13%	727	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8794	88.91%	100.00%	100%	Clonal
MP19	SMCHD1	p.Asn373Tyr	missense_variant	18	2697106	A	T	14.00%	350	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0589	54.13%	90.60%	71%	Subclonal
MP19	DSG4	p.Trp3Arg	missense_variant	18	28956881	T	A	5.69%	615	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7964	69.23%	100.00%	100%	Clonal
MP19	ASXL3	p.Ile462Ile	synonymous_variant	18	31318754	C	T	49.03%	259	.	.	.		.	.	.		TRUE	.	0.2289	96.16%	100.00%	100%	Clonal
MP19	MYO5B	p.Pro619Thr	missense_variant	18	47463665	G	T	16.16%	99	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5648	50.06%	98.62%	82%	Clonal
MP19	ZNF236	p.Leu1600Leu	synonymous_variant	18	74659500	C	T	24.40%	250	.	.	.		.	.	.		TRUE	.	0.8883	84.43%	100.00%	100%	Clonal
MP19	ZNF560	p.His566His	synonymous_variant	19	9577925	G	A	39.83%	241	.	.	.		.	.	.			.	0.7669	95.08%	100.00%	100%	Clonal
MP19	AP1M2	p.Asp323fs	frameshift_variant	19	10687938	CTGGTCTTGA ATCTGGGGGA G	C	5.20%	558	A	.	.		.	.	.			Indeterminate	0.0000	21.65%	44.28%	32%	Subclonal
MP19	ZNF564	p.Lys312Asn	missense_variant	19	12637986	T	G	21.07%	242	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8707	82.94%	100.00%	100%	Clonal
MP19	ZNF14	p.Asn528Ser	missense_variant	19	19822507	T	C	8.15%	184	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0002	25.02%	65.62%	41%	Subclonal
MP19	ZNF383	p.Pro52Thr	missense_variant	19	37726898	C	A	4.20%	238	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	15.92%	53.00%	30%	Subclonal
MP19	CYP2A6	p.Ile268Ile	synonymous_variant	19	41352807	A	G	8.26%	121	.	.	.		.	.	.			.	0.1878	31.80%	93.80%	58%	Subclonal
MP19	ZNF226	p.Arg30Gly	missense_variant	19	44676313	A	G	11.64%	438	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4656	62.74%	98.07%	82%	Subclonal
MP19	EML2	p.Trp734Leu	missense_variant	19	46117958	C	A	13.96%	308	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7983	70.98%	100.00%	99%	Clonal
MP19	SIGLEC8	p.Glu33Lys	missense_variant	19	51961545	C	T	5.08%	610	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0002	35.87%	71.31%	51%	Subclonal
MP19	NLRP7	p.Phe448Phe	synonymous_variant	19	55450843	G	A	3.95%	811	.	.	.		.	.	.			.	0.0000	27.85%	55.11%	40%	Subclonal
MP19	ZNF135	p.Glu627Glu	synonymous_variant	19	58579661	A	G	3.47%	346	.	.	.		.	.	.			.	0.0000	15.71%	47.68%	28%	Subclonal
MP19	REM1	p.Arg267Arg	synonymous_variant	20	30072137	C	T	27.07%	665	.	.	.		.	.	.			.	0.9416	96.70%	100.00%	100%	Clonal
MP19	PLCG1	p.Asp1165His	missense_variant	20	39802390	G	C	36.02%	855	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.8575	98.18%	100.00%	100%	Clonal
MP19	FAM65C	p.Thr435Thr	synonymous_variant	20	49218963	G	A	54.20%	655	.	.	.		.	.	.			.	0.4049	98.52%	100.00%	100%	Clonal
MP19	MYT1	p.Ser50Asn	missense_variant	20	62836450	G	A	12.02%	491	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8752	78.82%	100.00%	100%	Clonal
MP19	KRTAP8-1	p.Asn47Asn	synonymous_variant	21	32185398	G	A	55.47%	786	.	.	.		.	.	.		TRUE	.	0.5813	98.85%	100.00%	100%	Clonal
MP19	DEPDC5	p.Thr889Ser	missense_variant	22	32239663	C	G	11.90%	311	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1687	52.70%	94.20%	72%	Subclonal
MP19	TRIOBP	p.Val1652Phe	missense_variant	22	38131297	G	T	5.48%	821	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	28.68%	50.87%	39%	Subclonal
MP19	TCF20	p.Gln939His	missense_variant	22	42608495	T	A	11.19%	545	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2794	61.82%	96.42%	79%	Subclonal
MP19	TCF20	p.Trp820Cys	missense_variant	22	42608852	C	A	8.17%	355	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0069	40.24%	80.76%	58%	Subclonal
MP19	CHDC2	p.Lys164Thr	missense_variant	X	36103505	A	C	19.58%	475	N	.	Passenger		.	.	.			Likely passenger	0.3448	90.22%	100.00%	100%	Clonal
MP19	ZNF630	p.Glu223Lys	missense_variant	X	47919164	C	T	4.01%	274	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	15.58%	49.37%	28%	Subclonal
MP19	GRIPAP1	p.Glu801*	stop_gained	X	48831599	C	A	7.83%	345	D	.	.		.	.	.			Indeterminate	0.0039	38.04%	78.39%	55%	Subclonal
MP19	CYLC1	p.Gly592Gly	synonymous_variant	X	83129492	G	T	12.76%	337	.	.	.		.	.	.			.	0.3104	57.84%	96.67%	78%	Subclonal
MP19	OR13H1	p.Tyr258*	stop_gained	X	130678821	T	A	8.16%	441	D	.	.		.	.	.			Indeterminate	0.0018	41.68%	78.03%	58%	Subclonal
MP19	GPR112	p.Ile2810Thr	missense_variant	X	135482129	T	C	16.76%	185	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8518	73.74%	100.00%	100%	Clonal
MP19	SLITRK2	p.Ser601Leu	missense_variant	X	144905745	C	T	21.05%	437	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1338	91.18%	100.00%	100%	Clonal
MP19	ARHGAP4	p.Val591Val	synonymous_variant	X	153176404	G	A	44.14%	478	.	.	.		.	.	.			.	0.8229	97.69%	100.00%	100%	Clonal
MP21	SCNN1D	p.Pro157Thr	missense_variant	1	1220955	C	A	37.64%	433	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8801	96.63%	100.00%	100%	Clonal
MP21	HES5	p.Lys73Arg	missense_variant	1	2461287	T	C	58.00%	531	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.2522	98.07%	100.00%	100%	Clonal
MP21	SRSF4	p.Arg125Cys	missense_variant	1	29481413	G	A	76.18%	424	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0009	98.36%	100.00%	100%	Clonal
MP21	KLF17	p.Tyr343Tyr	synonymous_variant	1	44596287	T	C	4.21%	856	.	.	.		.	.	.		TRUE	.	0.0000	8.87%	17.21%	13%	Subclonal
MP21	CYB5RL	p.Glu49Asp	missense_variant	1	54661143	C	G	75.20%	375	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0209	98.20%	100.00%	100%	Clonal
MP21	ABCA4	p.Gly1508Ser	missense_variant	1	94495018	C	T	7.08%	226	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0000	13.06%	33.83%	22%	Subclonal
MP21	SELENBP1	p.Ile432Met	missense_variant	1	151337488	G	C	12.50%	960	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9299	87.28%	100.00%	100%	Clonal
MP21	THBS3	p.Gly656Ala	missense_variant	1	155168307	C	G	14.27%	876	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.6169	91.03%	100.00%	100%	Clonal
MP21	OR6K6	p.Arg247Arg	synonymous_variant	1	158725346	G	A	15.02%	812	.	.	.		.	.	.			.	0.9223	85.13%	100.00%	100%	Clonal
MP21	OLFML2B	p.Arg278Gln	missense_variant	1	161970022	C	T	23.80%	895	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4455	96.39%	100.00%	100%	Clonal
MP21	FMO1	p.Pro404Pro	synonymous_variant	1	171252299	A	G	19.50%	477	.	.	.		.	.	.		TRUE	.	0.9181	86.95%	100.00%	100%	Clonal
MP21	HLX	p.Ser461Ser	synonymous_variant	1	221057962	G	C	57.84%	925	.	.	.		.	.	.			.	0.0337	99.02%	100.00%	100%	Clonal
MP21	TAF5L	p.Glu236Asp	missense_variant	1	229738206	C	G	3.30%	938	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	16.06%	32.41%	23%	Subclonal
MP21	PREB	p.Ala36Ala	synonymous_variant	2	27357182	G	A	3.97%	831	.	.	.		.	.	.		TRUE	.	0.0000	8.18%	16.51%	12%	Subclonal
MP21	GFPT1	p.Gln404His	missense_variant	2	69565689	T	A	2.71%	738	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.39%	20.56%	14%	Subclonal
MP21	KCNJ3	p.Ser420Ile	missense_variant	2	155711578	G	T	37.96%	245	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9795	93.83%	100.00%	100%	Clonal
MP21	MYO3B	p.Glu1152Lys	missense_variant	2	171371514	G	A	67.55%	379	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9866	98.06%	100.00%	100%	Clonal
MP21	TTN	p.Lys24139Glu	missense_variant	2	179438444	T	C	67.57%	296	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9862	97.46%	100.00%	100%	Clonal
MP21	ABCA12	p.Met1642Ile	missense_variant	2	215843579	C	A	69.14%	243	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9762	97.15%	100.00%	100%	Clonal
MP21	RPSA	p.Val252Val	synonymous_variant	3	39453515	A	G	4.55%	110	.	.	.		.	.	.		TRUE	.	0.0000	5.63%	30.78%	14%	Subclonal
MP21	BFSP2	p.Val8Met	missense_variant	3	133118949	G	A	30.48%	853	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	96.88%	100.00%	100%	Clonal
MP21	NLGN1	p.Pro309Ser	missense_variant	3	173996716	C	T	11.38%	659	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7539	72.65%	100.00%	92%	Clonal
MP21	GRID2	p.Ser816Ser	synonymous_variant	4	94690448	A	G	6.29%	350	.	.	.		.	.	.		TRUE	.	0.0000	12.33%	28.13%	19%	Subclonal
MP21	MARCH6	p.Gln166*	stop_gained	5	10390532	C	T	8.70%	345	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	18.37%	36.76%	27%	Subclonal
MP21	SLC22A5	p.Phe513Phe	synonymous_variant	5	131729456	C	T	65.60%	593	.	.	.		.	.	.		TRUE	.	0.9929	98.44%	100.00%	100%	Clonal
MP21	GABRA6	p.Ala410Thr	missense_variant	5	161128645	G	A	77.50%	689	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5090	99.02%	100.00%	100%	Clonal
MP21	ADAMTS2	p.Arg1047His	missense_variant	5	178548700	C	T	82.60%	885	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0475	99.02%	100.00%	100%	Clonal
MP21	CUL7	p.Glu163*	stop_gained	6	43020196	C	A	37.43%	887	A	.	.		.	.	.			Indeterminate	0.9791	98.06%	100.00%	100%	Clonal
MP21	CEP162	p.Asp1070Asp	synonymous_variant	6	84862683	A	G	50.67%	750	.	.	.		.	.	.			.	0.4822	98.53%	100.00%	100%	Clonal
MP21	KIAA1324L	p.Pro876Pro	synonymous_variant	7	86526879	A	C	61.48%	122	.	.	.		.	.	.		TRUE	.	0.9776	93.38%	100.00%	100%	Clonal
MP21	SPDYE6	p.Pro297Leu	missense_variant	7	101988983	G	A	10.00%	280	.	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	21.04%	42.68%	31%	Subclonal
MP21	KMT2C	p.Leu736Leu	synonymous_variant	7	151945313	A	G	21.43%	28	.	.	.		true	true	true		TRUE	.	0.7164	41.98%	100.00%	100%	Clonal
MP21	TNFRSF10C	p.Pro202Pro	synonymous_variant	8	22974370	G	A	12.24%	245	.	.	.		.	.	.			.	0.0236	43.68%	85.15%	62%	Subclonal
MP21	CHRNA2	p.Leu66Leu	synonymous_variant	8	27327374	G	C	34.60%	896	.	.	.		.	.	.			.	0.5275	97.70%	100.00%	100%	Clonal
MP21	INTS9	p.Ala319Thr	missense_variant	8	28651406	C	T	3.43%	699	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.24%	25.13%	17%	Subclonal
MP21	PKHD1L1	p.Trp2625Arg	missense_variant	8	110476934	T	C	3.09%	777	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.16%	27.14%	19%	Subclonal
MP21	KIAA2026	p.Glu946Gln	missense_variant	9	5923160	C	G	4.24%	543	N	.	Passenger		.	.	.		TRUE	Likely passenger	0.0000	8.19%	18.78%	13%	Subclonal
MP21	GCNT1	p.Leu203Arg	missense_variant	9	79117905	T	G	40.97%	576	D	PASSENGER/OTHER	Driver		.	.	.	TRUE		Likely pathogenic	0.9842	97.45%	100.00%	100%	Clonal
MP21	GNAQ	p.Thr96Ser	missense_variant	9	80537112	T	A	10.05%	219	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0016	33.65%	74.20%	51%	Subclonal
MP21	RBP3	p.Arg665Arg	synonymous_variant	10	48388883	C	A	73.72%	643	.	.	.		.	.	.		TRUE	.	0.0037	99.01%	100.00%	100%	Clonal
MP21	SFTPA1	p.Arg109Arg	synonymous_variant	10	81372177	G	A	11.46%	855	.	.	.		.	.	.		TRUE	.	0.0000	47.59%	69.29%	58%	Subclonal
MP21	LDB3	p.Lys243Arg	missense_variant	10	88446864	A	G	32.39%	880	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0078	97.27%	100.00%	100%	Clonal
MP21	SFRP5	p.Arg237Arg	synonymous_variant	10	99527514	G	A	42.39%	762	.	.	.		.	.	.		TRUE	.	0.9607	98.12%	100.00%	100%	Clonal
MP21	CYP2E1	p.Phe189fs	frameshift_variant	10	135345703	ATTTTGACTAC AATGATGAGA AG	A	5.98%	836	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	13.44%	23.47%	18%	Subclonal
MP21	MS4A4A	p.Thr213Ile	missense_variant	11	60073664	C	T	27.57%	653	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0015	94.76%	100.00%	100%	Clonal
MP21	FADS2	p.Arg114Trp	missense_variant	11	61607827	C	T	40.74%	653	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9859	97.78%	100.00%	100%	Clonal
MP21	ZBTB3	p.Glu66Glu	synonymous_variant	11	62521089	C	T	40.71%	899	.	.	.		.	.	.			.	0.0003	98.05%	100.00%	100%	Clonal
MP21	KCNK4	p.Ala326Val	missense_variant	11	64066993	C	T	44.24%	886	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6104	98.34%	100.00%	100%	Clonal
MP21	CDC42BPG	p.Val1060Leu	missense_variant	11	64599103	C	G	37.64%	898	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9819	98.07%	100.00%	100%	Clonal
MP21	SSH3	p.Gly180Gly	synonymous_variant	11	67074845	C	A	33.22%	846	.	.	.		.	.	.			.	0.0782	97.31%	100.00%	100%	Clonal
MP21	USP28	p.Asp265Tyr	missense_variant	11	113702682	C	A	24.64%	280	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0571	60.69%	91.32%	76%	Subclonal
MP21	SCNN1A	p.Arg198Ser	missense_variant	12	6472876	C	A	24.68%	782	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3776	93.62%	100.00%	100%	Clonal
MP21	GRIP1	p.Leu794Phe	missense_variant	12	66773143	C	G	67.20%	189	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9858	96.23%	100.00%	100%	Clonal
MP21	TRHDE	p.Leu48Leu	synonymous_variant	12	72666702	C	T	63.94%	771	.	.	.		.	.	.		TRUE	.	0.9918	98.93%	100.00%	100%	Clonal
MP21	STAB2	p.Val1621Met	missense_variant	12	104121054	G	A	69.46%	740	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8941	99.01%	100.00%	100%	Clonal
MP21	POTEG	p.Lys142Lys	synonymous_variant	14	19553842	G	A	14.29%	56	.	.	.		.	.	.			.	0.4931	36.15%	97.90%	72%	Subclonal
MP21	GPX2	p.Leu185fs	frameshift_variant	14	65406211	TGGCAACTTT AAGGA	T	29.57%	1018	.	.	.		.	.	.		TRUE	Likely pathogenic	0.4662	81.76%	98.08%	91%	Subclonal
MP21	MAP3K9	p.Asp389Tyr	missense_variant	14	71215707	C	A	43.97%	257	D	CANCER	Driver		.	.	.			Likely pathogenic	0.9487	95.37%	100.00%	100%	Clonal
MP21	INO80	p.Leu204Leu	synonymous_variant	15	41379806	T	A	7.07%	184	.	.	.		.	.	.		TRUE	.	0.0000	12.34%	35.44%	22%	Subclonal
MP21	MYEF2	p.Gly384Arg	missense_variant	15	48444128	C	G	2.85%	527	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	4.81%	13.77%	9%	Subclonal
MP21	NOX5	p.Thr713Thr	synonymous_variant	15	69347813	C	A	8.67%	323	.	.	.		.	.	.		TRUE	.	0.0000	24.19%	49.31%	35%	Subclonal
MP21	CCNF	p.Phe15Phe	synonymous_variant	16	2481159	C	T	3.11%	579	.	.	.		.	.	.		TRUE	.	0.0000	9.49%	24.13%	16%	Subclonal
MP21	ITGAX	p.Arg842Arg	synonymous_variant	16	31388137	T	A	40.85%	913	.	.	.		.	.	.			.	0.9862	98.22%	100.00%	100%	Clonal
MP21	ABCC12	p.Phe174Ser	missense_variant	16	48174734	A	G	13.74%	473	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	43.97%	69.21%	56%	Subclonal
MP21	ABCC11	p.Lys411Lys	synonymous_variant	16	48248807	T	C	52.16%	464	.	.	.		.	.	.		TRUE	.	0.9755	97.75%	100.00%	100%	Clonal
MP21	FTO	p.Pro470Thr	missense_variant	16	54145717	C	A	54.71%	223	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9417	96.01%	100.00%	100%	Clonal
MP21	SMG6	p.Leu19Leu	synonymous_variant	17	2206960	G	A	71.71%	304	.	.	.		.	.	.		TRUE	.	0.8554	97.88%	100.00%	100%	Clonal
MP21	TNK1	p.Tyr330Tyr	synonymous_variant	17	7287926	C	T	75.82%	790	.	.	.		.	.	.		TRUE	.	0.0000	99.02%	100.00%	100%	Clonal
MP21	TP53	p.Val173Gly	missense_variant	17	7578412	A	C	71.84%	870	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.0310	99.02%	100.00%	100%	Clonal
MP21	C1QTNF1	p.Lys213*	stop_gained	17	77043961	A	T	82.13%	901	D	.	.		.	.	.		TRUE	Likely pathogenic	0.6211	99.02%	100.00%	100%	Clonal
MP21	HGS	p.Ala756Thr	missense_variant	17	79668580	G	A	30.25%	734	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9589	97.03%	100.00%	100%	Clonal
MP21	MOCOS	p.Met655Leu	missense_variant	18	33828887	A	T	4.33%	624	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	14.64%	31.01%	22%	Subclonal
MP21	SETBP1	c.486+2T>C	splice_donor_variant	18	42281799	T	C	3.16%	506	D	.	.		true	true	.			Likely pathogenic	0.0000	9.40%	25.22%	16%	Subclonal
MP21	PNPLA6	p.Arg442His	missense_variant	19	7607492	G	A	4.19%	907	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.0000	18.12%	34.06%	25%	Subclonal
MP21	ARRDC2	p.Glu334Gln	missense_variant	19	18121155	G	C	39.81%	751	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0335	98.10%	100.00%	100%	Clonal
MP21	KIAA1683	p.His674His	synonymous_variant	19	18376328	A	G	39.96%	896	.	.	.		.	.	.			.	0.0058	98.26%	100.00%	100%	Clonal
MP21	TMEM161A	p.Met203fs	frameshift_variant	19	19232616	A	ACTAAG	9.97%	1414	A	.	.		.	.	.			Indeterminate	0.0000	51.16%	70.14%	60%	Subclonal
MP21	SEC23B	p.Thr381Ser	missense_variant	20	18511356	C	G	3.26%	583	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	5.99%	14.93%	10%	Subclonal
MP21	PCIF1	p.Ile456Val	missense_variant	20	44574692	A	G	39.26%	889	N	.	Passenger		.	.	.			Likely passenger	0.9902	98.13%	100.00%	100%	Clonal
MP21	RNF114	p.Tyr113Tyr	synonymous_variant	20	48561966	C	T	39.25%	456	.	.	.		.	.	.			.	0.9864	96.69%	100.00%	100%	Clonal
MP21	COL20A1	p.Ile550Met	missense_variant	20	61943087	C	G	39.73%	886	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9901	98.14%	100.00%	100%	Clonal
MP21	RUNX1	p.Ser77Gly	missense_variant	21	36259262	T	C	70.71%	478	D	CANCER	Passenger		true	true	true	TRUE	TRUE	Likely pathogenic	0.8389	98.34%	100.00%	100%	Clonal
MP21	IGLL1	p.Ala174Val	missense_variant	22	23915574	G	A	7.66%	248	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	14.73%	35.26%	23%	Subclonal
MP21	CRYBB1	p.Gly111Trp	missense_variant	22	27003954	C	A	60.51%	785	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7825	98.65%	100.00%	100%	Clonal
MP21	DEPDC5	p.Arg165Cys	missense_variant	22	32179902	C	T	42.54%	315	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1632	93.23%	100.00%	100%	Clonal
MP21	DEPDC5	c.1871-1G>A	splice_acceptor_variant	22	32217487	G	A	50.32%	157	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0466	92.11%	100.00%	100%	Clonal
MP21	CCDC120	p.Ser325Leu	missense_variant	X	48923289	C	T	8.95%	838	D	.	Passenger		.	.	true		TRUE	Likely pathogenic	0.0000	21.53%	33.51%	27%	Subclonal
MP21	TSR2	p.Arg9*	stop_gained	X	54466879	C	T	8.82%	782	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	21.07%	33.32%	27%	Subclonal
MP21	ERCC6L	p.Phe717Phe	synonymous_variant	X	71426466	G	A	21.56%	436	.	.	.		.	.	.			.	0.9221	84.55%	100.00%	100%	Clonal
MP21	COL4A6	c.2567-1G>A	splice_acceptor_variant	X	107420242	C	T	66.75%	421	D	.	.		.	.	.		TRUE	Likely pathogenic	0.9899	98.12%	100.00%	100%	Clonal
MP27	ALDH4A1	p.Val329Met	missense_variant	1	19204062	C	T	3.87%	181	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	10.76%	45.16%	23%	Subclonal
MP27	NBL1	p.Met49Lys	missense_variant	1	19981564	T	A	13.92%	158	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6580	53.81%	98.54%	82%	Clonal
MP27	KPNA6	p.Glu350Asp	missense_variant	1	32631765	G	T	31.81%	525	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7654	97.02%	100.00%	100%	Clonal
MP27	CSMD2	p.Arg3132Lys	missense_variant	1	34006792	C	T	39.34%	272	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5017	95.81%	100.00%	100%	Clonal
MP27	NBPF8	p.Leu363Leu	synonymous_variant	1	148025763	G	A	15.87%	63	.	.	.		.	.	.			.	0.9181	61.49%	100.00%	100%	Clonal
MP27	FLG2	p.Gly1114Gly	synonymous_variant	1	152326920	G	A	4.88%	533	.	.	.		.	.	.			.	0.0237	39.38%	83.08%	58%	Subclonal
MP27	UBQLN4	p.Arg407His	missense_variant	1	156012611	C	T	10.84%	166	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8665	66.33%	100.00%	100%	Clonal
MP27	RRNAD1	p.Leu257Leu	synonymous_variant	1	156703935	C	T	5.22%	230	.	.	.		.	.	.			.	0.3022	35.28%	94.90%	62%	Subclonal
MP27	FAM78B	p.Thr119Thr	synonymous_variant	1	166039907	T	C	12.16%	296	.	.	.		.	.	.			.	0.8647	80.22%	100.00%	100%	Clonal
MP27	CHI3L1	p.Thr82Arg	missense_variant	1	203154324	G	C	34.41%	186	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7520	92.88%	100.00%	100%	Clonal
MP27	DNAH14	p.Ala3107Pro	missense_variant	1	225512026	G	C	8.31%	361	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3808	51.65%	96.35%	74%	Subclonal
MP27	SIPA1L2	p.Lys524Gln	missense_variant	1	232629320	T	G	42.65%	340	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6553	97.04%	100.00%	100%	Clonal
MP27	DNAH6	p.Val1752Ile	missense_variant	2	84880618	G	A	41.09%	331	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5246	96.66%	100.00%	100%	Clonal
MP27	CNGA3	p.Ala469Thr	missense_variant	2	99013038	G	A	29.07%	172	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8222	90.35%	100.00%	100%	Clonal
MP27	IL18R1	p.Ser290Ser	synonymous_variant	2	103003381	C	T	6.55%	168	.	.	.		.	.	.		TRUE	.	0.0012	21.37%	66.23%	39%	Subclonal
MP27	TUBA3D	p.Gly162Ser	missense_variant	2	132237750	G	A	10.00%	50	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4326	24.92%	96.46%	59%	Subclonal
MP27	SCN2A	p.Gly1937Ala	missense_variant	2	166246126	G	C	5.61%	321	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0077	31.36%	76.62%	50%	Subclonal
MP27	PPIG	p.His133Asn	missense_variant	2	170470993	C	A	12.71%	598	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9290	82.93%	100.00%	100%	Clonal
MP27	SLC11A1	p.Glu79Asp	missense_variant	2	219249052	G	T	12.68%	489	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9076	83.87%	100.00%	100%	Clonal
MP27	CAND2	p.Glu861Val	missense_variant	3	12859013	A	T	19.81%	212	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9142	77.76%	100.00%	100%	Clonal
MP27	KLF15	p.Ser293Leu	missense_variant	3	126070888	G	A	4.03%	273	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0004	19.76%	62.29%	36%	Subclonal
MP27	CP	p.Ser474Arg	missense_variant	3	148917580	T	G	15.31%	405	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8017	85.90%	100.00%	100%	Clonal
MP27	AP2M1	p.Ile222Val	missense_variant	3	183898971	A	G	5.45%	624	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0640	46.19%	88.28%	65%	Subclonal
MP27	RTP1	p.Val21Val	synonymous_variant	3	186915366	G	T	30.81%	675	.	.	.		.	.	.			.	0.4895	97.65%	100.00%	100%	Clonal
MP27	SST	p.Ala9Pro	missense_variant	3	187388055	C	G	29.96%	257	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6066	94.16%	100.00%	100%	Clonal
MP27	DHX15	p.Val510Val	synonymous_variant	4	24542527	A	T	33.99%	306	.	.	.		.	.	.			.	0.7949	95.39%	100.00%	100%	Clonal
MP27	CCDC149	p.Gln156*	stop_gained	4	24839801	G	A	11.46%	157	A	.	.		.	.	.			Indeterminate	0.8120	59.50%	100.00%	100%	Clonal
MP27	N4BP2	p.Ala651Ala	synonymous_variant	4	40121684	A	G	29.55%	176	.	.	.		.	.	.			.	0.7953	90.77%	100.00%	100%	Clonal
MP27	FAM13A	p.Asp391Tyr	missense_variant	4	89709004	C	A	33.33%	183	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9370	91.63%	100.00%	100%	Clonal
MP27	PCDH18	p.Ser782Phe	missense_variant	4	138450898	G	A	31.37%	408	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9670	95.53%	100.00%	100%	Clonal
MP27	MROH2B	c.4651+1G>A	splice_donor_variant	5	40998713	C	T	65.43%	81	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	92.60%	100.00%	100%	Clonal
MP27	NNT	p.Asn3Ile	missense_variant	5	43609305	A	T	36.45%	310	D	.	Passenger		.	.	.			Indeterminate	0.7049	95.93%	100.00%	100%	Clonal
MP27	GPR98	p.Lys5789Glu	missense_variant	5	90149261	A	G	3.93%	178	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	10.97%	45.91%	23%	Subclonal
MP27	PCDHA8	p.Gly97Arg	missense_variant	5	140221195	G	C	10.96%	73	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4492	32.51%	96.72%	64%	Subclonal
MP27	TENM2	p.Arg60Gln	missense_variant	5	166712021	G	A	16.09%	87	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7767	53.40%	100.00%	95%	Clonal
MP27	GABRP	p.Ile355del	disruptive_inframe_deletion	5	170238998	TATC	T	55.92%	363	D	.	.	Neutral	.	.	.		TRUE	Likely pathogenic	0.0000	97.75%	100.00%	100%	Clonal
MP27	MAPK14	p.Pro318Pro	synonymous_variant	6	36075344	A	C	7.14%	588	D	PASSENGER/OTHER	.		.	.	.			.	0.0156	46.86%	83.93%	63%	Subclonal
MP27	MAPK14	p.Val319Leu	missense_variant	6	36075345	G	C	7.22%	582	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0201	47.34%	84.77%	64%	Subclonal
MP27	RP9	p.Arg110Cys	missense_variant	7	33136960	G	A	39.87%	153	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6217	92.98%	100.00%	100%	Clonal
MP27	ABCB1	p.Arg157Gly	missense_variant	7	87196162	G	C	4.15%	265	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0007	20.37%	64.14%	37%	Subclonal
MP27	PRRT4	p.Ser851Tyr	missense_variant	7	127991058	G	T	6.93%	202	D	.	Passenger		.	.	.			Indeterminate	0.2390	36.62%	93.59%	62%	Subclonal
MP27	CNOT4	p.Leu240Pro	missense_variant	7	135095367	A	G	27.99%	343	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7103	94.53%	100.00%	100%	Clonal
MP27	KMT2C	p.Asp4530His	missense_variant	7	151845424	C	G	3.23%	465	D	PASSENGER/OTHER	Passenger		true	true	true		TRUE	Likely pathogenic	0.0000	11.11%	30.42%	19%	Subclonal
MP27	HR	p.Leu1043Leu	synonymous_variant	8	21976547	G	C	41.78%	383	.	.	.		.	.	.			.	0.5810	97.15%	100.00%	100%	Clonal
MP27	LOXL2	p.Leu437Leu	synonymous_variant	8	23177559	G	A	17.01%	582	.	.	.		.	.	.			.	0.2113	91.64%	100.00%	100%	Clonal
MP27	ADAM9	p.Arg202Leu	missense_variant	8	38874932	G	T	13.75%	291	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9044	77.89%	100.00%	100%	Clonal
MP27	CALB1	p.Leu218Pro	missense_variant	8	91072876	A	G	8.90%	191	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6114	48.63%	98.35%	79%	Clonal
MP27	OXR1	p.Ser270Leu	missense_variant	8	107715264	C	T	26.44%	295	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9052	93.19%	100.00%	100%	Clonal
MP27	EEF1D	p.Arg276_Arg281 del	disruptive_inframe_deletion	8	144671407	TTGCGGCCCC GCCGGTCTC	T	13.21%	1014	P	.	.	Deleterious	.	.	.			Indeterminate	0.2732	93.75%	100.00%	100%	Clonal
MP27	DOCK8	p.Asn642Ser	missense_variant	9	371484	A	G	14.40%	250	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8965	77.74%	100.00%	100%	Clonal
MP27	FAM154A	p.Ser321Pro	missense_variant	9	18928514	A	G	17.79%	208	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8957	82.55%	100.00%	100%	Clonal
MP27	TAF1L	p.Arg823*	stop_gained	9	32633111	G	A	37.67%	454	D	.	.		.	.	.			Indeterminate	0.5119	97.19%	100.00%	100%	Clonal
MP27	TAF1L	p.Ser576Cys	missense_variant	9	32633851	G	C	6.86%	656	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0033	45.40%	79.93%	61%	Subclonal
MP27	TJP2	p.Lys869*	stop_gained	9	71855009	A	T	37.08%	383	A	.	.		.	.	.			Indeterminate	0.6334	96.67%	100.00%	100%	Clonal
MP27	PRUNE2	p.Cys313Cys	synonymous_variant	9	79326251	A	G	42.07%	328	.	.	.		.	.	.			.	0.6212	96.75%	100.00%	100%	Clonal
MP27	HSDL2	p.Ile72Val	missense_variant	9	115167936	A	G	68.35%	376	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	98.21%	100.00%	100%	Clonal
MP27	PRRC2B	p.Gln2043His	missense_variant	9	134363387	G	T	6.25%	272	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0081	30.65%	76.53%	49%	Subclonal
MP27	ARHGAP21	p.Gln763Glu	missense_variant	10	24908537	G	C	11.65%	412	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8826	74.15%	100.00%	100%	Clonal
MP27	LYZL2	p.Ser19Tyr	missense_variant	10	30918579	G	T	46.67%	270	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2159	96.70%	100.00%	100%	Clonal
MP27	OR5AR1	p.Phe104fs	frameshift_variant	11	56431466	CT	C	31.53%	647	D	.	.		.	.	.			Indeterminate	0.7328	97.37%	100.00%	100%	Clonal
MP27	EEF1G	p.Gly318Cys	missense_variant	11	62327832	C	A	14.53%	234	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8937	77.17%	100.00%	100%	Clonal
MP27	SAC3D1	p.Pro211Leu	missense_variant	11	64811754	C	T	3.46%	549	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	19.32%	46.94%	31%	Subclonal
MP27	C11orf87	p.Pro167_Pro169 del	disruptive_inframe_deletion	11	109294851	TCCGCCTCCA	T	13.43%	633	P	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.9217	81.56%	100.00%	100%	Clonal
MP27	AMICA1	c.912-1G>A	splice_acceptor_variant	11	118068807	C	T	3.49%	401	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	16.08%	45.00%	28%	Subclonal
MP27	ADIPOR2	p.Gly280Gly	synonymous_variant	12	1893047	A	G	22.47%	485	.	.	.		.	.	.			.	0.6269	95.21%	100.00%	100%	Clonal
MP27	IFFO1	p.Lys90Glu	missense_variant	12	6664928	T	C	11.11%	693	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8191	87.17%	100.00%	100%	Clonal
MP27	ETV6	p.Pro25Arg	missense_variant	12	11905424	C	G	34.59%	370	N	PASSENGER/OTHER	Passenger		true	.	.	TRUE		Likely passenger	0.8011	96.23%	100.00%	100%	Clonal
MP27	FKBP11	c.318-1G>A	splice_acceptor_variant	12	49317636	C	T	5.00%	240	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	16.55%	49.71%	29%	Subclonal
MP27	KRT5	p.Lys405Asn	missense_variant	12	52910894	T	A	46.94%	49	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.7743	82.63%	100.00%	100%	Clonal

MP27	*SUOX*	p.Gly54fs	frameshift_variant	12	56396433	CAGGGATGGAG	C	40.14%	416	A	.	.		.	.	.		TRUE	Likely pathogenic	0.6565	96.86%	100.00%	100%	Clonal			
MP27	*LRRIQ1*	p.Trp752*	stop_gained	12	85450826	G	A	13.54%	347	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9115	79.53%	100.00%	100%	Clonal			
MP27	*SPPL3*	p.Ala208Ala	synonymous_variant	12	121206277	G	A	50.88%	228	.	.	.		.	.	.		TRUE	.	0.0000	96.11%	100.00%	100%	Clonal			
MP27	*CLIP1*	p.Glu960*	stop_gained	12	122812963	C	A	5.66%	106	A	.	.		true	.	.		TRUE	Likely pathogenic	0.0068	15.20%	68.81%	33%	Subclonal			
MP27	*PROZ*	p.Leu119Val	missense_variant	13	113817352	C	G	3.08%	585	N	CANCER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	22.81%	56.67%	37%	Subclonal			
MP27	*RNF212B*	p.Lys57Asn	missense_variant	14	23713548	G	C	28.08%	292	D	.	Passenger		.	.	.			Indeterminate	0.7627	93.72%	100.00%	100%	Clonal			
MP27	*EFS*	p.Arg505Ser	missense_variant	14	23826606	C	G	4.29%	396	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	23.54%	59.62%	38%	Subclonal			
MP27	*BMP4*	p.Ser133Ile	missense_variant	14	54417579	C	A	3.43%	350	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0000	11.17%	34.18%	20%	Subclonal			
MP27	*VSX2*	p.Ile296Ile	synonymous_variant	14	74727424	C	A	33.19%	226	.	.	.		.	.	.		TRUE	.	0.9770	92.36%	100.00%	100%	Clonal			
MP27	*CPSF2*	p.Glu475Ala	missense_variant	14	92621649	A	C	60.33%	184	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	96.18%	100.00%	100%	Clonal			
MP27	*RCOR1*	p.Met164Ile	missense_variant	14	103167661	G	A	31.06%	132	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9636	86.44%	100.00%	100%	Clonal			
MP27	*EID1*	p.Ala49Pro	missense_variant	15	49170518	G	C	56.20%	258	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	97.02%	100.00%	100%	Clonal			
MP27	*KIF7*	p.Pro543Arg	missense_variant	15	90190221	G	C	80.70%	399	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	98.58%	100.00%	100%	Clonal			
MP27	*ZNF774*	p.Ala264Ala	synonymous_variant	15	90903855	G	A	75.04%	629	.	.	.		.	.	.		TRUE	.	0.0159	99.02%	100.00%	100%	Clonal			
MP27	*ADAMTS17*	p.Lys535Lys	synonymous_variant	15	100672328	C	T	11.71%	316	.	.	.		.	.	.		TRUE	.	0.8704	81.33%	100.00%	100%	Clonal			
MP27	*E4F1*	p.His457Tyr	missense_variant	16	2283985	C	T	14.02%	264	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9003	77.37%	100.00%	100%	Clonal			
MP27	*SLX4*	p.Ala1358Gly	missense_variant	16	3639566	G	C	12.26%	212	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8619	67.79%	100.00%	100%	Clonal			
MP27	*DNAH3*	p.Ala3421Pro	missense_variant	16	20974945	C	G	11.78%	535	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7282	86.32%	100.00%	100%	Clonal			
MP27	*ADCY7*	p.Pro720Leu	missense_variant	16	50343556	C	T	5.21%	96	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0070	13.05%	67.70%	31%	Subclonal			
MP27	*PAFAH1B1*	p.Arg89Gln	missense_variant	17	2570359	G	A	6.67%	90	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0405	18.01%	79.60%	39%	Subclonal			
MP27	*TP53*	p.Cys176Phe	missense_variant	17	7578403	C	A	52.19%	366	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.0000	97.48%	100.00%	100%	Clonal			
MP27	*ADORA2B*	p.Arg215Leu	missense_variant	17	15878301	G	T	11.84%	245	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2305	48.72%	93.73%	70%	Subclonal			
MP27	*KRTAP4-6*	p.Ile191Ile	synonymous_variant	17	39296167	A	G	13.33%	45	.	.	.		.	.	.		TRUE	.	0.7055	37.69%	98.85%	92%	Clonal			
MP27	*SAP30BP*	p.Lys202Asn	missense_variant	17	73700840	G	C	36.51%	430	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.6911	97.03%	100.00%	100%	Clonal			
MP27	*MRPL38*	p.Arg58Leu	missense_variant	17	73900695	C	A	6.43%	451	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0090	39.65%	80.12%	57%	Subclonal			
MP27	*FBF1*	p.Arg756Cys	missense_variant	17	73914087	G	A	3.48%	230	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0004	15.44%	59.08%	31%	Subclonal			
MP27	*PALM*	p.Arg33Leu	missense_variant	19	727048	G	T	9.40%	117	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1536	31.00%	90.32%	55%	Subclonal			
MP27	*RASAL3*	p.Glu924Lys	missense_variant	19	15563527	C	T	20.17%	238	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9206	80.06%	100.00%	100%	Clonal			
MP27	*CHERP*	p.Trp472Cys	missense_variant	19	16636378	C	G	10.71%	140	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2507	38.35%	93.64%	63%	Subclonal			
MP27	*ZNF429*	p.Thr243Ser	missense_variant	19	21719583	C	G	60.00%	120	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	94.27%	100.00%	100%	Clonal			
MP27	*CYP2A6*	p.Leu73Leu	synonymous_variant	19	41355849	A	G	26.25%	80	.	.	.		.	.	.		TRUE	.	0.9310	79.07%	100.00%	100%	Clonal			
MP27	*PHLDB3*	p.Arg545Cys	missense_variant	19	43983598	G	A	7.61%	460	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1124	48.57%	90.83%	68%	Subclonal			
MP27	*SHANK1*	p.Leu132Leu	synonymous_variant	19	51219595	C	G	62.66%	241	.	.	.		.	.	.		TRUE	.	0.0029	97.22%	100.00%	100%	Clonal			
MP27	*FAM71E2*	p.Glu45*	stop_gained	19	55874302	C	A	33.81%	494	A	.	.		.	.	.		TRUE	Likely pathogenic	0.4497	97.00%	100.00%	100%	Clonal			
MP27	*ZNF586*	p.Arg310Gln	missense_variant	19	58290884	G	A	3.65%	356	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	16.50%	47.94%	29%	Subclonal			
MP27	*SLC52A3*	p.Val415Met	missense_variant	20	741837	C	T	13.03%	261	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8925	73.91%	100.00%	100%	Clonal			
MP27	*CST1*	p.Thr77Thr	synonymous_variant	20	23729764	G	A	37.66%	154	.	.	.		.	.	.			.	0.6655	92.44%	100.00%	100%	Clonal			
MP27	*ASXL1*	p.Asn57Ser	missense_variant	20	30956844	A	G	5.88%	306	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.0181	32.95%	80.19%	52%	Subclonal			
MP27	*CDH4*	p.Ala344Ala	synonymous_variant	20	60448938	G	C	4.98%	261	.	.	.		.	.	.			.	0.0061	25.70%	73.46%	44%	Subclonal			
MP27	*COL6A2*	p.Ile759Phe	missense_variant	21	47546004	A	T	12.06%	572	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9146	79.84%	100.00%	100%	Clonal			
MP27	*TANGO2*	p.Arg108Gly	missense_variant	22	20040041	C	G	37.71%	175	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6556	93.29%	100.00%	100%	Clonal			
MP27	*SCARF2*	p.Arg390Cys	missense_variant	22	20784750	G	A	35.12%	205	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7471	93.64%	100.00%	100%	Clonal			
MP27	*PI4KA*	p.Phe1738Leu	missense_variant	22	21073013	A	C	18.63%	102	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9295	73.01%	100.00%	100%	Clonal			
MP27	*PPM1F*	p.Lys8Asn	missense_variant	22	22300397	C	A	35.60%	250	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7450	94.83%	100.00%	100%	Clonal			
MP27	*CABIN1*	p.Arg1807Gln	missense_variant	22	24563019	G	A	4.00%	175	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0081	17.10%	70.60%	36%	Subclonal			
MP27	*TTC28*	p.Val1638Ile	missense_variant	22	28394735	C	T	12.63%	578	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9267	82.26%	100.00%	100%	Clonal			
MP27	*PKDREJ*	p.Ala237Glu	missense_variant	22	46658510	G	T	48.68%	717	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1901	98.56%	100.00%	100%	Clonal			
MP27	*FAM47A*	p.Lys663Thr	missense_variant	X	34148408	T	G	37.40%	393	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5859	96.83%	100.00%	100%	Clonal			
MP27	*GPKOW*	p.Arg25Leu	missense_variant	X	48979999	C	A	36.10%	698	D	.	Passenger		.	.	.			Indeterminate	0.7155	98.05%	100.00%	100%	Clonal			
MP27	*CCDC22*	p.Ser447Ser	synonymous_variant	X	49105105	T	A	32.22%	509	.	.	.		.	.	.			.	0.7933	97.01%	100.00%	100%	Clonal			
MP27	*HSD17B10*	p.Glu249Glu	synonymous_variant	X	53458391	C	T	24.80%	367	.	.	.		.	.	.			.	0.9763	93.30%	100.00%	100%	Clonal			
MP27	*IL13RA2*	p.Asn220Asn	synonymous_variant	X	114245253	G	A	10.23%	264	.	.	.		.	.	.			.	0.8676	68.89%	100.00%	100%	Clonal			
MP27	*GPR101*	p.Gln80Gln	synonymous_variant	X	136113594	C	T	8.84%	249	.	.	.		.	.	.			.	0.7944	60.20%	100.00%	96%	Clonal			
MP27	*SLITRK4*	p.Val724Met	missense_variant	X	142716755	C	T	9.39%	479	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8711	72.59%	100.00%	100%	Clonal			
MP27	*MAGEA8*	p.Gly266Gly	synonymous_variant	X	149013844	C	A	9.87%	466	.	.	.		.	.	.			.	0.8917	75.01%	100.00%	100%	Clonal			
MP7	*PANK4*	p.Pro520Pro	synonymous_variant	1	2445456	C	T	21.32%	319	.	.	.		.	.	.			.	0.8795	79.24%	100.00%	100%	Clonal			
MP7	*MTOR*	p.Ala1510Ala	synonymous_variant	1	11210223	G	T	32.47%	77	.	.	.		.	true	true			.	0.9022	78.29%	100.00%	100%	Clonal			
MP7	*CDCP2*	p.Thr286Thr	synonymous_variant	1	54605685	G	T	29.29%	239	.	.	.		.	.	.			.	0.9137	83.83%	100.00%	100%	Clonal			
MP7	*L1TD1*	p.Lys588Thr	missense_variant	1	62676209	A	C	20.88%	407	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2143	66.18%	95.59%	81%	Subclonal			
MP7	*HFM1*	p.Arg841Gln	missense_variant	1	91788662	C	T	19.54%	87	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4503	47.76%	97.72%	76%	Subclonal			
MP7	*DENND2C*	p.Cys707Tyr	missense_variant	1	115142058	C	T	36.36%	77	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8401	78.54%	100.00%	100%	Clonal			
MP7	*SV2A*	p.Gly304Gly	synonymous_variant	1	149882421	G	A	37.20%	250	.	.	.		.	.	.			.	0.0471	91.80%	100.00%	100%	Clonal			
MP7	*UCK2*	p.Val126Val	synonymous_variant	1	165865448	C	A	27.21%	272	.	.	.		.	.	.			.	0.7400	88.09%	100.00%	100%	Clonal			
MP7	*RABGAP1L*	p.Gly499Gly	synonymous_variant	1	174340148	T	G	19.89%	181	.	.	.		.	.	.			.	0.7882	68.51%	100.00%	97%	Clonal			
MP7	*SOX13*	p.Gln195Lys	missense_variant	1	204085799	C	A	10.81%	74	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0123	21.32%	76.48%	42%	Subclonal			
MP7	*PLEKHA6*	p.Gly679Arg	missense_variant	1	204214129	C	T	37.04%	54	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8574	73.54%	100.00%	100%	Clonal			
MP7	*LYST*	p.Ala3799Ser	missense_variant	1	235826251	C	A	4.64%	237	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	9.67%	30.95%	18%	Subclonal			
MP7	*APOB*	p.Ser2854Ala	missense_variant	2	21231180	A	C	48.88%	446	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.4960	97.77%	100.00%	100%	Clonal			
MP7	*SPAST*	p.Lys290Asn	missense_variant	2	32339894	G	T	14.57%	247	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.6176	61.71%	98.82%	86%	Clonal			
MP7	*PRKD3*	p.Ser333Ile	missense_variant	2	37507063	C	A	37.63%	93	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9613	85.11%	100.00%	100%	Clonal			
MP7	*TTC7A*	p.Lys227Asn	missense_variant	2	47205963	A	T	22.28%	606	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9325	87.43%	100.00%	100%	Clonal			
MP7	*MOGS*	p.Pro775Leu	missense_variant	2	74688592	G	A	3.04%	428	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	6.39%	19.40%	12%	Subclonal			
MP7	*CCDC142*	p.Gln643Gln	synonymous_variant	2	74702089	C	T	11.81%	271	.	.	.		.	.	.		TRUE	.	0.0000	32.41%	62.29%	46%	Subclonal			
MP7	*EIF2AK3*	p.Cys788Cys	synonymous_variant	2	88874637	A	G	8.86%	316	.	.	.		.	.	.		TRUE	.	0.0000	29.77%	60.51%	43%	Subclonal			
MP7	*SH3RF3*	p.Gly863Glu	missense_variant	2	110259187	G	A	43.49%	676	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9722	98.05%	100.00%	100%	Clonal			
MP7	*LRP1B*	p.Thr1714Lys	missense_variant	2	141597628	G	T	7.46%	201	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	21.90%	57.77%	36%	Subclonal			
MP7	*NEB*	p.Arg6723Leu	missense_variant	2	152404242	C	A	12.50%	248	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0124	43.16%	83.27%	61%	Subclonal			
MP7	*PKP4*	p.Ala39Glu	missense_variant	2	159389812	C	A	23.33%	90	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8258	67.12%	100.00%	100%	Clonal			
MP7	*METTL21A*	p.Gln115Glu	missense_variant	2	208478084	G	C	20.23%	351	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8441	77.02%	100.00%	99%	Clonal			
MP7	*NUP210*	p.Arg1871His	missense_variant	3	13359233	C	T	28.32%	279	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4602	89.39%	100.00%	100%	Clonal			
MP7	*STAB1*	p.Gly1393Glu	missense_variant	3	52550405	G	A	22.96%	392	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6429	73.09%	98.92%	89%	Clonal			
MP7	*CASR*	p.Asn468Ser	missense_variant	3	121994684	A	G	45.18%	301	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1452	96.37%	100.00%	100%	Clonal			
MP7	*TOPBP1*	p.Ser1274del	disruptive_inframe_deletion	3	133335705	AGAG	A	26.11%	157	D	.	.	Deleterious	.	.	.			Indeterminate	0.8175	84.11%	100.00%	100%	Clonal			
MP7	*PIK3CA*	p.His1047Arg	missense_variant	3	178952085	A	G	54.40%	364	D	CANCER	Driver		true	true	true			Likely pathogenic	0.3788	97.63%	100.00%	100%	Clonal			
MP7	*HSD17B13*	p.Ser21Ser	synonymous_variant	4	88243931	C	T	27.85%	316	.	.	.		.	.	.			.	0.4699	90.03%	100.00%	100%	Clonal			
MP7	*IRX1*	p.Thr141Met	missense_variant	5	3599484	C	T	41.92%	458	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1082	97.23%	100.00%	100%	Clonal			
MP7	*DAB2*	p.Arg126Cys	missense_variant	5	39390632	G	A	4.02%	174	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.20%	46.90%	24%	Subclonal			
MP7	*HAPLN1*	p.Leu145*	stop_gained	5	82948310	A	C	3.55%	310	A	.	.		.	.	.			Indeterminate	0.0000	9.27%	29.92%	17%	Subclonal			
MP7	*SLCO4C1*	p.Pro694Ala	missense_variant	5	101572657	G	C	14.80%	196	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2345	50.66%	95.19%	72%	Subclonal			
MP7	*ANKHD1*	p.Ser2109_Arg2111del	inframe_deletion	5	139908854	CATCACCCAG	C	15.29%	471	D	.	.	Deleterious	.	.	.			Indeterminate	0.0525	59.54%	90.98%	75%	Subclonal			
MP7	*SRA1*	p.Val53Ala	missense_variant	5	139936761	A	G	42.56%	531	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9824	97.37%	100.00%	100%	Clonal			
MP7	*PCDHB8*	p.Ala720Val	missense_variant	5	140559774	C	T	33.33%	60	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9540	77.28%	100.00%	100%	Clonal			
MP7	*KIF4B*	p.Glu576Asp	missense_variant	5	154395147	A	C	17.98%	356	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6325	68.96%	98.88%	88%	Clonal			
MP7	*CLINT1*	p.Gln335*	stop_gained	5	157230667	G	A	22.44%	352	A	.	.		.	.	.			Indeterminate	0.9091	83.07%	100.00%	100%	Clonal			
MP7	*FAM184A*	p.Ser415Thr	missense_variant	6	119341232	A	T	25.75%	167	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8282	72.70%	100.00%	100%	Clonal			
MP7	*MED23*	p.Tyr472Ser	missense_variant	6	131926578	T	G	8.63%	139	D	.	Passenger		.	.	true		TRUE	Likely pathogenic	0.0000	19.03%	55.67%	33%	Subclonal			
MP7	*AUTS2*	p.Arg1119Gln	missense_variant	7	70255558	G	A	38.29%	679	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8247	97.84%	100.00%	100%	Clonal			
MP7	*SPDYE2*	p.Lys107Lys	synonymous_variant	7	102194966	G	A	22.05%	127	.	.	.		.	.	.			.	0.8606	75.17%	100.00%	100%	Clonal			
MP7	*C7orf60*	p.Pro229Ser	missense_variant	7	112462332	G	A	34.13%	208	D	.	Passenger		.	.	.			Indeterminate	0.9749	92.18%	100.00%	100%	Clonal			
MP7	*PRSS1*	p.Glu85Glu	synonymous_variant	7	142459679	G	A	4.15%	554	.	.	.		.	.	.			.	0.0000	15.89%	35.67%	24%	Subclonal			
MP7	*SGK223*	p.Ser743Arg	missense_variant	8	8197079	G	T	18.94%	301	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7504	71.06%	100.00%	92%	Clonal			
MP7	*PCMTD1*	p.Asn257Lys	missense_variant	8	52733214	A	C	3.72%	188	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.46%	35.97%	18%	Subclonal			
MP7	*NOV*	p.Val199Val	synonymous_variant	8	120431405	C	G	22.49%	169	.	.	.		.	.	.			.	0.8627	74.65%	100.00%	100%	Clonal			
MP7	*TLE4*	p.Cys53fs	frameshift_variant	9	82189802	GT	G	20.71%	338	A	.	.		.	.	.			Indeterminate	0.8630	78.12%	100.00%	100%	Clonal			
MP7	*GOLGA1*	p.Ala46Asp	missense_variant	9	127693684	G	T	19.89%	181	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7882	68.51%	100.00%	97%	Clonal			
MP7	*GLE1*	p.Lys157Arg	missense_variant	9	131284984	A	G	19.05%	168	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2429	53.04%	95.41%	74%	Subclonal			
MP7	*PARD3*	p.Arg1088Trp	missense_variant	10	34558751	G	A	51.58%	380	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0119	97.38%	100.00%	100%	Clonal			
MP7	*RET*	p.Arg112His	missense_variant	10	43596168	G	A	4.62%	130	N	CANCER	Passenger		true	.	.		TRUE	Likely passenger	0.0000	10.10%	46.80%	23%	Subclonal			
MP7	*NPY4R*	p.Thr202Thr	synonymous_variant	10	47087389	C	T	27.57%	555	.	.	.		.	.	.			.	0.0554	93.52%	100.00%	100%	Clonal			
MP7	*NPFFR1*	p.Leu399Ile	missense_variant	10	72014811	G	T	29.12%	261	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9170	84.42%	100.00%	100%	Clonal			
MP7	*POLR3A*	p.Pro532Leu	missense_variant	10	79770276	G	A	5.42%	332	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	12.96%	32.08%	21%	Subclonal			
MP7	*TMEM180*	p.Leu143Met	missense_variant	10	104230597	C	A	53.43%	715	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9851	98.32%	100.00%	100%	Clonal			
MP7	*MRPL17*	p.Gln160*	stop_gained	11	6703399	G	A	32.98%	285	D	.	.		.	.	.			Indeterminate	0.5278	92.63%	100.00%	100%	Clonal			
MP7	*DBX1*	p.Gly12Arg	missense_variant	11	20181837	C	T	19.79%	379	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9115	84.38%	100.00%	100%	Clonal			
MP7	*CLP1*	p.Pro271Pro	synonymous_variant	11	57428443	C	A	37.08%	418	.	.	.		.	.	.			.	0.9587	96.36%	100.00%	100%	Clonal			
MP7	*CDC42BPG*	p.Ala98Ala	synonymous_variant	11	64609164	G	T	7.54%	451	.	.	.		.	.	.			.	0.0000	20.59%	39.64%	29%	Subclonal			
MP7	*OR8D4*	p.Arg53Cys	missense_variant	11	123777295	C	T	35.81%	363	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8859	95.05%	100.00%	100%	Clonal			
MP7	*FOXRED1*	p.Gly114Val	missense_variant	11	126142898	G	T	38.42%	544	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9717	97.05%	100.00%	100%	Clonal			
MP7	*IQSEC3*	p.Arg349Trp	missense_variant	12	247574	C	T	4.97%	362	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	11.81%	29.46%	19%	Subclonal			
MP7	*KIF5A*	p.Met300fs	frameshift_variant	12	57963115	CTA	C	33.19%	901	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0013	96.18%	100.00%	100%	Clonal			
MP7	*TMCC3*	p.Pro249Pro	synonymous_variant	12	94975646	G	C	20.47%	557	.	.	.		.	.	.			.	0.8801	81.94%	100.00%	100%	Clonal			
MP7	*TMEM132B*	p.Gln977Lys	missense_variant	12	126138948	C	A	35.48%	217	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9218	91.99%	100.00%	100%	Clonal			
MP7	*PSPC1*	p.Glu368fs	frameshift_variant	13	20304433	TTC	T	42.49%	353	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9806	96.26%	100.00%	100%	Clonal			
MP7	*TMCO3*	p.Leu481Val	missense_variant	13	114188457	C	G	13.54%	325	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0156	49.44%	85.66%	66%	Subclonal			
MP7	*FAM177A1*	p.Thr114Ile	missense_variant	14	35546357	C	T	14.09%	504	D	.	Passenger		.	.	.			Indeterminate	0.0038	54.69%	84.32%	69%	Subclonal			
MP7	*AHNAK2*	p.Glu825Ala	missense_variant	14	105419314	T	G	10.71%	84	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0972	27.65%	89.32%	52%	Subclonal			
MP7	*MYO5A*	p.Arg874Trp	missense_variant	15	52664518	G	A	4.23%	142	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.0000	9.19%	42.93%	21%	Subclonal			
MP7	*RAB40C*	p.Ala38Thr	missense_variant	16	640403	G	A	5.00%	320	N	CANCER	Passenger		.	.	.			Likely passenger	0.0000	17.79%	46.33%	29%	Subclonal			
MP7	*RAB40C*	p.Ala39Ala	synonymous_variant	16	640408	A	C	4.67%	300	.	.	.		.	.	.			.	0.0000	16.05%	44.64%	27%	Subclonal			
MP7	*ERN2*	p.Phe772Leu	missense_variant	16	23703581	A	C	11.17%	376	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0199	48.70%	86.06%	66%	Subclonal			
MP7	*KIAA0556*	p.Glu499Lys	missense_variant	16	27720131	G	A	22.12%	529	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5752	91.09%	100.00%	100%	Clonal			
MP7	*ZNF629*	p.Glu648Asp	missense_variant	16	30793705	C	G	10.02%	479	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	36.77%	63.06%	49%	Subclonal			
MP7	*ZNF629*	p.Asp601His	missense_variant	16	30793848	C	G	9.96%	683	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	38.16%	60.11%	49%	Subclonal			
MP7	*ZNF629*	p.Gln588Gln	synonymous_variant	16	30793885	C	T	9.12%	724	.	.	.		.	.	.			.	0.0000	34.74%	55.26%	44%	Subclonal			
MP7	*ZNF629*	p.Leu560Leu	synonymous_variant	16	30793969	C	T	11.89%	732	.	.	.		.	.	.			.	0.0000	47.00%	69.86%	58%	Subclonal			
MP7	*ZNF629*	p.Leu385Leu	synonymous_variant	16	30794494	C	T	12.18%	731	.	.	.		.	.	.			.	0.0000	48.24%	71.41%	59%	Subclonal			
MP7	*TP53*	p.Cys135fs	frameshift_variant	17	7578526	CA	C	48.77%	570	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9739	97.90%	100.00%	100%	Clonal			
MP7	*KCNAB3*	p.Arg244fs	frameshift_variant	17	7827562	GT	G	46.49%	555	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8332	97.50%	100.00%	100%	Clonal			
MP7	*NCOR1*	p.Ser1855Arg	missense_variant	17	15965031	G	T	57.23%	311	D	PASSENGER/OTHER	Passenger		.	true	true		TRUE	Likely pathogenic	0.9072	97.15%	100.00%	100%	Clonal			
MP7	*KRTAP1-1*	p.Thr19Thr	synonymous_variant	17	39197593	G	T	39.13%	69	.	.	.		.	.	.		TRUE	.	0.9619	82.16%	100.00%	100%	Clonal			
MP7	*KRTAP4-9*	p.Val46Val	synonymous_variant	17	39261778	A	G	44.07%	59	.	.	.		.	.	.		TRUE	.	0.9560	82.90%	100.00%	100%	Clonal			
MP7	*SDK2*	p.Ser487Ser	synonymous_variant	17	71427660	T	G	27.64%	550	.	.	.		.	.	.		TRUE	.	0.9372	88.19%	100.00%	100%	Clonal			
MP7	*ZNF493*	p.Val107Val	synonymous_variant	19	21605782	G	A	26.00%	50	.	.	.		.	.	.		TRUE	.	0.7414	55.41%	100.00%	100%	Clonal			
MP7	*APLP1*	p.Ser235Ile	missense_variant	19	36362792	G	T	4.53%	685	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	21.55%	43.19%	31%	Subclonal			
MP7	*ZNF529*	p.Gly113Gly	synonymous_variant	19	37039121	G	A	12.32%	633	.	.	.		.	.	.			.	0.4914	68.01%	98.16%	85%	Subclonal			
MP7	*SPRED3*	p.Arg296Cys	missense_variant	19	38886438	C	T	58.40%	250	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4320	97.10%	100.00%	100%	Clonal			
MP7	*SMG9*	p.Glu362Lys	missense_variant	19	44238559	C	T	15.69%	51	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.2700	31.10%	95.35%	61%	Subclonal			
MP7	*LILRA4*	p.Gly191Cys	missense_variant	19	54849291	C	A	9.31%	204	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0003	29.05%	68.21%	45%	Subclonal			
MP7	*ZNF579*	p.Glu237Lys	missense_variant	19	56090297	C	T	26.96%	701	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0394	94.31%	100.00%	100%	Clonal			
MP7	*ZNF587B*	p.Ser191Ile	missense_variant	19	58352614	G	T	32.89%	149	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8358	87.20%	100.00%	100%	Clonal			
MP7	*ATRN*	p.Leu1291Ile	missense_variant	20	3614965	C	A	34.98%	203	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9735	92.31%	100.00%	100%	Clonal			
MP7	*CDH22*	p.Thr562Thr	synonymous_variant	20	44806814	C	T	32.20%	764	.	.	.		.	.	.			.	0.9768	97.27%	100.00%	100%	Clonal			
MP7	*DOK5*	p.Glu206Val	missense_variant	20	53226944	A	T	31.86%	339	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9723	94.28%	100.00%	100%	Clonal			
MP7	*KRTAP10-2*	p.Ser78Leu	missense_variant	21	45971109	G	A	12.77%	94	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2162	35.86%	94.35%	62%	Subclonal			
MP7	*KRTAP10-2*	p.Pro64Ser	missense_variant	21	45971152	G	A	19.20%	125	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7324	61.48%	100.00%	94%	Clonal			
MP7	*KRTAP10-2*	p.Ala60Ala	synonymous_variant	21	45971162	C	T	18.52%	135	.	.	.		.	.	.			.	0.6979	60.35%	100.00%	90%	Clonal			
MP7	*DGCR14*	p.Tyr43Cys	missense_variant	22	19132026	T	C	18.57%	210	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7131	65.94%	100.00%	91%	Clonal			
MP7	*PKDREJ*	p.Val1137Ile	missense_variant	22	46655811	C	T	25.08%	299	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8981	86.27%	100.00%	100%	Clonal			
MP7	*APOOL*	p.Thr199fs	frameshift_variant	X	84329106	G	GA	18.52%	378	A	.	.		.	.	.			Indeterminate	0.8976	81.22%	100.00%	100%	Clonal			
MP8	*NPHP4*	p.Gln10Arg	missense_variant	1	6046321	T	C	5.61%	107	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	9.89%	45.48%	22%	Subclonal			
MP8	*TAS1R2*	p.Leu402Ile	missense_variant	1	19180760	G	T	11.02%	118	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0007	25.35%	70.03%	43%	Subclonal			
MP8	*CSMD2*	p.Pro1257Arg	missense_variant	1	34164508	G	C	4.17%	240	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	8.49%	28.95%	16%	Subclonal			
MP8	*ABCA4*	p.Thr867Ser	missense_variant	1	94517243	T	A	7.14%	140	N	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Likely passenger	0.0001	19.02%	61.88%	35%	Subclonal			
MP8	*CDC14A*	p.Ala415Pro	missense_variant	1	100960479	G	C	5.93%	236	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	17.16%	47.39%	29%	Subclonal			
MP8	*CDC14A*	p.Ala415Val	missense_variant	1	100960480	C	T	5.56%	234	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.72%	45.22%	27%	Subclonal			
MP8	*OLFM3*	p.Thr293Thr	synonymous_variant	1	102270352	A	T	5.00%	320	.	.	.		.	.	.			.	0.0000	11.71%	30.82%	20%	Subclonal			
MP8	*DDX20*	p.Asp772His	missense_variant	1	112309360	G	C	19.90%	206	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2158	58.41%	96.77%	78%	Subclonal			
MP8	*PEX11B*	p.Glu117Gly	missense_variant	1	145518248	A	G	14.97%	167	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2122	50.37%	96.59%	74%	Subclonal			
MP8	*HRNR*	p.Arg648Ser	missense_variant	1	152192163	G	T	12.99%	77	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1884	34.93%	95.92%	64%	Subclonal			
MP8	*KPRP*	p.Ser223Ser	synonymous_variant	1	152732733	C	A	42.36%	576	.	.	.		.	.	.			.	0.9679	97.57%	100.00%	100%	Clonal			
MP8	*SPRR3*	p.Gly73Gly	synonymous_variant	1	152975715	C	T	17.44%	86	.	.	.		.	.	.			.	0.4838	51.12%	98.87%	86%	Subclonal			
MP8	*PKLR*	p.Pro262Pro	synonymous_variant	1	155264452	G	C	18.60%	602	.	.	.		.	.	.			.	0.5981	76.40%	100.00%	92%	Clonal			
MP8	*INSRR*	p.Glu1030Val	missense_variant	1	156812833	T	A	2.90%	483	D	CANCER	Driver		true	.	.			Likely pathogenic	0.0000	8.10%	23.20%	14%	Subclonal			
MP8	*LY9*	p.Thr506Met	missense_variant	1	160793273	C	T	4.38%	160	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	10.18%	42.65%	22%	Subclonal			
MP8	*DUSP27*	p.Ala439Thr	missense_variant	1	167095683	G	A	8.29%	579	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	24.28%	42.01%	33%	Subclonal			
MP8	*CACNA1E*	p.Tyr528Tyr	synonymous_variant	1	181687249	T	C	7.84%	153	.	.	.		.	.	.		TRUE	.	0.0000	17.44%	51.44%	31%	Subclonal			
MP8	*HMCN1*	p.Gln4802Lys	missense_variant	1	186114672	C	A	10.08%	238	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	26.52%	56.76%	40%	Subclonal			
MP8	*HLX*	p.Gly314Gly	synonymous_variant	1	221055675	C	T	3.12%	481	.	.	.		.	.	.		TRUE	.	0.0000	8.91%	24.58%	15%	Subclonal			
MP8	*ACTA1*	p.Val154Met	missense_variant	1	229568173	C	T	39.46%	560	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9743	97.20%	100.00%	100%	Clonal			
MP8	*CAD*	p.Gly132Ala	missense_variant	2	27445104	G	C	3.90%	410	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.05%	24.02%	15%	Subclonal			
MP8	*RFX8*	p.Ser455Ser	synonymous_variant	2	102014067	T	G	17.74%	186	.	.	.		.	.	.			.	0.0623	50.27%	92.07%	70%	Subclonal			
MP8	*R3HDM1*	p.Gly64Ala	missense_variant	2	136373741	G	C	19.43%	175	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2021	55.37%	96.51%	76%	Subclonal			
MP8	*LOC100996693*	p.Pro177His	missense_variant	2	220362535	C	A	20.63%	189	.	.	Passenger		.	.	.			Indeterminate	0.3189	60.07%	97.88%	81%	Subclonal			
MP8	*ECEL1*	p.Arg663Gln	missense_variant	2	233346217	C	T	31.46%	89	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6783	64.29%	100.00%	92%	Clonal			
MP8	*SRGAP3*	p.Arg25Arg	synonymous_variant	3	9166594	G	A	53.79%	132	.	.	.		true	.	.	TRUE	TRUE	.	0.2314	93.68%	100.00%	100%	Clonal			
MP8	*BBX*	p.Leu58Phe	missense_variant	3	107435463	C	T	15.00%	180	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0049	40.87%	81.76%	59%	Subclonal			
MP8	*POGLUT1*	p.Ala21Ala	synonymous_variant	3	119187931	G	C	22.67%	300	.	.	.		.	.	.			.	0.5246	70.88%	100.00%	89%	Clonal			
MP8	*ATP11B*	p.Ser788*	stop_gained	3	182597394	C	G	29.13%	127	A	.	.		.	.	.			Indeterminate	0.7254	82.04%	100.00%	100%	Clonal			
MP8	*MUC4*	p.His4205Gln	missense_variant	3	195505836	G	C	21.05%	38	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4366	40.65%	98.64%	83%	Subclonal			
MP8	*ZFYVE28*	p.Leu741Leu	synonymous_variant	4	2275000	C	A	13.02%	192	.	.	.		.	.	.		TRUE	.	0.0000	25.83%	53.77%	38%	Subclonal			
MP8	*SH3TC1*	p.Trp705*	stop_gained	4	8229535	G	A	28.60%	437	A	.	.		.	.	.		TRUE	Likely pathogenic	0.1511	71.42%	95.64%	84%	Subclonal			
MP8	*HTRA3*	p.Asn304Asn	synonymous_variant	4	8294056	C	T	29.00%	100	.	.	.		.	.	.		TRUE	.	0.5385	60.33%	98.72%	85%	Clonal			
MP8	*ARHGAP10*	c.250+1G>C	splice_donor_variant	4	148743974	G	C	7.05%	539	D	.	.		.	.	.			Indeterminate	0.0000	19.87%	36.94%	28%	Subclonal			
MP8	*TRIML2*	p.Val336Val	synonymous_variant	4	189012683	C	T	35.81%	310	.	.	.		.	.	.		TRUE	.	0.9017	85.61%	100.00%	100%	Clonal			
MP8	*DTWD2*	p.Gln120Gln	synonymous_variant	5	118274935	C	T	41.11%	90	.	.	.		.	.	.		TRUE	.	0.8690	79.57%	100.00%	100%	Clonal			
MP8	*RNF39*	p.Ala377Thr	missense_variant	6	30039022	C	T	21.95%	328	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8338	81.62%	100.00%	100%	Clonal			
MP8	*ZNF451*	p.Gln369Lys	missense_variant	6	57011988	C	A	9.86%	345	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	27.55%	52.40%	39%	Subclonal			
MP8	*RIMS1*	p.Arg1316Cys	missense_variant	6	73017056	C	T	11.52%	191	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	29.94%	65.65%	45%	Subclonal			
MP8	*ECT2L*	p.Ser445Cys	missense_variant	6	139186175	C	G	10.26%	78	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.0555	25.77%	89.16%	51%	Subclonal			
MP8	*SYNE1*	p.Leu1268Gln	missense_variant	6	152765580	A	T	14.04%	114	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0154	34.27%	83.94%	55%	Subclonal			
MP8	*DGKB*	p.Cys339Trp	missense_variant	7	14722196	A	C	5.61%	196	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	12.03%	37.89%	22%	Subclonal			
MP8	*IL6*	p.Ile151Met	missense_variant	7	22769261	C	G	25.08%	307	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7582	78.22%	100.00%	99%	Clonal			
MP8	*STK31*	p.Thr766Lys	missense_variant	7	23826149	C	A	25.11%	223	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7343	75.10%	100.00%	99%	Clonal			
MP8	*ADCYAP1R1*	p.Thr119Met	missense_variant	7	31123783	C	T	4.82%	249	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	10.45%	31.86%	19%	Subclonal			
MP8	*ELN*	p.Gly57Arg	missense_variant	7	73452042	G	C	25.63%	238	D	PASSENGER/OTHER	Passenger		true	.	.	TRUE		Likely pathogenic	0.8222	85.04%	100.00%	100%	Clonal			
MP8	*GRM8*	p.Thr670Thr	synonymous_variant	7	126173426	T	G	31.37%	357	.	.	.		.	.	.			.	0.6769	77.53%	100.00%	92%	Clonal			
MP8	*PDGFRL*	p.Pro188Arg	missense_variant	8	17486053	C	G	28.70%	446	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1583	71.81%	95.76%	84%	Subclonal			
MP8	*RHOBTB2*	p.Val174Ile	missense_variant	8	22863630	G	A	5.26%	95	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	6.29%	33.88%	15%	Subclonal			
MP8	*KCTD9*	p.Val278Val	synonymous_variant	8	25290931	G	C	32.69%	52	.	.	.		.	.	.		TRUE	.	0.6872	59.02%	100.00%	96%	Clonal			
MP8	*PCMTD1*	p.Val281Ala	missense_variant	8	52733143	A	G	3.09%	421	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	6.62%	19.96%	12%	Subclonal			
MP8	*MYBL1*	p.Gln732Glu	missense_variant	8	67476997	G	C	4.96%	423	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.63%	36.35%	24%	Subclonal			
MP8	*RGS22*	p.Arg405Thr	missense_variant	8	101075782	C	G	3.20%	375	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	8.59%	26.67%	16%	Subclonal			
MP8	*SLC25A32*	p.Glu24Gln	missense_variant	8	104427096	C	G	19.37%	382	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6984	75.53%	100.00%	95%	Clonal			
MP8	*DCAF13*	p.Ala15Ala	synonymous_variant	8	104427263	A	T	26.89%	264	.	.	.		.	.	.			.	0.6918	87.65%	100.00%	100%	Clonal			
MP8	*SCRIB*	p.Gly1191Ser	missense_variant	8	144885585	C	T	17.67%	515	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2570	90.11%	100.00%	100%	Clonal			
MP8	*PLEC*	p.Val3615Val	synonymous_variant	8	144993555	C	T	15.21%	309	.	.	.		.	.	.			.	0.8178	79.78%	100.00%	100%	Clonal			
MP8	*DMRT3*	p.Ser320Ser	synonymous_variant	9	990546	C	A	4.53%	729	.	.	.		.	.	.			.	0.0000	25.22%	49.39%	36%	Subclonal			
MP8	*IFNA7*	p.Ala42Gly	missense_variant	9	21202040	G	C	13.89%	36	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1599	23.47%	95.01%	55%	Subclonal			
MP8	*MAMDC2*	c.421-1G>C	splice_acceptor_variant	9	72724635	G	C	28.24%	255	D	.	.		.	.	.		TRUE	Likely pathogenic	0.2798	67.00%	96.94%	83%	Subclonal			
MP8	*AKNA*	p.Val497Val	synonymous_variant	9	117130801	G	C	5.95%	168	.	.	.		.	.	.		TRUE	.	0.0000	12.41%	41.20%	23%	Subclonal			
MP8	*ABL1*	p.Gly697Ser	missense_variant	9	133759709	G	A	28.19%	408	N	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely passenger	0.8862	87.38%	100.00%	100%	Clonal			
MP8	*ITIH5*	p.Pro49His	missense_variant	10	7684043	G	T	13.60%	125	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1467	42.18%	95.03%	67%	Subclonal			
MP8	*SVIL*	p.Asp219Tyr	missense_variant	10	29839698	C	A	8.30%	542	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	30.37%	53.40%	41%	Subclonal			
MP8	*JMJD1C*	p.Val2235Leu	missense_variant	10	64946011	C	G	31.00%	100	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6606	64.77%	100.00%	91%	Clonal			
MP8	*C11orf49*	p.Arg80Trp	missense_variant	11	47074027	C	T	3.80%	237	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.44%	27.24%	15%	Subclonal			
MP8	*OR5M11*	p.Tyr126Cys	missense_variant	11	56310357	T	C	21.84%	261	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4235	66.97%	98.60%	86%	Subclonal			
MP8	*TAF6L*	p.Pro227Leu	missense_variant	11	62549658	C	T	9.55%	555	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.46%	47.77%	38%	Subclonal			
MP8	*CCDC85B*	p.Asp202Asp	synonymous_variant	11	65658860	T	C	24.71%	603	.	.	.		.	.	.			.	0.7736	82.66%	100.00%	97%	Clonal			
MP8	*CATSPER1*	p.Ala90Thr	missense_variant	11	65793583	C	T	26.53%	524	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8689	86.24%	100.00%	100%	Clonal			
MP8	*KDM2A*	p.Lys310*	stop_gained	11	66986845	A	T	25.26%	190	A	.	.		.	.	.			Indeterminate	0.7283	73.69%	100.00%	99%	Clonal			
MP8	*P2RY2*	p.Arg151Arg	synonymous_variant	11	72945657	C	G	18.41%	630	.	.	.		.	.	.			.	0.0004	60.70%	84.50%	72%	Subclonal			
MP8	*OR10S1*	p.Ala238_Ala245del	disruptive_inframe_deletion	11	123847664	GGCTGTGCGGATGCGCAACACAGCT	G	11.78%	331	P	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.0000	25.12%	45.53%	35%	Subclonal			
MP8	*ROBO3*	p.Thr623Asn	missense_variant	11	124744049	C	A	30.84%	214	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6468	72.25%	100.00%	90%	Clonal			
MP8	*ARNTL2*	p.Asp625Asn	missense_variant	12	27573427	G	A	6.15%	195	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.53%	40.58%	24%	Subclonal			
MP8	*KIAA1551*	p.Cys1172Trp	missense_variant	12	32137405	C	G	4.79%	188	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	9.55%	34.27%	19%	Subclonal			
MP8	*HDAC7*	p.Asp306Glu	missense_variant	12	48189539	G	T	26.79%	224	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8051	79.06%	100.00%	100%	Clonal			
MP8	*KRT81*	p.Gln380Gln	synonymous_variant	12	52680993	C	T	10.45%	67	.	.	.		.	.	.			.	0.0828	25.11%	91.51%	51%	Subclonal			
MP8	*ZNF740*	c.374-1G>C	splice_acceptor_variant	12	53580174	G	C	41.56%	154	D	.	.		.	.	.		TRUE	Likely pathogenic	0.6600	90.42%	100.00%	100%	Clonal			
MP8	*COPZ1*	p.Asp82His	missense_variant	12	54737059	G	C	11.20%	366	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	32.37%	57.85%	44%	Subclonal			
MP8	*EP400*	p.Gln2742Gln	synonymous_variant	12	132547138	A	G	3.02%	431	.	.	.		.	.	.		TRUE	.	0.0000	6.44%	19.54%	12%	Subclonal			
MP8	*MTUS2*	p.Gly850Glu	missense_variant	13	29674982	G	A	34.87%	195	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8514	79.90%	100.00%	100%	Clonal			

MP8	*MAB21L1*	p.Glu67Asp	missense_variant	13	36050075	C	G	27.43%	288	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1368	65.66%	94.92%	80%	Subclonal			
MP8	*CGRRF1*	p.Arg185Gln	missense_variant	14	54997752	G	A	4.35%	161	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	5.79%	24.97%	13%	Subclonal			
MP8	*SLC8A3*	p.Phe833Phe	synonymous_variant	14	70512949	G	A	4.55%	176	.	.	.		.	.	.		TRUE	.	0.0000	6.34%	25.00%	13%	Subclonal			
MP8	*ADAM21*	p.Pro40Leu	missense_variant	14	70924335	C	T	24.14%	87	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1921	47.35%	95.11%	71%	Subclonal			
MP8	*BAHD1*	p.Glu660Lys	missense_variant	15	40756672	G	A	9.47%	169	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	22.80%	57.79%	37%	Subclonal			
MP8	*JMJD7*	p.Val188Met	missense_variant	15	42128378	G	A	29.66%	118	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8003	76.44%	100.00%	100%	Clonal			
MP8	*PLA2G4F*	p.Phe145Leu	missense_variant	15	42446305	G	C	15.65%	147	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0226	41.41%	86.98%	61%	Subclonal			
MP8	*HDC*	p.Tyr322Cys	missense_variant	15	50544703	T	C	10.58%	397	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	22.70%	40.52%	31%	Subclonal			
MP8	*GLDN*	p.Pro252Thr	missense_variant	15	51689732	C	A	29.77%	215	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8543	83.91%	100.00%	100%	Clonal			
MP8	*MYO5C*	p.Ser630Cys	missense_variant	15	52539205	T	A	10.26%	117	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0003	23.07%	66.65%	40%	Subclonal			
MP8	*HCN4*	p.Arg372Arg	synonymous_variant	15	73635819	C	T	18.57%	280	.	.	.		.	.	.			.	0.0423	56.28%	91.52%	73%	Subclonal			
MP8	*PLIN1*	p.Asp418Asp	synonymous_variant	15	90209129	G	A	23.79%	206	.	.	.		.	.	.			.	0.6421	70.66%	100.00%	93%	Clonal			
MP8	*FBXL16*	p.Cys115Gly	missense_variant	16	747063	A	C	39.49%	314	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0109	94.26%	100.00%	100%	Clonal			
MP8	*CRAMP1L*	p.Ala500Thr	missense_variant	16	1706256	G	A	10.48%	372	N	.	Passenger		.	.	.		TRUE	Likely passenger	0.0000	30.04%	54.59%	41%	Subclonal			
MP8	*FBRS*	p.His90Leu	missense_variant	16	30678265	A	T	26.77%	198	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7925	77.63%	100.00%	100%	Clonal			
MP8	*ZNF423*	p.Glu823*	stop_gained	16	49670596	C	A	18.63%	263	A	.	.		.	.	.			Indeterminate	0.0542	56.05%	92.22%	73%	Subclonal			
MP8	*CTCF*	p.Pro696fs	frameshift_variant	16	67671675	AGCCC	A	12.15%	535	D	.	.		.	true	true	TRUE		Likely pathogenic	0.0000	37.39%	59.21%	48%	Subclonal			
MP8	*MLYCD*	p.Ser344Ser	synonymous_variant	16	83948644	G	A	28.21%	397	.	.	.		.	.	.			.	0.8847	87.21%	100.00%	100%	Clonal			
MP8	*ABR*	p.His320His	synonymous_variant	17	973265	G	A	3.13%	351	.	.	.		.	.	.		TRUE	.	0.0000	6.41%	21.21%	12%	Subclonal			
MP8	*OR3A3*	p.Phe286Ser	missense_variant	17	3324718	T	C	23.27%	202	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5987	68.97%	100.00%	91%	Clonal			
MP8	*NLRP1*	p.Ala438Ser	missense_variant	17	5462704	C	A	37.66%	316	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0017	93.60%	100.00%	100%	Clonal			
MP8	*TP53*	p.Arg248Gln	missense_variant	17	7577538	C	T	30.46%	197	A	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.8493	83.95%	100.00%	100%	Clonal			
MP8	*LLGL1*	p.Pro178Ala	missense_variant	17	18137231	C	G	16.85%	445	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	39.49%	59.89%	49%	Subclonal			
MP8	*KLHL11*	p.Val382Val	synonymous_variant	17	40010973	A	C	45.88%	340	.	.	.		.	.	.		TRUE	.	0.8254	96.61%	100.00%	100%	Clonal			
MP8	*GRIN2C*	p.Glu134Lys	missense_variant	17	72848750	C	T	20.59%	204	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.7320	72.60%	100.00%	100%	Clonal			
MP8	*LAMA3*	p.Thr1323Thr	synonymous_variant	18	21427465	G	A	28.26%	545	.	.	.		.	.	.			.	0.9028	89.66%	100.00%	100%	Clonal			
MP8	*TRAPPC8*	p.Lys447Asn	missense_variant	18	29487471	C	G	15.63%	224	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0032	44.52%	81.83%	61%	Subclonal			
MP8	*TCF4*	p.Pro17Pro	synonymous_variant	18	53303078	G	T	11.01%	227	.	.	.		.	.	.	TRUE		.	0.0000	29.28%	61.43%	43%	Subclonal			
MP8	*SF3A2*	p.Gly342Gly	synonymous_variant	19	2248176	G	A	4.52%	221	.	.	.		.	.	.			.	0.0000	9.29%	31.45%	18%	Subclonal			
MP8	*EEF2*	p.Cys369*	stop_gained	19	3980882	G	T	8.05%	323	A	.	.		.	.	.			Indeterminate	0.0000	26.92%	56.38%	40%	Subclonal			
MP8	*CAMSAP3*	p.Leu424Phe	missense_variant	19	7676468	C	T	24.32%	440	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8571	88.87%	100.00%	100%	Clonal			
MP8	*ZNF763*	p.Ser27Ser	synonymous_variant	19	12087921	G	C	11.27%	71	.	.	.		.	.	.			.	0.1080	28.31%	93.15%	56%	Subclonal			
MP8	*DAND5*	p.Val158Met	missense_variant	19	13084350	G	A	22.08%	693	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8947	88.43%	100.00%	100%	Clonal			
MP8	*NR2F6*	p.Glu329Asp	missense_variant	19	17343389	C	G	11.11%	162	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0107	34.81%	82.47%	55%	Subclonal			
MP8	*MAP1S*	p.Gly251Arg	missense_variant	19	17836944	G	A	22.81%	583	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8922	88.61%	100.00%	100%	Clonal			
MP8	*HPN*	p.Leu171Phe	missense_variant	19	35551309	G	C	35.57%	596	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	95.74%	100.00%	100%	Clonal			
MP8	*SPTBN4*	p.Val1951Ile	missense_variant	19	41066245	G	A	31.97%	638	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1386	94.32%	100.00%	100%	Clonal			
MP8	*ZNF227*	p.Glu222Lys	missense_variant	19	44739247	G	A	47.58%	227	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7385	95.37%	100.00%	100%	Clonal			
MP8	*FKRP*	p.Leu491Leu	synonymous_variant	19	47260180	G	C	6.99%	415	.	.	.		.	.	.		TRUE	.	0.0000	23.72%	48.09%	34%	Subclonal			
MP8	*PTOV1*	p.Lys210Asn	missense_variant	19	50360303	G	C	3.65%	274	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.37%	25.40%	14%	Subclonal			
MP8	*A1BG*	p.Val492Val	synonymous_variant	19	58858723	C	A	21.81%	243	.	.	.		.	.	.		TRUE	.	0.4290	66.23%	98.63%	86%	Subclonal			
MP8	*ASXL1*	p.Lys523Asn	missense_variant	20	31021570	G	C	3.38%	325	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.0000	8.96%	28.87%	17%	Subclonal			
MP8	*SCAND1*	p.Ser101Tyr	missense_variant	20	34542094	G	T	10.31%	97	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0328	27.75%	86.30%	51%	Subclonal			
MP8	*SRC*	p.His25Tyr	missense_variant	20	36012629	C	T	26.17%	554	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3001	92.58%	100.00%	100%	Clonal			
MP8	*DHX35*	p.Leu463Leu	synonymous_variant	20	37643564	G	C	24.60%	313	.	.	.		.	.	.		TRUE	.	0.7272	77.11%	100.00%	97%	Clonal			
MP8	*OSBPL2*	p.Ala438Pro	missense_variant	20	60866821	G	C	9.42%	191	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	23.30%	56.12%	37%	Subclonal			
MP8	*LAMA5*	p.Arg3550Pro	missense_variant	20	60885319	C	G	21.79%	280	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4055	67.38%	98.51%	86%	Subclonal			
MP8	*SYNJ1*	p.Pro821Pro	synonymous_variant	21	34030141	C	T	11.43%	105	.	.	.		.	.	.			.	0.0023	25.79%	73.85%	45%	Subclonal			
MP8	*TRAPPC10*	p.Ala55Thr	missense_variant	21	45457686	G	A	15.61%	237	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0022	44.89%	81.14%	61%	Subclonal			
MP8	*GGT5*	p.Leu559Leu	synonymous_variant	22	24616027	G	A	23.44%	337	.	.	.		.	.	.			.	0.6198	74.32%	100.00%	92%	Clonal			
MP8	*MYO18B*	p.Ser71Pro	missense_variant	22	26164094	T	C	19.88%	503	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0306	64.82%	92.01%	78%	Subclonal			
MP8	*WWC3*	p.Pro733Pro	synonymous_variant	X	10096120	A	C	24.38%	365	.	.	.		.	.	.			.	0.7186	77.85%	100.00%	96%	Clonal			
MP8	*ARHGAP6*	p.Thr108Thr	synonymous_variant	X	11682625	G	C	7.83%	460	.	.	.		.	.	.			.	0.0000	21.96%	41.35%	31%	Subclonal			
MP8	*PIGA*	p.Ser330Thr	missense_variant	X	15342986	C	G	25.68%	183	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7442	74.27%	100.00%	100%	Clonal			
MP8	*CNKSR2*	p.Ala798Thr	missense_variant	X	21627435	G	A	21.48%	461	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2390	70.05%	97.30%	84%	Subclonal			
MP8	*CYLC1*	p.Thr152Ser	missense_variant	X	83128170	A	T	8.77%	114	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	18.62%	60.04%	34%	Subclonal			
MP8	*PAK3*	p.Phe413Phe	synonymous_variant	X	110439090	C	T	10.34%	87	.	.	.		.	.	.			.	0.0024	21.43%	72.22%	41%	Subclonal			
MP8	*RBMXL3*	p.Gly962Gly	synonymous_variant	X	114426890	G	T	2.88%	695	.	.	.		.	.	.			.	0.0000	6.87%	16.82%	11%	Subclonal			
MP8	*TENM1*	p.Trp248Cys	missense_variant	X	123870839	C	G	35.56%	270	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0972	91.54%	100.00%	100%	Clonal			
MP8	*MAGEC1*	p.Pro232Leu	missense_variant	X	140993885	C	T	21.21%	33	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4384	38.75%	98.65%	83%	Subclonal			
MP8	*MAGEA11*	p.Glu24Glu	synonymous_variant	X	148794891	G	A	10.58%	104	.	.	.		.	.	.			.	0.0010	23.24%	70.08%	42%	Subclonal			
MP8	*DNASE1L1*	p.Leu29Arg	missense_variant	X	153633824	A	C	10.00%	460	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.0000	29.28%	50.91%	39%	Subclonal			
MP8	*ATP6AP1*	p.Ala386Ser	missense_variant	X	153663804	G	T	4.87%	411	N	.	Passenger		.	.	.			Likely passenger	0.0000	12.02%	28.60%	19%	Subclonal			
MTC01	*HSPG2*	p.Gly4252Arg	missense_variant	1	22150863	C	T	18.11%	392	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5737	68.69%	98.54%	86%	Clonal			
MTC01	*SPRR3*	p.Gly73Gly	synonymous_variant	1	152975715	C	T	15.71%	140	.	.	.		.	.	.			.	0.3995	49.69%	97.17%	75%	Subclonal			
MTC01	*CHRNB2*	p.Arg41His	missense_variant	1	154541995	G	A	17.94%	379	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5463	67.73%	98.38%	85%	Clonal			
MTC01	*KCNK3*	p.Gly272Ser	missense_variant	2	26951065	G	A	9.69%	382	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	33.30%	61.63%	46%	Subclonal			
MTC01	*LRP2*	p.Lys2620Lys	synonymous_variant	2	170060637	T	C	3.79%	264	.	.	.		.	.	.			.	0.0000	9.40%	31.95%	18%	Subclonal			
MTC01	*PDCD10*	p.Thr144Lys	missense_variant	3	167405446	G	T	26.45%	242	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8884	85.47%	100.00%	100%	Clonal			
MTC01	*PIK3CA*	p.His1047Arg	missense_variant	3	178952085	A	G	29.52%	376	D	CANCER	Driver		true	true	true			Likely pathogenic	0.0713	92.23%	100.00%	100%	Clonal	TRUE	ATCTCTTCATAAATCTTTTCTCAAT	ACAGTGCAGTGTGGAATCCA
MTC01	*MUC4*	p.Val1001Glu	missense_variant	3	195515449	A	T	12.00%	50	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2841	26.22%	95.35%	57%	Subclonal			
MTC01	*SLC12A2*	p.Arg482Arg	synonymous_variant	5	127474326	A	G	18.25%	378	.	.	.		.	.	.			.	0.6053	68.99%	98.70%	87%	Clonal			
MTC01	*TREML2*	p.Trp104Gly	missense_variant	6	41165913	A	C	21.43%	70	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7636	57.65%	100.00%	100%	Clonal			
MTC01	*GPR126*	p.Leu911Leu	synonymous_variant	6	142736996	G	T	24.19%	277	.	.	.		.	.	.		TRUE	.	0.9139	83.28%	100.00%	100%	Clonal			
MTC01	*RUNDC3B*	p.Thr373Thr	synonymous_variant	7	87436799	G	A	3.95%	380	.	.	.		.	.	.			.	0.0000	13.38%	36.39%	23%	Subclonal			
MTC01	*MCM10*	p.Lys763Lys	synonymous_variant	10	13243468	A	G	24.44%	180	.	.	.		.	.	.			.	0.8930	78.77%	100.00%	100%	Clonal			
MTC01	*GBF1*	p.Glu48Glu	synonymous_variant	10	104019854	G	A	19.35%	310	.	.	.		.	.	.			.	0.7557	71.38%	100.00%	92%	Clonal			
MTC01	*NEURL1*	p.Arg323His	missense_variant	10	105344611	G	A	19.39%	294	D	.	Passenger		.	.	.			Indeterminate	0.7578	71.00%	100.00%	92%	Clonal			
MTC01	*OTOG*	p.Pro2430Pro	synonymous_variant	11	17655408	G	A	7.00%	100	.	.	.		.	.	.			.	0.0015	16.05%	64.86%	33%	Subclonal			
MTC01	*AIP*	p.Tyr261*	stop_gained	11	67257924	C	G	20.56%	107	D	.	.		.	.	.			Indeterminate	0.7708	62.18%	100.00%	98%	Clonal			
MTC01	*PVRL1*	p.Arg451His	missense_variant	11	119535659	C	T	22.46%	334	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9034	81.52%	100.00%	100%	Clonal			
MTC01	*TAS2R30*	p.Trp35Ser	missense_variant	12	11286740	C	G	25.00%	76	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8364	66.90%	100.00%	100%	Clonal			
MTC01	*KRAS*	p.Ala59Gly	missense_variant	12	25380282	G	C	6.94%	72	D	CANCER	Passenger		true	true	true			Likely pathogenic	0.0096	14.11%	71.75%	33%	Subclonal	TRUE	TTATTTATGGCAAATACACAAAGAAAG	TTTCTCCCTTCTCAGGATTCC
MTC01	*PFDN5*	p.Val79Met	missense_variant	12	53691661	G	A	21.46%	261	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8630	76.29%	100.00%	100%	Clonal			
MTC01	*RCBTB1*	p.Asp39Asn	missense_variant	13	50141301	C	T	24.62%	65	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8182	63.35%	100.00%	100%	Clonal			
MTC01	*PAPLN*	p.Leu6Pro	missense_variant	14	73706503	T	C	15.19%	79	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4446	41.33%	97.55%	72%	Subclonal			
MTC01	*AXIN1*	p.Ser57Leu	missense_variant	16	396856	G	A	19.57%	700	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.7774	78.87%	100.00%	93%	Clonal			
MTC01	*LCAT*	p.Pro167Pro	synonymous_variant	16	67976596	G	A	23.43%	495	.	.	.		.	.	.			.	0.9339	87.26%	100.00%	100%	Clonal			
MTC01	*KSR1*	p.Val416Val	synonymous_variant	17	25931733	G	T	21.93%	374	.	.	.		.	.	.			.	0.8979	81.30%	100.00%	100%	Clonal			
MTC01	*KRT40*	p.Gly239Ala	missense_variant	17	39137375	C	G	19.00%	579	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6938	75.25%	100.00%	90%	Clonal			
MTC01	*SH2D3A*	p.Pro71Arg	missense_variant	19	6760856	G	C	20.47%	215	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8125	71.17%	100.00%	97%	Clonal			
MTC01	*ZNF358*	p.Leu50Val	missense_variant	19	7584276	C	G	19.76%	678	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8027	79.38%	100.00%	94%	Clonal			
MTC01	*GPR64*	p.Gly767Gly	synonymous_variant	X	19018008	C	T	20.00%	220	.	.	.		.	.	.			.	0.7900	69.98%	100.00%	95%	Clonal			
MTC01	*MBTPS2*	p.Tyr251Tyr	synonymous_variant	X	21886667	C	T	7.44%	309	.	.	.		.	.	.			.	0.0000	23.35%	51.43%	35%	Subclonal			
MTC01	*NR0B1*	p.Ala96Ala	synonymous_variant	X	30327193	C	T	5.95%	723	.	.	.		.	.	.			.	0.0000	20.61%	37.13%	28%	Subclonal			
MTC01	*GLRA4*	p.Leu414Leu	synonymous_variant	X	102962284	G	C	20.00%	340	.	.	.		.	.	.			.	0.8089	74.53%	100.00%	95%	Clonal			
MTC03	*HES3*	p.Glu166Lys	missense_variant	1	6305502	G	A	29.29%	280	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9165	82.52%	100.00%	100%	Clonal			
MTC03	*SPATA21*	p.Ser123*	stop_gained	1	16736315	G	C	27.33%	150	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8376	71.63%	100.00%	98%	Clonal			
MTC03	*DLGAP3*	p.Phe47Phe	synonymous_variant	1	35370844	G	A	28.95%	190	.	.	.		.	.	.		TRUE	.	0.8902	77.88%	100.00%	100%	Clonal			
MTC03	*ZMYM4*	p.Pro57Pro	synonymous_variant	1	35824611	G	A	32.38%	488	.	.	.		.	.	.		TRUE	.	0.9243	91.51%	100.00%	100%	Clonal			
MTC03	*SF3A3*	p.Glu187Gln	missense_variant	1	38446389	C	G	32.20%	59	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.8518	67.14%	100.00%	100%	Clonal			
MTC03	*TIE1*	p.Glu1061Gln	missense_variant	1	43787099	G	C	29.36%	545	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9450	88.12%	100.00%	100%	Clonal			
MTC03	*FOXD3*	p.Gly387Gly	synonymous_variant	1	63789890	C	G	16.01%	556	.	.	.		.	.	.			.	0.9133	82.16%	100.00%	100%	Clonal			
MTC03	*EVI5*	p.Asp342His	missense_variant	1	93160884	C	G	6.25%	272	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.70%	34.71%	22%	Subclonal			
MTC03	*FAM19A3*	p.Arg117Thr	missense_variant	1	113266651	G	C	45.83%	48	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.8985	72.32%	100.00%	100%	Clonal			
MTC03	*IVL*	p.Pro42Thr	missense_variant	1	152882397	C	A	7.67%	326	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	23.66%	50.45%	35%	Subclonal			
MTC03	*SHC1*	p.Leu173Leu	synonymous_variant	1	154941901	G	C	21.86%	215	.	.	.		.	.	.			.	0.8566	73.66%	100.00%	100%	Clonal			
MTC03	*ARHGEF2*	p.Asp718His	missense_variant	1	155921730	C	G	18.06%	454	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4038	67.44%	97.24%	83%	Subclonal			
MTC03	*C1orf61*	p.Tyr124Ser	missense_variant	1	156376924	T	G	10.45%	201	N	.	Passenger		.	.	.			Likely passenger	0.0005	31.44%	70.55%	48%	Subclonal			
MTC03	*SPTA1*	p.Leu1512Leu	synonymous_variant	1	158612673	C	T	30.88%	489	.	.	.		.	.	.			.	0.0030	94.20%	100.00%	100%	Clonal			
MTC03	*ADCY10*	p.Asp305Asn	missense_variant	1	167852782	C	T	16.54%	260	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2775	57.01%	95.62%	76%	Subclonal			
MTC03	*SELL*	p.Phe31Phe	synonymous_variant	1	169679608	G	A	4.03%	471	.	.	.		.	.	.			.	0.0000	11.44%	28.07%	19%	Subclonal			
MTC03	*RC3H1*	p.Ile1098Val	missense_variant	1	173907972	T	C	17.06%	293	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3335	60.08%	96.40%	78%	Subclonal			
MTC03	*GLUL*	p.Asp122His	missense_variant	1	182355502	C	G	22.22%	153	D	.	Passenger		.	.	.			Indeterminate	0.8906	77.05%	100.00%	100%	Clonal			
MTC03	*TROVE2*	p.Phe506Phe	synonymous_variant	1	193053762	C	T	16.54%	520	.	.	.		.	.	.			.	0.0550	62.01%	91.17%	76%	Subclonal			
MTC03	*RCOR3*	p.Arg391His	missense_variant	1	211486158	G	A	4.17%	551	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.35%	27.94%	19%	Subclonal			
MTC03	*TAF1A*	p.Gln369Glu	missense_variant	1	222734841	G	C	14.71%	374	D	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0109	52.27%	85.25%	68%	Subclonal			
MTC03	*DISP1*	p.Glu459Gln	missense_variant	1	223176114	G	C	15.80%	462	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0256	58.17%	88.67%	73%	Subclonal			
MTC03	*SUSD4*	p.Ser231Ser	synonymous_variant	1	223438003	C	T	6.67%	360	.	.	.		.	.	.			.	0.0000	20.31%	44.25%	31%	Subclonal			
MTC03	*PCNXL2*	p.Glu2087Gln	missense_variant	1	233120205	C	G	39.72%	360	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9198	95.69%	100.00%	100%	Clonal			
MTC03	*ZNF672*	p.Asp157Asn	missense_variant	1	249141942	G	A	17.92%	212	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5610	60.49%	98.28%	82%	Clonal			
MTC03	*RAD51AP2*	p.Glu371Lys	missense_variant	2	17698572	C	T	20.35%	285	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7997	72.13%	100.00%	94%	Clonal			
MTC03	*NT5C1B*	p.Glu154Lys	missense_variant	2	18767549	C	T	22.90%	393	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9169	82.75%	100.00%	100%	Clonal			
MTC03	*OTOF*	p.Glu1867Gln	missense_variant	2	26683833	C	G	25.81%	403	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9260	88.46%	100.00%	100%	Clonal			
MTC03	*ALK*	p.Arg317Thr	missense_variant	2	29917718	C	G	14.29%	98	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.2850	39.46%	95.21%	66%	Subclonal			
MTC03	*CAPN14*	p.Ile226Ile	synonymous_variant	2	31423365	G	A	17.74%	124	.	.	.		.	.	.			.	0.5963	54.00%	98.48%	82%	Clonal			
MTC03	*BIRC6*	p.Pro4357Thr	missense_variant	2	32774473	C	A	8.55%	339	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	27.22%	54.77%	39%	Subclonal			
MTC03	*BIRC6*	p.Ser4358Phe	missense_variant	2	32774477	C	T	8.47%	354	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	27.13%	53.95%	39%	Subclonal			
MTC03	*SLC8A1*	p.Gln109Glu	missense_variant	2	40657096	G	C	14.08%	483	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0005	51.27%	79.82%	65%	Subclonal			
MTC03	*ZFP36L2*	p.Glu249Lys	missense_variant	2	43452198	C	T	15.60%	391	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0380	56.24%	89.15%	72%	Subclonal			
MTC03	*THADA*	p.Leu568Leu	synonymous_variant	2	43801500	A	C	24.55%	110	.	.	.		.	.	.			.	0.8665	71.04%	100.00%	100%	Clonal			
MTC03	*MSH6*	p.Phe1103Val	missense_variant	2	48030693	T	G	9.25%	508	D	CANCER	Passenger		true	.	.	TRUE		Likely pathogenic	0.0000	31.83%	55.08%	43%	Subclonal			
MTC03	*USP34*	p.Glu2441Lys	missense_variant	2	61456009	C	T	21.95%	442	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8980	81.28%	100.00%	100%	Clonal			
MTC03	*AAK1*	p.Thr241Met	missense_variant	2	69757773	G	A	10.42%	192	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0007	31.05%	70.98%	48%	Subclonal			
MTC03	*SEMA4C*	p.Arg473Lys	missense_variant	2	97529444	C	T	18.55%	415	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5473	68.79%	98.24%	85%	Clonal			
MTC03	*RANBP2*	p.Glu2897Lys	missense_variant	2	109397814	G	A	15.63%	192	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2387	50.83%	94.76%	72%	Subclonal			
MTC03	*EDAR*	p.Leu412Leu	synonymous_variant	2	109513474	G	A	19.84%	383	.	.	.		.	.	.			.	0.7595	73.10%	100.00%	91%	Clonal			
MTC03	*SH3RF3*	p.Ala505Ala	synonymous_variant	2	110049068	G	A	4.77%	440	.	.	.		.	.	.			.	0.0000	14.01%	32.57%	22%	Subclonal			
MTC03	*CNTNAP5*	p.Glu469Lys	missense_variant	2	125281960	G	A	13.41%	164	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0662	41.07%	88.24%	62%	Subclonal			
MTC03	*MYO7B*	p.Ile178Ile	synonymous_variant	2	128327427	C	T	21.91%	251	.	.	.		.	.	.			.	0.8673	75.57%	100.00%	100%	Clonal			
MTC03	*LRP1B*	p.Ala225Val	missense_variant	2	141986928	G	A	21.54%	130	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8143	66.31%	100.00%	99%	Clonal			
MTC03	*FAP*	p.Asp268Asn	missense_variant	2	163072472	C	T	19.61%	255	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7403	68.44%	100.00%	90%	Clonal			
MTC03	*SCN3A*	p.Val753Val	synonymous_variant	2	165994521	C	A	17.15%	484	.	.	.		.	.	.			.	0.1614	64.10%	94.24%	79%	Subclonal			
MTC03	*SCN1A*	p.Phe536Phe	synonymous_variant	2	166901607	G	A	20.34%	413	.	.	.		.	.	.	TRUE		.	0.8069	75.51%	100.00%	94%	Clonal			
MTC03	*NOSTRIN*	p.Lys15Lys	synonymous_variant	2	169668094	G	A	23.44%	128	.	.	.		.	.	.			.	0.8601	70.86%	100.00%	100%	Clonal			
MTC03	*SP5*	p.Ile43Ile	synonymous_variant	2	171572846	C	T	23.40%	470	.	.	.		.	.	.			.	0.9331	85.50%	100.00%	100%	Clonal			
MTC03	*TTN*	p.Arg18037Gln	missense_variant	2	179469794	C	T	18.41%	766	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2946	72.21%	96.49%	85%	Subclonal			
MTC03	*TTN*	p.Val2843Val	synonymous_variant	2	179634899	G	A	25.18%	564	.	.	.		.	.	.			.	0.9366	90.15%	100.00%	100%	Clonal			
MTC03	*CCDC141*	p.Asp255His	missense_variant	2	179825974	C	G	21.94%	196	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8534	72.77%	100.00%	100%	Clonal			
MTC03	*FSIP2*	p.Val2033Val	synonymous_variant	2	186657695	C	G	20.49%	405	.	.	.		.	.	.			.	0.8190	75.91%	100.00%	94%	Clonal			
MTC03	*MDH1B*	p.Leu450Leu	synonymous_variant	2	207611019	G	A	19.55%	133	.	.	.		.	.	.			.	0.7279	60.78%	100.00%	90%	Clonal			
MTC03	*IKZF2*	p.Glu70Gln	missense_variant	2	213921755	C	G	16.25%	320	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1555	57.47%	93.53%	75%	Subclonal			
MTC03	*RUFY4*	p.Lys199Asn	missense_variant	2	218938605	G	T	9.25%	335	A	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	29.86%	58.55%	43%	Subclonal			
MTC03	*TTLL4*	p.Ser1081Phe	missense_variant	2	219617892	C	T	21.98%	182	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8500	71.98%	100.00%	100%	Clonal			
MTC03	*COL6A3*	p.Leu1033Met	missense_variant	2	238283637	G	T	15.04%	512	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0031	55.60%	84.08%	69%	Subclonal			
MTC03	*MKRN2*	p.Arg361Trp	missense_variant	3	12623419	C	T	23.48%	626	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9447	87.98%	100.00%	100%	Clonal			
MTC03	*TGFBR2*	p.Asp60Asn	missense_variant	3	30686247	G	A	22.31%	399	N	CANCER	Passenger		.	true	true			Likely passenger	0.9039	81.35%	100.00%	100%	Clonal			
MTC03	*PLCD1*	p.Arg551*	stop_gained	3	38050781	G	A	21.35%	342	A	.	.		.	.	.			Indeterminate	0.8623	77.13%	100.00%	98%	Clonal			
MTC03	*SCN10A*	p.Gln640Glu	missense_variant	3	38783970	G	C	21.89%	507	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9026	82.30%	100.00%	100%	Clonal			
MTC03	*SCAP*	p.Leu109Leu	synonymous_variant	3	47470086	G	A	35.82%	282	.	.	.		.	.	.		TRUE	.	0.6825	90.77%	100.00%	100%	Clonal			
MTC03	*IMPDH2*	p.Phe431Phe	synonymous_variant	3	49062331	G	A	31.92%	354	.	.	.		.	.	.		TRUE	.	0.9397	88.74%	100.00%	100%	Clonal			
MTC03	*LAMB2*	p.Ser709Cys	missense_variant	3	49163823	G	C	28.36%	201	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8815	77.26%	100.00%	100%	Clonal			
MTC03	*ZBTB20*	p.Phe671Leu	missense_variant	3	114058065	G	C	20.62%	417	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8293	76.59%	100.00%	95%	Clonal			
MTC03	*GPR156*	p.Glu390Lys	missense_variant	3	119887156	C	T	21.78%	303	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8734	77.21%	100.00%	100%	Clonal			
MTC03	*FSTL1*	p.Glu132Gln	missense_variant	3	120128447	C	G	22.85%	337	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9082	81.15%	100.00%	100%	Clonal	TRUE	CCTGAATAGTCTTCCTCCTACCTCT	CCTGACTGCTCCAGCTGAC
MTC03	*GOLGB1*	p.Glu1325Gln	missense_variant	3	121415397	C	G	22.22%	504	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9126	83.19%	100.00%	100%	Clonal			
MTC03	*EFCAB12*	p.Gly459Ser	missense_variant	3	129123121	C	T	25.75%	400	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9273	88.33%	100.00%	100%	Clonal			
MTC03	*DNAJC13*	p.Glu67Lys	missense_variant	3	132166219	G	A	41.20%	415	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9573	96.43%	100.00%	100%	Clonal			
MTC03	*ZIC1*	p.Phe167Phe	synonymous_variant	3	147128400	C	T	19.64%	718	.	.	.		.	.	.			.	0.6901	76.99%	98.97%	90%	Clonal			
MTC03	*HTR3D*	p.Glu412Glu	synonymous_variant	3	183756634	G	A	10.34%	174	.	.	.		.	.	.			.	0.0013	30.13%	71.98%	48%	Subclonal			
MTC03	*GAK*	p.Asp777Asn	missense_variant	4	862393	C	T	19.61%	255	N	CANCER	Passenger		.	.	.		TRUE	Likely passenger	0.0405	54.19%	88.96%	71%	Subclonal			
MTC03	*LIMCH1*	p.Ser478Phe	missense_variant	4	41648678	C	T	25.77%	392	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.7901	76.93%	100.00%	93%	Clonal			
MTC03	*SHISA3*	p.Gly103Ser	missense_variant	4	42403058	G	A	52.76%	489	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9561	97.75%	100.00%	100%	Clonal			
MTC03	*SLC10A4*	p.Arg87Trp	missense_variant	4	48485837	C	T	23.81%	105	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6644	58.46%	98.85%	86%	Clonal			
MTC03	*CEP135*	p.Arg832Lys	missense_variant	4	56876059	G	A	23.38%	402	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9261	84.10%	100.00%	100%	Clonal			
MTC03	*KIAA1211*	p.Ser822Ser	synonymous_variant	4	57182134	C	T	2.47%	768	.	.	.		.	.	.			.	0.0000	6.81%	17.12%	11%	Subclonal			
MTC03	*AMBN*	p.Met285Ile	missense_variant	4	71471958	G	A	20.20%	589	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9400	87.73%	100.00%	100%	Clonal			
MTC03	*TRAM1L1*	p.Asp285Asn	missense_variant	4	118005697	C	T	24.05%	420	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5281	72.09%	98.14%	87%	Clonal			
MTC03	*SYNPO2*	p.Leu959Leu	synonymous_variant	4	119952807	C	T	25.85%	441	.	.	.		.	.	.		TRUE	.	0.7965	78.05%	100.00%	93%	Clonal			
MTC03	*NR3C2*	p.Glu381Lys	missense_variant	4	149356872	C	T	20.14%	581	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9396	87.47%	100.00%	100%	Clonal			
MTC03	*GFM2*	p.Glu573Gln	missense_variant	5	74026190	C	G	29.48%	268	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9172	82.47%	100.00%	100%	Clonal			
MTC03	*TTC37*	p.Gln1411Glu	missense_variant	5	94814128	G	C	22.45%	147	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5178	58.38%	97.98%	81%	Clonal			
MTC03	*CAST*	p.Leu349Phe	missense_variant	5	96078428	C	T	23.31%	326	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.4529	67.94%	97.62%	84%	Subclonal			
MTC03	*AQPEP*	p.Glu41Gln	missense_variant	5	115298435	G	C	32.13%	277	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9343	86.99%	100.00%	100%	Clonal			
MTC03	*VDAC1*	p.Leu97Leu	synonymous_variant	5	133326578	C	T	27.69%	65	.	.	.		.	.	.		TRUE	.	0.7917	60.72%	100.00%	100%	Clonal			
MTC03	*PCDHA5*	p.Ser266Leu	missense_variant	5	140202157	C	T	30.43%	460	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9478	88.68%	100.00%	100%	Clonal			
MTC03	*PCYOX1L*	p.Glu121Gln	missense_variant	5	148743664	G	C	59.90%	197	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9369	95.93%	100.00%	100%	Clonal			
MTC03	*GRIA1*	p.Thr81Ala	missense_variant	5	152873616	A	G	4.84%	186	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	8.82%	31.68%	17%	Subclonal			
MTC03	*UIMC1*	p.Ser198*	stop_gained	5	176396163	G	C	19.83%	590	A	.	.		.	.	.			Indeterminate	0.9390	86.95%	100.00%	100%	Clonal			
MTC03	*KIF13A*	p.Arg621Gln	missense_variant	6	17817389	C	T	26.06%	376	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9208	88.26%	100.00%	100%	Clonal			
MTC03	*FAM65B*	p.Ala333Val	missense_variant	6	24848332	G	A	23.55%	276	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9101	80.75%	100.00%	100%	Clonal			
MTC03	*HIST1H4E*	p.Glu64Gln	missense_variant	6	26205062	G	C	2.86%	768	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.0000	8.22%	19.30%	13%	Subclonal			
MTC03	*ZNF391*	p.Ser262*	stop_gained	6	27368934	C	G	21.85%	302	D	.	.		.	.	.			Indeterminate	0.8757	77.38%	100.00%	100%	Clonal			
MTC03	*NKAPL*	p.Lys178Lys	synonymous_variant	6	28227683	G	A	21.04%	366	.	.	.		.	.	.			.	0.8504	76.80%	100.00%	97%	Clonal			
MTC03	*SLC44A4*	p.Lys706Asn	missense_variant	6	31831419	C	G	20.95%	296	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8364	74.44%	100.00%	96%	Clonal			
MTC03	*LEMD2*	p.Trp461Ser	missense_variant	6	33740535	C	G	27.19%	228	D	.	Passenger		.	.	.			Indeterminate	0.9036	85.10%	100.00%	100%	Clonal			
MTC03	*RAB44*	p.Val958Met	missense_variant	6	36696552	G	A	19.77%	177	D	.	Passenger		.	.	.			Indeterminate	0.7489	65.03%	100.00%	91%	Clonal			
MTC03	*LRFN2*	p.Asp353His	missense_variant	6	40399796	C	G	24.37%	279	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9204	82.59%	100.00%	100%	Clonal			
MTC03	*YIPF3*	p.Gln217Gln	synonymous_variant	6	43480822	C	T	3.29%	365	.	.	.		.	.	.			.	0.0000	8.23%	25.54%	15%	Subclonal			
MTC03	*MEP1A*	p.Asp249Asn	missense_variant	6	46793197	G	A	20.42%	431	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8142	76.17%	100.00%	94%	Clonal			
MTC03	*ICK*	p.Leu75Val	missense_variant	6	52897386	G	C	22.31%	121	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8316	67.33%	100.00%	100%	Clonal			
MTC03	*RIMS1*	p.Arg1113Arg	synonymous_variant	6	72975693	G	A	7.17%	293	.	.	.		.	.	.			.	0.0000	16.55%	38.02%	26%	Subclonal			
MTC03	*MB21D1*	p.Glu509Lys	missense_variant	6	74134994	C	T	24.06%	133	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6748	61.92%	98.90%	87%	Clonal			
MTC03	*COL12A1*	p.Ile711Ile	synonymous_variant	6	75890686	A	T	4.81%	187	.	.	.		.	.	.			.	0.0000	8.76%	31.51%	17%	Subclonal			
MTC03	*UFL1*	p.Leu739Leu	synonymous_variant	6	97001211	A	T	5.77%	416	.	.	.		.	.	.			.	0.0000	17.47%	38.34%	27%	Subclonal			
MTC03	*TSPYL4*	p.Pro71Pro	synonymous_variant	6	116574959	G	A	22.69%	692	.	.	.		.	.	.			.	0.9370	86.89%	100.00%	100%	Clonal			
MTC03	*LTV1*	p.Asp153His	missense_variant	6	144178499	G	C	19.53%	430	D	.	Passenger		.	.	.			Indeterminate	0.7176	72.91%	100.00%	90%	Clonal			
MTC03	*UTRN*	p.Glu344Lys	missense_variant	6	144757245	G	A	34.60%	396	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0492	94.72%	100.00%	100%	Clonal			
MTC03	*SYNJ2*	p.Ser87Cys	missense_variant	6	158449833	C	G	21.28%	517	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8771	80.56%	100.00%	98%	Clonal			
MTC03	*HOXA9*	p.Ile252Ile	synonymous_variant	7	27203285	G	A	16.19%	451	.	.	.		true	.	.			.	0.0533	59.61%	90.67%	74%	Subclonal			
MTC03	*ADCY1*	p.Leu837Leu	synonymous_variant	7	45743031	C	T	18.71%	294	.	.	.		.	.	.			.	0.8853	77.02%	100.00%	100%	Clonal			
MTC03	*AUTS2*	p.Gln111*	stop_gained	7	69364293	C	T	36.36%	132	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8751	84.18%	100.00%	100%	Clonal			
MTC03	*AKAP9*	p.Glu2659Asp	missense_variant	7	91709424	G	C	3.40%	852	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.0017	36.69%	75.08%	53%	Subclonal			
MTC03	*MUC17*	p.Val719Val	synonymous_variant	7	100676854	G	C	29.52%	393	.	.	.		.	.	true			.	0.9347	85.96%	100.00%	100%	Clonal			
MTC03	*RELN*	p.Gly1513Glu	missense_variant	7	103212681	C	T	25.42%	240	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.7649	71.77%	100.00%	91%	Clonal			
MTC03	*SPAM1*	p.Phe494Phe	synonymous_variant	7	123599975	C	T	27.41%	270	.	.	.		.	.	.		TRUE	.	0.8708	78.11%	100.00%	99%	Clonal			
MTC03	*PAX4*	p.Gln272Lys	missense_variant	7	127251664	G	T	26.58%	79	A	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7767	61.36%	100.00%	96%	Clonal			
MTC03	*WDR91*	p.Phe628Phe	synonymous_variant	7	134871919	G	A	25.93%	54	.	PASSENGER/OTHER	.		.	.	.		TRUE	.	0.7344	54.08%	100.00%	93%	Clonal			
MTC03	*DLC1*	p.Ser163Cys	missense_variant	8	13357093	G	C	21.89%	498	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9015	82.14%	100.00%	100%	Clonal			
MTC03	*TNFRSF10B*	p.Thr384Thr	synonymous_variant	8	22880355	C	G	5.79%	570	.	.	.		.	.	.			.	0.0000	18.58%	36.40%	27%	Subclonal			
MTC03	*MBOAT4*	p.Val399Val	synonymous_variant	8	29989570	G	C	6.17%	389	N	.	.		.	.	.			.	0.0000	14.53%	31.94%	22%	Subclonal			
MTC03	*PLAT*	p.Ser80*	stop_gained	8	42046466	G	T	26.97%	89	A	.	.		.	.	.			Indeterminate	0.8736	72.21%	100.00%	100%	Clonal			
MTC03	*PRKDC*	p.Ser2532*	stop_gained	8	48749936	G	T	24.80%	125	A	.	.		.	.	.			Indeterminate	0.8787	73.44%	100.00%	100%	Clonal			
MTC03	*EFCAB1*	p.Trp89Ser	missense_variant	8	49643152	C	G	21.85%	357	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8842	79.05%	100.00%	100%	Clonal			
MTC03	*CNGB3*	p.Leu628Leu	synonymous_variant	8	87591380	G	A	15.24%	328	.	.	.		.	.	.			.	0.6236	64.89%	98.66%	85%	Clonal			
MTC03	*TP53INP1*	p.Gly227Ala	missense_variant	8	95942750	C	G	17.41%	902	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8834	82.70%	100.00%	97%	Clonal			
MTC03	*GRINA*	p.Glu4Lys	missense_variant	8	145065401	G	A	17.97%	295	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8612	74.66%	100.00%	100%	Clonal			
MTC03	*TONSL*	p.Asp405Asn	missense_variant	8	145665811	C	T	19.49%	390	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9176	82.26%	100.00%	100%	Clonal			
MTC03	*GPT*	p.Leu95Leu	synonymous_variant	8	145730186	G	A	15.14%	773	.	.	.		.	.	.			.	0.3993	71.01%	97.29%	85%	Subclonal			
MTC03	*ZNF517*	p.His368Leu	missense_variant	8	146033404	A	T	5.02%	279	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	16.43%	45.68%	28%	Subclonal			
MTC03	*FAM221B*	p.Gln76Glu	missense_variant	9	35825933	G	C	28.19%	408	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9127	83.53%	100.00%	100%	Clonal			
MTC03	*CCDC180*	p.Leu752Leu	synonymous_variant	9	100092899	G	A	29.72%	212	.	.	.		.	.	.		TRUE	.	0.9086	80.55%	100.00%	100%	Clonal			
MTC03	*OR13C5*	p.Arg244Cys	missense_variant	9	107360965	G	A	29.72%	434	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9408	87.10%	100.00%	100%	Clonal			
MTC03	*OR13C5*	p.Ile181Asn	missense_variant	9	107361153	A	T	34.38%	288	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8699	89.73%	100.00%	100%	Clonal			
MTC03	*SVEP1*	p.Phe127Leu	missense_variant	9	113341443	G	C	28.31%	537	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9268	85.90%	100.00%	100%	Clonal			
MTC03	*CDK9*	p.Lys96Lys	synonymous_variant	9	130550248	G	A	33.26%	487	.	.	.		.	.	.		TRUE	.	0.8528	92.33%	100.00%	100%	Clonal			
MTC03	*SPTAN1*	p.Glu1782Lys	missense_variant	9	131378106	G	A	24.75%	303	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6951	71.87%	98.99%	89%	Clonal			
MTC03	*HMCN2*	p.Arg4330Arg	synonymous_variant	9	133306770	C	T	22.73%	66	.	.	.		.	.	.		TRUE	.	0.6135	49.70%	98.57%	82%	Clonal			
MTC03	*ABCA2*	p.Leu1350Leu	synonymous_variant	9	139909185	G	C	28.95%	190	.	.	.		.	.	.		TRUE	.	0.8902	77.88%	100.00%	100%	Clonal			
MTC03	*ASB13*	p.Asp13Asn	missense_variant	10	5708478	C	T	9.20%	87	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0003	16.70%	61.12%	33%	Subclonal			
MTC03	*ITIH2*	p.Glu821Gln	missense_variant	10	7786806	G	C	19.27%	275	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0196	53.63%	87.02%	69%	Subclonal			
MTC03	*DHTKD1*	p.Ile452Ile	synonymous_variant	10	12136268	C	T	15.29%	170	.	.	.		.	.	.			.	0.0021	37.88%	76.77%	55%	Subclonal			
MTC03	*ANK3*	p.Asp2027Asn	missense_variant	10	61834560	C	T	32.64%	435	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0010	94.41%	100.00%	100%	Clonal			
MTC03	*USP54*	p.Ser358Tyr	missense_variant	10	75296098	G	T	5.61%	374	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	12.85%	29.85%	20%	Subclonal			
MTC03	*IFIT1*	p.Leu222Phe	missense_variant	10	91162696	C	T	15.20%	296	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	41.11%	70.54%	55%	Subclonal			

MTC03	NOLC1	p.Asp170Asn	missense_variant	10	103917872	G	A	38.34%	313	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0492	93.05%	100.00%	100%	Clonal			
MTC03	CHST15	p.Phe116Phe	synonymous_variant	10	125805381	G	A	37.26%	416	.	.	.		.	.	.		TRUE	.	0.0311	94.08%	100.00%	100%	Clonal			
MTC03	MKI67	p.Val157Val	synonymous_variant	10	129914201	T	G	7.57%	185	.	.	.		.	.	.		TRUE	.	0.0000	16.00%	43.78%	27%	Subclonal			
MTC03	DNHD1	p.Ser1914Leu	missense_variant	11	6567910	C	T	13.89%	72	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0447	27.42%	84.01%	50%	Subclonal			
MTC03	OR10A2	p.Glu283Glu	synonymous_variant	11	6891834	G	A	32.23%	363	.	.	.		.	.	.			.	0.9365	89.30%	100.00%	100%	Clonal			
MTC03	SYT9	p.Lys411Asn	missense_variant	11	7439255	G	C	25.73%	412	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7860	77.18%	100.00%	93%	Clonal			
MTC03	E2F8	p.Glu148Lys	missense_variant	11	19258870	C	T	24.86%	185	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7261	67.67%	100.00%	89%	Clonal			
MTC03	KIAA1549L	p.Ser311*	stop_gained	11	33564932	C	G	25.92%	787	A	.	.		.	.	.			Indeterminate	0.7860	81.93%	100.00%	93%	Clonal			
MTC03	KIAA1549L	p.Ser404Leu	missense_variant	11	33565211	C	T	30.81%	344	N	.	Passenger		.	.	.			Likely passenger	0.9401	87.02%	100.00%	100%	Clonal			
MTC03	ABTB2	p.Glu324Gln	missense_variant	11	34226151	C	G	29.94%	157	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8946	77.55%	100.00%	100%	Clonal			
MTC03	OR8J1	p.Ser188Cys	missense_variant	11	56128285	C	G	17.49%	406	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8563	76.34%	100.00%	98%	Clonal			
MTC03	MS4A6A	p.Leu129Leu	synonymous_variant	11	59945769	T	C	2.41%	582	.	PASSENGER/OTHER	.		.	.	.			.	0.0000	7.54%	21.88%	13%	Subclonal			
MTC03	MYRF	p.Gln397His	missense_variant	11	61541514	G	C	15.94%	320	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7217	67.71%	100.00%	89%	Clonal			
MTC03	RTN3	p.Pro230Leu	missense_variant	11	63486663	C	T	16.67%	576	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8036	76.19%	100.00%	93%	Clonal			
MTC03	RCE1	p.Leu131Leu	synonymous_variant	11	66611777	G	A	18.69%	610	.	.	.		.	.	.			.	0.9229	84.18%	100.00%	100%	Clonal			
MTC03	C2CD3	p.Phe781Phe	synonymous_variant	11	73814413	G	A	19.72%	720	.	.	.		.	.	.			.	0.9448	88.25%	100.00%	100%	Clonal			
MTC03	RSF1	p.Arg602Thr	missense_variant	11	77412469	C	G	18.27%	635	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9124	83.19%	100.00%	100%	Clonal			
MTC03	FAT3	p.Pro413Ala	missense_variant	11	92086515	C	G	20.35%	634	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9412	88.60%	100.00%	100%	Clonal			
MTC03	TMPRSS13	p.Gln83Arg	missense_variant	11	117789327	T	C	41.67%	36	P	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9110	72.61%	100.00%	100%	Clonal			
MTC03	MSANTD2	p.Ala331Thr	missense_variant	11	124637605	C	T	3.00%	367	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.26%	23.81%	14%	Subclonal			
MTC03	PRMT8	p.Ser31Pro	missense_variant	12	3649787	T	C	13.48%	89	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5335	42.80%	98.05%	75%	Clonal			
MTC03	CLEC4A	p.Ser49Leu	missense_variant	12	8278220	C	T	13.04%	276	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2340	53.07%	94.77%	73%	Subclonal			
MTC03	PIK3C2G	p.Glu172Gln	missense_variant	12	18435529	G	C	16.87%	581	N	CANCER	Passenger		.	.	.			Likely passenger	0.8247	77.13%	100.00%	94%	Clonal	TRUE	TTCCAGATTCAGTATTTTAGCTCCA	AAAGATGGTTCCACAATGTTCAC
MTC03	SOX5	p.Ser486Asn	missense_variant	12	23716223	C	T	16.32%	190	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7495	63.41%	100.00%	91%	Clonal			
MTC03	MANSC4	p.Thr163Thr	synonymous_variant	12	27916205	C	T	13.33%	375	.	.	.		.	.	.			.	0.1812	56.95%	94.00%	75%	Subclonal			
MTC03	ANO6	p.Gln348Glu	missense_variant	12	45751188	C	G	10.00%	70	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0034	17.44%	68.75%	36%	Subclonal			
MTC03	SCAF11	p.Leu1005Val	missense_variant	12	46320471	G	C	11.24%	436	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	30.45%	51.86%	40%	Subclonal			
MTC03	SCAF11	p.Leu69Phe	missense_variant	12	46355497	G	A	17.96%	167	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0406	45.88%	87.32%	65%	Subclonal			
MTC03	TUBA1B	p.Gly134fs	frameshift_variant	12	49522698	C	CT	16.31%	141	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0185	39.55%	83.18%	59%	Subclonal			
MTC03	MAP3K12	p.Asp403Asn	missense_variant	12	53878082	C	T	23.40%	235	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.5508	65.61%	98.24%	84%	Clonal			
MTC03	ATF7	p.Asn230His	missense_variant	12	53926380	T	G	7.63%	118	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	14.25%	49.41%	27%	Subclonal			
MTC03	LRIG3	p.Val179Val	synonymous_variant	12	59283900	G	A	14.03%	385	.	.	.		true	.	.		TRUE	.	0.0000	38.76%	63.75%	50%	Subclonal			
MTC03	CAND1	p.Val375Ile	missense_variant	12	67696225	G	A	3.82%	706	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	14.28%	30.36%	21%	Subclonal			
MTC03	TMEM19	p.Asp247Asn	missense_variant	12	72092781	G	A	16.12%	490	D	.	Passenger		.	.	.			Indeterminate	0.7349	72.43%	100.00%	90%	Clonal			
MTC03	RASSF9	p.Asp208Glu	missense_variant	12	86199164	A	T	7.33%	341	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	17.54%	37.66%	26%	Subclonal			
MTC03	SLC17A8	p.Pro16Ala	missense_variant	12	100751215	C	G	8.61%	337	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	21.30%	42.98%	31%	Subclonal			
MTC03	UTP20	p.Ser151Ser	synonymous_variant	12	101680225	G	A	13.46%	260	.	.	.		.	.	.		TRUE	.	0.0000	34.94%	64.81%	48%	Subclonal			
MTC03	SH2B3	p.Glu523Lys	missense_variant	12	111885945	G	A	22.04%	313	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.2267	63.52%	95.23%	79%	Subclonal			
MTC03	TMEM116	p.Gln276Glu	missense_variant	12	112369613	G	C	32.38%	105	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8937	76.37%	100.00%	100%	Clonal			
MTC03	DNAH10	p.Leu3966Leu	synonymous_variant	12	124413080	C	G	14.88%	383	.	.	.		.	.	.		TRUE	.	0.0000	41.47%	67.13%	54%	Subclonal			
MTC03	ZDHHC20	p.Phe21Phe	synonymous_variant	13	22033248	G	A	18.05%	133	.	.	.		.	.	.			.	0.6188	55.85%	98.61%	83%	Clonal			
MTC03	AMER2	p.Arg282Gly	missense_variant	13	25744914	G	C	21.24%	193	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2849	57.23%	95.73%	76%	Subclonal			
MTC03	MTUS2	p.Ser702Cys	missense_variant	13	29600910	C	G	30.23%	387	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9410	87.06%	100.00%	100%	Clonal			
MTC03	RFC3	p.Leu223Leu	synonymous_variant	13	34404951	C	T	20.69%	203	.	.	.		.	.	.			.	0.1936	55.92%	94.21%	74%	Subclonal			
MTC03	CCNA1	p.Leu455Leu	synonymous_variant	13	37016769	C	T	26.56%	128	.	.	.		.	.	.			.	0.8036	67.89%	100.00%	96%	Clonal			
MTC03	NALCN	p.Lys1334Lys	synonymous_variant	13	101726966	C	T	16.36%	385	.	.	.		.	.	.			.	0.1121	59.28%	92.66%	75%	Subclonal			
MTC03	ARHGEF7	p.Leu375Leu	synonymous_variant	13	111920006	C	T	14.07%	462	.	.	.		.	.	.			.	0.0007	51.00%	80.14%	65%	Subclonal			
MTC03	SUPT16H	p.Glu841Gln	missense_variant	14	21825495	C	G	21.83%	284	D	.	Passenger		.	.	.			Indeterminate	0.8715	76.68%	100.00%	100%	Clonal			
MTC03	CHD8	p.Glu1718Lys	missense_variant	14	21863487	C	T	19.70%	396	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.7422	72.84%	100.00%	91%	Clonal	TRUE	CAGAATTCAGTGAATAATTCCCC	GAAAGTGATTTCAGAGTGCCAAC
MTC03	MIS18BP1	p.Glu482Lys	missense_variant	14	45700494	C	T	21.60%	125	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8136	65.94%	100.00%	99%	Clonal			
MTC03	MGAT2	p.Pro171Pro	synonymous_variant	14	50088499	G	T	2.83%	954	.	.	.		.	.	.			.	0.0000	8.42%	18.33%	13%	Subclonal			
MTC03	NID2	p.Asp783His	missense_variant	14	52496319	C	G	29.39%	262	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6556	88.94%	100.00%	100%	Clonal			
MTC03	MTHFD1	p.Glu158Lys	missense_variant	14	64882451	G	A	24.94%	445	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9383	88.01%	100.00%	100%	Clonal			
MTC03	PCNX	p.Ser2003Phe	missense_variant	14	71570299	C	T	21.92%	616	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9118	83.94%	100.00%	100%	Clonal			
MTC03	ITPK1	c.671-1G>A	splice_acceptor_variant	14	93418359	C	T	18.78%	543	D	.	.		.	.	.			Indeterminate	0.5369	71.65%	98.20%	86%	Clonal			
MTC03	THBS1	p.Glu62*	stop_gained	15	39874510	G	T	24.65%	357	A	.	.		.	.	.		TRUE	Likely pathogenic	0.6660	72.84%	98.86%	89%	Clonal			
MTC03	MFAP1	p.Glu366Gln	missense_variant	15	44097615	C	G	16.10%	267	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0002	43.33%	75.03%	58%	Subclonal			
MTC03	WDR76	p.Ser429*	stop_gained	15	44149238	C	G	15.82%	354	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	44.08%	71.43%	57%	Subclonal			
MTC03	ALDH1A2	p.Thr430Arg	missense_variant	15	58253455	G	C	7.44%	215	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0000	16.22%	41.78%	27%	Subclonal			
MTC03	C2CD4A	p.Arg15Trp	missense_variant	15	62359855	C	T	26.02%	342	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8106	76.57%	100.00%	94%	Clonal			
MTC03	IQCH	p.Phe389Phe	synonymous_variant	15	67664862	C	T	17.64%	516	.	.	.		.	.	.			.	0.8756	79.16%	100.00%	99%	Clonal			
MTC03	IQCH	p.Leu390Phe	missense_variant	15	67664863	C	T	17.31%	520	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8565	77.99%	100.00%	97%	Clonal			
MTC03	NOX5	p.Leu479Leu	synonymous_variant	15	69331262	G	A	20.97%	453	.	.	.		.	.	.			.	0.8549	78.47%	100.00%	96%	Clonal			
MTC03	UBL7	p.Ser349Leu	missense_variant	15	74740898	G	A	25.52%	239	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7725	72.04%	100.00%	92%	Clonal			
MTC03	AGBL1	p.Leu895Val	missense_variant	15	87097595	C	G	14.87%	417	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	41.87%	66.46%	53%	Subclonal			
MTC03	IQGAP1	p.Leu978Ser	missense_variant	15	91020043	T	C	39.51%	329	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9150	95.27%	100.00%	100%	Clonal			
MTC03	MCTP2	p.Ser798Phe	missense_variant	15	95013594	C	T	11.53%	503	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6804	67.51%	98.94%	88%	Clonal			
MTC03	CERS3	p.Ser48Cys	missense_variant	15	101041945	G	C	13.19%	675	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8832	79.34%	100.00%	100%	Clonal			
MTC03	RPUSD1	p.Glu124*	stop_gained	16	837116	C	A	17.89%	503	A	.	.		.	.	.			Indeterminate	0.3202	67.44%	96.51%	82%	Subclonal			
MTC03	C16orf59	p.Ser120Phe	missense_variant	16	2510979	C	T	19.42%	726	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6372	76.16%	98.75%	89%	Clonal			
MTC03	TIGD7	p.Glu362Gln	missense_variant	16	3349531	C	G	17.58%	455	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2815	65.47%	96.00%	81%	Subclonal			
MTC03	TIGD7	p.Gln192Glu	missense_variant	16	3350041	G	C	20.22%	356	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7952	73.82%	100.00%	93%	Clonal			
MTC03	NLRC3	p.Leu864Leu	synonymous_variant	16	3599153	C	T	18.64%	295	.	.	.		.	.	.			.	0.6205	66.31%	98.64%	86%	Clonal			
MTC03	XYLT1	p.Arg286His	missense_variant	16	17352901	C	T	46.94%	98	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8330	88.09%	100.00%	100%	Clonal			
MTC03	ARL6IP1	p.Leu171Phe	missense_variant	16	18804675	G	A	15.84%	101	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0478	35.52%	85.93%	57%	Subclonal			
MTC03	DNAH3	p.Glu2414Gln	missense_variant	16	20996824	C	G	19.88%	322	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0204	56.64%	87.87%	72%	Subclonal			
MTC03	NUPR1	p.Lys65Asn	missense_variant	16	28549448	C	G	14.85%	330	D	.	Passenger		.	.	.			Indeterminate	0.0254	52.03%	87.16%	68%	Subclonal			
MTC03	RNF40	p.Ser621Ser	synonymous_variant	16	30779735	C	T	21.38%	435	.	.	.		.	.	.			.	0.8749	79.43%	100.00%	98%	Clonal			
MTC03	CHD9	p.Glu2423Gln	missense_variant	16	53348381	G	C	9.49%	253	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	29.24%	62.65%	44%	Subclonal			
MTC03	FTO	p.Leu44Leu	synonymous_variant	16	53859784	G	C	14.86%	175	.	.	.		.	.	.			.	0.1715	47.08%	93.11%	68%	Subclonal			
MTC03	BBS2	p.His470Asn	missense_variant	16	56533809	G	T	15.92%	333	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0993	56.41%	91.91%	73%	Subclonal			
MTC03	DUS2	p.Glu138Gln	missense_variant	16	68095011	G	C	15.77%	241	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1818	53.32%	93.78%	72%	Subclonal			
MTC03	PMFBP1	p.Arg881Gln	missense_variant	16	72157496	C	T	16.54%	635	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0234	63.17%	89.70%	76%	Subclonal			
MTC03	GLG1	p.Arg208Pro	missense_variant	16	74537580	C	G	19.63%	326	D	.	Passenger		.	.	.			Indeterminate	0.7398	70.91%	100.00%	90%	Clonal			
MTC03	FA2H	p.Gln133His	missense_variant	16	74761249	C	G	7.10%	155	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	18.07%	55.89%	33%	Subclonal			
MTC03	CDH13	p.Glu520Lys	missense_variant	16	83711945	G	A	17.10%	573	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0971	64.99%	92.98%	79%	Subclonal			
MTC03	PIEZO1	p.Leu2478Leu	synonymous_variant	16	88782145	G	C	16.06%	467	D	PASSENGER/OTHER	.		.	.	.			.	0.0380	59.31%	89.80%	74%	Subclonal			
MTC03	OR1G1	p.Met163Ile	missense_variant	17	3030357	C	G	27.18%	504	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8878	82.72%	100.00%	98%	Clonal			
MTC03	SHPK	p.Pro415Ala	missense_variant	17	3514048	G	C	30.95%	294	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9352	85.85%	100.00%	100%	Clonal			
MTC03	CAMTA2	p.Glu975Gln	missense_variant	17	4873786	C	G	29.03%	217	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8992	79.48%	100.00%	100%	Clonal			
MTC03	MYOCD	p.Pro696Ala	missense_variant	17	12659758	C	G	26.82%	358	D	PASSENGER/OTHER	Passenger		.	.	true		TRUE	Likely pathogenic	0.8587	79.13%	100.00%	96%	Clonal			
MTC03	ELAC2	p.Asp35Asn	missense_variant	17	12921162	C	T	8.21%	207	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	18.22%	45.43%	30%	Subclonal			
MTC03	NATD1	p.Glu58Lys	missense_variant	17	21147469	C	T	34.03%	288	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8919	89.39%	100.00%	100%	Clonal			
MTC03	GAS2L2	p.Arg506Gln	missense_variant	17	34072999	C	T	41.21%	182	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9379	83.65%	100.00%	100%	Clonal			
MTC03	BRCA1	p.Asp1527His	missense_variant	17	41226507	C	G	40.51%	158	N	CANCER	Passenger		true	true	true	TRUE	TRUE	Likely passenger	0.9262	81.29%	100.00%	100%	Clonal			
MTC03	CDC27	p.Ser93Ser	synonymous_variant	17	45247381	A	G	4.81%	104	.	.	.		.	.	true			.	0.0000	9.26%	48.98%	22%	Subclonal			
MTC03	TRIM25	p.Glu483Gln	missense_variant	17	54969507	C	G	8.81%	261	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	26.89%	58.73%	41%	Subclonal			
MTC03	OR4D2	p.Thr288Asn	missense_variant	17	56247879	C	A	5.83%	823	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	24.27%	42.34%	33%	Subclonal			
MTC03	CLTC	p.Gln10Glu	missense_variant	17	57697520	C	G	20.90%	531	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.9323	88.25%	100.00%	100%	Clonal			
MTC03	TANC2	p.Ser398*	stop_gained	17	61392004	C	G	8.52%	962	A	.	.		.	.	.		TRUE	Likely pathogenic	0.3746	65.86%	96.97%	82%	Subclonal			
MTC03	HELZ	p.Leu392Leu	synonymous_variant	17	65175029	C	T	7.63%	249	.	.	.		.	.	.		TRUE	.	0.0000	22.26%	52.90%	35%	Subclonal			
MTC03	CEP295NL	p.Leu107Leu	synonymous_variant	17	76888265	G	A	26.85%	581	.	.	.		.	.	.		TRUE	.	0.8751	82.82%	100.00%	97%	Clonal			
MTC03	EMILIN2	p.Glu832Lys	missense_variant	18	2906915	G	A	20.90%	67	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7483	54.48%	100.00%	96%	Clonal			
MTC03	ROCK1	p.Ser533*	stop_gained	18	18586700	G	C	7.56%	410	A	.	.		.	.	.			Indeterminate	0.0001	35.04%	69.00%	50%	Subclonal			
MTC03	RIOK3	p.Val419Val	synonymous_variant	18	21057145	C	G	5.36%	261	.	.	.		.	.	.			.	0.0000	20.87%	57.59%	35%	Subclonal			
MTC03	ST8SIA5	p.Lys224Met	missense_variant	18	44260465	T	A	20.27%	74	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4383	44.80%	97.26%	73%	Subclonal			
MTC03	FBXO15	p.Ile211Ile	synonymous_variant	18	71796792	G	A	20.51%	78	.	.	.		.	.	.		TRUE	.	0.4481	46.06%	97.36%	74%	Subclonal			
MTC03	MED16	p.Leu337Leu	synonymous_variant	19	881689	G	C	7.63%	262	.	.	.		.	.	.			.	0.0000	22.51%	52.39%	35%	Subclonal			
MTC03	DOT1L	p.Leu334Leu	synonymous_variant	19	2208972	C	G	18.63%	161	.	.	.		.	.	.			.	0.6622	60.10%	98.84%	86%	Clonal			
MTC03	ACSBG2	p.Leu410Val	missense_variant	19	6183189	C	G	19.42%	551	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6776	74.31%	98.92%	89%	Clonal			
MTC03	ZNF561	p.Gln323Glu	missense_variant	19	9721370	G	C	25.30%	166	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9011	78.31%	100.00%	100%	Clonal			
MTC03	ILF3	p.Trp48*	stop_gained	19	10781790	G	A	23.01%	578	A	.	.		.	.	.			Indeterminate	0.9357	86.29%	100.00%	100%	Clonal			
MTC03	PODNL1	p.Gln85Glu	missense_variant	19	14047267	G	C	22.67%	247	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8872	77.41%	100.00%	100%	Clonal			
MTC03	MYO9B	p.Ter2158Serext*?	stop_lost	19	17323118	G	C	25.78%	128	D	.	.		.	.	.		TRUE	Indeterminate	0.7726	65.99%	100.00%	93%	Clonal			
MTC03	ABHD8	p.Glu232Gln	missense_variant	19	17411732	C	G	27.29%	469	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8899	82.47%	100.00%	98%	Clonal			
MTC03	FAM129C	p.Asp574Asp	synonymous_variant	19	17657569	C	T	25.00%	232	.	.	.		.	.	.		TRUE	.	0.7325	70.26%	100.00%	90%	Clonal			
MTC03	KLHL26	p.Asp129Tyr	missense_variant	19	18778592	G	T	27.18%	401	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8794	81.01%	100.00%	98%	Clonal			
MTC03	ZNF100	p.His423Asp	missense_variant	19	21909847	G	C	20.59%	34	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5377	35.49%	98.06%	74%	Clonal			
MTC03	KMT2B	p.Asp2635Asn	missense_variant	19	36229213	G	A	21.18%	576	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9240	89.37%	100.00%	100%	Clonal			
MTC03	SERTAD3	p.Phe133Leu	missense_variant	19	40947589	G	C	7.30%	137	N	.	Passenger		.	.	.			Likely passenger	0.0000	14.06%	45.98%	26%	Subclonal			
MTC03	CYP2F1	p.Leu37Leu	synonymous_variant	19	41622204	C	T	29.41%	323	.	.	.		.	.	.			.	0.9250	84.09%	100.00%	100%	Clonal			
MTC03	MEGF8	p.Arg1004Arg	synonymous_variant	19	42855824	G	A	27.48%	222	.	.	.		.	.	.			.	0.8634	76.33%	100.00%	99%	Clonal			
MTC03	PHLDB3	p.Ala278Ala	synonymous_variant	19	43999764	A	G	14.29%	119	.	.	.		.	.	.			.	0.0065	32.36%	77.55%	51%	Subclonal			
MTC03	IRGQ	p.Asp332His	missense_variant	19	44097056	C	G	24.86%	551	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6373	76.45%	98.75%	89%	Clonal			
MTC03	IRGQ	p.Glu310Lys	missense_variant	19	44097122	C	T	32.74%	339	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9281	89.35%	100.00%	100%	Clonal			
MTC03	C19orf68	p.Val197Val	synonymous_variant	19	48697912	G	A	33.33%	150	.	.	.		.	.	.			.	0.9141	82.25%	100.00%	100%	Clonal			
MTC03	KLK2	p.Ile226Met	missense_variant	19	51381707	C	G	24.69%	162	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.7154	65.81%	100.00%	89%	Clonal			
MTC03	LILRA2	p.Glu370Gln	missense_variant	19	55087429	G	C	25.42%	240	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7649	71.77%	100.00%	91%	Clonal			
MTC03	PEG3	p.Glu43Lys	missense_variant	19	57335897	C	T	7.58%	264	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	17.36%	40.59%	27%	Subclonal			
MTC03	ZNF551	p.Ser386Cys	missense_variant	19	58198800	C	G	5.84%	257	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	12.36%	33.37%	21%	Subclonal			
MTC03	NOP56	p.Glu474Gln	missense_variant	20	2638575	G	C	36.84%	38	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8895	69.38%	100.00%	100%	Clonal			
MTC03	SLC23A2	p.Pro408Pro	synonymous_variant	20	4850578	T	G	10.93%	183	.	.	.		.	.	.			.	0.0022	32.61%	74.37%	50%	Subclonal			
MTC03	SNX5	p.Pro5Thr	missense_variant	20	17949056	G	T	26.19%	126	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8909	76.17%	100.00%	100%	Clonal			
MTC03	TPX2	p.Glu266Gln	missense_variant	20	30365355	G	C	19.32%	264	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7122	67.77%	100.00%	89%	Clonal			
MTC03	BPIFB3	p.Asp260Asn	missense_variant	20	31652505	G	A	16.72%	574	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0519	63.37%	91.31%	77%	Subclonal			
MTC03	CEP250	p.Glu1421Lys	missense_variant	20	34090458	G	A	17.75%	462	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3168	66.27%	96.43%	82%	Subclonal			
MTC03	JPH2	p.Pro551Leu	missense_variant	20	42744663	G	A	27.54%	138	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8955	79.60%	100.00%	100%	Clonal			
MTC03	LSM14B	p.Gln295Gln	synonymous_variant	20	60706461	G	A	29.45%	146	.	.	.		.	.	.			.	0.8559	82.89%	100.00%	100%	Clonal			
MTC03	PSMA7	p.Glu170Lys	missense_variant	20	60713310	C	T	14.54%	399	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0055	52.02%	83.80%	67%	Subclonal			
MTC03	RTEL1	p.Pro1146Leu	missense_variant	20	62326512	C	T	8.86%	553	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	30.61%	52.51%	41%	Subclonal			
MTC03	DONSON	p.Ser363Cys	missense_variant	21	34954320	G	C	35.84%	346	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.4773	92.19%	100.00%	100%	Clonal			
MTC03	CECR2	p.Glu708Lys	missense_variant	22	18022080	G	A	23.71%	797	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9534	90.10%	100.00%	100%	Clonal			
MTC03	ATP6V1E1	p.Asn185His	missense_variant	22	18077360	T	G	7.91%	139	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0002	20.21%	62.13%	36%	Subclonal			
MTC03	SRRD	p.Arg129Lys	missense_variant	22	26884130	G	A	19.92%	512	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7622	75.73%	100.00%	92%	Clonal			
MTC03	AP1B1	p.Ala77Ala	synonymous_variant	22	29755861	G	A	43.42%	403	.	.	.		.	.	.			.	0.9717	96.71%	100.00%	100%	Clonal			
MTC03	MPST	p.Glu298Gln	missense_variant	22	37425493	G	C	20.81%	322	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8324	74.84%	100.00%	96%	Clonal			
MTC03	PLXNB2	p.Ile1699Ile	synonymous_variant	22	50716119	G	A	18.92%	518	.	.	.		.	.	.			.	0.5810	71.89%	98.45%	87%	Clonal			
MTC03	ARSE	p.Glu476Glu	synonymous_variant	X	2854841	C	T	5.24%	401	.	.	.		.	.	.			.	0.0000	15.38%	35.72%	24%	Subclonal			
MTC03	ACE2	p.Ile694Ile	synonymous_variant	X	15584408	G	A	23.19%	470	.	.	.		.	.	.			.	0.9301	85.05%	100.00%	100%	Clonal			
MTC03	RBBP7	p.Leu237Gln	missense_variant	X	16875736	A	T	18.39%	310	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5722	65.76%	98.37%	85%	Clonal			
MTC03	DCAF8L1	p.Lys377Asn	missense_variant	X	27998321	C	A	15.49%	226	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1655	51.68%	93.29%	71%	Subclonal			
MTC03	GPR34	p.Met189Ile	missense_variant	X	41555453	G	A	18.03%	466	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3851	67.47%	97.07%	83%	Subclonal			
MTC03	CCDC22	p.Gln306*	stop_gained	X	49103963	C	T	5.92%	355	A	.	.		.	.	.			Indeterminate	0.5835	51.72%	98.44%	80%	Clonal			
MTC03	ZXDB	p.Ser327Ser	synonymous_variant	X	57619462	G	A	18.70%	246	.	.	.		.	.	.		TRUE	.	0.6458	64.82%	98.76%	86%	Clonal			
MTC03	ACRC	p.Ser204*	stop_gained	X	70823738	C	G	22.73%	44	A	.	.		.	.	.		TRUE	Likely pathogenic	0.7593	51.28%	100.00%	100%	Clonal			
MTC03	PHKA1	p.Val162Val	synonymous_variant	X	71904399	G	A	24.38%	160	.	.	.		.	.	.		TRUE	.	0.8898	76.02%	100.00%	100%	Clonal			
MTC03	ABCB7	p.Met442Ile	missense_variant	X	74290242	C	G	23.92%	209	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9001	78.41%	100.00%	100%	Clonal			
MTC03	TNMD	p.Ser28Ser	synonymous_variant	X	99840263	A	G	13.55%	251	.	.	.		.	.	.		TRUE	.	0.0143	44.86%	83.73%	62%	Subclonal			
MTC03	FRMPD3	p.Arg1213Trp	missense_variant	X	106844807	C	T	12.86%	412	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	45.35%	75.12%	59%	Subclonal			
MTC03	ATG4A	p.Gln88Glu	missense_variant	X	107374558	C	G	25.12%	211	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9124	80.94%	100.00%	100%	Clonal			
MTC03	XIAP	p.Gln398*	stop_gained	X	123034435	C	T	26.17%	107	A	.	.		.	.	.		TRUE	Likely pathogenic	0.8808	73.72%	100.00%	100%	Clonal			
MTC03	GPR112	p.Met340Ile	missense_variant	X	135426885	G	C	27.90%	552	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3765	93.01%	100.00%	100%	Clonal			
MTC03	GPR112	p.Pro367Arg	missense_variant	X	135426965	C	G	10.02%	539	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	35.19%	58.58%	46%	Subclonal			
MTC03	MAGEA12	p.Ser43Cys	missense_variant	X	151900673	G	C	14.18%	282	P	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0199	48.22%	85.58%	65%	Subclonal			
MTC03	DUSP9	p.Arg322Arg	synonymous_variant	X	152915571	G	A	19.07%	430	.	.	.		.	.	.			.	0.6433	71.11%	98.76%	88%	Clonal			
MTC03	GDI1	p.Leu14Leu	synonymous_variant	X	153665642	C	T	18.18%	297	.	.	.		.	.	.			.	0.5443	64.59%	98.19%	84%	Clonal			
MTC04	RSG1	p.Arg221Trp	missense_variant	1	16558659	G	A	3.44%	262	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	8.70%	31.64%	17%	Subclonal			
MTC04	TMCO4	p.Pro556Pro	synonymous_variant	1	20009770	G	A	68.54%	480	.	.	.		.	.	.			.	0.0000	98.51%	100.00%	100%	Clonal			
MTC04	PLA2G5	p.Val115Ile	missense_variant	1	20417111	G	A	53.90%	154	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1015	94.55%	100.00%	100%	Clonal			
MTC04	RPA2	p.Glu260Gln	missense_variant	1	28218733	C	G	49.25%	67	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9162	86.95%	100.00%	100%	Clonal			
MTC04	KCNA2	p.Trp232Leu	missense_variant	1	111146710	C	A	25.57%	790	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9489	96.49%	100.00%	100%	Clonal			
MTC04	GDAP2	p.Gly5Asp	missense_variant	1	118462967	C	T	29.68%	502	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9845	96.06%	100.00%	100%	Clonal			
MTC04	POGZ	p.Leu549Phe	missense_variant	1	151395904	C	G	7.52%	532	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6632	60.44%	98.45%	83%	Clonal			
MTC04	DENND4B	p.Asp481Val	missense_variant	1	153912967	T	A	8.01%	599	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7694	65.85%	100.00%	88%	Clonal			
MTC04	CD84	p.Lys303Asn	missense_variant	1	160520728	C	A	18.25%	274	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9762	88.57%	100.00%	100%	Clonal			
MTC04	ARHGAP30	p.Ala185Ala	synonymous_variant	1	161023157	G	T	19.47%	226	.	.	.		.	.	.			.	0.9696	87.82%	100.00%	100%	Clonal			
MTC04	ADAMTS4	p.Gln319Gln	synonymous_variant	1	161166347	C	T	8.73%	790	.	.	.		.	.	.			.	0.8741	74.37%	100.00%	96%	Clonal			
MTC04	CFH	c.2057-2A>T	splice_acceptor_variant	1	196695889	A	T	28.52%	561	D	.	.		.	.	.			Indeterminate	0.1673	96.64%	100.00%	100%	Clonal			
MTC04	MYOG	p.Lys74Met	missense_variant	1	203054869	T	A	2.38%	839	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.0000	13.48%	32.49%	22%	Subclonal			
MTC04	FAM177B	p.Asp4Glu	missense_variant	1	222919899	C	G	16.57%	332	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7592	86.32%	100.00%	100%	Clonal			
MTC04	EXO1	p.Leu206Phe	missense_variant	1	242021880	C	T	51.55%	741	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2112	98.74%	100.00%	100%	Clonal			
MTC04	OR2G3	p.Val29Glu	missense_variant	1	247768973	T	A	3.55%	704	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	21.33%	46.35%	32%	Subclonal			
MTC04	IL1B	p.Ser58Gly	missense_variant	2	113591080	T	C	11.07%	289	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5446	55.13%	97.51%	78%	Clonal			
MTC04	NCKAP5	p.Asp1420Asp	synonymous_variant	2	133540124	G	A	28.67%	457	.	.	.		.	.	.			.	0.9865	95.36%	100.00%	100%	Clonal			
MTC04	XIRP2	p.His2051Gln	missense_variant	2	168104055	T	A	26.75%	587	N	PASSENGER/OTHER	Passenger		.	.	true			Likely passenger	0.9820	95.88%	100.00%	100%	Clonal			
MTC04	TLK1	p.Lys412Asn	missense_variant	2	171884849	C	A	29.83%	181	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9768	90.10%	100.00%	100%	Clonal			
MTC04	COL3A1	p.Arg562Gln	missense_variant	2	189861146	G	A	33.63%	223	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.9233	93.17%	100.00%	100%	Clonal			
MTC04	GIGYF2	p.Pro392Leu	missense_variant	2	233655986	C	T	21.60%	625	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0423	93.84%	100.00%	100%	Clonal			
MTC04	NEU2	p.Ala207Val	missense_variant	2	233899244	C	T	33.33%	624	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7131	97.25%	100.00%	100%	Clonal			
MTC04	USP40	p.Gln964His	missense_variant	2	234402129	C	G	30.70%	417	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9766	95.51%	100.00%	100%	Clonal			
MTC04	BBX	p.Ser544Ser	synonymous_variant	3	107492200	A	G	37.22%	583	.	.	.		.	.	.			.	0.5848	97.65%	100.00%	100%	Clonal			
MTC04	CLSTN2	p.Arg591Ser	missense_variant	3	140275453	G	T	47.08%	291	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4964	96.99%	100.00%	100%	Clonal			
MTC04	SSR3	p.Gly183Ser	missense_variant	3	156261003	C	T	24.12%	398	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.4541	94.85%	100.00%	100%	Clonal			
MTC04	CHRD	p.Asp414Glu	missense_variant	3	184101128	T	A	20.46%	518	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7902	94.89%	100.00%	100%	Clonal			
MTC04	DGKG	p.Thr308Ile	missense_variant	3	185990120	G	A	22.57%	567	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.3355	95.97%	100.00%	100%	Clonal			
MTC04	TMEM128	p.Val158Ile	missense_variant	4	4239589	C	T	10.53%	114	D	.	Passenger		.	.	.			Indeterminate	0.5986	41.81%	97.89%	74%	Clonal			
MTC04	ADH1C	p.Phe199Leu	missense_variant	4	100264183	A	T	42.00%	100	.	.	Passenger		.	.	.		TRUE	Indeterminate	0.9764	88.36%	100.00%	100%	Clonal			
MTC04	CXXC4	p.Ser189Trp	missense_variant	4	105412394	G	C	2.95%	373	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.88%	25.65%	15%	Subclonal			
MTC04	TTC29	p.Pro3Ser	missense_variant	4	147863801	G	A	7.06%	170	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	20.14%	59.47%	35%	Subclonal			
MTC04	SEMA5A	p.Leu297Leu	synonymous_variant	5	9202110	G	A	22.51%	391	.	.	.		.	.	.	TRUE		.	0.9822	93.22%	100.00%	100%	Clonal			
MTC04	PDZD2	p.Thr1544Lys	missense_variant	5	32088185	C	A	26.22%	904	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5656	97.47%	100.00%	100%	Clonal			
MTC04	PCDHGA5	p.Gly377Glu	missense_variant	5	140745027	G	A	60.74%	731	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.3855	99.01%	100.00%	100%	Clonal			
MTC04	DNAH8	p.Asp3533Tyr	missense_variant	6	38889217	G	T	24.55%	387	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9667	94.10%	100.00%	100%	Clonal			
MTC04	GLYATL3	p.Asp69His	missense_variant	6	49485161	G	C	25.26%	669	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9208	96.53%	100.00%	100%	Clonal			
MTC04	PKHD1	p.Ser3744Ser	synonymous_variant	6	51513961	G	C	23.22%	491	.	.	.		.	.	.			.	0.9815	94.78%	100.00%	100%	Clonal			
MTC04	FOXO3	p.Ser411Ser	synonymous_variant	6	108985269	C	T	3.82%	419	.	.	.		true	.	.			.	0.0000	18.53%	48.56%	31%	Subclonal			
MTC04	FOXO3	p.Phe414Tyr	missense_variant	6	108985277	T	A	3.49%	372	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0000	16.08%	46.73%	28%	Subclonal			
MTC04	ROS1	p.Pro1539Ser	missense_variant	6	117663617	G	A	26.39%	610	N	CANCER	Passenger		true	.	.			Likely passenger	0.9815	96.25%	100.00%	100%	Clonal			
MTC04	SDK1	p.Gly1093Arg	missense_variant	7	4119169	G	C	12.71%	409	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7883	67.66%	100.00%	89%	Clonal			
MTC04	BBS9	p.Arg407Arg	synonymous_variant	7	33380531	A	G	28.69%	474	.	.	.		.	.	.		TRUE	.	0.9867	95.52%	100.00%	100%	Clonal			
MTC04	ASNS	p.Val339Phe	missense_variant	7	97486017	C	A	22.73%	286	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9789	91.19%	100.00%	100%	Clonal			
MTC04	ZSCAN25	p.Asp35Asn	missense_variant	7	99217332	G	A	27.25%	767	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2390	97.26%	100.00%	100%	Clonal			
MTC04	ZAN	p.Leu773Pro	missense_variant	7	100350046	T	C	10.63%	395	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8540	68.94%	100.00%	96%	Clonal			
MTC04	ACHE	p.Ala283Asp	missense_variant	7	100491006	G	T	4.55%	308	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.74%	52.06%	32%	Subclonal			
MTC04	FBXO25	p.Leu233Leu	synonymous_variant	8	408407	G	A	40.63%	320	.	.	.		.	.	.		TRUE	.	0.9874	95.67%	100.00%	100%	Clonal			
MTC04	CSMD1	p.Gly716Gly	synonymous_variant	8	3263667	C	A	51.56%	320	.	.	.		.	.	.		TRUE	.	0.0099	97.08%	100.00%	100%	Clonal			
MTC04	CPQ	p.Val331Val	synonymous_variant	8	98041662	G	A	22.54%	426	.	.	.		.	.	.			.	0.9567	94.15%	100.00%	100%	Clonal			
MTC04	TRHR	p.Asp85Glu	missense_variant	8	110099996	C	G	17.48%	927	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9823	96.13%	100.00%	100%	Clonal			
MTC04	PKHD1L1	p.Cys3811Cys	synonymous_variant	8	110523043	C	T	17.06%	211	.	.	.		.	.	.			.	0.9709	85.10%	100.00%	100%	Clonal			
MTC04	FOXD4	p.Ser107Tyr	missense_variant	9	117800	G	T	5.00%	100	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0004	10.58%	55.63%	25%	Subclonal			
MTC04	GNAQ	p.Asp35Asp	synonymous_variant	9	80646047	G	A	11.56%	147	.	.	.		true	.	.			.	0.6877	50.00%	98.55%	81%	Clonal			
MTC04	FOXE1	p.Thr321Met	missense_variant	9	100617158	C	T	28.69%	481	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2525	96.18%	100.00%	100%	Clonal			
MTC04	LPAR1	p.Asn27Lys	missense_variant	9	113704413	G	T	49.64%	280	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5676	96.65%	100.00%	100%	Clonal			
MTC04	PMPCA	p.Ser305Cys	missense_variant	9	139312485	C	G	58.63%	336	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7486	97.82%	100.00%	100%	Clonal			
MTC04	CASC10	p.Ala34Ala	synonymous_variant	10	21784838	A	T	68.57%	70	.	.	.		.	.	.		TRUE	.	0.1943	92.15%	100.00%	100%	Clonal			
MTC04	SPAG6	p.Lys405Arg	missense_variant	10	22690106	A	G	6.35%	315	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0003	28.70%	66.95%	45%	Subclonal			
MTC04	ANK3	p.Ser2623Phe	missense_variant	10	61832771	G	A	50.32%	316	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0613	97.00%	100.00%	100%	Clonal			
MTC04	DDX21	p.Ser632*	stop_gained	10	70737437	C	G	36.75%	166	A	.	.		.	.	.			Indeterminate	0.7616	92.17%	100.00%	100%	Clonal			
MTC04	CALHM2	p.Ile5Ile	synonymous_variant	10	105209684	G	A	20.86%	561	.	.	.		.	.	.			.	0.0331	92.60%	100.00%	100%	Clonal			
MTC04	NRAP	p.Ala1225Ala	synonymous_variant	10	115368200	C	T	32.45%	379	.	.	.		.	.	.			.	0.9390	95.53%	100.00%	100%	Clonal			
MTC04	ATRNL1	p.Ala1220Thr	missense_variant	10	117278776	G	A	30.94%	459	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9735	96.03%	100.00%	100%	Clonal			
MTC04	PNLIPRP1	p.Ser48Cys	missense_variant	10	118351375	A	T	46.47%	680	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6736	98.34%	100.00%	100%	Clonal			
MTC04	PPAPDC1A	p.Pro132Thr	missense_variant	10	122280556	C	A	42.92%	466	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7272	97.68%	100.00%	100%	Clonal			
MTC04	CLRN3	p.Thr127Lys	missense_variant	10	129681989	G	T	15.82%	158	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9047	74.85%	100.00%	100%	Clonal			
MTC04	CLRN3	p.Leu124Leu	synonymous_variant	10	129681997	C	A	15.03%	173	.	.	.		.	.	.			.	0.8990	74.30%	100.00%	100%	Clonal			
MTC04	OR52B2	p.Ala119Ala	synonymous_variant	11	6191200	G	A	5.83%	309	.	.	.		.	.	.		TRUE	.	0.0000	18.22%	44.82%	29%	Subclonal			
MTC04	ATG13	p.Gln249Gln	synonymous_variant	11	46680993	A	G	26.18%	191	.	.	.		.	.	.			.	0.9743	88.29%	100.00%	100%	Clonal			
MTC04	OR5L1	p.Lys80Lys	synonymous_variant	11	55579182	A	G	6.41%	156	.	.	.		.	.	.			.	0.0307	24.40%	79.10%	45%	Subclonal			
MTC04	C11orf88	p.Ala27Ala	synonymous_variant	11	111385590	T	A	31.73%	561	.	.	.		.	.	.			.	0.9500	96.81%	100.00%	100%	Clonal			
MTC04	PUS3	p.Leu457Ile	missense_variant	11	125763757	G	T	32.63%	426	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9220	96.08%	100.00%	100%	Clonal			
MTC04	LRTM2	p.Arg106Pro	missense_variant	12	1940350	G	C	17.65%	759	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9294	95.62%	100.00%	100%	Clonal			
MTC04	NOP2	p.Val59Gly	missense_variant	12	6675757	A	C	5.41%	148	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	13.53%	51.26%	27%	Subclonal			
MTC04	ADAMTS20	p.Arg644Lys	missense_variant	12	43846328	C	T	51.11%	405	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0024	97.53%	100.00%	100%	Clonal			
MTC04	XPO4	p.Val222Leu	missense_variant	13	21417097	C	A	43.38%	325	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9720	96.19%	100.00%	100%	Clonal			

MTC04	PPP1R36	p.Lys76Thr	missense_variant	14	65031513	A	C	53.49%	258	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0040	96.56%	100.00%	100%	Clonal			
MTC04	SERPINA12	p.Thr81Thr	synonymous_variant	14	94964492	T	A	11.84%	659	.	.	.		.	.	.		TRUE	.	0.5412	66.73%	97.61%	83%	Clonal			
MTC04	ERN2	p.Leu706Pro	missense_variant	16	23706176	A	G	13.53%	436	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8629	72.50%	100.00%	95%	Clonal			
MTC04	CES5A	c.638+1G>A	splice_donor_variant	16	55903522	C	T	4.51%	133	D	.	.		.	.	.			Indeterminate	0.0047	14.41%	66.08%	32%	Subclonal			
MTC04	SLC12A4	p.Asp320Gly	missense_variant	16	67985905	T	C	34.68%	447	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5458	96.52%	100.00%	100%	Clonal			
MTC04	TANGO6	p.Lys143Gln	missense_variant	16	68894119	A	C	30.78%	575	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9747	96.68%	100.00%	100%	Clonal			
MTC04	FGF11	p.Val181Phe	missense_variant	17	7346045	G	T	32.46%	268	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9515	93.94%	100.00%	100%	Clonal			
MTC04	TP53	p.Glu198*	stop_gained	17	7578257	C	A	26.56%	305	A	.	.		true	true	true	TRUE		Likely pathogenic	0.9788	92.37%	100.00%	100%	Clonal	TRUE	GACAACCACCCTTAACCCCTC	CTGGTTGCCCAGGGTCCC
MTC04	TP53	p.Tyr107*	stop_gained	17	7579366	G	T	31.01%	345	A	.	.		true	true	true	TRUE		Likely pathogenic	0.9733	94.80%	100.00%	100%	Clonal	TRUE	CCAGGCATTGAAGTCTCATGG	CCCTGCACCAGCAGCTCCTA
MTC04	RAI1	p.Val1189Val	synonymous_variant	17	17699829	C	A	31.84%	581	.	.	.		.	.	.	TRUE	TRUE	.	0.9431	97.00%	100.00%	100%	Clonal			
MTC04	EFCAB5	p.Val1240Ile	missense_variant	17	28417473	G	A	24.06%	212	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9702	89.51%	100.00%	100%	Clonal			
MTC04	RHBDL3	p.Leu370Gln	missense_variant	17	30648142	T	A	48.38%	649	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3080	98.35%	100.00%	100%	Clonal			
MTC04	EME1	p.Asn233Lys	missense_variant	17	48453268	T	A	2.51%	716	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	10.72%	27.17%	18%	Subclonal			
MTC04	MPO	p.Gln367Leu	missense_variant	17	56355292	T	A	6.21%	531	N	PASSENGER/OTHER	Passenger		.	.	true		TRUE	Likely passenger	0.0000	30.86%	59.90%	44%	Subclonal			
MTC04	SRSF2	p.Lys172Arg	missense_variant	17	74732394	T	C	7.55%	914	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.1835	59.72%	93.33%	76%	Subclonal			
MTC04	LAMA1	p.Ile98Val	missense_variant	18	7080027	T	C	33.82%	207	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9212	92.75%	100.00%	100%	Clonal			
MTC04	CYP4F12	p.Glu352Glu	synonymous_variant	19	15795948	G	A	34.50%	200	.	.	.		.	.	.			.	0.8934	92.74%	100.00%	100%	Clonal			
MTC04	HAPLN4	p.Ala181Ala	synonymous_variant	19	19369606	C	G	34.63%	361	.	.	.		.	.	.			.	0.7128	95.83%	100.00%	100%	Clonal			
MTC04	FCGBP	p.Ala633Thr	missense_variant	19	40424306	C	T	32.89%	821	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6780	97.94%	100.00%	100%	Clonal			
MTC04	ZNF541	p.Ala1306Thr	missense_variant	19	48024606	C	T	7.08%	438	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	34.88%	68.84%	50%	Subclonal			
MTC04	USP29	p.Phe703Leu	missense_variant	19	57642152	C	A	29.50%	478	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9850	95.81%	100.00%	100%	Clonal			
MTC04	PAK7	p.Leu584Met	missense_variant	20	9525135	A	T	16.46%	395	D	PASSENGER/OTHER	Driver		.	.	.			Likely pathogenic	0.9358	82.38%	100.00%	100%	Clonal			
MTC04	ZNF831	p.Ala597Ser	missense_variant	20	57767863	G	T	62.03%	374	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	98.08%	100.00%	100%	Clonal			
MTC04	ITGB2	p.Glu220Gln	missense_variant	21	46321490	C	G	22.83%	622	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9848	95.65%	100.00%	100%	Clonal			
MTC04	YDJC	p.Glu23Lys	missense_variant	22	21984237	C	T	30.48%	105	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9691	84.74%	100.00%	100%	Clonal			
MTC04	ASB11	p.Ala48Val	missense_variant	X	15333585	G	A	9.38%	352	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7146	59.66%	98.75%	85%	Clonal			
MTC04	PDK3	p.Gly78Gly	synonymous_variant	X	24512986	A	G	48.42%	285	.	.	.		.	.	.		TRUE	.	0.5030	96.36%	100.00%	100%	Clonal			
MTC04	SHROOM4	p.Leu1065Phe	missense_variant	X	50350947	C	A	9.41%	510	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0244	49.91%	85.52%	66%	Subclonal			
MTC04	AMER1	p.Pro750Ala	missense_variant	X	63410919	G	C	14.42%	527	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.9142	78.49%	100.00%	100%	Clonal	TRUE	AAGAGGTTCCCATTGCTGG	CTGCCTGATGCAGCTCTTC
MTC04	FLJ44635	p.Met101Val	missense_variant	X	71379980	A	G	30.08%	133	.	.	Passenger		.	.	.			Indeterminate	0.9730	87.23%	100.00%	100%	Clonal			
MTC04	MAGEE1	p.Leu627Ile	missense_variant	X	75650202	C	A	10.89%	606	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2275	60.26%	94.05%	76%	Subclonal			
MTC04	PNCK	p.Pro423Leu	missense_variant	X	152935925	G	A	29.13%	103	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9498	84.42%	100.00%	100%	Clonal			
MTC06	CELA2A	p.Leu90Ile	missense_variant	1	15789268	C	A	24.48%	290	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9384	82.73%	100.00%	100%	Clonal			
MTC06	RSC1A1	p.Ala345Val	missense_variant	1	15987397	C	T	6.59%	258	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	18.39%	46.23%	30%	Subclonal			
MTC06	AHDC1	p.Ser135Phe	missense_variant	1	27878223	G	A	22.78%	417	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9316	82.36%	100.00%	100%	Clonal			
MTC06	FAM167B	p.Pro143Ala	missense_variant	1	32714137	C	G	29.03%	62	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8881	68.99%	100.00%	100%	Clonal			
MTC06	CDCP2	p.His231His	synonymous_variant	1	54606841	G	A	53.64%	371	.	.	.		.	.	.			.	0.6653	97.58%	100.00%	100%	Clonal			
MTC06	DOCK7	p.Arg77Arg	synonymous_variant	1	63119744	C	T	15.76%	330	.	.	.		.	.	.			.	0.7346	66.58%	98.90%	87%	Clonal			
MTC06	RPAP2	p.Ile227Val	missense_variant	1	92789156	A	G	7.67%	313	.	.	Passenger		.	.	.			Indeterminate	0.0000	28.37%	61.28%	42%	Subclonal			
MTC06	ABCA4	p.Pro2259Leu	missense_variant	1	94461705	G	A	18.09%	282	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.8879	74.04%	100.00%	100%	Clonal			
MTC06	ABCA4	p.Pro2259Thr	missense_variant	1	94461706	G	T	17.99%	289	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.8860	74.01%	100.00%	100%	Clonal			
MTC06	S1PR1	p.Leu214Leu	synonymous_variant	1	101705182	G	T	50.99%	406	.	.	.		.	.	.			.	0.4780	97.62%	100.00%	100%	Clonal			
MTC06	COL11A1	p.Arg774Gln	missense_variant	1	103461555	C	T	22.60%	146	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9111	76.81%	100.00%	100%	Clonal			
MTC06	CELSR2	p.Val968Val	synonymous_variant	1	109795605	C	T	37.73%	379	.	.	.		.	.	.			.	0.9693	96.07%	100.00%	100%	Clonal			
MTC06	TRIM33	p.Trp889Cys	missense_variant	1	114948133	C	A	35.78%	721	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.9815	97.51%	100.00%	100%	Clonal			
MTC06	RPTN	p.Gly554Gly	synonymous_variant	1	152127913	G	T	16.53%	750	.	.	.		.	.	.			.	0.8569	90.33%	100.00%	100%	Clonal			
MTC06	HRNR	p.Gly2017Gly	synonymous_variant	1	152188054	C	T	3.83%	470	.	.	.		.	.	.			.	0.0000	17.94%	44.53%	29%	Subclonal			
MTC06	TMEM79	p.Arg275Gln	missense_variant	1	156256117	G	A	40.94%	381	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5794	97.02%	100.00%	100%	Clonal			
MTC06	TTC24	p.Ala379Ala	synonymous_variant	1	156553227	A	G	10.51%	514	.	.	.		.	.	.			.	0.4423	60.77%	96.83%	79%	Subclonal			
MTC06	PRCC	p.Met426Ile	missense_variant	1	156764555	G	T	11.95%	452	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.7895	68.44%	100.00%	90%	Clonal			
MTC06	SH2D2A	p.Ser356Phe	missense_variant	1	156777103	G	A	16.67%	186	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9061	75.34%	100.00%	100%	Clonal			
MTC06	KIRREL	p.Pro41His	missense_variant	1	158045972	C	A	11.06%	425	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6425	62.59%	98.38%	83%	Clonal			
MTC06	SPTA1	p.Asn1613Lys	missense_variant	1	158609696	G	T	12.38%	735	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8440	75.40%	100.00%	93%	Clonal			
MTC06	PYHIN1	p.Thr81Pro	missense_variant	1	158906941	A	C	32.39%	213	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7902	92.70%	100.00%	100%	Clonal			
MTC06	MAEL	p.Trp225Arg	missense_variant	1	166974337	T	C	30.80%	250	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8872	93.19%	100.00%	100%	Clonal			
MTC06	CCDC181	p.Glu440Lys	missense_variant	1	169366527	C	T	13.07%	199	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8408	64.06%	100.00%	98%	Clonal			
MTC06	C1orf105	p.Lys7Asn	missense_variant	1	172390046	G	T	25.30%	328	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9627	92.62%	100.00%	100%	Clonal			
MTC06	ZNF648	p.Thr440Met	missense_variant	1	182025827	G	A	13.92%	237	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7971	63.77%	100.00%	91%	Clonal			
MTC06	SMG7	p.Gln795Gln	synonymous_variant	1	183515253	G	A	14.73%	713	.	.	.		.	.	.			.	0.8857	78.68%	100.00%	96%	Clonal			
MTC06	HMCN1	p.Ser3921Leu	missense_variant	1	186086669	C	T	3.59%	334	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.10%	39.85%	23%	Subclonal			
MTC06	CAMSAP2	p.His391Asp	missense_variant	1	200816366	C	G	4.55%	198	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.40%	54.48%	30%	Subclonal			
MTC06	GNPAT	p.Arg163Gln	missense_variant	1	231398518	G	A	21.60%	287	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9512	90.08%	100.00%	100%	Clonal			
MTC06	EGLN1	p.Asp278Ala	missense_variant	1	231556802	T	G	34.43%	941	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6622	98.22%	100.00%	100%	Clonal			
MTC06	SIPA1L2	p.Glu915Lys	missense_variant	1	232600663	C	T	13.21%	636	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9409	83.95%	100.00%	100%	Clonal			
MTC06	NTPCR	p.Asp100Tyr	missense_variant	1	233105658	G	T	12.31%	463	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9100	76.93%	100.00%	100%	Clonal			
MTC06	RYR2	p.Leu308Val	missense_variant	1	237586465	C	G	8.91%	505	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3643	56.87%	95.92%	76%	Subclonal			
MTC06	MAP1LC3C	p.Tyr105Cys	missense_variant	1	242159595	T	C	12.02%	832	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9253	81.53%	100.00%	100%	Clonal			
MTC06	TFB2M	p.His148His	synonymous_variant	1	246720795	G	A	28.05%	303	.	.	.		.	.	.			.	0.5131	94.31%	100.00%	100%	Clonal			
MTC06	ZNF695	p.Glu12Gln	missense_variant	1	247163346	C	G	9.97%	371	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8855	71.28%	100.00%	100%	Clonal			
MTC06	LOC653602	c.442+1G>T	splice_donor_variant	2	14775769	G	T	27.55%	559	.	.	.		.	.	.			Indeterminate	0.6667	92.49%	100.00%	100%	Clonal			
MTC06	KCNS3	p.Asp70Asp	synonymous_variant	2	18112485	T	C	16.40%	378	.	.	.		.	.	.			.	0.1169	58.50%	91.89%	74%	Subclonal			
MTC06	OTOF	p.Arg810_Ala814del	inframe_deletion	2	26700120	GGGCCCGCAGCATCCT	G	16.37%	281	.	.	.	Deleterious	.	.	.			Indeterminate	0.2260	56.20%	93.92%	74%	Subclonal			
MTC06	XPO1	p.Lys1023Asn	missense_variant	2	61708320	C	G	10.69%	131	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.0122	28.99%	77.19%	48%	Subclonal			
MTC06	PELI1	p.Asp33Gly	missense_variant	2	64331938	T	C	22.66%	128	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8728	68.46%	100.00%	100%	Clonal			
MTC06	ELMOD3	p.Ser27Cys	missense_variant	2	85589334	C	G	23.23%	254	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9188	78.52%	100.00%	100%	Clonal			
MTC06	IL36G	p.Cys85Ser	missense_variant	2	113737678	T	A	12.60%	262	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0023	40.87%	77.37%	57%	Subclonal			
MTC06	AMER3	p.Asp128His	missense_variant	2	131520027	G	C	14.83%	681	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8914	78.79%	100.00%	97%	Clonal			
MTC06	ITGB6	p.Glu689Lys	missense_variant	2	160968627	C	T	6.08%	296	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	24.96%	60.99%	40%	Subclonal			
MTC06	SCN3A	p.Asp918Asn	missense_variant	2	165986620	C	T	13.23%	257	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7359	61.46%	98.91%	86%	Clonal			
MTC06	ZNF804A	p.Leu1191Val	missense_variant	2	185803694	C	G	7.72%	816	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	39.25%	63.29%	50%	Subclonal			
MTC06	TMEM194B	p.Arg356Trp	missense_variant	2	191375151	G	A	7.27%	399	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	32.95%	66.48%	48%	Subclonal			
MTC06	DNAH7	p.Pro3563Pro	synonymous_variant	2	196659089	C	T	9.04%	188	.	.	.		.	.	.			.	0.1216	37.01%	89.27%	59%	Subclonal			
MTC06	RAPH1	p.Val450Val	synonymous_variant	2	204319216	A	C	2.82%	248	.	.	.		.	.	.			.	0.0000	8.60%	36.80%	18%	Subclonal			
MTC06	PTPRN	p.Glu284Glu	synonymous_variant	2	220167001	C	T	52.28%	285	.	.	.		.	.	.			.	0.1315	97.05%	100.00%	100%	Clonal			
MTC06	SPP2	p.Asn23Lys	missense_variant	2	234959499	C	A	4.01%	524	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	16.76%	39.03%	26%	Subclonal			
MTC06	BSN	p.Ala355Val	missense_variant	3	49680131	C	T	62.50%	216	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9072	96.40%	100.00%	100%	Clonal			
MTC06	TMF1	p.Gln747Pro	missense_variant	3	69084178	T	G	4.05%	346	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	8.11%	23.11%	14%	Subclonal			
MTC06	ZIC4	p.Trp225Cys	missense_variant	3	147113802	C	G	22.60%	500	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9347	83.45%	100.00%	100%	Clonal			
MTC06	PHC3	p.Ser497Ala	missense_variant	3	169846771	A	C	3.37%	505	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.33%	34.32%	22%	Subclonal			
MTC06	VPS8	p.Leu455Val	missense_variant	3	184580823	C	G	16.03%	237	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8907	72.19%	100.00%	100%	Clonal			
MTC06	MUC4	p.Pro2192Ser	missense_variant	3	195511877	G	A	13.89%	36	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7118	34.33%	98.77%	91%	Clonal			
MTC06	PAK2	p.Ser109Ser	synonymous_variant	3	196529926	C	A	7.09%	141	.	.	.		.	.	.			.	0.0393	25.17%	80.97%	46%	Subclonal			
MTC06	CRMP1	p.Ala395Thr	missense_variant	4	5841376	C	T	23.65%	203	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9145	76.93%	100.00%	100%	Clonal			
MTC06	N4BP2	p.Ser105Cys	missense_variant	4	40103779	C	G	26.70%	206	N	CANCER	Passenger		.	.	.			Likely passenger	0.8533	72.72%	100.00%	94%	Clonal			
MTC06	EPHA5	p.Gly82Glu	missense_variant	4	66509082	C	T	12.82%	234	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6922	58.42%	98.67%	84%	Clonal			
MTC06	HELQ	p.Gly763Ala	missense_variant	4	84352824	C	G	17.42%	155	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5825	54.73%	97.91%	79%	Clonal			
MTC06	PAPSS1	p.Asp211Asn	missense_variant	4	108603209	C	T	23.04%	191	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9019	74.72%	100.00%	100%	Clonal			
MTC06	KIAA1109	p.Thr4939Ala	missense_variant	4	123283199	A	G	20.57%	141	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8174	64.04%	100.00%	93%	Clonal			
MTC06	USP38	p.Ala619Pro	missense_variant	4	144134984	G	C	17.35%	438	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2345	63.39%	94.61%	79%	Subclonal			
MTC06	GRIA2	p.Phe71Ile	missense_variant	4	158142941	T	A	32.81%	128	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9263	79.11%	100.00%	100%	Clonal			
MTC06	IRX1	p.Leu142Phe	missense_variant	5	3599486	C	T	6.56%	320	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	23.52%	53.90%	36%	Subclonal			
MTC06	RHOBTB3	p.Val463Ile	missense_variant	5	95116060	G	A	6.72%	595	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	32.06%	58.52%	44%	Subclonal			
MTC06	RGMB	p.Leu44Phe	missense_variant	5	98109783	G	C	12.03%	349	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4909	58.36%	97.22%	79%	Subclonal			
MTC06	APC	p.Val915Val	synonymous_variant	5	112174036	G	C	22.76%	615	.	.	.		true	true	true	TRUE		.	0.0052	93.93%	100.00%	100%	Clonal			
MTC06	DMXL1	p.Glu1187Asp	missense_variant	5	118485083	G	C	27.02%	581	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8805	95.59%	100.00%	100%	Clonal			
MTC06	SRFBP1	p.Glu336Gln	missense_variant	5	121356436	G	C	6.24%	529	D	.	Passenger		.	.	.			Indeterminate	0.0000	28.79%	55.92%	41%	Subclonal			
MTC06	CSNK1G3	p.Ala410Thr	missense_variant	5	122940463	G	A	25.81%	248	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8804	89.81%	100.00%	100%	Clonal			
MTC06	PCDHB2	p.Met383Ile	missense_variant	5	140475523	G	A	4.02%	373	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	10.64%	29.11%	18%	Subclonal			
MTC06	PCDHB3	p.Gly427Gly	synonymous_variant	5	140481514	G	C	3.96%	278	.	.	.		.	.	.		TRUE	.	0.0000	9.63%	30.99%	18%	Subclonal			
MTC06	SH3TC2	p.Arg1163Thr	missense_variant	5	148386631	C	G	24.59%	244	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9326	81.11%	100.00%	100%	Clonal			
MTC06	ZNF346	p.Cys139Arg	missense_variant	5	176471432	T	C	43.09%	181	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9689	93.06%	100.00%	100%	Clonal			
MTC06	HIST1H3J	p.Met1?	start_lost	6	27858570	T	C	16.78%	435	.	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8366	73.57%	100.00%	93%	Clonal			
MTC06	OR5V1	p.Ser93Cys	missense_variant	6	29323695	G	C	19.23%	390	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9300	81.12%	100.00%	100%	Clonal			
MTC06	OR2H1	p.Asn3Tyr	missense_variant	6	29429553	A	T	13.40%	418	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1612	57.41%	92.79%	74%	Subclonal			
MTC06	UBD	p.Ser65Thr	missense_variant	6	29523962	A	T	17.13%	467	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8637	75.65%	100.00%	95%	Clonal			
MTC06	HLA-DPB1	p.Tyr87His	missense_variant	6	33048607	T	C	20.40%	598	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9529	87.92%	100.00%	100%	Clonal			
MTC06	DNAH8	p.Ala4576Glu	missense_variant	6	38994334	C	A	13.01%	369	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6866	64.11%	98.64%	85%	Clonal			
MTC06	ZC2HC1B	p.Ala191Pro	missense_variant	6	144224262	G	C	20.46%	303	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0439	57.15%	89.05%	72%	Subclonal			
MTC06	RAB32	p.Arg217Thr	missense_variant	6	146875713	G	C	28.75%	240	N	CANCER	Passenger		.	.	.			Likely passenger	0.9157	79.13%	100.00%	100%	Clonal			
MTC06	CYP2W1	p.Leu79Leu	synonymous_variant	7	1024110	G	A	17.22%	151	.	.	.		.	.	.			.	0.8257	63.16%	100.00%	95%	Clonal			
MTC06	STK31	p.Ala600Ala	synonymous_variant	7	23810710	C	A	3.80%	184	.	.	.		.	.	.			.	0.0000	8.06%	34.16%	17%	Subclonal			
MTC06	PKD1L1	p.Glu786Lys	missense_variant	7	47933572	C	T	25.00%	200	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9273	79.61%	100.00%	100%	Clonal			
MTC06	ABCA13	p.Leu4412Val	missense_variant	7	48528884	C	G	25.36%	280	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9408	84.03%	100.00%	100%	Clonal			
MTC06	DDC	p.Ala278Glu	missense_variant	7	50566889	G	T	40.26%	154	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9498	90.94%	100.00%	100%	Clonal			
MTC06	PCLO	p.Ala461Asp	missense_variant	7	82784575	G	T	28.94%	311	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9460	93.86%	100.00%	100%	Clonal			
MTC06	CCDC132	p.Ser595*	stop_gained	7	92940513	C	A	12.68%	410	A	.	.		.	.	.			Indeterminate	0.8551	71.38%	100.00%	96%	Clonal			
MTC06	KPNA7	p.Ser477Ser	synonymous_variant	7	98775576	C	T	10.22%	225	.	.	.		.	.	.			.	0.7475	56.88%	98.98%	87%	Clonal			
MTC06	MCM7	p.Val304Val	synonymous_variant	7	99695530	C	G	3.78%	502	.	.	.		.	.	.			.	0.0000	20.35%	49.33%	32%	Subclonal			
MTC06	MUC17	p.Ser3674Leu	missense_variant	7	100685718	C	T	13.11%	862	N	PASSENGER/OTHER	Passenger		.	.	true			Likely passenger	0.9493	86.38%	100.00%	100%	Clonal			
MTC06	COL26A1	p.Trp85Cys	missense_variant	7	101063354	G	T	3.38%	296	N	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.38%	51.62%	29%	Subclonal			
MTC06	COL26A1	p.Pro86Thr	missense_variant	7	101063355	C	A	3.38%	296	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	15.38%	51.62%	29%	Subclonal			
MTC06	AKR1B15	p.Lys126Met	missense_variant	7	134254223	A	T	16.12%	614	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9262	87.96%	100.00%	100%	Clonal			
MTC06	STRA8	p.Ile166Met	missense_variant	7	134931220	C	G	2.78%	792	N	.	Passenger		.	.	.			Likely passenger	0.0000	13.38%	30.92%	21%	Subclonal			
MTC06	KCNU1	p.Arg156Thr	missense_variant	8	36662802	G	C	33.86%	127	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7408	65.53%	98.64%	86%	Clonal			
MTC06	KCNU1	p.Arg156Ser	missense_variant	8	36662803	G	C	33.59%	128	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7218	65.06%	98.52%	85%	Clonal			
MTC06	NSMAF	p.Asp841Glu	missense_variant	8	59499033	G	C	15.34%	176	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7154	58.12%	98.80%	85%	Clonal			
MTC06	C8orf34	p.Leu492Leu	synonymous_variant	8	69699696	T	C	7.18%	780	.	.	.		.	.	.			.	0.6025	63.51%	98.14%	83%	Clonal			
MTC06	HEY1	p.Ile65Met	missense_variant	8	80679298	G	C	8.87%	834	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.9097	78.24%	100.00%	100%	Clonal			
MTC06	LRRCC1	p.Leu220Pro	missense_variant	8	86027449	T	C	8.53%	692	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8779	73.85%	100.00%	98%	Clonal			
MTC06	CTHRC1	p.Ala26Ala	synonymous_variant	8	104383962	G	A	23.75%	240	.	.	.		.	.	.			.	0.5755	91.45%	100.00%	100%	Clonal			
MTC06	TMEM74	p.Glu258*	stop_gained	8	109796556	C	A	9.18%	915	D	.	.		.	.	.			Indeterminate	0.9277	81.12%	100.00%	100%	Clonal			
MTC06	TRPS1	p.Ser1133Ser	synonymous_variant	8	116426737	G	C	8.00%	750	.	.	.		.	.	.	TRUE		.	0.8216	70.56%	100.00%	92%	Clonal			
MTC06	AGO2	p.Leu100Leu	synonymous_variant	8	141582947	T	C	5.88%	255	.	.	.		.	.	.			.	0.4243	40.87%	96.36%	68%	Subclonal			
MTC06	TSNARE1	c.823+1G>T	splice_donor_variant	8	143413114	C	A	6.62%	861	D	.	.		.	.	.			Indeterminate	0.7798	68.26%	100.00%	90%	Clonal			
MTC06	BAI1	p.Ile983Met	missense_variant	8	143602211	C	G	6.18%	922	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6312	64.22%	98.34%	84%	Clonal			
MTC06	DGAT1	c.1160+1G>T	splice_donor_variant	8	145540849	C	A	7.41%	958	D	.	.		.	.	.			Indeterminate	0.8967	76.70%	100.00%	100%	Clonal			
MTC06	FBXL6	p.Thr102Lys	missense_variant	8	145581803	G	T	7.89%	786	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9156	78.13%	100.00%	100%	Clonal			
MTC06	PLIN2	p.Ile96Met	missense_variant	9	19123584	A	C	39.71%	272	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9395	95.09%	100.00%	100%	Clonal			
MTC06	LINGO2	p.Ala172Ala	synonymous_variant	9	27950154	T	A	18.99%	716	.	.	.		.	.	.			.	0.9481	85.89%	100.00%	100%	Clonal			
MTC06	LINGO2	p.Ile92Met	missense_variant	9	27950394	G	C	36.13%	548	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9792	97.02%	100.00%	100%	Clonal			
MTC06	TAF1L	p.Arg1356Arg	synonymous_variant	9	32631510	G	A	17.99%	567	.	.	.		.	.	.			.	0.9138	80.67%	100.00%	100%	Clonal			
MTC06	NFX1	p.His835Pro	missense_variant	9	33351637	A	C	17.89%	503	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9056	79.26%	100.00%	99%	Clonal			
MTC06	DAB2IP	p.Val529Val	synonymous_variant	9	124528983	C	T	29.11%	158	.	.	.		.	.	.		TRUE	.	0.9030	75.32%	100.00%	100%	Clonal			
MTC06	NTMT1	p.Trp133Cys	missense_variant	9	132396569	G	C	32.50%	80	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9019	72.05%	100.00%	100%	Clonal			
MTC06	UBAC1	p.Arg282Gln	missense_variant	9	138836905	C	T	24.44%	446	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9517	86.66%	100.00%	100%	Clonal			
MTC06	MLLT10	p.Leu596Ser	missense_variant	10	22002788	T	C	7.79%	308	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0000	23.53%	50.92%	35%	Subclonal			
MTC06	RET	p.Asp1031Tyr	missense_variant	10	43622074	G	T	6.32%	95	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0000	10.05%	45.85%	22%	Subclonal			
MTC06	ARHGAP22	p.Gly474Arg	missense_variant	10	49658800	C	T	10.94%	320	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	27.69%	51.95%	39%	Subclonal			
MTC06	ANK3	p.Glu431Gln	missense_variant	10	61965552	C	G	3.45%	290	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	6.20%	21.55%	12%	Subclonal			
MTC06	CHUK	p.Met272Val	missense_variant	10	101977871	T	C	26.64%	214	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9312	83.25%	100.00%	100%	Clonal			
MTC06	PKD2L1	p.Arg343Cys	missense_variant	10	102056895	G	A	2.73%	439	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	6.63%	20.89%	12%	Subclonal			
MTC06	KNDC1	p.Val1164Ala	missense_variant	10	135020369	T	C	24.22%	289	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6376	68.74%	98.35%	86%	Clonal			
MTC06	OR52E2	p.Arg264His	missense_variant	11	5080067	C	T	32.86%	140	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9299	80.28%	100.00%	100%	Clonal			
MTC06	EIF4G2	p.Arg259Arg	synonymous_variant	11	10825063	C	T	33.94%	109	.	.	.		.	.	.			.	0.9225	78.58%	100.00%	100%	Clonal			
MTC06	SOX6	p.Gln403Leu	missense_variant	11	16077380	T	A	24.19%	186	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.6942	64.82%	98.67%	86%	Clonal			
MTC06	NCR3LG1	p.Pro431Ala	missense_variant	11	17393985	C	G	14.24%	337	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	38.11%	64.52%	50%	Subclonal			
MTC06	GAS2	p.Ser11Ser	synonymous_variant	11	22696448	T	C	7.78%	167	.	.	.		.	.	.			.	0.0000	20.48%	57.87%	35%	Subclonal			
MTC06	TNKS1BP1	p.Lys269Asn	missense_variant	11	57081355	C	A	32.08%	53	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8908	70.28%	100.00%	100%	Clonal			
MTC06	OR6Q1	p.Pro160Ser	missense_variant	11	57798902	C	T	17.78%	613	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1869	67.32%	94.31%	81%	Subclonal			
MTC06	PYGM	p.Val643Val	synonymous_variant	11	64518837	G	A	21.49%	121	.	.	.		.	.	.			.	0.8414	64.59%	100.00%	97%	Clonal			
MTC06	MYEOV	p.Val88Val	synonymous_variant	11	69063181	T	C	22.51%	271	.	.	.		.	.	.			.	0.9082	77.39%	100.00%	100%	Clonal			
MTC06	PHOX2A	p.Arg273Leu	missense_variant	11	71950830	C	A	35.51%	107	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8283	67.20%	100.00%	90%	Clonal			
MTC06	FAT3	p.Ile3265Met	missense_variant	11	92565101	T	G	41.13%	231	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9558	84.62%	100.00%	100%	Clonal			
MTC06	BCL9L	p.Ile3Val	missense_variant	11	118780642	T	C	31.15%	260	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9453	84.39%	100.00%	100%	Clonal			
MTC06	OR10G9	p.Arg260Thr	missense_variant	11	123894498	G	C	24.41%	254	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6831	68.26%	98.61%	86%	Clonal			
MTC06	PRMT8	p.Asp246Asn	missense_variant	12	3686060	G	A	27.60%	192	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8805	74.21%	100.00%	98%	Clonal			
MTC06	MRPL51	p.Gly82Arg	missense_variant	12	6601580	C	G	25.62%	203	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7998	69.69%	100.00%	91%	Clonal			
MTC06	TAS2R43	p.Ser175Leu	missense_variant	12	11244305	G	A	26.44%	261	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8469	74.31%	100.00%	93%	Clonal			
MTC06	PDZRN4	p.Gly705Glu	missense_variant	12	41966695	G	A	26.96%	293	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8735	76.75%	100.00%	95%	Clonal			
MTC06	KRT2	p.Arg197Gln	missense_variant	12	53044333	C	T	20.75%	53	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7747	49.75%	100.00%	94%	Clonal			
MTC06	TENC1	p.Arg1363Gln	missense_variant	12	53457198	G	A	25.65%	386	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9461	87.49%	100.00%	100%	Clonal			
MTC06	SHMT2	p.Arg217Arg	synonymous_variant	12	57626292	G	T	21.70%	401	.	.	.		.	.	.			.	0.9017	78.96%	100.00%	98%	Clonal			
MTC06	PTPRB	p.Thr1044Ile	missense_variant	12	70965045	G	A	30.35%	201	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.7378	87.14%	100.00%	100%	Clonal			
MTC06	CCDC38	p.Leu429Leu	synonymous_variant	12	96266230	C	T	35.83%	120	.	.	.		.	.	.		TRUE	.	0.9174	82.13%	100.00%	100%	Clonal			
MTC06	KSR2	p.Glu605Asp	missense_variant	12	117962974	C	G	32.13%	249	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9469	85.44%	100.00%	100%	Clonal			
MTC06	IFT88	p.Val587Val	synonymous_variant	13	21217645	G	T	8.53%	375	.	.	.		.	.	.			.	0.0000	27.23%	53.02%	39%	Subclonal			
MTC06	RFXAP	p.Ala105Gly	missense_variant	13	37393808	C	G	24.02%	229	N	.	Passenger		.	.	.			Likely passenger	0.9247	79.18%	100.00%	100%	Clonal			
MTC06	KLF12	p.Ser238Thr	missense_variant	13	74387382	C	G	3.68%	136	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	5.22%	28.89%	13%	Subclonal			
MTC06	SLITRK1	p.Ile179Ile	synonymous_variant	13	84455106	G	A	29.21%	202	.	.	.		.	.	.		TRUE	.	0.9158	78.29%	100.00%	100%	Clonal			
MTC06	ARGLU1	p.Glu221Lys	missense_variant	13	107196505	C	T	29.23%	65	D	.	Passenger		.	.	.		TRUE	Indeterminate	0.8548	63.11%	100.00%	100%	Clonal			
MTC06	ZNF219	p.Ala534Ala	synonymous_variant	14	21559262	C	A	39.29%	196	.	.	.		.	.	.			.	0.9482	93.22%	100.00%	100%	Clonal			
MTC06	DHRS4	p.Arg26Leu	missense_variant	14	24423074	G	T	31.66%	338	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8956	93.97%	100.00%	100%	Clonal			
MTC06	LRRC16B	p.Gln445Pro	missense_variant	14	24527375	A	C	18.72%	219	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8926	73.02%	100.00%	100%	Clonal			
MTC06	RNF31	p.Lys640Asn	missense_variant	14	24620876	G	C	16.46%	243	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8035	66.34%	100.00%	91%	Clonal			
MTC06	PNN	p.Phe431Leu	missense_variant	14	39650206	T	G	19.58%	383	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9344	81.91%	100.00%	100%	Clonal			
MTC06	ADAM21	p.Arg96His	missense_variant	14	70924503	G	A	5.10%	98	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	7.45%	39.79%	18%	Subclonal			
MTC06	EVL	p.His81fs	frameshift_variant	14	100563878	CA	C	30.97%	155	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9239	78.56%	100.00%	100%	Clonal			
MTC06	HERC2	p.Ser4474Cys	missense_variant	15	28361999	G	C	4.53%	309	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	9.15%	25.88%	16%	Subclonal			
MTC06	THBS1	p.Asp935His	missense_variant	15	39885236	G	C	42.64%	265	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.9665	87.71%	100.00%	100%	Clonal			
MTC06	TYRO3	p.Gln84His	missense_variant	15	41853452	G	C	41.67%	96	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9310	76.34%	100.00%	100%	Clonal			
MTC06	SPTBN5	p.Ser193Arg	missense_variant	15	42180206	G	C	7.87%	89	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	9.40%	38.49%	20%	Subclonal			
MTC06	UBR1	p.Cys1635Tyr	missense_variant	15	43244578	C	T	29.11%	158	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9030	75.32%	100.00%	100%	Clonal			
MTC06	LRRC49	p.Val410Val	synonymous_variant	15	71300763	C	T	25.97%	154	.	.	.		.	.	.		TRUE	.	0.8157	67.74%	100.00%	92%	Clonal			
MTC06	AKAP13	p.Gly1076Val	missense_variant	15	86124526	G	T	9.39%	735	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	48.42%	76.06%	61%	Subclonal			
MTC06	FANCI	p.Val372Val	synonymous_variant	15	89819945	T	G	11.54%	104	.	.	.		.	.	.		TRUE	.	0.6055	42.60%	98.07%	75%	Clonal			
MTC06	IGF1R	p.Tyr643Asn	missense_variant	15	99459291	T	A	23.92%	761	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9745	96.50%	100.00%	100%	Clonal			
MTC06	WDR90	p.Ser1728Ser	synonymous_variant	16	717526	C	T	19.19%	172	D	.	.		.	.	.			.	0.7445	62.05%	98.95%	87%	Clonal			
MTC06	SOX8	p.Gly381Ala	missense_variant	16	1035187	G	C	46.90%	258	N	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Likely passenger	0.9621	95.62%	100.00%	100%	Clonal			
MTC06	CASKIN1	p.Val856Met	missense_variant	16	2230803	C	T	40.65%	155	N	CANCER	Passenger		.	.	.			Likely passenger	0.9539	91.13%	100.00%	100%	Clonal			
MTC06	C16orf89	p.Pro55Pro	synonymous_variant	16	5115745	A	C	22.08%	317	.	.	.		.	.	.			.	0.9045	77.85%	100.00%	100%	Clonal			
MTC06	ZP2	p.Tyr428His	missense_variant	16	21213430	A	G	28.05%	435	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7137	91.35%	100.00%	100%	Clonal			
MTC06	RABEP2	p.Asp556Glu	missense_variant	16	28916306	A	C	20.74%	188	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8356	68.14%	100.00%	94%	Clonal			
MTC06	FUS	p.Gly15Arg	missense_variant	16	31193838	G	C	20.81%	197	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.8402	68.90%	100.00%	94%	Clonal			
MTC06	ITGAM	p.Pro51Thr	missense_variant	16	31276732	C	A	20.00%	225	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8004	67.74%	100.00%	91%	Clonal			
MTC06	CES5A	p.Arg564Trp	missense_variant	16	55880488	G	A	26.17%	321	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9395	86.65%	100.00%	100%	Clonal			
MTC06	LRRC36	p.Glu628Lys	missense_variant	16	67412567	G	A	4.14%	145	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	8.31%	39.09%	19%	Subclonal			
MTC06	DPEP3	p.Gly121Cys	missense_variant	16	68013998	C	A	23.02%	126	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8788	69.13%	100.00%	100%	Clonal			
MTC06	TANGO6	p.Gly441Glu	missense_variant	16	68914478	G	A	16.95%	177	D	.	Passenger		.	.	.			Indeterminate	0.4925	54.37%	97.17%	77%	Subclonal			
MTC06	ST3GAL2	p.Ala210Thr	missense_variant	16	70422355	C	T	23.53%	153	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8983	73.06%	100.00%	100%	Clonal			
MTC06	RFWD3	p.Ser735Trp	missense_variant	16	74657947	G	C	19.89%	186	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7918	65.29%	100.00%	90%	Clonal			
MTC06	MAF	p.Pro110fs	frameshift_variant	16	79633469	CG	C	22.30%	278	A	.	.		true	.	.			Likely pathogenic	0.9045	77.12%	100.00%	100%	Clonal			
MTC06	PKD1L2	p.Ile472Ile	synonymous_variant	16	81232394	G	A	23.73%	177	.	.	.		.	.	.			.	0.9088	75.41%	100.00%	100%	Clonal			
MTC06	VMO1	p.Ala191Gly	missense_variant	17	4688694	G	C	61.08%	185	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9521	95.74%	100.00%	100%	Clonal			
MTC06	KCTD11	p.Gly182Glu	missense_variant	17	7256806	G	A	9.04%	166	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	19.20%	50.36%	32%	Subclonal			
MTC06	TP53	p.Arg273His	missense_variant	17	7577120	C	T	60.71%	140	A	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.9581	94.41%	100.00%	100%	Clonal	TRUE	CATAACTGCACCCTTGGTCTC	GGACCTGATTTCCTTACTGCC
MTC06	MYH10	p.Gly795Ala	missense_variant	17	8422069	C	G	28.97%	290	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9269	81.40%	100.00%	100%	Clonal			
MTC06	DNAH9	p.Met715Ile	missense_variant	17	11554433	G	A	28.07%	285	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9082	79.25%	100.00%	99%	Clonal			
MTC06	RAI1	p.Asp1365Asn	missense_variant	17	17700355	G	A	29.23%	260	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.9268	80.94%	100.00%	100%	Clonal			
MTC06	MYO15A	p.Ser717Ser	synonymous_variant	17	18024265	C	T	35.71%	112	.	.	.		.	.	.		TRUE	.	0.9183	81.13%	100.00%	100%	Clonal			
MTC06	FLII	p.Met323Leu	missense_variant	17	18156661	T	A	29.85%	201	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9243	79.50%	100.00%	100%	Clonal			
MTC06	MMP28	p.Phe299Leu	missense_variant	17	34095349	G	C	31.74%	167	.	.	Passenger		.	.	.		TRUE	Indeterminate	0.9323	80.69%	100.00%	100%	Clonal			
MTC06	KRT20	p.Asp189Gly	missense_variant	17	39036930	T	C	29.00%	100	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8772	69.17%	100.00%	100%	Clonal			
MTC06	ABCC3	p.Ala853Ala	synonymous_variant	17	48750979	C	G	24.62%	195	.	.	.		.	.	.		TRUE	.	0.9233	78.54%	100.00%	100%	Clonal			
MTC06	RNF213	p.Ala4450Gly	missense_variant	17	78350264	C	G	16.79%	262	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8268	68.49%	100.00%	93%	Clonal			
MTC06	ENDOV	p.Pro9Leu	missense_variant	17	78389020	C	T	17.50%	240	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8589	70.11%	100.00%	97%	Clonal			
MTC06	CNDP1	p.Ala205Ala	synonymous_variant	18	72234527	C	A	21.99%	291	.	.	.		.	.	.		TRUE	.	0.8984	76.72%	100.00%	100%	Clonal			
MTC06	ZNF407	p.Gly265Gly	synonymous_variant	18	72343770	C	T	18.26%	553	.	.	.		.	.	.		TRUE	.	0.3741	68.70%	96.45%	83%	Subclonal			
MTC06	ZNF516	p.Val336Val	synonymous_variant	18	74154003	G	C	25.92%	463	.	.	.		.	.	.		TRUE	.	0.9410	89.36%	100.00%	100%	Clonal			
MTC06	DOT1L	p.Ala1284Gly	missense_variant	19	2226371	C	G	41.79%	481	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9690	97.04%	100.00%	100%	Clonal			
MTC06	AMH	p.Glu343Gln	missense_variant	19	2251300	G	C	13.16%	38	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.4536	25.39%	96.52%	60%	Subclonal			
MTC06	DHPS	p.Asn298Asn	synonymous_variant	19	12786951	G	A	24.59%	61	.	PASSENGER/OTHER	.		.	.	.		TRUE	.	0.8548	60.86%	100.00%	100%	Clonal			
MTC06	ZNF431	p.Glu163Glu	synonymous_variant	19	21365595	G	A	3.94%	203	.	.	.		.	.	.		TRUE	.	0.0000	8.71%	33.88%	18%	Subclonal			
MTC06	ZNF570	p.Glu439Glu	synonymous_variant	19	37975673	G	A	23.98%	221	.	.	.		.	.	.			.	0.9227	78.69%	100.00%	100%	Clonal			
MTC06	ATP1A3	p.Thr45Arg	missense_variant	19	42492528	G	C	7.45%	322	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	22.47%	48.74%	34%	Subclonal			

MTC06	ZNF180	p.Arg457Gly	missense_variant	19	44981329	T	C	13.02%	192	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0255	40.27%	83.36%	59%	Subclonal			
MTC06	SULT2A1	p.Ser2Leu	missense_variant	19	48389510	G	A	14.04%	235	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0355	45.69%	85.81%	64%	Subclonal			
MTC06	IL4I1	p.Ala247Ala	synonymous_variant	19	50394326	G	T	21.98%	323	.	.	.		.	.	.			.	0.9024	77.74%	100.00%	100%	Clonal			
MTC06	SHANK1	p.Val103Leu	missense_variant	19	51219684	C	G	21.35%	192	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8599	70.22%	100.00%	97%	Clonal			
MTC06	LILRB3	p.Pro620Pro	synonymous_variant	19	54721001	T	C	20.19%	213	.	.	.		.	.	.			.	0.8113	67.78%	100.00%	92%	Clonal			
MTC06	ZNF805	p.Phe442Phe	synonymous_variant	19	57765513	C	T	23.15%	203	.	.	.		.	.	.			.	0.9069	75.75%	100.00%	100%	Clonal			
MTC06	ZNF211	p.Gly320Arg	missense_variant	19	58152617	G	A	12.12%	396	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	41.53%	70.76%	55%	Subclonal			
MTC06	EBF4	p.Pro516Pro	synonymous_variant	20	2736292	G	A	36.96%	92	.	.	.		.	.	.			.	0.9029	83.80%	100.00%	100%	Clonal			
MTC06	MACROD2	p.Gly99Glu	missense_variant	20	14474149	G	A	27.05%	122	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9139	76.79%	100.00%	100%	Clonal			
MTC06	ACTR5	p.Asp114Glu	missense_variant	20	37377463	C	G	24.31%	181	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9169	77.00%	100.00%	100%	Clonal			
MTC06	CHD6	p.Arg838Cys	missense_variant	20	40102114	G	A	22.28%	184	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8844	72.31%	100.00%	100%	Clonal			
MTC06	PTPRT	p.His173Leu	missense_variant	20	41408908	T	A	19.58%	240	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7696	67.00%	100.00%	89%	Clonal			
MTC06	R3HDML	p.Thr251Thr	synonymous_variant	20	42979423	G	A	49.59%	242	.	.	.		.	.	.			.	0.8947	95.80%	100.00%	100%	Clonal			
MTC06	ATP9A	p.Arg348fs	frameshift_variant	20	50287789	CA	C	20.63%	315	A	.	.		.	.	.			Indeterminate	0.8450	73.28%	100.00%	94%	Clonal			
MTC06	CDH4	p.Glu71Lys	missense_variant	20	60318660	G	A	19.39%	263	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7498	67.21%	98.98%	88%	Clonal			
MTC06	ITSN1	p.Gln632Gln	synonymous_variant	21	35166716	G	A	20.98%	205	.	.	.		.	.	.		TRUE	.	0.8485	69.86%	100.00%	95%	Clonal			
MTC06	MCM3AP	p.Val1020Ala	missense_variant	21	47685410	A	G	9.43%	53	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3280	22.36%	94.51%	52%	Subclonal			
MTC06	TANGO2	p.Ala112Val	missense_variant	22	20040054	C	T	19.63%	163	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9067	76.67%	100.00%	100%	Clonal			
MTC06	DRICH1	p.Gly56Gly	synonymous_variant	22	23974043	G	A	18.12%	149	.	.	.		.	.	.			.	0.8979	71.75%	100.00%	100%	Clonal			
MTC06	HDAC10	p.Asp468Asp	synonymous_variant	22	50686139	A	G	12.46%	289	.	.	.		.	.	.			.	0.8264	66.19%	100.00%	94%	Clonal			
MTC06	ACR	p.Leu10Pro	missense_variant	22	51176692	T	C	12.50%	248	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8229	64.46%	100.00%	94%	Clonal			
MTC06	PRKX	p.Pro312Pro	synonymous_variant	X	3533871	C	T	56.51%	292	.	.	.		.	.	.		TRUE	.	0.9815	96.82%	100.00%	100%	Clonal			
MTC06	ATP6AP2	p.Leu184Val	missense_variant	X	40457948	C	G	27.27%	99	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8420	65.37%	100.00%	96%	Clonal	TRUE	ATCCTGTGCCTTGCTTGGTA	TATTCAAGGATTCTCTAGAAACCAAAA
MTC06	KDM5C	p.Gly1535Arg	missense_variant	X	53222229	C	G	20.86%	187	N	PASSENGER/OTHER	Passenger		true	true	true			Likely passenger	0.8401	68.41%	100.00%	95%	Clonal			
MTC06	ZC3H12B	p.Ala568Gly	missense_variant	X	64722281	C	G	20.10%	418	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8050	73.91%	100.00%	91%	Clonal			
MTC06	MAGT1	p.Arg214Thr	missense_variant	X	77112357	C	G	23.26%	86	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6776	53.73%	98.55%	82%	Clonal			
MTC06	ZNF449	p.His429His	synonymous_variant	X	134494731	T	C	22.16%	379	.	.	.		.	.	.			.	0.9140	79.81%	100.00%	100%	Clonal			
MTC06	MAGEC1	p.Arg204Pro	missense_variant	X	140993801	G	C	6.19%	113	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	13.44%	55.02%	28%	Subclonal			
MTC07	TNFRSF8	p.Glu252Lys	missense_variant	1	12172032	G	A	35.62%	292	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.4738	93.61%	100.00%	100%	Clonal			
MTC07	CROCC	p.Ala704Thr	missense_variant	1	17272075	G	A	14.00%	50	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1414	31.62%	97.07%	66%	Subclonal			
MTC07	NR0B2	p.Arg238His	missense_variant	1	27238397	C	T	15.48%	336	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6071	75.46%	100.00%	100%	Clonal			
MTC07	COL11A1	c.2233-2A>T	splice_acceptor_variant	1	103462682	T	A	33.80%	361	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0504	94.11%	100.00%	100%	Clonal			
MTC07	VPS45	p.Gly127Gly	synonymous_variant	1	150049005	T	C	22.96%	257	.	.	.		.	.	.			.	0.4190	87.86%	100.00%	100%	Clonal			
MTC07	SPRR3	p.Gly73Gly	synonymous_variant	1	152975715	C	T	23.78%	143	.	.	.		.	.	.			.	0.7386	82.03%	100.00%	100%	Clonal			
MTC07	NUP210L	p.Val1502Leu	missense_variant	1	153994614	C	G	4.88%	451	N	PASSENGER/OTHER	Passenger		.	.	true			Likely passenger	0.0000	21.22%	48.13%	33%	Subclonal			
MTC07	OR10R2	p.Ser237Phe	missense_variant	1	158450377	C	T	22.55%	479	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5221	90.25%	100.00%	100%	Clonal			
MTC07	CFH	p.Ile734Thr	missense_variant	1	196696035	T	C	29.78%	272	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7252	91.90%	100.00%	100%	Clonal			
MTC07	CR2	p.Cys875*	stop_gained	1	207648470	C	A	7.20%	389	A	.	.		.	.	.			Indeterminate	0.0000	28.11%	57.53%	41%	Subclonal			
MTC07	CENPF	p.Glu2851Gln	missense_variant	1	214830341	G	C	13.97%	451	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4633	72.22%	100.00%	93%	Subclonal			
MTC07	NLRP3	p.Met277Val	missense_variant	1	247587574	A	G	6.67%	615	N	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Likely passenger	0.0000	32.60%	59.12%	45%	Subclonal			
MTC07	OR2W5	p.Pro202His	missense_variant	1	247655034	C	A	3.02%	463	.	.	Passenger		.	.	.			Indeterminate	0.0000	11.63%	32.97%	20%	Subclonal			
MTC07	CTNNA2	p.Arg120Cys	missense_variant	2	80085198	C	T	10.26%	117	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0410	33.49%	91.95%	58%	Subclonal			
MTC07	GLI2	p.Thr351Thr	synonymous_variant	2	121728176	C	A	4.11%	146	.	.	.		.	.	.			.	0.0000	10.47%	48.78%	23%	Subclonal			
MTC07	TTN	p.Cys9277*	stop_gained	2	179576726	G	T	26.20%	229	A	.	.		.	.	.			Indeterminate	0.2856	87.85%	100.00%	100%	Clonal			
MTC07	ITGAV	p.Val258Leu	missense_variant	2	187501806	G	C	12.75%	345	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0369	54.28%	93.04%	72%	Subclonal			
MTC07	COL5A2	p.Arg1294His	missense_variant	2	189904042	C	T	26.92%	26	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5608	51.61%	100.00%	100%	Clonal			
MTC07	IKZF2	p.Thr11Arg	missense_variant	2	214013322	G	C	15.58%	231	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3542	63.57%	100.00%	89%	Subclonal			
MTC07	COL4A3	p.Arg1432Pro	missense_variant	2	228172468	G	C	6.25%	128	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0005	17.91%	66.83%	36%	Subclonal			
MTC07	RBM44	p.Glu449Lys	missense_variant	2	238726904	G	A	3.92%	332	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	12.64%	36.91%	22%	Subclonal			
MTC07	QRICH1	p.Ser315Ser	synonymous_variant	3	49094688	A	G	4.01%	299	.	.	.		.	.	.		TRUE	.	0.0000	10.36%	31.74%	19%	Subclonal			
MTC07	WNT5A	p.Ala167Thr	missense_variant	3	55508550	C	T	14.91%	161	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0669	47.35%	94.73%	70%	Subclonal	TRUE	CGGGCGTCCACGAACTCCTT	CGAGACGGCCTTCACATACG
MTC07	A4GNT	p.Arg233Lys	missense_variant	3	137843431	C	T	21.27%	489	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7495	88.59%	100.00%	100%	Clonal			
MTC07	FOXL2	p.Gly240Ser	missense_variant	3	138664847	C	T	4.50%	333	N	PASSENGER/OTHER	Passenger		true	.	.	TRUE		Likely passenger	0.0000	15.18%	40.97%	26%	Subclonal			
MTC07	AHSG	c.410-2A>C	splice_acceptor_variant	3	186334974	A	C	9.26%	108	D	.	.		.	.	.			Indeterminate	0.0242	28.69%	88.74%	53%	Subclonal			
MTC07	MUC4	p.Thr2180Thr	synonymous_variant	3	195511911	G	A	18.52%	27	.	.	.		.	.	.			.	0.3496	37.48%	100.00%	100%	Subclonal			
MTC07	ASIC5	p.Trp90Leu	missense_variant	4	156784678	C	A	9.90%	394	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	41.16%	74.80%	56%	Subclonal			
MTC07	TERT	p.Ala801Pro	missense_variant	5	1271301	C	G	8.88%	349	N	PASSENGER/OTHER	Passenger		true	.	.	TRUE		Likely passenger	0.0000	35.49%	69.61%	50%	Subclonal			
MTC07	NIPAL4	p.Ser454Leu	missense_variant	5	156899928	C	T	44.79%	413	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0074	97.21%	100.00%	100%	Clonal			
MTC07	PAK1IP1	p.Ala219Ser	missense_variant	6	10704992	G	T	25.43%	232	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7306	83.12%	100.00%	100%	Clonal			
MTC07	TMEM170B	p.Trp37Cys	missense_variant	6	11565912	G	C	8.04%	112	D	.	Passenger		.	.	.			Indeterminate	0.0004	19.74%	67.75%	38%	Subclonal			
MTC07	SIRT5	p.Pro68Gln	missense_variant	6	13588650	C	A	3.97%	126	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.69%	41.41%	19%	Subclonal			
MTC07	MUC21	p.Ala162Ala	synonymous_variant	6	30954438	C	T	12.74%	212	.	.	.		.	.	.			.	0.4652	64.29%	100.00%	98%	Subclonal			
MTC07	T	p.Ile410Ile	synonymous_variant	6	166571881	G	A	34.56%	353	.	.	.		.	.	.			.	0.1369	94.25%	100.00%	100%	Clonal			
MTC07	NUDCD3	p.Asn274Lys	missense_variant	7	44432049	G	T	7.59%	290	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.33%	63.28%	43%	Subclonal			
MTC07	ZNF277	p.Lys84Arg	missense_variant	7	111927087	A	G	27.66%	394	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1076	93.15%	100.00%	100%	Clonal			
MTC07	POLB	p.Gly305Glu	missense_variant	8	42229081	G	A	17.56%	262	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6831	78.93%	100.00%	100%	Clonal			
MTC07	CYP7B1	p.Tyr89Tyr	synonymous_variant	8	65528831	G	A	20.48%	83	.	.	.		.	.	.			.	0.7153	70.34%	100.00%	100%	Clonal			
MTC07	ZFHX4	p.Ser1304*	stop_gained	8	77762545	C	G	6.21%	419	A	.	.		.	.	.			Indeterminate	0.0000	32.35%	68.18%	48%	Subclonal			
MTC07	RSPO2	p.Leu186Leu	synonymous_variant	8	108970366	C	T	3.87%	284	.	.	.		true	.	.			.	0.0000	16.34%	51.76%	30%	Subclonal			
MTC07	KIAA2026	p.Val659Phe	missense_variant	9	5968256	C	A	3.39%	443	N	.	Passenger		.	.	.			Likely passenger	0.0000	11.25%	30.83%	19%	Subclonal			
MTC07	FRMPD1	p.Ser587Ser	synonymous_variant	9	37740286	C	T	4.59%	305	.	.	.		.	.	.			.	0.0000	15.22%	42.46%	26%	Subclonal			
MTC07	FANCC	p.Ile504Thr	missense_variant	9	97869370	A	G	12.38%	105	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.1412	41.12%	97.13%	70%	Subclonal			
MTC07	SVEP1	p.Tyr2741His	missense_variant	9	113169659	A	G	3.02%	430	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.40%	33.62%	20%	Subclonal			
MTC07	MUSK	p.Pro765Arg	missense_variant	9	113562952	C	G	7.91%	670	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	40.26%	67.71%	53%	Subclonal			
MTC07	ODF2	p.Arg360Trp	missense_variant	9	131243901	C	T	17.31%	283	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5405	72.64%	100.00%	98%	Clonal			
MTC07	ITGA8	p.Met754Thr	missense_variant	10	15634254	A	G	9.02%	255	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0004	34.15%	74.37%	51%	Subclonal			
MTC07	UBQLN3	p.Pro565Pro	synonymous_variant	11	5529094	G	T	11.11%	243	.	.	.		.	.	.		TRUE	.	0.0001	35.84%	72.96%	52%	Subclonal			
MTC07	CCDC85B	p.Gly145Gly	synonymous_variant	11	65658689	C	T	5.03%	199	.	.	.		.	.	.			.	0.0000	15.26%	50.67%	29%	Subclonal			
MTC07	RSF1	p.Arg1206Gln	missense_variant	11	77383221	C	T	26.94%	245	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8854	90.64%	100.00%	100%	Clonal			
MTC07	TENM4	p.Glu2765Lys	missense_variant	11	78369120	C	T	20.90%	670	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0129	93.18%	100.00%	100%	Clonal			
MTC07	OR4D5	p.Val158Leu	missense_variant	11	123810795	G	C	11.41%	263	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	37.50%	73.60%	53%	Subclonal			
MTC07	OR10G4	p.Leu212Leu	synonymous_variant	11	123886917	G	A	24.32%	74	.	.	.		.	.	.		TRUE	.	0.5382	64.66%	100.00%	100%	Clonal			
MTC07	CRACR2A	p.Lys659Asn	missense_variant	12	3728494	C	G	18.50%	173	N	CANCER	Passenger		.	.	.			Likely passenger	0.5620	70.24%	100.00%	100%	Clonal			
MTC07	DYRK4	p.Asn514Asn	synonymous_variant	12	4722898	C	T	11.11%	261	.	.	.		.	.	.			.	0.0103	44.15%	87.18%	63%	Subclonal			
MTC07	VWF	p.Arg2507Trp	missense_variant	12	6080794	G	A	8.84%	147	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0061	29.42%	81.72%	50%	Subclonal			
MTC07	VWF	p.Cys633Cys	synonymous_variant	12	6166069	G	A	21.31%	61	.	.	.		.	.	.			.	0.5133	59.93%	100.00%	100%	Clonal			
MTC07	PRB4	p.Gly107Gly	synonymous_variant	12	11461596	T	G	17.02%	47	.	.	.		.	.	.			.	0.3508	44.46%	100.00%	97%	Subclonal			
MTC07	LRRK2	p.Ser1036Arg	missense_variant	12	40692054	A	C	4.92%	264	N	PASSENGER/OTHER	Passenger		.	true	.			Likely passenger	0.0000	21.92%	62.83%	38%	Subclonal			
MTC07	MON2	p.Gln859Glu	missense_variant	12	62938786	C	G	38.17%	131	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8791	88.77%	100.00%	100%	Clonal			
MTC07	HECTD4	p.Gly1732Ala	missense_variant	12	112673436	C	G	3.14%	255	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.09%	27.90%	15%	Subclonal			
MTC07	DNAJC3	p.Glu125Glu	synonymous_variant	13	96377488	A	G	3.41%	264	.	.	.		.	.	.		TRUE	.	0.0000	9.86%	35.59%	19%	Subclonal			
MTC07	OR4K13	p.Arg232Gln	missense_variant	14	20502223	C	T	30.95%	349	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0096	92.48%	100.00%	100%	Clonal			
MTC07	ARHGEF40	p.Cys1287Cys	synonymous_variant	14	21552983	C	T	42.13%	178	.	.	.		.	.	.		TRUE	.	0.9351	92.79%	100.00%	100%	Clonal			
MTC07	DNAAF2	p.Pro651Pro	synonymous_variant	14	50094784	T	C	3.47%	144	.	.	.		.	.	.		TRUE	.	0.0000	6.65%	36.33%	16%	Subclonal			
MTC07	TRMT5	p.Asn480Asn	synonymous_variant	14	61442197	A	G	3.54%	198	.	.	.		.	.	.		TRUE	.	0.0000	7.67%	32.81%	17%	Subclonal			
MTC07	DCAF4	p.Ile463Val	missense_variant	14	73425412	A	G	13.77%	276	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1392	57.29%	97.24%	78%	Subclonal			
MTC07	PTPN21	p.Glu734Lys	missense_variant	14	88945575	C	T	19.68%	249	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6728	78.31%	100.00%	100%	Clonal			
MTC07	BEGAIN	p.Arg58Leu	missense_variant	14	101012841	C	A	22.73%	264	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8526	89.37%	100.00%	100%	Clonal			
MTC07	SEMA6D	p.Arg99Leu	missense_variant	15	48053368	G	T	29.81%	463	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0073	93.49%	100.00%	100%	Clonal			
MTC07	MYO5C	p.His1434Tyr	missense_variant	15	52500837	G	A	5.06%	158	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	11.75%	44.80%	24%	Subclonal			
MTC07	CHSY1	p.Lys111Lys	synonymous_variant	15	101775770	C	T	10.08%	248	.	.	.		.	.	.		TRUE	.	0.0000	31.98%	67.23%	47%	Subclonal			
MTC07	ERN2	p.Ser538Arg	missense_variant	16	23711917	T	G	19.16%	261	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6562	77.50%	100.00%	100%	Clonal			
MTC07	ABCC11	p.Gly501Arg	missense_variant	16	48244966	C	G	27.96%	447	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0925	94.05%	100.00%	100%	Clonal			
MTC07	MTHFSD	p.Gly72Gly	synonymous_variant	16	86585660	G	A	3.42%	234	.	.	.		.	.	.		TRUE	.	0.0000	9.50%	36.98%	19%	Subclonal			
MTC07	ACSF3	p.Pro130Ser	missense_variant	16	89167477	C	T	5.39%	297	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.55%	48.22%	31%	Subclonal			
MTC07	MNT	p.Asp152Asp	synonymous_variant	17	2298366	G	A	12.12%	66	.	.	.		.	.	.		TRUE	.	0.0619	28.97%	93.78%	57%	Subclonal			
MTC07	TP53	p.His193Leu	missense_variant	17	7578271	T	A	42.21%	199	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.9384	93.47%	100.00%	100%	Clonal	TRUE	GACAACCACCCTTAACCCCTC	CTGGTTGCCCAGGGTCCC
MTC07	TAOK1	p.Arg433His	missense_variant	17	27829701	G	A	38.16%	228	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.8630	93.10%	100.00%	100%	Clonal			
MTC07	AKAP1	p.Ser847Arg	missense_variant	17	55195780	A	C	3.59%	306	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	11.07%	35.43%	20%	Subclonal			
MTC07	CASKIN2	p.Arg522His	missense_variant	17	73499946	C	T	7.60%	263	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0010	32.85%	76.02%	51%	Subclonal			
MTC07	RNF157	p.Pro408Leu	missense_variant	17	74155497	G	A	4.21%	309	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	16.14%	46.72%	28%	Subclonal			
MTC07	CBX4	p.Val253Val	synonymous_variant	17	77808682	G	C	54.99%	682	.	.	.		.	.	.		TRUE	.	0.0133	98.62%	100.00%	100%	Clonal			
MTC07	BAHCC1	p.Arg1389Gln	missense_variant	17	79419058	G	A	44.44%	90	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.1976	89.33%	100.00%	100%	Clonal			
MTC07	POTEC	p.Ala119Thr	missense_variant	18	14542791	C	T	18.75%	32	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.2908	37.23%	98.76%	88%	Subclonal			
MTC07	KLHL14	p.Val376Met	missense_variant	18	30275459	C	T	35.02%	237	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7442	93.79%	100.00%	100%	Clonal			
MTC07	SETBP1	p.Ser763Cys	missense_variant	18	42531593	C	G	35.05%	368	D	CANCER	Passenger		true	true	.		TRUE	Likely pathogenic	0.1938	94.62%	100.00%	100%	Clonal			
MTC07	SETBP1	p.Ser763Ser	synonymous_variant	18	42531594	C	A	35.08%	362	.	.	.		true	true	.		TRUE	.	0.2096	94.55%	100.00%	100%	Clonal			
MTC07	CPAMD8	p.Asn314Asn	synonymous_variant	19	17111290	G	A	20.00%	230	.	.	.		.	.	.			.	0.5967	85.03%	100.00%	100%	Clonal			
MTC07	JAK3	p.Arg402Arg	synonymous_variant	19	17951087	G	A	3.63%	358	.	.	.		true	.	.			.	0.0000	16.01%	46.48%	28%	Subclonal			
MTC07	ZNF222	p.Tyr381*	stop_gained	19	44536850	C	A	5.93%	455	D	.	.		.	.	.			Indeterminate	0.0000	22.90%	47.80%	34%	Subclonal			
MTC07	GPR4	p.Lys299Met	missense_variant	19	46094229	T	A	24.40%	291	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3618	88.24%	100.00%	100%	Clonal			
MTC07	ARHGAP35	p.Ile640fs	frameshift_variant	19	47423849	AAT	A	17.59%	415	A	.	.		.	true	true			Likely pathogenic	0.6082	77.73%	100.00%	100%	Clonal			
MTC07	NLRP12	p.Arg134His	missense_variant	19	54314512	C	T	18.61%	274	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6333	76.53%	100.00%	100%	Clonal			
MTC07	MAVS	p.Glu410Asp	missense_variant	20	3846401	G	C	11.54%	182	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0018	35.49%	79.05%	54%	Subclonal			
MTC07	DEFB118	p.Glu24Gly	missense_variant	20	29960672	A	G	30.17%	179	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9157	89.89%	100.00%	100%	Clonal			
MTC07	SLCO4A1	p.His191Gln	missense_variant	20	61288379	C	A	11.56%	199	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1807	51.40%	97.84%	77%	Subclonal			
MTC07	PMM1	p.Ala78Ala	synonymous_variant	22	41980579	G	A	10.89%	303	.	.	.		.	.	.		TRUE	.	0.0039	44.21%	84.07%	62%	Subclonal			
MTC07	SYN1	p.Pro470Ala	missense_variant	X	47433975	G	C	10.00%	110	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0040	26.23%	78.97%	47%	Subclonal			
MTC07	STARD8	p.Thr274Ala	missense_variant	X	67937576	A	G	5.20%	327	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	14.87%	37.76%	24%	Subclonal			
MTC07	GLRA4	p.Gln345*	stop_gained	X	102968498	G	A	21.77%	248	D	.	.		.	.	.			Indeterminate	0.6066	75.93%	100.00%	100%	Clonal			
MTC07	PAK3	p.Arg534Cys	missense_variant	X	110459733	C	T	14.06%	249	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0099	47.68%	87.80%	66%	Subclonal			
MTC11	ESPN	p.Gly251Asp	missense_variant	1	6500762	G	A	16.67%	48	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7538	51.92%	100.00%	100%	Clonal			
MTC11	EPHA2	p.Gly377Arg	missense_variant	1	16464531	C	T	6.63%	181	N	PASSENGER/OTHER	Passenger		.	.	true			Likely passenger	0.0751	31.29%	89.31%	55%	Subclonal			
MTC11	ARID1A	p.Glu1779_Glu1780del	disruptive_inframe_deletion	1	27105720	AGAAGAG	A	6.01%	416	P	.	.	Deleterious	true	true	true			Likely pathogenic	0.0004	33.43%	71.52%	50%	Subclonal			
MTC11	ZNF362	p.Leu386Leu	synonymous_variant	1	33764542	G	A	24.40%	168	.	.	.		.	.	.			.	0.9457	86.87%	100.00%	100%	Clonal			
MTC11	USP1	p.Pro315Leu	missense_variant	1	62910795	C	T	8.13%	283	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1508	44.72%	93.83%	67%	Subclonal			
MTC11	CRNN	p.Pro400Pro	synonymous_variant	1	152382358	C	T	6.49%	462	.	.	.		.	.	.			.	0.0136	42.02%	83.74%	60%	Subclonal			
MTC11	SPRR3	p.Gly73Gly	synonymous_variant	1	152975715	C	T	11.63%	129	.	.	.		.	.	.			.	0.7253	58.21%	100.00%	100%	Clonal			
MTC11	ADAR	p.Asn692Asp	missense_variant	1	154569604	T	C	7.76%	361	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.2231	49.61%	95.67%	72%	Subclonal			
MTC11	EFNA4	p.Gly121Arg	missense_variant	1	155039453	G	C	11.85%	270	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8094	71.10%	100.00%	100%	Clonal			
MTC11	OLFML2B	p.Thr28Thr	synonymous_variant	1	161993137	T	C	3.15%	445	.	.	.		.	.	.			.	0.0000	17.04%	47.74%	29%	Subclonal			
MTC11	CEP350	p.Glu1056Asp	missense_variant	1	179990077	A	T	3.75%	347	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.02%	57.84%	35%	Subclonal			
MTC11	ZBTB41	p.Gln84Gln	synonymous_variant	1	197169352	T	C	4.56%	241	.	.	.		.	.	.			.	0.0045	23.44%	73.32%	42%	Subclonal			
MTC11	PPP1R12B	p.Ser474Ile	missense_variant	1	202407115	G	T	3.76%	372	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	20.47%	57.04%	35%	Subclonal			
MTC11	SRBD1	p.Pro354Pro	synonymous_variant	2	45807024	A	G	9.02%	266	.	.	.		.	.	.			.	0.3321	49.97%	97.16%	74%	Subclonal			
MTC11	RTN4	p.Ser603Leu	missense_variant	2	55253427	G	A	15.73%	286	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8519	81.23%	100.00%	100%	Clonal			
MTC11	KDM3A	p.Asn880Lys	missense_variant	2	86709180	C	G	12.96%	378	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8378	75.96%	100.00%	100%	Clonal			
MTC11	MBD5	p.Arg200*	stop_gained	2	149226110	C	T	3.22%	404	A	.	.		.	.	.			Indeterminate	0.0000	15.19%	44.31%	27%	Subclonal			
MTC11	TTN	p.Thr7938Thr	synonymous_variant	2	179584405	T	G	7.67%	391	.	.	.		.	.	.			.	0.0356	44.35%	87.67%	63%	Subclonal			
MTC11	TTN	p.Gly3359Gly	synonymous_variant	2	179628941	C	G	13.39%	239	.	.	.		.	.	.			.	0.8144	71.52%	100.00%	100%	Clonal			
MTC11	ICA1L	p.Met166Lys	missense_variant	2	203684485	A	T	23.45%	290	D	.	Passenger		.	.	.			Indeterminate	0.9567	91.22%	100.00%	100%	Clonal			
MTC11	PARD3B	p.Leu643Phe	missense_variant	2	206058019	G	C	14.93%	67	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7360	54.32%	100.00%	100%	Clonal			
MTC11	POMGNT2	p.Leu19Leu	synonymous_variant	3	43122867	C	T	6.77%	266	.	.	.		.	.	.			.	0.0292	35.29%	85.06%	56%	Subclonal			
MTC11	ROBO1	p.Ser600Gly	missense_variant	3	78717285	T	C	3.62%	276	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.0000	16.01%	53.49%	30%	Subclonal			
MTC11	CD96	p.Thr141Thr	synonymous_variant	3	111286374	A	T	10.96%	73	.	PASSENGER/OTHER	.		.	.	.			.	0.5851	42.12%	98.91%	90%	Clonal			
MTC11	U2SURP	p.Lys962Asn	missense_variant	3	142773896	A	T	4.19%	167	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0032	16.64%	68.72%	35%	Subclonal			
MTC11	ZBBX	p.Thr624Thr	synonymous_variant	3	167016100	T	C	9.89%	263	.	.	.		.	.	.			.	0.4982	55.25%	98.48%	82%	Subclonal			
MTC11	VWA5B2	p.Asp1185His	missense_variant	3	183959650	G	C	7.83%	447	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0299	46.46%	87.44%	65%	Subclonal			
MTC11	MAP3K13	p.Ser695Ile	missense_variant	3	185191203	G	T	8.41%	345	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1475	48.34%	93.91%	69%	Subclonal			
MTC11	MUC4	p.Pro2194Leu	missense_variant	3	195511870	G	A	18.18%	33	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7535	46.89%	100.00%	100%	Clonal			
MTC11	EVC	p.Val119Gly	missense_variant	4	5731089	T	G	6.56%	122	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1461	27.41%	92.91%	54%	Subclonal			
MTC11	SLIT2	p.Pro1324Arg	missense_variant	4	20618656	C	G	6.06%	198	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0045	25.07%	74.10%	44%	Subclonal			
MTC11	NWD2	p.Asp446Val	missense_variant	4	37444947	A	T	17.56%	393	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8552	85.80%	100.00%	100%	Clonal			
MTC11	COL25A1	p.Val620Ile	missense_variant	4	109740473	C	T	11.16%	251	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6736	61.98%	100.00%	92%	Clonal			
MTC11	FREM3	p.Phe290Tyr	missense_variant	4	144620960	A	T	7.65%	353	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0478	43.39%	88.67%	63%	Subclonal			
MTC11	TRIM2	p.Gly100Val	missense_variant	4	154197128	G	T	5.33%	319	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0005	27.28%	68.60%	44%	Subclonal			
MTC11	NPR3	p.Ser475Ser	synonymous_variant	5	32783133	A	G	9.09%	264	.	.	.		.	.	.			.	0.7431	63.95%	100.00%	100%	Clonal			
MTC11	C7	p.Val346Ile	missense_variant	5	40950059	G	A	9.16%	273	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7512	64.85%	100.00%	100%	Clonal			
MTC11	MAP3K1	p.Ile216Asn	missense_variant	5	56155555	T	A	13.04%	115	D	CANCER	Passenger		.	true	true			Likely pathogenic	0.6596	54.17%	100.00%	95%	Clonal			
MTC11	ZFYVE16	p.Tyr73Cys	missense_variant	5	79732722	A	G	15.79%	285	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8582	77.67%	100.00%	100%	Clonal			
MTC11	FTMT	p.Leu164Val	missense_variant	5	121188148	C	G	9.78%	317	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1667	50.10%	94.49%	71%	Subclonal			
MTC11	PCDHA12	p.Pro543Pro	synonymous_variant	5	140256686	G	A	22.73%	66	.	.	.		.	.	.		TRUE	.	0.8307	66.37%	100.00%	100%	Clonal			
MTC11	PDE6A	p.Lys372Lys	synonymous_variant	5	149279085	T	C	6.33%	221	.	.	.		.	.	.			.	0.1039	34.89%	91.43%	59%	Subclonal			
MTC11	SOX30	p.Gly118Arg	missense_variant	5	157078735	C	G	13.25%	332	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8614	79.23%	100.00%	100%	Clonal			
MTC11	CREBRF	p.Gln591*	stop_gained	5	172550172	C	T	5.75%	226	D	.	.		.	.	.			Indeterminate	0.0473	31.06%	86.70%	53%	Subclonal			
MTC11	MRS2	p.Leu45Leu	synonymous_variant	6	24403409	G	A	10.53%	171	.	.	.		.	.	.			.	0.5934	53.41%	98.94%	87%	Clonal			
MTC11	HIST1H2BN	p.Arg30Cys	missense_variant	6	27806527	C	T	4.52%	199	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0021	19.49%	68.56%	37%	Subclonal			
MTC11	PRRC2A	p.Pro800His	missense_variant	6	31598512	C	A	20.00%	195	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8843	84.03%	100.00%	100%	Clonal			
MTC11	PSMB8	p.Tyr208Tyr	synonymous_variant	6	32809426	G	A	7.60%	329	.	.	.		.	.	.			.	0.0545	42.48%	89.08%	63%	Subclonal			
MTC11	DEF6	p.Ser568*	stop_gained	6	35288994	C	A	25.00%	56	D	.	.		.	.	.			Indeterminate	0.8345	72.37%	100.00%	100%	Clonal			
MTC11	COL9A1	p.Glu491Asp	missense_variant	6	70966501	T	A	9.35%	214	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4263	49.59%	97.99%	77%	Subclonal			
MTC11	CASP8AP2	p.Ser212Thr	missense_variant	6	90572062	T	A	8.44%	379	.	.	Passenger		.	.	.			Indeterminate	0.1304	49.40%	93.48%	70%	Subclonal			
MTC11	SP4	p.Gln493*	stop_gained	7	21470260	C	T	4.55%	483	A	.	.		.	.	.			Indeterminate	0.0003	30.61%	69.25%	47%	Subclonal			
MTC11	AEBP1	p.Pro289Thr	missense_variant	7	44147608	C	A	32.48%	157	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2197	91.37%	100.00%	100%	Clonal			
MTC11	ABCA13	p.Thr2471Ala	missense_variant	7	48318202	A	G	6.68%	404	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1497	47.04%	93.93%	69%	Subclonal			
MTC11	VWC2	p.Pro118Leu	missense_variant	7	49815384	C	T	7.52%	452	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3395	55.05%	97.30%	77%	Subclonal			
MTC11	PCLO	p.Lys1240Met	missense_variant	7	82595385	T	A	3.60%	333	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0002	20.92%	62.99%	37%	Subclonal			
MTC11	SEMA3A	p.Arg516Trp	missense_variant	7	83610743	G	A	18.56%	194	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9397	84.49%	100.00%	100%	Clonal			
MTC11	EN2	p.His312Gln	missense_variant	7	155255316	C	G	4.07%	172	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0098	18.16%	74.64%	38%	Subclonal			
MTC11	ADAMTSL1	p.Asn1342Lys	missense_variant	9	18826373	C	G	2.95%	271	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	10.53%	40.94%	21%	Subclonal			
MTC11	BAG1	p.Lys74Lys	synonymous_variant	9	33264451	C	T	12.17%	263	.	.	.		.	.	.	TRUE		.	0.6241	61.72%	100.00%	88%	Clonal			
MTC11	SETX	p.Glu1873*	stop_gained	9	135173631	C	A	6.64%	241	A	.	.		.	.	.			Indeterminate	0.1233	37.78%	92.52%	61%	Subclonal			
MTC11	ABCA2	p.Leu1977Val	missense_variant	9	139905722	G	C	7.74%	504	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1314	52.37%	93.71%	72%	Subclonal			
MTC11	NEBL	p.Leu97His	missense_variant	10	21177105	A	T	6.98%	172	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2482	36.78%	95.86%	65%	Subclonal			
MTC11	KIF5B	p.Glu349Lys	missense_variant	10	32323684	C	T	9.33%	75	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.5507	38.54%	98.75%	86%	Clonal			
MTC11	MBL2	p.Leu115Leu	synonymous_variant	10	54529035	C	T	18.10%	116	.	.	.		.	.	.		TRUE	.	0.8189	70.34%	100.00%	100%	Clonal			
MTC11	DLG5	p.Asn679Ser	missense_variant	10	79589262	T	C	3.58%	810	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6752	62.59%	100.00%	94%	Clonal			
MTC11	BTAF1	p.Tyr1269Phe	missense_variant	10	93768025	A	T	10.89%	101	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.4959	43.01%	98.44%	79%	Subclonal			
MTC11	NOLC1	p.Ser83Leu	missense_variant	10	103917017	C	T	10.34%	261	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.3207	51.61%	97.03%	75%	Subclonal			
MTC11	MUC2	p.Lys1394Arg	missense_variant	11	1092362	A	G	8.84%	181	P	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3671	44.64%	97.48%	73%	Subclonal			
MTC11	NRXN2	p.Arg485Cys	missense_variant	11	64435067	G	A	3.21%	405	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.16%	44.19%	27%	Subclonal			
MTC11	MRPL49	p.Lys164Glu	missense_variant	11	64893333	A	G	8.57%	350	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1739	49.59%	94.66%	71%	Subclonal			
MTC11	SIPA1	p.Ser346*	stop_gained	11	65412478	C	A	9.94%	181	A	.	.		.	.	.			Indeterminate	0.5263	51.04%	98.62%	82%	Clonal			
MTC11	TENM4	p.Leu1864Met	missense_variant	11	78383281	G	T	5.44%	349	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	25.08%	60.06%	39%	Subclonal			
MTC11	PPP2R1B	p.Pro615Pro	synonymous_variant	11	111608238	G	T	9.77%	174	.	.	.		.	.	.		TRUE	.	0.3087	44.20%	96.82%	71%	Subclonal			
MTC11	PPP2R1B	p.Ser612Ile	missense_variant	11	111608248	C	A	10.34%	174	N	CANCER	Passenger		.	.	.		TRUE	Likely passenger	0.3933	47.27%	97.71%	75%	Subclonal	TRUE	GACCCCAGGCTTCCGGGC	GGGAGGGATGTGCCCTGGTC
MTC11	PRB4	p.Pro50Thr	missense_variant	12	11461769	G	T	15.24%	105	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8169	66.63%	100.00%	100%	Clonal			
MTC11	FOXN4	p.Ala337Ala	synonymous_variant	12	109719495	C	T	3.03%	363	.	.	.		.	.	.			.	0.0000	13.63%	43.62%	25%	Subclonal			
MTC11	BORA	p.Asp256Ala	missense_variant	13	73319149	A	C	13.16%	190	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7834	67.19%	100.00%	100%	Clonal			
MTC11	CHAMP1	p.Gly722Ser	missense_variant	13	115091481	G	A	13.79%	319	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8525	76.99%	100.00%	100%	Clonal			
MTC11	MYH7	p.Leu714Ile	missense_variant	14	23895195	G	T	5.85%	188	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0260	26.92%	82.63%	48%	Subclonal			
MTC11	DHRS2	p.Lys140Arg	missense_variant	14	24109103	A	G	9.30%	215	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4185	49.38%	97.93%	77%	Subclonal			
MTC11	FOXG1	p.Pro445Pro	synonymous_variant	14	29237820	G	A	17.34%	369	.	.	.		.	.	.			.	0.5546	87.27%	100.00%	100%	Clonal			
MTC11	EXD2	p.Gly106Gly	synonymous_variant	14	69676505	A	C	9.14%	186	.	.	.		.	.	.			.	0.4100	46.73%	97.86%	75%	Subclonal			
MTC11	GOLGA6C	p.Asp652Val	missense_variant	15	75562413	A	T	13.95%	43	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6651	42.30%	100.00%	100%	Clonal			
MTC11	ARNT2	p.Arg76Trp	missense_variant	15	80762590	C	T	24.62%	394	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9632	93.89%	100.00%	100%	Clonal			
MTC11	UNC45A	p.Cys446Cys	synonymous_variant	15	91489982	T	C	8.46%	449	.	.	.		.	.	.			.	0.0934	50.95%	92.28%	70%	Subclonal			
MTC11	TBL3	p.Ala471Val	missense_variant	16	2026934	C	T	11.33%	309	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7956	70.57%	100.00%	100%	Clonal			
MTC11	HS3ST2	p.Ala282Ser	missense_variant	16	22926623	G	T	6.97%	445	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0452	45.37%	88.76%	64%	Subclonal			
MTC11	CDH8	p.Ala30Ser	missense_variant	16	62055220	C	A	7.39%	284	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0071	35.06%	79.52%	54%	Subclonal			
MTC11	DLG4	p.Ser10Leu	missense_variant	17	7121949	G	A	16.90%	284	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7768	83.65%	100.00%	100%	Clonal			
MTC11	SARM1	p.Thr479Met	missense_variant	17	26712106	C	T	8.29%	410	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5568	60.17%	98.79%	85%	Clonal			
MTC11	EFCAB5	p.Leu466Leu	synonymous_variant	17	28380370	G	A	9.28%	291	.	.	.		.	.	.			.	0.7010	62.73%	100.00%	95%	Clonal			
MTC11	RPL23	p.Lys109Thr	missense_variant	17	37006629	T	G	12.55%	231	D	.	Passenger		.	.	.			Indeterminate	0.8197	71.63%	100.00%	100%	Clonal			
MTC11	JUP	p.Val405Phe	missense_variant	17	39919519	C	A	8.99%	367	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5167	58.79%	98.59%	83%	Clonal			
MTC11	RPS6KB1	p.Glu45Asp	missense_variant	17	57970680	G	T	21.18%	203	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7705	84.30%	100.00%	100%	Clonal			
MTC11	HEATR6	p.Gln940Gln	synonymous_variant	17	58123540	T	C	16.51%	218	.	.	.		.	.	.			.	0.8492	76.18%	100.00%	100%	Clonal			
MTC11	ENGASE	p.Ala112Ala	synonymous_variant	17	77073866	G	A	20.61%	165	.	.	.		.	.	.			.	0.8134	80.79%	100.00%	100%	Clonal			
MTC11	CBLN2	p.Gly83Asp	missense_variant	18	70209148	C	T	3.76%	213	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0002	15.50%	59.21%	31%	Subclonal			
MTC11	IZUMO4	p.His115Leu	missense_variant	19	2097468	A	T	28.63%	482	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.1422	96.21%	100.00%	100%	Clonal			
MTC11	CERS4	p.Glu291Gln	missense_variant	19	8326594	G	C	6.08%	395	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0103	37.68%	81.57%	56%	Subclonal			
MTC11	ICAM5	p.Lys607Arg	missense_variant	19	10404824	A	G	2.56%	585	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	14.03%	38.26%	24%	Subclonal			
MTC11	BRD4	p.Pro860Ala	missense_variant	19	15355045	G	C	10.14%	148	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.6490	53.54%	100.00%	94%	Clonal			
MTC11	GMIP	p.Leu542Phe	missense_variant	19	19745959	G	A	5.00%	340	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0016	28.71%	72.25%	46%	Subclonal			
MTC11	DACT3	p.Gly571Asp	missense_variant	19	47151917	C	T	3.49%	315	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0003	19.77%	62.50%	36%	Subclonal			
MTC11	SPIB	p.Ala67Thr	missense_variant	19	50926154	G	A	9.32%	118	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6353	48.96%	100.00%	96%	Clonal			
MTC11	MYBPC2	p.Gly14Cys	missense_variant	19	50938438	G	T	4.74%	190	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0546	25.49%	86.71%	49%	Subclonal			
MTC11	C20orf194	p.Ala261Val	missense_variant	20	3329179	G	A	12.99%	154	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7552	63.16%	100.00%	100%	Clonal			
MTC11	DDX27	p.Val87Ile	missense_variant	20	47838061	G	A	18.54%	151	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9124	79.90%	100.00%	100%	Clonal			
MTC11	SALL4	p.Ser580Tyr	missense_variant	20	50407283	G	T	12.36%	518	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.8798	81.48%	100.00%	100%	Clonal			
MTC11	CSTF1	p.Pro227Ser	missense_variant	20	54974056	C	T	7.47%	281	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2257	45.17%	95.61%	69%	Subclonal			
MTC11	RPS21	p.Arg71*	stop_gained	20	60963389	C	T	8.19%	403	D	.	.		.	.	.			Indeterminate	0.3018	53.89%	96.87%	76%	Subclonal			
MTC11	SON	p.Thr2225Arg	missense_variant	21	34939479	C	G	10.00%	90	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6527	47.36%	100.00%	100%	Clonal			
MTC11	BACE2	p.Val417Val	synonymous_variant	21	42629201	C	A	14.06%	64	.	.	.		.	.	.		TRUE	.	0.7051	50.77%	100.00%	100%	Clonal			

MTC11	LIMK2	p.Asp88Val	missense_variant	22	31655180	A	T	11.82%	203	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7167	62.40%	100.00%	98%	Clonal			
MTC11	PKDREJ	p.Glu283Lys	missense_variant	22	46658373	C	T	7.97%	464	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4664	59.00%	98.31%	82%	Subclonal			
MTC11	IRS4	p.Ser918Ser	synonymous_variant	X	107976821	A	G	4.89%	327	.	.	.		.	.	.			.	0.0001	24.64%	63.90%	40%	Subclonal			
MTC11	IRS4	p.Ser918Pro	missense_variant	X	107976823	A	G	4.72%	318	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	23.37%	62.56%	39%	Subclonal			
MTC12	VPS13D	p.Arg1692Gln	missense_variant	1	12343234	G	A	5.60%	125	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.19%	50.24%	26%	Subclonal			
MTC12	ZNF683	p.Asn154Ser	missense_variant	1	26691576	T	C	18.10%	105	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4687	52.78%	98.63%	83%	Subclonal			
MTC12	HMGCS2	p.Val124fs	frameshift_variant	1	120306981	CCA	C	23.53%	153	A	.	.		.	.	.		TRUE	Likely pathogenic	0.5355	61.45%	98.53%	84%	Clonal			
MTC12	GORAB	p.Ile263Val	missense_variant	1	170521205	A	G	22.75%	211	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7922	75.49%	100.00%	100%	Clonal			
MTC12	SHISA4	p.Val99Met	missense_variant	1	201859631	G	A	13.44%	186	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0215	41.90%	86.31%	61%	Subclonal			
MTC12	OR14C36	p.Ala145Ala	synonymous_variant	1	248512511	C	T	24.64%	138	.	.	.		.	.	.			.	0.8020	74.30%	100.00%	100%	Clonal			
MTC12	RAB3GAP1	p.Lys389*	stop_gained	2	135888220	A	T	18.79%	165	A	.	.		.	.	.			Indeterminate	0.5128	60.55%	98.85%	86%	Clonal			
MTC12	SLC39A10	p.Glu65*	stop_gained	2	196544959	G	T	10.05%	199	A	.	.		.	.	.			Indeterminate	0.0001	29.70%	68.09%	46%	Subclonal			
MTC12	AOX1	p.Gly1276Trp	missense_variant	2	201534325	G	T	22.95%	61	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6682	57.55%	100.00%	100%	Clonal			
MTC12	FGD5	p.Gly443Glu	missense_variant	3	14861906	G	A	4.29%	210	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	7.65%	27.83%	15%	Subclonal			
MTC12	PLCD1	p.Cys593*	stop_gained	3	38050540	G	T	20.83%	24	A	.	.		.	.	.		TRUE	Likely pathogenic	0.4808	30.76%	98.14%	74%	Subclonal			
MTC12	ZBTB38	p.Ala589Val	missense_variant	3	141162996	C	T	3.11%	289	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	7.10%	26.01%	14%	Subclonal			
MTC12	ARHGEF26	p.Pro841Thr	missense_variant	3	153973167	C	A	17.60%	125	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.4152	53.28%	98.32%	80%	Subclonal			
MTC12	SORCS2	p.Thr553Pro	missense_variant	4	7698990	A	C	27.14%	70	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7684	68.27%	100.00%	100%	Clonal			
MTC12	FHDC1	p.Met815Thr	missense_variant	4	153896887	T	C	13.19%	273	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0023	43.73%	80.42%	60%	Subclonal			
MTC12	PIK3R1	p.Asp281Val	missense_variant	5	67576760	A	T	18.57%	70	D	PASSENGER/OTHER	Passenger		true	true	true	TRUE		Likely pathogenic	0.5028	48.64%	98.80%	85%	Clonal	TRUE	TGCAGATGCTATCACACACATT	AATGTTAAATGCTCAAAAAGCATTAC
MTC12	UTP15	p.Ile387Lys	missense_variant	5	72874855	T	A	17.07%	123	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3667	51.29%	97.97%	78%	Subclonal			
MTC12	TRERF1	p.Ser1120Arg	missense_variant	6	42196386	G	T	3.40%	147	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	6.33%	34.71%	16%	Subclonal			
MTC12	NT5C3A	p.Ala285Val	missense_variant	7	33055337	G	A	17.02%	47	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4226	38.46%	98.35%	78%	Subclonal			
MTC12	NACAD	p.Lys618Lys	synonymous_variant	7	45123925	C	T	15.00%	40	.	.	.		.	.	.			.	0.3339	30.92%	97.63%	68%	Subclonal			
MTC12	SEMA3A	p.Glu479Lys	missense_variant	7	83631288	C	T	20.11%	189	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6328	66.51%	100.00%	92%	Clonal			
MTC12	LAMB1	p.Tyr663Tyr	synonymous_variant	7	107601771	A	G	26.25%	160	.	.	.		.	.	.			.	0.8384	79.32%	100.00%	100%	Clonal			
MTC12	LAMB4	p.Arg308Lys	missense_variant	7	107745012	C	T	22.68%	194	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7817	74.30%	100.00%	100%	Clonal			
MTC12	KMT2C	p.Glu765Gly	missense_variant	7	151945225	T	C	16.13%	31	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.3914	30.21%	98.12%	74%	Subclonal			
MTC12	ACTR3B	p.Thr162Thr	synonymous_variant	7	152513619	G	A	13.46%	52	.	.	.		.	.	.			.	0.2266	29.84%	96.16%	61%	Subclonal			
MTC12	ANK1	p.Leu163Ser	missense_variant	8	41584805	A	G	22.08%	77	D	CANCER	Driver		.	.	.			Likely pathogenic	0.6664	59.49%	100.00%	100%	Clonal			
MTC12	CHRNA6	p.Leu41Leu	synonymous_variant	8	42620304	C	T	25.00%	88	.	.	.		.	.	.			.	0.7602	68.21%	100.00%	100%	Clonal			
MTC12	KDM4C	p.Cys861Arg	missense_variant	9	7103841	T	C	14.52%	62	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2617	34.96%	96.78%	66%	Subclonal			
MTC12	PTEN	p.Leu112Gln	missense_variant	10	89692851	T	A	32.77%	119	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.8781	78.37%	100.00%	100%	Clonal	TRUE	GGTTATCTTTTTACCACAGTTGCAC	AAATTTGCCCCGATGTAATAAAT
MTC12	PRKCDBP	p.Ala94Thr	missense_variant	11	6341427	C	T	21.98%	91	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6798	61.93%	100.00%	100%	Clonal			
MTC12	FAM180B	p.Ser75Tyr	missense_variant	11	47609658	C	A	5.43%	129	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.79%	48.73%	25%	Subclonal			
MTC12	ANO1	p.Ile201Met	missense_variant	11	69950167	C	G	15.67%	217	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1086	51.70%	93.76%	72%	Subclonal			
MTC12	FAT3	p.Ser1563Ile	missense_variant	11	92526009	G	T	18.46%	195	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4667	61.23%	98.63%	84%	Subclonal			
MTC12	CNTN5	p.Arg580Thr	missense_variant	11	100064250	G	C	16.22%	74	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3524	42.34%	97.83%	74%	Subclonal			
MTC12	OR6M1	p.Tyr58His	missense_variant	11	123676886	A	G	16.67%	174	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2644	53.49%	96.98%	76%	Subclonal			
MTC12	CDON	p.Asp185Glu	missense_variant	11	125888310	G	C	7.14%	84	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0017	14.91%	66.72%	33%	Subclonal			
MTC12	SLC6A12	p.Lys369Met	missense_variant	12	306018	T	A	7.29%	96	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0008	16.07%	64.80%	33%	Subclonal			
MTC12	OVCH1	p.Ser695Ser	synonymous_variant	12	29617480	C	T	28.17%	71	.	.	.		.	.	.			.	0.7812	70.21%	100.00%	100%	Clonal			
MTC12	KLHL1	p.Ala289Val	missense_variant	13	70514320	G	A	38.24%	34	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8053	64.67%	100.00%	100%	Clonal			
MTC12	STON2	p.Val651Met	missense_variant	14	81743704	C	T	40.32%	310	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8979	95.75%	100.00%	100%	Clonal			
MTC12	UNC79	p.Val1900Gly	missense_variant	14	94120117	T	G	55.56%	36	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4672	81.42%	100.00%	100%	Clonal			
MTC12	APBA2	p.Gly359Trp	missense_variant	15	29385283	G	T	4.51%	133	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.08%	33.36%	16%	Subclonal			
MTC12	ZNF609	p.Pro1090Pro	synonymous_variant	15	64968323	G	A	5.76%	139	.	.	.		.	.	.		TRUE	.	0.0000	10.13%	38.56%	21%	Subclonal			
MTC12	TBC1D2B	p.Leu888Phe	missense_variant	15	78293995	G	A	16.28%	129	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2814	49.05%	97.15%	74%	Subclonal			
MTC12	ARNT2	p.Pro607Leu	missense_variant	15	80873647	C	T	20.56%	214	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6741	69.39%	100.00%	94%	Clonal			
MTC12	TBL3	p.Val446Val	synonymous_variant	16	2026860	G	A	13.95%	172	.	.	.		.	.	.			.	0.0457	43.19%	89.50%	64%	Subclonal			
MTC12	TEKT5	p.Thr116Thr	synonymous_variant	16	10788383	C	T	5.36%	112	.	.	.		.	.	.			.	0.0000	11.04%	50.65%	24%	Subclonal			
MTC12	TNRC6A	p.Gln1310Glu	missense_variant	16	24816116	C	G	10.87%	92	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0279	27.13%	84.55%	50%	Subclonal			
MTC12	RPGRIP1L	p.Val1021Ile	missense_variant	16	53671766	C	T	12.09%	91	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0631	31.07%	89.65%	55%	Subclonal			
MTC12	SLC6A2	p.Ala105Ala	synonymous_variant	16	55703517	G	A	20.00%	95	.	.	.		.	.	.			.	0.5933	57.23%	100.00%	91%	Clonal			
MTC12	TP53	p.Arg306*	stop_gained	17	7577022	G	A	35.08%	191	A	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.8819	86.61%	100.00%	100%	Clonal	TRUE	CATAACTGCACCCTTGGTCTC	GGACCTGATTTCCTTACTGCC
MTC12	TMEM88	p.Pro139Leu	missense_variant	17	7758968	C	T	32.41%	145	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8886	80.33%	100.00%	100%	Clonal			
MTC12	CEP112	p.Ser192Leu	missense_variant	17	64125931	G	A	28.74%	87	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8007	74.45%	100.00%	100%	Clonal			
MTC12	DNAH17	p.Thr1434Thr	synonymous_variant	17	76503822	T	A	4.40%	159	.	.	.		.	.	.			.	0.0000	9.44%	39.72%	20%	Subclonal			
MTC12	NOTCH3	p.Glu309Lys	missense_variant	19	15302346	C	T	15.00%	220	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0001	38.34%	71.98%	53%	Subclonal			
MTC12	NOTCH3	p.Cys291Tyr	missense_variant	19	15302399	C	T	11.94%	201	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	28.62%	60.71%	43%	Subclonal			
MTC12	NOTCH3	p.Gly289Asp	missense_variant	19	15302405	C	T	10.55%	199	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	24.52%	55.14%	38%	Subclonal			
MTC12	NOTCH3	p.Leu280Leu	synonymous_variant	19	15302431	C	T	7.83%	166	.	.	.		.	.	.		TRUE	.	0.0000	16.11%	45.67%	28%	Subclonal			
MTC12	NOTCH3	p.Asp276Asn	missense_variant	19	15302445	C	T	8.47%	177	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.13%	47.72%	30%	Subclonal			
MTC12	PGLYRP2	p.Pro85Leu	missense_variant	19	15587227	G	A	23.97%	242	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5254	67.06%	98.49%	85%	Clonal			
MTC12	ZNF492	p.Ala40Thr	missense_variant	19	22836805	G	A	10.39%	77	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0017	18.80%	67.98%	37%	Subclonal			
MTC12	ZNF30	p.Arg476Gln	missense_variant	19	35435294	G	A	13.67%	139	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0642	40.32%	90.66%	62%	Subclonal			
MTC12	ZFP30	p.Asn41Ser	missense_variant	19	38135525	T	C	20.25%	79	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5946	55.18%	100.00%	92%	Clonal			
MTC12	RYR1	p.Thr99Met	missense_variant	19	38934223	C	T	15.31%	98	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.2442	42.68%	96.59%	70%	Subclonal			
MTC12	ZNF610	p.Val151Gly	missense_variant	19	52869083	T	G	14.45%	173	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4079	54.50%	98.29%	80%	Subclonal			
MTC12	XKR7	p.Pro465His	missense_variant	20	30584914	C	A	10.45%	220	D	.	Passenger		.	.	.			Indeterminate	0.0001	31.84%	68.93%	48%	Subclonal			
MTC12	AP1B1	p.Ala376Asp	missense_variant	22	29747188	G	T	5.47%	128	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	11.90%	49.09%	25%	Subclonal			
MTC12	CFP	p.Lys154Arg	missense_variant	X	47486983	T	C	10.79%	139	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0045	29.99%	77.28%	49%	Subclonal			
MTC12	NLGN3	p.Arg97Leu	missense_variant	X	70367889	G	T	17.87%	207	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3847	59.69%	98.14%	82%	Subclonal			
MTC12	NLGN3	p.Arg97Arg	synonymous_variant	X	70367890	G	T	17.96%	206	.	.	.		.	.	.			.	0.3970	59.98%	98.22%	82%	Subclonal			
MTC12	ITGB1BP2	p.Leu228Ser	missense_variant	X	70524080	T	C	4.03%	149	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	8.15%	38.34%	18%	Subclonal			
MTC12	TFDP3	p.Glu400Gln	missense_variant	X	132351090	C	G	2.92%	240	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.50%	32.31%	16%	Subclonal			
MTC12	FGF13	p.Val242Met	missense_variant	X	137715055	C	T	11.11%	108	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1460	35.54%	94.30%	62%	Subclonal			
MTC13	GSTM5	p.Arg187Cys	missense_variant	1	110257854	C	T	3.29%	243	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	4.33%	17.82%	9%	Subclonal			
MTC13	GON4L	p.Pro1984Leu	missense_variant	1	155722273	G	A	7.45%	94	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.87%	56.10%	29%	Subclonal			
MTC13	SLAMF9	p.Ala32Ala	synonymous_variant	1	159923394	C	T	5.56%	396	.	.	.		.	.	.			.	0.0000	13.88%	31.61%	22%	Subclonal			
MTC13	RYR2	p.Lys3282Gln	missense_variant	1	237870512	A	C	7.27%	605	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.67%	36.84%	28%	Subclonal			
MTC13	TFB2M	p.Arg39Arg	synonymous_variant	1	246729324	C	T	4.86%	556	.	.	.		.	.	.			.	0.0000	12.50%	26.59%	19%	Subclonal			
MTC13	FAHD2B	p.Pro63Pro	synonymous_variant	2	97757255	T	C	39.13%	23	.	.	.		.	.	.			.	0.6211	58.68%	100.00%	100%	Clonal			
MTC13	ERBB4	p.Met322Ile	missense_variant	2	212578291	C	A	3.51%	228	D	CANCER	Passenger		.	true	.			Likely pathogenic	0.0000	6.48%	25.76%	14%	Subclonal			
MTC13	DNAJB8	p.Arg206Arg	synonymous_variant	3	128181471	G	A	2.90%	448	.	.	.		.	.	.			.	0.0000	4.35%	13.66%	8%	Subclonal			
MTC13	LPHN3	p.Pro457Pro	synonymous_variant	4	62758468	G	A	6.91%	304	.	.	.		.	.	.			.	0.0000	12.63%	29.26%	20%	Subclonal			
MTC13	GAB1	p.Gln163*	stop_gained	4	144354763	C	T	12.39%	234	A	.	.		.	.	.			Indeterminate	0.0000	24.76%	49.13%	36%	Subclonal			
MTC13	FAM13B	p.Arg688Cys	missense_variant	5	137284676	G	A	29.88%	164	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2670	66.47%	98.64%	86%	Subclonal			
MTC13	CTNNA1	p.Leu780Leu	synonymous_variant	5	138268308	G	A	4.53%	353	.	.	.		.	.	.			.	0.0000	7.56%	20.37%	13%	Subclonal			
MTC13	HMGXB3	p.Ser1105Leu	missense_variant	5	149429927	C	T	3.32%	241	N	.	Passenger		.	.	.			Likely passenger	0.0000	4.37%	17.95%	10%	Subclonal			
MTC13	NSD1	p.Leu598Leu	synonymous_variant	5	176637192	T	C	2.69%	335	.	.	.		true	true	true	TRUE		.	0.0000	3.55%	13.95%	8%	Subclonal			
MTC13	MUC21	p.Ala237Ala	synonymous_variant	6	30954663	C	T	10.48%	124	.	.	.		.	.	.			.	0.0000	17.50%	48.81%	30%	Subclonal			
MTC13	MUC21	p.Pro248Thr	missense_variant	6	30954694	C	A	20.18%	109	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0028	39.06%	82.01%	58%	Subclonal			
MTC13	MUC21	p.Glu274Asp	missense_variant	6	30954774	G	C	5.03%	179	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	7.23%	26.22%	14%	Subclonal			
MTC13	AGMO	p.Pro264Pro	synonymous_variant	7	15430326	G	T	10.60%	217	.	.	.		.	.	.			.	0.0000	27.34%	59.28%	41%	Subclonal			
MTC13	NME8	p.Gln482His	missense_variant	7	37934114	G	T	4.82%	249	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	10.32%	31.46%	19%	Subclonal			
MTC13	GIMAP6	p.Asp180Asp	synonymous_variant	7	150325356	G	A	2.78%	431	N	.	.		.	.	.			.	0.0000	5.71%	18.13%	11%	Subclonal			
MTC13	ACTR3B	p.Thr162Thr	synonymous_variant	7	152513619	G	A	35.61%	132	.	.	.		.	.	.			.	0.5512	84.89%	100.00%	100%	Clonal			
MTC13	SLC18A1	p.Ala30Thr	missense_variant	8	20038388	C	T	12.40%	121	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	21.60%	55.55%	36%	Subclonal			
MTC13	OTUD6B	p.Pro13Ala	missense_variant	8	92082559	C	G	14.05%	242	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	29.00%	54.20%	40%	Subclonal			
MTC13	TRAPPC9	p.Ile1086Ile	synonymous_variant	8	140922391	G	A	6.52%	184	.	.	.		.	.	.			.	0.0000	10.39%	31.35%	19%	Subclonal			
MTC13	LHX2	p.Ala189Ala	synonymous_variant	9	126777644	G	A	16.95%	295	.	.	.		.	.	.			.	0.0000	37.21%	61.85%	49%	Subclonal			
MTC13	EHMT1	p.Ala34Ala	synonymous_variant	9	140611094	C	T	36.70%	109	.	.	.		.	.	.	TRUE		.	0.6289	75.66%	100.00%	100%	Clonal			
MTC13	PIDD1	p.Pro372Ser	missense_variant	11	802257	G	A	4.41%	136	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	5.44%	26.25%	13%	Subclonal			
MTC13	OR52I1	p.Phe16Leu	missense_variant	11	4615316	C	A	35.07%	288	.	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6880	82.93%	100.00%	100%	Clonal			
MTC13	OR5M11	p.His56His	synonymous_variant	11	56310566	G	A	9.68%	248	.	.	.		.	.	.			.	0.0000	18.47%	39.82%	28%	Subclonal			
MTC13	DDX11	p.Val745Val	synonymous_variant	12	31255209	G	A	4.96%	121	.	.	.		.	.	.			.	0.0000	8.54%	39.83%	19%	Subclonal			
MTC13	DDX11	p.Ala751Ala	synonymous_variant	12	31255227	A	G	6.94%	144	.	.	.		.	.	.			.	0.0000	14.40%	47.29%	27%	Subclonal			
MTC13	KRT18	p.Leu16Leu	synonymous_variant	12	53343005	G	A	6.00%	100	.	.	.		.	.	.			.	0.0000	10.46%	47.92%	23%	Subclonal			
MTC13	KRT18	p.Gly17Asp	missense_variant	12	53343007	G	A	5.88%	102	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	10.25%	47.00%	23%	Subclonal			
MTC13	STAB2	p.Asp780Asn	missense_variant	12	104064552	G	A	12.22%	311	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	34.54%	62.85%	47%	Subclonal			
MTC13	FRY	p.Gly1400Arg	missense_variant	13	32783169	G	A	3.60%	250	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	5.06%	18.80%	10%	Subclonal			
MTC13	PAPLN	p.Ser166Phe	missense_variant	14	73717646	C	T	3.66%	191	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	4.68%	20.73%	11%	Subclonal			
MTC13	ANGEL1	p.Trp223Gly	missense_variant	14	77274474	A	C	3.85%	130	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	4.35%	24.52%	11%	Subclonal			
MTC13	NARFL	p.Arg42His	missense_variant	16	789680	C	T	26.74%	273	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0186	62.35%	92.19%	77%	Subclonal			
MTC13	NSMCE1	p.Thr38Arg	missense_variant	16	27268779	G	C	7.22%	97	P	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.40%	54.45%	28%	Subclonal			
MTC13	C17orf97	p.Glu340Lys	missense_variant	17	263652	G	A	4.76%	147	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	8.63%	36.37%	18%	Subclonal			
MTC13	ADAM11	p.Gly59Arg	missense_variant	17	42837203	G	A	10.85%	212	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.03%	60.65%	42%	Subclonal			
MTC13	NPEPPS	p.Leu354Leu	synonymous_variant	17	45664677	C	T	5.49%	91	.	.	.		.	.	.			.	0.0000	8.93%	46.93%	21%	Subclonal			
MTC13	BZRAP1	p.Arg270Arg	synonymous_variant	17	56402306	G	T	11.07%	244	.	.	.		.	.	.			.	0.0000	29.46%	60.12%	43%	Subclonal			
MTC13	CHERP	p.Gln320*	stop_gained	19	16640630	G	A	10.61%	198	D	.	.		.	.	.			Indeterminate	0.0000	19.81%	44.65%	31%	Subclonal			
MTC13	ZNF585B	p.Arg389Lys	missense_variant	19	37677273	C	T	43.43%	99	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7095	82.69%	100.00%	100%	Clonal			
MTC13	KLK2	p.Arg167Cys	missense_variant	19	51380133	C	T	8.89%	360	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.0000	17.84%	34.87%	26%	Subclonal			
MTC13	NLRP7	p.Thr414Met	missense_variant	19	55450946	G	A	17.84%	342	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	40.21%	63.58%	51%	Subclonal			
MTC13	PTPRT	p.Gly745Ala	missense_variant	20	40877462	C	G	8.24%	170	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	18.86%	51.31%	32%	Subclonal			
MTC14	SKI	p.Val484_Glu485del	disruptive_inframe_deletion	1	2235512	CGGAGGT	C	22.63%	190	P	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.6696	69.98%	100.00%	95%	Clonal			
MTC14	RERE	p.Ala921Val	missense_variant	1	8420805	G	A	7.89%	152	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	18.81%	55.34%	33%	Subclonal			
MTC14	HSPG2	p.Pro2769Pro	synonymous_variant	1	22172953	G	A	13.79%	58	.	.	.		.	.	.		TRUE	.	0.0104	22.57%	78.96%	44%	Subclonal			
MTC14	SZT2	p.Phe2872Leu	missense_variant	1	43909427	T	C	6.58%	76	D	.	Passenger		.	.	.			Indeterminate	0.0005	11.72%	60.39%	28%	Subclonal			
MTC14	CRYZ	p.Leu327His	missense_variant	1	75171990	A	T	20.50%	200	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4779	63.91%	98.80%	86%	Subclonal			
MTC14	HENMT1	p.Arg290Gln	missense_variant	1	109191501	C	T	6.61%	227	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	16.53%	44.08%	28%	Subclonal			
MTC14	CSF1	p.Asp77Glu	missense_variant	1	110459920	T	G	5.38%	279	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.33%	35.94%	23%	Subclonal			
MTC14	FLG2	p.Gly236Gly	synonymous_variant	1	152329554	A	T	5.09%	923	.	.	.		.	.	.			.	0.0000	23.35%	41.06%	32%	Subclonal			
MTC14	CHRNB2	p.Asp27Asp	synonymous_variant	1	154541954	T	C	35.45%	457	.	.	.		.	.	.			.	0.9237	96.49%	100.00%	100%	Clonal			
MTC14	ATP1A2	p.Gly142Arg	missense_variant	1	160093775	G	C	14.94%	328	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.6292	69.28%	100.00%	93%	Clonal			
MTC14	OLFML2B	p.Tyr735Cys	missense_variant	1	161953517	T	C	3.27%	551	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	12.38%	31.14%	20%	Subclonal			
MTC14	PPP2R5A	p.Ser484Asn	missense_variant	1	212534102	G	A	50.00%	104	N	.	Passenger		.	.	.			Likely passenger	0.9544	90.69%	100.00%	100%	Clonal	TRUE	AATTAGAGGAGCTAAAGCTAAAGAAAG	CATATTTCAAAAAAGCATACAAAACTC
MTC14	USH2A	p.Lys1031Lys	synonymous_variant	1	216390793	C	T	50.47%	212	.	.	.		.	.	.			.	0.9596	95.20%	100.00%	100%	Clonal			
MTC14	SNAP47	p.Gln342His	missense_variant	1	227947089	G	C	58.09%	513	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7230	98.24%	100.00%	100%	Clonal			
MTC14	KIDINS220	p.Arg381Trp	missense_variant	2	8934075	G	A	4.30%	372	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	18.75%	48.96%	31%	Subclonal			
MTC14	FAM179A	p.Leu49Leu	synonymous_variant	2	29222054	C	G	7.09%	141	.	.	.		.	.	.			.	0.0004	19.93%	64.83%	37%	Subclonal			
MTC14	FAM179A	p.Leu737Leu	synonymous_variant	2	29256415	G	A	16.67%	120	.	.	.		.	.	.			.	0.5077	55.36%	98.93%	87%	Clonal			
MTC14	FAM179A	p.Pro738Thr	missense_variant	2	29256416	C	A	16.67%	120	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5077	55.36%	98.93%	87%	Clonal			
MTC14	BIRC6	p.Arg1788Lys	missense_variant	2	32692599	G	A	18.88%	286	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1969	61.43%	96.48%	79%	Subclonal			
MTC14	FSHR	p.Met520Leu	missense_variant	2	49190402	T	A	49.38%	322	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.0006	95.87%	100.00%	100%	Clonal			
MTC14	BCL11A	p.Pro35Pro	synonymous_variant	2	60773386	C	T	56.25%	144	.	.	.		true	.	.		TRUE	.	0.9186	93.43%	100.00%	100%	Clonal			
MTC14	GMCL1	p.Ser139Cys	missense_variant	2	70066620	C	G	9.55%	199	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	19.35%	45.69%	31%	Subclonal			
MTC14	LRRTM1	p.Ala153Pro	missense_variant	2	80530488	C	G	11.67%	377	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	36.49%	63.78%	49%	Subclonal			
MTC14	VAMP5	p.Ala13Glu	missense_variant	2	85818882	C	A	27.05%	414	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8895	87.95%	100.00%	100%	Clonal			
MTC14	MAP3K19	p.Arg885*	stop_gained	2	135743789	G	A	12.46%	289	A	.	.		.	.	.		TRUE	Likely pathogenic	0.0000	37.89%	69.90%	52%	Subclonal			
MTC14	NEB	p.Asp2648Ala	missense_variant	2	152500345	T	G	13.04%	46	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.1426	25.29%	94.32%	55%	Subclonal			
MTC14	FAP	p.Leu90Leu	synonymous_variant	2	163082008	C	T	5.00%	340	.	.	.		.	.	.		TRUE	.	0.0000	12.73%	32.53%	21%	Subclonal			
MTC14	CPS1	p.Arg727Gln	missense_variant	2	211471635	G	A	6.71%	149	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	15.10%	49.55%	28%	Subclonal			
MTC14	SLC23A3	p.Leu578Leu	synonymous_variant	2	220026754	C	T	77.66%	188	.	.	.		.	.	.		TRUE	.	0.2697	97.16%	100.00%	100%	Clonal			
MTC14	COL4A4	p.Arg1272Ile	missense_variant	2	227896663	C	A	43.52%	108	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9434	88.66%	100.00%	100%	Clonal			
MTC14	ATG16L1	p.Lys222Gln	missense_variant	2	234178670	A	C	12.07%	58	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0720	24.77%	90.43%	51%	Subclonal			
MTC14	TMEM43	p.Glu294Glu	synonymous_variant	3	14177408	G	A	12.93%	232	.	.	.		.	.	.		TRUE	.	0.0003	38.20%	74.52%	54%	Subclonal			
MTC14	IP6K2	p.Ser412Thr	missense_variant	3	48725752	C	G	5.87%	375	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	15.95%	36.13%	25%	Subclonal			
MTC14	APEH	p.Ser638Arg	missense_variant	3	49720306	C	A	42.81%	320	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9021	95.53%	100.00%	100%	Clonal			
MTC14	ESYT3	p.Pro48Thr	missense_variant	3	138153782	C	A	6.15%	325	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	28.50%	66.57%	44%	Subclonal			
MTC14	FNDC3B	p.Gly364Val	missense_variant	3	172025182	G	T	6.20%	548	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	22.77%	43.93%	32%	Subclonal			
MTC14	SLIT2	p.Ala505Gly	missense_variant	4	20530623	C	G	3.31%	181	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	6.06%	29.04%	14%	Subclonal			
MTC14	PPARGC1A	p.Pro376Ala	missense_variant	4	23815980	G	C	16.42%	268	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0224	51.84%	88.77%	69%	Subclonal			
MTC14	SULT1E1	p.Glu245Lys	missense_variant	4	70709918	C	T	19.13%	115	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0201	41.08%	86.39%	61%	Subclonal			
MTC14	THAP9	p.Gly22Asp	missense_variant	4	83822020	G	A	11.63%	129	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0031	29.72%	76.33%	49%	Subclonal			
MTC14	SLC25A4	p.Glu30Asp	missense_variant	4	186064616	G	C	32.63%	190	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8691	91.84%	100.00%	100%	Clonal			
MTC14	TRIO	p.Gly2780Gly	synonymous_variant	5	14502695	G	C	5.68%	264	.	.	.		.	.	.		TRUE	.	0.0000	14.14%	37.97%	24%	Subclonal			
MTC14	XRCC4	p.Glu212Lys	missense_variant	5	82499522	G	A	67.98%	203	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9266	96.57%	100.00%	100%	Clonal			
MTC14	TBC1D7	p.Gly213Gly	synonymous_variant	6	13307858	T	G	8.91%	348	.	.	.		.	.	.		TRUE	.	0.0000	26.17%	51.46%	37%	Subclonal			
MTC14	ATF6B	p.Pro13Ser	missense_variant	6	32095948	G	A	10.44%	182	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0993	41.59%	93.18%	65%	Subclonal			
MTC14	HLA-DRB5	p.Ser24Phe	missense_variant	6	32497931	G	A	24.32%	37	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7585	56.87%	100.00%	100%	Clonal			
MTC14	C6orf106	p.Glu135Lys	missense_variant	6	34614486	C	T	5.58%	394	D	.	Passenger		.	.	.			Indeterminate	0.0000	22.57%	51.00%	35%	Subclonal			
MTC14	COL19A1	p.Ile885Leu	missense_variant	6	70886442	A	T	4.17%	192	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	6.35%	25.10%	13%	Subclonal			
MTC14	C6orf57	p.Leu48Arg	missense_variant	6	71289195	T	G	72.47%	178	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4766	96.51%	100.00%	100%	Clonal			
MTC14	SLC22A1	p.Ile403Met	missense_variant	6	160560832	C	G	61.64%	73	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9640	89.80%	100.00%	100%	Clonal			
MTC14	DNAH11	c.6546+1G>T	splice_donor_variant	7	21745156	G	T	7.90%	367	D	.	.		.	.	.			Indeterminate	0.0000	22.87%	46.20%	33%	Subclonal			
MTC14	MUC3A	p.Ser469Cys	missense_variant	7	100550824	A	T	8.57%	70	.	.	.		.	.	.			Indeterminate	0.0049	16.51%	72.70%	36%	Subclonal			
MTC14	MUC12	p.Thr240Thr	synonymous_variant	7	100634564	C	G	37.65%	85	.	.	.		.	.	.			.	0.8113	82.35%	100.00%	100%	Clonal			
MTC14	CUX1	p.Glu850Lys	missense_variant	7	101845092	G	A	6.79%	221	D	PASSENGER/OTHER	Passenger		true	.	true			Likely pathogenic	0.0000	17.04%	45.27%	28%	Subclonal			
MTC14	DLD	p.Thr319Ser	missense_variant	7	107557319	C	G	50.00%	206	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9632	95.04%	100.00%	100%	Clonal			
MTC14	LAMB1	p.Ser1365Ser	synonymous_variant	7	107575953	G	A	6.38%	329	.	.	.		.	.	.			.	0.0000	17.22%	39.67%	27%	Subclonal			
MTC14	FLNC	p.Ala2220Ser	missense_variant	7	128494201	G	T	5.65%	230	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	13.54%	39.09%	24%	Subclonal			
MTC14	MKLN1	p.Ala66Ala	synonymous_variant	7	131071908	T	G	9.55%	178	.	.	.		.	.	.			.	0.0000	24.99%	61.52%	40%	Subclonal			
MTC14	RB1CC1	p.Asp336Tyr	missense_variant	8	53580748	C	A	4.41%	227	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	14.55%	48.59%	27%	Subclonal			
MTC14	ZFHX4	p.Gln2114His	missense_variant	8	77765499	G	T	3.24%	895	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	15.83%	32.74%	23%	Subclonal			
MTC14	PAG1	p.Leu116Val	missense_variant	8	81897541	G	C	5.49%	911	N	.	Passenger		.	.	.			Likely passenger	0.0000	42.23%	72.58%	56%	Subclonal			
MTC14	CHMP4C	p.Gln138*	stop_gained	8	82667648	C	T	22.19%	924	A	.	.		.	.	.			Indeterminate	0.8353	97.10%	100.00%	100%	Clonal			
MTC14	RUNX1T1	p.Leu523Leu	synonymous_variant	8	92983035	G	A	14.50%	476	.	.	.		true	.	.			.	0.4166	88.28%	100.00%	100%	Clonal			
MTC14	ESRP1	p.Arg175Pro	missense_variant	8	95674533	G	C	28.10%	484	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5335	96.26%	100.00%	100%	Clonal			
MTC14	NFX1	p.Glu777Ala	missense_variant	9	33344172	A	C	16.23%	154	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4670	56.99%	98.76%	84%	Subclonal			
MTC14	ABCA1	p.Glu1859Asp	missense_variant	9	107555511	T	G	13.42%	231	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	30.28%	58.45%	43%	Subclonal			
MTC14	CDK5RAP2	p.Val995Leu	missense_variant	9	123210215	C	G	15.57%	334	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0022	50.21%	82.83%	65%	Subclonal			
MTC14	OR1L8	p.Thr250Met	missense_variant	9	125330008	G	A	9.70%	268	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	27.69%	57.62%	41%	Subclonal			
MTC14	NOTCH1	p.Pro2514fs	frameshift_variant	9	139390648	CAG	C	79.31%	145	D	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.1718	96.46%	100.00%	100%	Clonal			
MTC14	SEC61A2	p.Glu459Gln	missense_variant	10	12206397	G	C	3.48%	345	D	.	Passenger		.	.	.			Indeterminate	0.0000	12.01%	36.58%	22%	Subclonal			
MTC14	HKDC1	p.Glu271Glu	synonymous_variant	10	71003059	G	A	25.61%	164	.	.	.		.	.	.		TRUE	.	0.7928	81.87%	100.00%	100%	Clonal			
MTC14	HKDC1	p.Asp272Tyr	missense_variant	10	71003060	G	T	25.93%	162	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7812	82.15%	100.00%	100%	Clonal			
MTC14	USP54	p.Glu558Gln	missense_variant	10	75290057	C	G	9.85%	518	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	38.86%	65.63%	51%	Subclonal			
MTC14	COMTD1	c.329-1G>A	splice_acceptor_variant	10	76994937	C	T	12.99%	231	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0590	47.61%	91.44%	68%	Subclonal			
MTC14	PTEN	p.Asp268Glu	missense_variant	10	89720653	C	A	19.15%	47	D	CANCER	Passenger		true	true	true	TRUE	TRUE	Likely pathogenic	0.5673	47.60%	100.00%	100%	Clonal			
MTC14	SORCS1	p.Lys476Lys	synonymous_variant	10	108448082	C	T	29.19%	161	.	.	.		.	.	.		TRUE	.	0.6540	70.74%	100.00%	93%	Clonal			
MTC14	IFITM5	p.Trp92Arg	missense_variant	11	298626	A	G	10.47%	344	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	24.02%	44.78%	33%	Subclonal			
MTC14	STIM1	p.Lys698Asn	missense_variant	11	4112746	G	C	37.73%	220	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8592	88.03%	100.00%	100%	Clonal			
MTC14	STIM1	p.Ala699Ser	missense_variant	11	4112747	G	T	37.33%	217	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8683	87.48%	100.00%	100%	Clonal			
MTC14	PAMR1	p.Val642Glu	missense_variant	11	35454193	A	T	45.45%	231	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0041	93.15%	100.00%	100%	Clonal			
MTC14	SSSCA1	p.Val71Val	synonymous_variant	11	65338398	G	C	2.67%	712	D	PASSENGER/OTHER	.		.	.	.			.	0.0000	11.89%	29.25%	19%	Subclonal			
MTC14	SLC29A2	p.Pro321Leu	missense_variant	11	66133608	G	A	22.17%	433	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8775	86.66%	100.00%	100%	Clonal			
MTC14	C2CD3	p.Arg1438His	missense_variant	11	73789450	C	T	47.49%	478	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0132	97.70%	100.00%	100%	Clonal			
MTC14	FAT3	p.Arg4002Cys	missense_variant	11	92600252	C	T	51.98%	252	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2566	96.37%	100.00%	100%	Clonal			
MTC14	HTR3A	p.Leu255Leu	synonymous_variant	11	113857281	G	A	82.45%	188	.	PASSENGER/OTHER	.		.	.	.		TRUE	.	0.0056	97.32%	100.00%	100%	Clonal			
MTC14	SLC6A12	p.Val238Leu	missense_variant	12	308097	C	A	65.85%	123	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2029	95.01%	100.00%	100%	Clonal			
MTC14	IPO8	p.Val862Ala	missense_variant	12	30790026	A	G	5.62%	516	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.04%	40.87%	29%	Subclonal			
MTC14	DIP2B	p.Arg634Gln	missense_variant	12	51089718	G	A	26.42%	386	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8811	86.29%	100.00%	100%	Clonal			
MTC14	CELA1	p.Arg236Arg	synonymous_variant	12	51723519	C	T	7.42%	229	.	.	.		.	.	.			.	0.0000	19.23%	48.07%	31%	Subclonal			
MTC14	OR10P1	p.Val306Leu	missense_variant	12	56031591	G	T	8.48%	330	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	24.43%	49.86%	36%	Subclonal			
MTC14	BEST3	c.153-2A>T	splice_acceptor_variant	12	70088246	T	A	4.98%	261	D	.	.		.	.	.			Indeterminate	0.0000	14.83%	42.83%	26%	Subclonal			
MTC14	SYT1	p.Ala167Gly	missense_variant	12	79689874	C	G	37.22%	180	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3832	90.15%	100.00%	100%	Clonal			
MTC14	MLXIP	p.Thr134Pro	missense_variant	12	122517159	A	C	4.62%	238	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	7.88%	25.38%	15%	Subclonal			
MTC14	EP400	p.Ala1649Thr	missense_variant	12	132510280	G	A	23.23%	99	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.2240	50.53%	96.62%	74%	Subclonal			
MTC14	SACS	p.Leu4120Phe	missense_variant	13	23905655	T	A	48.71%	388	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9764	97.09%	100.00%	100%	Clonal			
MTC14	CENPJ	p.Gly105Glu	missense_variant	13	25486850	C	T	4.53%	353	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	11.31%	29.88%	19%	Subclonal			
MTC14	USPL1	p.Asp683Tyr	missense_variant	13	31232261	G	T	18.93%	243	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2431	60.27%	97.05%	79%	Subclonal			
MTC14	RBM26	p.Glu22Asp	missense_variant	13	79979844	C	A	53.97%	378	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6836	97.40%	100.00%	100%	Clonal			
MTC14	SOX21	p.Ala21Val	missense_variant	13	95364242	G	A	8.69%	495	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	26.86%	47.79%	36%	Subclonal			
MTC14	SOX21	p.Phe15Leu	missense_variant	13	95364259	G	T	9.15%	503	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	28.57%	49.83%	38%	Subclonal			
MTC14	METTL21C	p.Thr229Ala	missense_variant	13	103338491	T	C	11.51%	391	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	36.11%	62.73%	48%	Subclonal			
MTC14	COL4A1	p.Pro899Ala	missense_variant	13	110830210	G	C	6.54%	153	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	14.67%	48.28%	27%	Subclonal			
MTC14	UPF3A	p.Gly57Gly	synonymous_variant	13	115047285	C	T	21.73%	382	.	.	.		.	.	.			.	0.6007	74.00%	100.00%	91%	Clonal			
MTC14	NDRG2	c.762-1_762insT	splice_acceptor_variant	14	21486973	C	CA	10.57%	265	.	.	.		.	.	.			Indeterminate	0.0000	23.22%	46.99%	34%	Subclonal			
MTC14	RTN1	p.Pro202Arg	missense_variant	14	60212836	G	C	22.09%	430	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8771	86.45%	100.00%	100%	Clonal			
MTC14	RYR3	p.Glu2674Asp	missense_variant	15	34040347	G	C	37.85%	177	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9614	91.83%	100.00%	100%	Clonal			
MTC14	TGM5	p.Ser582Ser	synonymous_variant	15	43527096	G	T	4.17%	168	.	.	.		.	.	.		TRUE	.	0.0000	6.10%	26.21%	13%	Subclonal			
MTC14	TLN2	p.Lys280Asn	missense_variant	15	62966077	G	C	4.61%	217	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	10.17%	34.25%	19%	Subclonal			
MTC14	DIS3L	p.Glu168Val	missense_variant	15	66601127	A	T	5.97%	201	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	14.07%	42.10%	25%	Subclonal			
MTC14	AAGAB	p.Gly158Arg	missense_variant	15	67524215	C	T	5.46%	458	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	15.16%	32.83%	23%	Subclonal			
MTC14	EFTUD1	p.Leu1028Val	missense_variant	15	82431091	G	C	75.07%	341	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5004	98.17%	100.00%	100%	Clonal			
MTC14	RCCD1	p.Thr360Thr	synonymous_variant	15	91504948	C	T	4.76%	210	.	.	.		.	.	.		TRUE	.	0.0000	10.51%	35.38%	20%	Subclonal			
MTC14	CACNA1H	p.Arg2130Gln	missense_variant	16	1270321	G	A	56.04%	439	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0895	98.02%	100.00%	100%	Clonal			
MTC14	ZKSCAN2	p.Val644Leu	missense_variant	16	25255157	C	G	10.44%	249	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	29.89%	61.91%	44%	Subclonal			
MTC14	CNGB1	p.Arg1082Cys	missense_variant	16	57921977	G	A	17.03%	229	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5432	64.58%	100.00%	89%	Clonal			
MTC14	CCDC113	p.Glu48Glu	synonymous_variant	16	58286673	G	A	41.82%	110	.	.	.		.	.	.			.	0.9383	89.38%	100.00%	100%	Clonal			
MTC14	LOC100129697	p.Val384Ile	missense_variant	16	89017676	G	A	22.75%	167	.	.	Passenger		true	.	.		TRUE	Likely pathogenic	0.0811	54.03%	93.20%	73%	Subclonal			
MTC14	TP53	p.Ile195Thr	missense_variant	17	7578265	A	G	79.49%	234	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.0500	97.76%	100.00%	100%	Clonal	TRUE	GACAACCACCCTTAACCCCTC	CTGGTTGCCCAGGGTCCC
MTC14	KDM6B	p.Val1512Val	synonymous_variant	17	7755880	G	T	4.91%	529	.	.	.		.	.	.		TRUE	.	0.0000	13.67%	29.36%	21%	Subclonal			

MTC14	MYH4	p.Val1749Leu	missense_variant	17	10348604	C	G	5.73%	157	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	12.39%	43.75%	24%	Subclonal			
MTC14	MAP2K3	p.Ser6Trp	missense_variant	17	21188249	C	G	17.06%	170	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0003	38.37%	74.47%	55%	Subclonal			
MTC14	CCL23	p.Val100Val	synonymous_variant	17	34340786	G	A	63.83%	94	.	.	.		.	.	.		TRUE	.	0.9678	92.32%	100.00%	100%	Clonal			
MTC14	DHX8	p.Ala957Ala	synonymous_variant	17	41597569	C	T	7.78%	167	.	.	.		.	.	.		TRUE	.	0.0000	14.29%	40.67%	25%	Subclonal			
MTC14	BRIP1	p.Asp674Gly	missense_variant	17	59853838	T	C	5.96%	386	D	PASSENGER/OTHER	Passenger		true	.	.		TRUE	Likely pathogenic	0.0000	20.34%	45.17%	31%	Subclonal			
MTC14	GGA3	p.Pro557Leu	missense_variant	17	73235566	G	A	6.90%	232	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.0000	21.89%	56.23%	36%	Subclonal			
MTC14	TNRC6C	p.Ala42Gly	missense_variant	17	76045268	C	G	14.32%	482	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0358	59.14%	91.33%	74%	Subclonal			
MTC14	AFMID	p.Arg238His	missense_variant	17	76201752	G	A	6.55%	534	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	24.21%	46.19%	34%	Subclonal			
MTC14	BAHCC1	p.Ala2465Val	missense_variant	17	79429851	C	T	3.39%	442	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	10.27%	28.22%	18%	Subclonal			
MTC14	LAMA1	p.Val116Ile	missense_variant	18	7050935	C	T	5.06%	237	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	8.90%	27.14%	16%	Subclonal			
MTC14	TRAPPC8	p.Ser1367Leu	missense_variant	18	29410926	G	A	72.69%	227	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.2185	97.21%	100.00%	100%	Clonal			
MTC14	CHERP	p.Gln797_Ser800del	disruptive_inframe_deletion	19	16631020	CGGGACCGCGACT	C	5.45%	165	D	.	.	Deleterious	.	.	.		TRUE	Likely pathogenic	0.0000	8.85%	31.64%	17%	Subclonal			
MTC14	ARHGAP35	p.Ala343Gly	missense_variant	19	47422960	C	G	21.57%	547	D	PASSENGER/OTHER	Passenger		.	true	true		TRUE	Likely pathogenic	0.8882	87.48%	100.00%	100%	Clonal			
MTC14	NLRP2	p.Arg717Ser	missense_variant	19	55496535	G	T	21.48%	149	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0455	49.53%	90.73%	69%	Subclonal			
MTC14	NLRP2	p.Ile718Val	missense_variant	19	55496536	A	G	21.09%	147	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0358	48.35%	89.72%	67%	Subclonal			
MTC14	C20orf194	p.Gly829Asp	missense_variant	20	3268278	C	T	4.26%	141	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.92%	37.16%	18%	Subclonal			
MTC14	ISM1	p.Asp181Asn	missense_variant	20	13260443	G	A	7.37%	312	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	20.35%	44.93%	31%	Subclonal			
MTC14	CFAP61	p.Tyr165Tyr	synonymous_variant	20	20056188	T	C	4.80%	271	.	.	.		.	.	.			.	0.0000	11.39%	33.24%	20%	Subclonal			
MTC14	CD93	p.Val416Ile	missense_variant	20	23065584	C	T	25.63%	476	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8822	86.54%	100.00%	100%	Clonal			
MTC14	CEP250	p.Leu1061Leu	synonymous_variant	20	34084421	G	C	9.86%	355	.	.	.		.	.	.			.	0.0000	29.63%	55.80%	41%	Subclonal			
MTC14	ZNF335	p.Gly47Trp	missense_variant	20	44599911	C	A	25.64%	234	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8241	79.87%	100.00%	100%	Clonal			
MTC14	FAM209A	c.250-1G>T	splice_acceptor_variant	20	55100859	G	T	4.00%	350	D	.	.		.	.	.			Indeterminate	0.0000	12.04%	33.83%	21%	Subclonal			
MTC14	LTN1	p.Met1009Ile	missense_variant	21	30329657	C	T	7.44%	215	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	19.03%	48.84%	31%	Subclonal			
MTC14	KRTAP10-11	p.Ser262Tyr	missense_variant	21	46067160	C	A	25.42%	295	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5312	90.43%	100.00%	100%	Clonal			
MTC14	SPECC1L	p.Ile1084Met	missense_variant	22	24808663	C	G	9.49%	137	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	23.24%	64.86%	40%	Subclonal			
MTC14	TTC28	p.Arg395Arg	synonymous_variant	22	28559336	C	T	7.07%	368	.	.	.		.	.	.			.	0.0000	19.99%	42.13%	30%	Subclonal			
MTC14	ZBED4	p.Glu532Gln	missense_variant	22	50278904	G	C	5.06%	395	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	13.37%	31.81%	21%	Subclonal			
MTC14	HDAC10	p.Arg104Gly	missense_variant	22	50688571	G	C	54.07%	246	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8255	96.25%	100.00%	100%	Clonal			
MTC14	WNK3	p.Pro318Leu	missense_variant	X	54334491	G	A	6.79%	265	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0000	22.13%	53.99%	35%	Subclonal			
MTC14	ABCB7	p.Thr647Ser	missense_variant	X	74280164	G	C	42.65%	279	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9184	95.55%	100.00%	100%	Clonal			
MTC14	COL4A6	p.Gln824His	missense_variant	X	107422008	C	G	43.93%	280	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8460	95.81%	100.00%	100%	Clonal			
MTC14	AFF2	p.Pro124Pro	synonymous_variant	X	147743620	A	T	3.43%	700	.	.	.		.	.	.			.	0.0000	11.51%	25.78%	18%	Subclonal			
MTC14	CETN2	p.Met57Leu	missense_variant	X	151997815	T	G	11.63%	215	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0165	41.15%	85.50%	60%	Subclonal			
MTC14	ZNF275	p.Ala153Pro	missense_variant	X	152612600	G	C	37.56%	607	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9767	97.24%	100.00%	100%	Clonal			
MTC14	G6PD	p.Arg423Cys	missense_variant	X	153760892	G	A	4.56%	636	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	16.12%	33.15%	24%	Subclonal			
MTC15	MST1P2	n.1656+2T>A	splice_donor_variant	1	16975289	T	A	35.71%	14	.	.	.		.	.	.			Indeterminate	0.8724	48.18%	100.00%	100%	Clonal			
MTC15	AK5	p.Thr115Asn	missense_variant	1	77759574	C	A	13.44%	372	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7287	66.69%	100.00%	88%	Clonal			
MTC15	DUSP27	p.Pro749Pro	synonymous_variant	1	167096615	G	A	15.60%	359	.	.	.		.	.	.			.	0.8867	75.92%	100.00%	100%	Clonal			
MTC15	LYPLAL1	p.Val209Val	synonymous_variant	1	219384983	T	G	15.40%	487	.	.	.		.	.	.			.	0.8948	78.38%	100.00%	100%	Clonal			
MTC15	OR2G6	p.Cys189Cys	synonymous_variant	1	248685514	T	C	14.84%	411	.	.	.		.	.	.			.	0.8594	74.32%	100.00%	97%	Clonal			
MTC15	PLEKHH2	p.Asn921Thr	missense_variant	2	43956816	A	C	17.28%	191	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8884	73.31%	100.00%	100%	Clonal			
MTC15	POLR2D	p.Asn102Ile	missense_variant	2	128608209	T	A	12.73%	55	D	.	Passenger		.	.	.			Indeterminate	0.6558	38.03%	98.65%	84%	Clonal			
MTC15	LRP1B	p.Leu4450Leu	synonymous_variant	2	140997076	G	A	14.89%	329	.	.	.		.	.	.			.	0.8515	72.12%	100.00%	98%	Clonal			
MTC15	PIK3CA	p.His1047Arg	missense_variant	3	178952085	A	G	15.98%	338	D	CANCER	Driver		true	true	true			Likely pathogenic	0.8952	76.59%	100.00%	100%	Clonal	TRUE	ATCTCTTCATAAATCTTTTCTCAAT	ACAGTGCAGTGTGGAATCCA
MTC15	CCDC39	p.Ala611Ala	synonymous_variant	3	180359822	C	T	13.10%	420	.	.	.		.	.	.			.	0.6668	66.07%	98.73%	86%	Clonal			
MTC15	FAT1	p.Val2168fs	frameshift_variant	4	187541235	TA	T	15.62%	634	A	.	.		.	.	true			Likely pathogenic	0.9151	81.73%	100.00%	100%	Clonal			
MTC15	SH3TC2	p.Leu784Leu	synonymous_variant	5	148406945	A	G	24.49%	543	.	.	.		.	.	.			.	0.9677	95.08%	100.00%	100%	Clonal			
MTC15	FGFR4	p.Leu446Leu	synonymous_variant	5	176520493	C	A	7.83%	651	A	.	.		.	.	.			.	0.0004	45.02%	76.37%	59%	Subclonal			
MTC15	SLC18B1	p.Val336Leu	missense_variant	6	133094211	C	G	16.04%	293	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8889	75.12%	100.00%	100%	Clonal			
MTC15	FNDC1	p.Gln1352Arg	missense_variant	6	159657334	A	G	17.23%	325	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9170	80.09%	100.00%	100%	Clonal			
MTC15	WIPI2	p.Thr215Thr	synonymous_variant	7	5257621	T	G	45.60%	386	.	.	.		.	.	.			.	0.3921	97.46%	100.00%	100%	Clonal			
MTC15	GAL3ST4	p.Pro232Thr	missense_variant	7	99758318	G	T	11.20%	375	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.2332	54.61%	94.44%	74%	Subclonal			
MTC15	PIK3CG	p.Ala676Thr	missense_variant	7	106513012	G	A	20.25%	321	D	CANCER	Passenger		.	true	.			Likely pathogenic	0.6295	88.57%	100.00%	100%	Clonal	TRUE	TCCATTTCCTTTTCCCTGATT	TAGGTCTACCAGTTAATTCTTGGCA
MTC15	RSPO2	p.Arg27Gly	missense_variant	8	109094788	T	C	12.01%	283	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.5113	56.55%	97.70%	79%	Clonal			
MTC15	EXT1	p.Cys334Ser	missense_variant	8	118849402	C	G	8.68%	311	D	PASSENGER/OTHER	Passenger		true	.	.			Likely pathogenic	0.0101	39.20%	80.49%	57%	Subclonal			
MTC15	TEK	p.Asp185Val	missense_variant	9	27169553	A	T	13.78%	225	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.7621	62.71%	100.00%	90%	Clonal			
MTC15	GSTO1	p.Leu75Val	missense_variant	10	106019413	C	G	41.41%	99	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6084	89.20%	100.00%	100%	Clonal			
MTC15	ATG2A	p.Ser1581Ser	synonymous_variant	11	64665763	C	T	13.45%	171	.	.	.		.	.	.			.	0.7301	57.74%	100.00%	88%	Clonal			
MTC15	MFAP5	p.Ala53Thr	missense_variant	12	8808026	C	T	14.41%	222	N	.	Passenger		.	.	.			Likely passenger	0.8051	65.31%	100.00%	95%	Clonal			
MTC15	CMKLR1	p.Val50Ile	missense_variant	12	108686592	C	T	15.16%	376	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8714	74.70%	100.00%	100%	Clonal			
MTC15	SACS	p.Leu4307fs	frameshift_variant	13	23905090	CTTTT	C	15.08%	590	D	.	.		.	.	.			Indeterminate	0.8891	78.94%	100.00%	99%	Clonal			
MTC15	MCF2L	p.Arg6Lys	missense_variant	13	113623710	G	A	13.40%	403	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7201	67.26%	98.99%	88%	Clonal			
MTC15	RTN1	p.Gly160Gly	synonymous_variant	14	60212961	G	T	12.31%	333	.	.	.		.	.	.			.	0.5411	59.71%	97.94%	81%	Clonal			
MTC15	VRK1	p.Asn294Lys	missense_variant	14	97322916	C	A	12.92%	387	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6421	64.36%	98.60%	85%	Clonal			
MTC15	CCNK	p.Asp59Asn	missense_variant	14	99959189	G	A	14.29%	133	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7716	57.65%	100.00%	94%	Clonal			
MTC15	MAGEL2	p.Cys1126Ser	missense_variant	15	23889513	C	G	13.72%	430	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7628	69.51%	100.00%	90%	Clonal			
MTC15	RYR3	p.Arg3562His	missense_variant	15	34110864	G	A	14.29%	91	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7494	51.70%	100.00%	94%	Clonal			
MTC15	TAOK1	p.Glu402Gly	missense_variant	17	27829608	A	G	6.88%	160	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0161	25.17%	77.38%	45%	Subclonal			
MTC15	NBR1	p.Glu2Gly	missense_variant	17	41327821	A	G	13.03%	284	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6829	61.83%	98.81%	86%	Clonal			
MTC15	ZNF397	p.Lys184Glu	missense_variant	18	32823251	A	G	2.61%	499	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	9.57%	28.46%	17%	Subclonal			
MTC15	ZNF536	p.Arg505Trp	missense_variant	19	30935982	C	T	13.07%	306	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6853	62.84%	98.82%	86%	Clonal			
MTC15	DEFB118	p.Asp83Asn	missense_variant	20	29960848	G	A	14.40%	361	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8255	71.03%	100.00%	95%	Clonal			
MTC15	SOGA1	p.Pro109Pro	synonymous_variant	20	35491421	C	T	17.05%	129	.	.	.		.	.	.			.	0.8580	66.63%	100.00%	100%	Clonal			
MTC15	CEBPB	p.Asp124Asp	synonymous_variant	20	48807942	C	T	17.78%	90	.	.	.		.	.	.			.	0.8441	62.45%	100.00%	100%	Clonal			
MTC15	SLC35E4	p.Gly104Gly	synonymous_variant	22	31032749	C	T	16.40%	445	.	.	.		.	.	.			.	0.9195	81.08%	100.00%	100%	Clonal			
MTC15	ENTHD1	p.Asn196Thr	missense_variant	22	40257775	T	G	8.75%	80	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.3209	27.81%	95.15%	57%	Subclonal			
MTC15	IL17REL	p.Leu332Leu	synonymous_variant	22	50435482	C	T	13.16%	114	.	.	.		.	.	.			.	0.7003	50.87%	98.90%	86%	Clonal			
MTC15	SHROOM4	p.Gly1268Gly	synonymous_variant	X	50345771	T	G	15.24%	105	.	.	.		.	.	.			.	0.7953	57.40%	100.00%	100%	Clonal			
MTC15	UPRT	p.Thr299Lys	missense_variant	X	74523312	C	A	7.25%	138	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.0455	25.86%	82.81%	48%	Subclonal			
MTC15	STAG2	p.Gln340Lys	missense_variant	X	123184971	C	A	14.71%	34	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.7028	35.58%	98.88%	97%	Clonal			
MTC15	NAA10	p.Leu162Leu	synonymous_variant	X	153195662	C	T	18.21%	302	.	.	.		.	.	.			.	0.9187	81.73%	100.00%	100%	Clonal			
MTC16	AGRN	p.Ser918Leu	missense_variant	1	981416	C	T	12.54%	287	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0477	47.92%	87.92%	66%	Subclonal			
MTC16	RAP1GAP	p.Asp392Asn	missense_variant	1	21936630	C	T	10.00%	350	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0001	37.81%	70.98%	53%	Subclonal			
MTC16	B4GALT2	p.Ile318Ile	synonymous_variant	1	44451192	C	T	8.80%	284	.	.	.		.	.	.			.	0.0046	37.32%	78.79%	55%	Subclonal			
MTC16	ZNF654	p.Thr552Ile	missense_variant	3	88190115	C	T	19.10%	199	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.8492	70.71%	100.00%	100%	Clonal			
MTC16	PIK3CA	p.Cys420Arg	missense_variant	3	178927980	T	C	26.32%	133	D	CANCER	Driver		true	true	true		TRUE	Likely pathogenic	0.8671	80.32%	100.00%	100%	Clonal	TRUE	GAGATGATTGTTGAATTTTCCTTTT	TCTAATCCATGAGGTACTGGCC
MTC16	CPZ	p.Asp391Asp	synonymous_variant	4	8609098	C	T	7.56%	238	.	.	.		.	.	.			.	0.0000	25.03%	60.73%	40%	Subclonal			
MTC16	PCDHB2	p.Arg231Gln	missense_variant	5	140475066	G	A	10.28%	360	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0001	39.23%	72.34%	54%	Subclonal			
MTC16	PAQR8	p.Arg231Pro	missense_variant	6	52268703	G	C	19.92%	266	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8908	76.72%	100.00%	100%	Clonal			
MTC16	T	p.Asn78Asn	synonymous_variant	6	166580317	G	A	3.13%	544	.	.	.		.	.	.			.	0.0000	11.81%	30.49%	20%	Subclonal			
MTC16	PCLO	p.Arg1579Lys	missense_variant	7	82585533	C	T	12.69%	268	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4205	56.96%	97.82%	79%	Subclonal			
MTC16	ZNF804B	p.Ile527Phe	missense_variant	7	88963875	A	T	5.68%	229	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	17.20%	49.32%	30%	Subclonal			
MTC16	DAB2IP	p.Ser848Arg	missense_variant	9	124535435	C	G	18.13%	386	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8378	74.83%	100.00%	95%	Clonal			
MTC16	PRRC2B	p.Arg1127Gln	missense_variant	9	134350896	G	A	13.97%	365	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1362	56.24%	92.76%	73%	Subclonal			
MTC16	PTEN	c.209+2T>C	splice_donor_variant	10	89685316	T	C	12.99%	77	D	.	.		true	true	true	TRUE		Likely pathogenic	0.5426	42.75%	98.59%	81%	Clonal	TRUE	CATTTTTGTTAATGGTGGCTTT	AACTCTACCTCACTCTAACAAGCAG
MTC16	PTEN	c.1027-1G>A	splice_acceptor_variant	10	89725043	G	A	14.47%	76	D	.	.		true	true	true	TRUE		Likely pathogenic	0.6286	47.84%	100.00%	91%	Clonal	TRUE	ATCTGCAAAATGGAATAAAAAATCTG	GATCAGGTTCATTGTCACTAACATCT
MTC16	CAPRIN2	p.Thr821Asn	missense_variant	12	30869444	G	T	22.87%	188	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9093	79.35%	100.00%	100%	Clonal			
MTC16	ATP2A2	p.Arg236Gly	missense_variant	12	110765433	C	G	25.33%	225	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE		Indeterminate	0.8585	85.40%	100.00%	100%	Clonal			
MTC16	TRPC4	p.Gln385Gln	synonymous_variant	13	38266215	C	T	18.64%	177	.	.	.		.	.	.			.	0.8491	74.36%	100.00%	100%	Clonal			
MTC16	OR4N4	p.Thr18Ile	missense_variant	15	22382525	C	T	13.16%	38	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.5367	32.33%	98.54%	82%	Clonal			
MTC16	CYFIP1	p.Arg550Arg	synonymous_variant	15	22955256	C	T	12.82%	78	.	PASSENGER/OTHER	.		.	.	.			.	0.5313	42.32%	98.52%	80%	Clonal			
MTC16	WFIKKN1	p.Arg339Arg	synonymous_variant	16	683427	C	T	13.37%	374	.	.	.		.	.	.		TRUE	.	0.0578	53.62%	89.62%	70%	Subclonal			
MTC16	GLG1	p.Ser229Asn	missense_variant	16	74537517	C	T	17.72%	237	D	.	Passenger		.	.	.			Indeterminate	0.8547	75.87%	100.00%	100%	Clonal			
MTC16	TP53	p.Val274Ala	missense_variant	17	7577117	A	G	27.06%	170	D	CANCER	Driver		true	true	true	TRUE	TRUE	Likely pathogenic	0.7768	84.36%	100.00%	100%	Clonal	TRUE	CATAACTGCACCCTTGGTCTC	GGACCTGATTTCCTTACTGCC
MTC16	LPPR3	p.Lys738Glu	missense_variant	19	812599	T	C	20.34%	59	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7832	59.37%	100.00%	100%	Clonal			
MTC16	MAP1S	p.Arg563His	missense_variant	19	17837881	G	A	17.52%	331	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8751	79.36%	100.00%	100%	Clonal			
MTC16	GATAD2A	p.Arg9Trp	missense_variant	19	19576179	C	T	10.29%	408	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0116	47.76%	84.70%	64%	Subclonal			
MTC16	NLRP11	p.Tyr524Tyr	synonymous_variant	19	56320404	G	A	27.08%	240	.	.	.		.	.	.		TRUE	.	0.5505	88.06%	100.00%	100%	Clonal			
MTC16	CDK5RAP1	p.Thr107Thr	synonymous_variant	20	31982909	G	A	3.72%	215	.	.	.		.	.	.			.	0.0000	13.43%	51.53%	27%	Subclonal			
MTC16	RFPL1	p.Arg198Arg	synonymous_variant	22	29837749	A	C	50.00%	14	.	.	.		.	.	.			.	0.4623	58.59%	100.00%	100%	Clonal			
MTC16	POLA1	p.Asn935Tyr	missense_variant	X	24766557	A	T	9.90%	202	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0060	33.77%	77.31%	52%	Subclonal			
MTC16	IQSEC2	p.Ser412Leu	missense_variant	X	53283878	G	A	10.90%	312	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0020	41.11%	77.58%	57%	Subclonal			
MTC17	HSPG2	p.Ala3778Asp	missense_variant	1	22158167	G	T	5.85%	188	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3739	34.31%	95.16%	62%	Subclonal			
MTC17	UBXN11	p.Arg289Cys	missense_variant	1	26610961	G	A	9.56%	136	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8203	53.49%	100.00%	100%	Clonal			
MTC17	SMPDL3B	p.Thr245Thr	synonymous_variant	1	28282239	G	A	23.81%	189	.	.	.		.	.	.		TRUE	.	0.8773	89.11%	100.00%	100%	Clonal			
MTC17	ZCCHC11	p.Arg1108Gln	missense_variant	1	52924120	C	T	5.71%	175	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8237	51.06%	100.00%	100%	Clonal			
MTC17	SCP2	p.Cys225Phe	missense_variant	1	53442441	G	T	4.88%	246	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7843	49.90%	100.00%	95%	Clonal			
MTC17	MYSM1	p.Glu370Lys	missense_variant	1	59147608	C	T	11.63%	215	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9542	78.29%	100.00%	100%	Clonal			
MTC17	TNNI3K	p.Lys252Thr	missense_variant	1	74808598	A	C	6.10%	164	N	CANCER	Passenger		.	.	.			Likely passenger	0.5719	37.56%	97.62%	70%	Clonal			
MTC17	RPAP2	c.1538+1G>C	splice_donor_variant	1	92799031	G	C	7.20%	125	.	.	.		.	.	.		TRUE	Likely pathogenic	0.5627	35.59%	97.46%	69%	Clonal			
MTC17	LCE1D	p.Gly68Gly	synonymous_variant	1	152770474	T	A	6.49%	77	.	.	.		.	.	.			.	0.7164	33.12%	98.69%	88%	Clonal			
MTC17	RRNAD1	p.Arg351Trp	missense_variant	1	156704215	C	T	5.98%	518	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.6560	56.56%	98.34%	81%	Clonal			
MTC17	METTL18	p.Thr295Thr	synonymous_variant	1	169761952	G	A	6.12%	147	.	.	.		.	.	.			.	0.6571	38.89%	98.32%	77%	Clonal			
MTC17	KCNH1	p.Ser819Ser	synonymous_variant	1	210857136	G	T	6.52%	445	.	.	.		.	.	.			.	0.6772	56.30%	98.48%	82%	Clonal			
MTC17	TTC13	p.Ile527Met	missense_variant	1	231061270	T	C	7.76%	116	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7814	45.80%	100.00%	97%	Clonal			
MTC17	MAP10	p.Phe711Phe	synonymous_variant	1	232942902	C	T	7.65%	183	.	.	.		.	.	.			.	0.8017	52.98%	100.00%	96%	Clonal			
MTC17	TARBP1	p.Gln719Glu	missense_variant	1	234573098	G	C	7.58%	264	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8167	58.22%	100.00%	95%	Clonal			
MTC17	NID1	p.Gly834Glu	missense_variant	1	236175247	C	T	14.49%	138	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9515	74.88%	100.00%	100%	Clonal			
MTC17	SPTBN1	p.Val1520Val	synonymous_variant	2	54873130	G	A	39.86%	276	.	.	.		.	.	.		TRUE	.	0.2028	96.13%	100.00%	100%	Clonal			
MTC17	SMYD1	p.Val114Gly	missense_variant	2	88387407	T	G	27.78%	54	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7428	75.23%	100.00%	100%	Clonal			
MTC17	NCKAP5	p.Gln1488Gln	synonymous_variant	2	133539920	T	C	11.94%	494	.	.	.		.	.	.		TRUE	.	0.7324	86.79%	100.00%	100%	Clonal			
MTC17	LRP1B	p.Pro1164Leu	missense_variant	2	141665475	G	A	6.02%	83	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6522	30.05%	98.26%	76%	Clonal			
MTC17	TTN	p.Ala31986Val	missense_variant	2	179408999	G	A	18.05%	277	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9678	88.83%	100.00%	100%	Clonal			
MTC17	UNC80	p.Asn2194Asn	synonymous_variant	2	210806078	C	T	35.82%	335	.	.	.		.	.	.		TRUE	.	0.3812	96.34%	100.00%	100%	Clonal			
MTC17	ERBB4	p.Gly725Gly	synonymous_variant	2	212488674	G	T	11.86%	118	.	.	.		.	true	.		TRUE	.	0.9074	64.71%	100.00%	100%	Clonal			
MTC17	PLCL2	p.Lys1020Asn	missense_variant	3	17084419	G	T	7.56%	172	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6857	45.34%	98.49%	80%	Clonal			
MTC17	NGLY1	p.Asp360Glu	missense_variant	3	25777564	G	T	15.49%	71	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9303	62.91%	100.00%	100%	Clonal			
MTC17	ITGA9	p.Arg564Trp	missense_variant	3	37670678	C	T	11.63%	43	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8343	40.65%	100.00%	100%	Clonal			
MTC17	GRM2	p.Ala6Val	missense_variant	3	51743016	C	T	38.83%	103	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.3561	90.07%	100.00%	100%	Clonal			
MTC17	PARP3	p.Ala7Thr	missense_variant	3	51976724	G	A	8.03%	274	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8086	58.66%	100.00%	93%	Clonal			
MTC17	PBRM1	p.Ala137Thr	missense_variant	3	52696268	C	T	12.40%	242	D	PASSENGER/OTHER	Passenger		true	true	true		TRUE	Likely pathogenic	0.8978	77.43%	100.00%	100%	Clonal			
MTC17	RPN1	p.Asp601Asn	missense_variant	3	128339277	C	T	7.75%	387	D	.	Passenger		true	.	.		TRUE	Likely pathogenic	0.8494	65.00%	100.00%	97%	Clonal			
MTC17	IFT122	p.Leu977Leu	synonymous_variant	3	129225379	C	G	9.27%	313	.	.	.		.	.	.		TRUE	.	0.9006	71.31%	100.00%	100%	Clonal			
MTC17	SI	p.Tyr1243Asp	missense_variant	3	164735368	A	C	15.81%	215	D	PASSENGER/OTHER	Passenger		.	.	.	TRUE	TRUE	Indeterminate	0.9641	84.03%	100.00%	100%	Clonal			
MTC17	PIK3CA	p.His1047Leu	missense_variant	3	178952085	A	T	65.23%	302	D	CANCER	Driver		true	true	true		TRUE	Likely pathogenic	0.2270	98.04%	100.00%	100%	Clonal	TRUE	ATCTCTTCATAAATCTTTTCTCAAT	ACAGTGCAGTGTGGAATCCA
MTC17	MUC4	p.Ser2855Ser	synonymous_variant	3	195509886	G	C	20.51%	39	.	.	.		.	.	.		TRUE	.	0.6933	62.00%	100.00%	100%	Clonal			
MTC17	MFI2	p.Cys172Cys	synonymous_variant	3	196749956	G	A	28.81%	236	.	.	.		.	.	.		TRUE	.	0.3121	93.99%	100.00%	100%	Clonal			
MTC17	NOP14	p.Gly89Arg	missense_variant	4	2959398	C	T	5.31%	113	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4945	27.63%	96.79%	61%	Subclonal			
MTC17	JAKMIP1	p.Tyr502Cys	missense_variant	4	6064094	T	C	11.11%	63	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8436	47.21%	100.00%	100%	Clonal			
MTC17	PSAPL1	p.Arg323Cys	missense_variant	4	7435640	G	A	5.46%	403	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.1729	41.53%	91.17%	63%	Subclonal			
MTC17	MMRN1	p.Gly1027Gly	synonymous_variant	4	90857912	C	A	6.82%	176	.	.	.		.	.	.		TRUE	.	0.5799	40.56%	97.66%	72%	Clonal			
MTC17	DCLK2	p.Arg121Cys	missense_variant	4	151000540	C	T	6.77%	502	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7289	60.04%	98.79%	85%	Clonal			
MTC17	FAT1	p.Glu4283Gln	missense_variant	4	187517847	C	G	9.43%	424	D	PASSENGER/OTHER	Passenger		.	.	true			Likely pathogenic	0.8082	65.10%	100.00%	90%	Clonal			
MTC17	SDHA	p.Ala148Ala	synonymous_variant	5	225665	C	A	6.72%	119	.	.	.		.	.	.			.	0.7488	41.89%	98.91%	91%	Clonal			
MTC17	TRIO	p.Ser52Ser	synonymous_variant	5	14143990	C	G	10.91%	110	.	.	.		.	.	.			.	0.8998	61.32%	100.00%	100%	Clonal			
MTC17	FBXL7	p.Arg480Cys	missense_variant	5	15937257	C	T	30.29%	416	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5770	96.38%	100.00%	100%	Clonal			
MTC17	RICTOR	p.Glu40Asp	missense_variant	5	39021216	C	G	4.19%	167	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.3798	27.30%	95.24%	57%	Subclonal			
MTC17	GPR98	p.Gln5069Glu	missense_variant	5	90106282	C	G	12.95%	193	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9033	73.64%	100.00%	100%	Clonal			
MTC17	YTHDC2	p.His79Arg	missense_variant	5	112851017	A	G	32.56%	86	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4200	85.45%	100.00%	100%	Clonal			
MTC17	FEM1C	p.Arg592His	missense_variant	5	114860084	C	T	10.63%	207	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.8822	65.94%	100.00%	100%	Clonal			
MTC17	BRD8	p.Gly225Cys	missense_variant	5	137503737	C	A	18.33%	60	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9243	65.95%	100.00%	100%	Clonal			
MTC17	BRD8	p.Ser224Phe	missense_variant	5	137503739	G	A	25.00%	64	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7572	76.17%	100.00%	100%	Clonal			
MTC17	PCDH1	p.Ser356Ser	synonymous_variant	5	141244828	T	G	25.27%	281	.	.	.		.	.	.			.	0.5331	93.38%	100.00%	100%	Clonal			
MTC17	GABRA6	p.Arg159Ser	missense_variant	5	161116290	G	T	13.22%	121	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9339	69.33%	100.00%	100%	Clonal			
MTC17	RARS	p.Asp324Gly	missense_variant	5	167929024	A	G	9.60%	125	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8567	56.88%	100.00%	100%	Clonal			
MTC17	SERPINB9	p.Ile359Ile	synonymous_variant	6	2890451	G	A	21.64%	305	.	.	.		.	.	.			.	0.8348	92.17%	100.00%	100%	Clonal			
MTC17	FAM50B	p.Arg115His	missense_variant	6	3850389	G	A	6.59%	501	N	.	Passenger		.	.	.			Likely passenger	0.4990	54.00%	97.04%	76%	Subclonal			
MTC17	PPP1R11	p.Gly104Gly	synonymous_variant	6	30037014	A	G	7.26%	234	.	.	.		.	.	.			.	0.7262	50.93%	98.77%	84%	Clonal			
MTC17	SPDEF	p.Ser324Pro	missense_variant	6	34506089	A	G	13.17%	486	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7126	87.91%	100.00%	100%	Clonal			
MTC17	PGK2	p.Gly130Gly	synonymous_variant	6	49754511	C	T	11.57%	389	.	.	.		.	.	.			.	0.8948	81.51%	100.00%	100%	Clonal			
MTC17	PHIP	p.Met429Val	missense_variant	6	79725451	T	C	16.67%	114	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9390	76.48%	100.00%	100%	Clonal			
MTC17	CNR1	p.Pro57Pro	synonymous_variant	6	88854823	G	C	31.70%	265	.	.	.		.	.	.			.	0.4067	94.52%	100.00%	100%	Clonal			
MTC17	FOXO3	p.Asp339Asp	synonymous_variant	6	108985053	T	C	7.59%	79	.	.	.		true	.	.		TRUE	.	0.6875	34.15%	98.48%	80%	Clonal			
MTC17	FAM184A	p.Asp182Asp	synonymous_variant	6	119345592	G	A	8.58%	268	.	.	.		.	.	.		TRUE	.	0.7971	58.33%	100.00%	91%	Clonal			
MTC17	MTFR2	p.Pro228Pro	synonymous_variant	6	136560789	G	A	12.12%	231	.	.	.		.	.	.			.	0.9008	75.90%	100.00%	100%	Clonal			
MTC17	DACT2	p.Ser417Tyr	missense_variant	6	168709187	G	T	10.21%	284	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9033	71.86%	100.00%	100%	Clonal			
MTC17	ITGB8	p.Ser25Trp	missense_variant	7	20371503	C	G	5.43%	442	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4966	49.14%	97.00%	74%	Subclonal			
MTC17	SEPT7	p.Glu27Ala	missense_variant	7	35872424	A	C	10.87%	92	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8910	57.38%	100.00%	100%	Clonal			
MTC17	URGCP	p.Ser896Ser	synonymous_variant	7	43916374	A	G	6.68%	524	.	.	.		.	.	.			.	0.8031	63.51%	100.00%	91%	Clonal			
MTC17	BAIAP2L1	p.Thr409Thr	synonymous_variant	7	97935765	G	A	8.17%	208	.	.	.		.	.	.			.	0.8589	60.90%	100.00%	100%	Clonal			
MTC17	RELN	p.Arg503Arg	synonymous_variant	7	103294587	T	G	7.96%	113	.	.	.		.	.	.	TRUE		.	0.8122	48.42%	100.00%	100%	Clonal			
MTC17	ZNF277	p.Leu159Leu	synonymous_variant	7	111958248	G	A	5.73%	192	.	.	.		.	.	.			.	0.6601	41.97%	98.35%	78%	Clonal			
MTC17	CPA2	p.Arg415Leu	missense_variant	7	129929571	G	T	3.24%	339	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0197	24.38%	76.69%	44%	Subclonal			
MTC17	AGBL3	p.Arg70His	missense_variant	7	134678328	G	A	6.12%	327	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7103	52.44%	98.69%	83%	Clonal			
MTC17	ZNF777	p.Ser707Leu	missense_variant	7	149129243	G	A	9.49%	453	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9114	79.84%	100.00%	100%	Clonal			
MTC17	TMEM176B	p.Ser258Leu	missense_variant	7	150488659	G	A	16.00%	100	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9414	72.92%	100.00%	100%	Clonal			
MTC17	KMT2C	p.Asp457Gly	missense_variant	7	151949730	T	C	4.71%	191	D	PASSENGER/OTHER	Passenger		true	true	true			Likely pathogenic	0.4690	33.19%	96.56%	64%	Subclonal			
MTC17	AGPAT5	p.His8Tyr	missense_variant	8	6566211	C	T	16.52%	224	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9547	83.77%	100.00%	100%	Clonal			
MTC17	SPIDR	p.His209His	synonymous_variant	8	48309037	C	T	4.31%	441	.	.	.		.	.	.			.	0.2186	39.98%	92.38%	63%	Subclonal			
MTC17	CRH	p.Glu54*	stop_gained	8	67089553	C	A	14.23%	260	D	.	.		.	.	.			Indeterminate	0.9585	83.91%	100.00%	100%	Clonal			
MTC17	SLCO5A1	p.Ile156Met	missense_variant	8	70744441	A	C	16.46%	571	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9759	93.49%	100.00%	100%	Clonal			
MTC17	RUNX1T1	p.Arg547Leu	missense_variant	8	92982962	C	A	4.10%	488	D	CANCER	Passenger		true	.	.			Likely pathogenic	0.0116	33.11%	77.82%	51%	Subclonal			
MTC17	ENPP2	p.Pro736Pro	synonymous_variant	8	120581476	A	C	15.59%	404	.	.	.		.	.	.			.	0.9732	90.34%	100.00%	100%	Clonal			
MTC17	COL14A1	p.Leu541Pro	missense_variant	8	121228614	T	C	8.37%	227	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8532	61.12%	100.00%	100%	Clonal			
MTC17	PLEC	p.Glu1151Lys	missense_variant	8	145003623	C	T	4.89%	307	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2604	37.04%	93.18%	61%	Subclonal			
MTC17	VPS13A	p.Leu2840Val	missense_variant	9	79983017	C	G	14.57%	151	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9539	76.58%	100.00%	100%	Clonal			
MTC17	DAPK1	p.Asp426Ala	missense_variant	9	90262266	A	C	7.80%	282	D	CANCER	Passenger		.	.	.		TRUE	Likely pathogenic	0.8361	60.81%	100.00%	98%	Clonal			
MTC17	SPATA31E1	p.Ala1376Val	missense_variant	9	90503529	C	T	6.15%	423	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5820	52.25%	97.77%	77%	Clonal			
MTC17	HMCN2	p.Ala3378Thr	missense_variant	9	133278211	G	A	6.11%	131	.	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.6571	37.15%	98.32%	77%	Clonal			
MTC17	EHMT1	p.Ala988Ala	synonymous_variant	9	140707554	T	G	14.29%	42	.	.	.		.	.	.	TRUE	TRUE	.	0.8924	48.74%	100.00%	100%	Clonal			
MTC17	IL2RA	p.Val153Ile	missense_variant	10	6063567	C	T	6.82%	381	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.4233	49.03%	96.12%	72%	Subclonal			
MTC17	CUBN	p.Val1884Met	missense_variant	10	16981045	C	T	15.56%	90	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9299	66.74%	100.00%	100%	Clonal			
MTC17	CHCHD1	p.Lys85Asn	missense_variant	10	75542843	G	C	12.90%	186	D	.	Passenger		.	.	.			Indeterminate	0.9030	72.88%	100.00%	100%	Clonal			
MTC17	SORCS1	p.Arg395Gln	missense_variant	10	108466352	C	T	22.77%	224	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9152	90.03%	100.00%	100%	Clonal			
MTC17	SMC3	p.Arg57Cys	missense_variant	10	112335132	C	T	7.06%	170	D	PASSENGER/OTHER	Passenger		.	true	true			Likely pathogenic	0.6206	41.80%	98.00%	74%	Clonal			
MTC17	CCDC172	p.Phe7Leu	missense_variant	10	118084544	T	A	6.78%	177	D	.	Passenger		.	.	.			Indeterminate	0.5728	40.35%	97.60%	72%	Clonal			
MTC17	CRACR2B	p.Val323Ile	missense_variant	11	831237	G	A	6.84%	380	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7470	57.39%	98.90%	86%	Clonal			
MTC17	KRTAP5-1	p.Val212Met	missense_variant	11	1605846	C	T	14.56%	206	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9591	81.37%	100.00%	100%	Clonal			
MTC17	OR52E8	p.Val54Val	synonymous_variant	11	5878771	C	T	8.27%	266	.	.	.		.	.	.			.	0.8587	63.05%	100.00%	100%	Clonal			
MTC17	PLEKHA7	p.Arg958Arg	synonymous_variant	11	16812620	G	T	8.82%	272	.	.	.		.	.	.			.	0.8814	66.72%	100.00%	100%	Clonal			
MTC17	PHF21A	p.Ser324Arg	missense_variant	11	45986887	G	T	16.98%	106	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9467	75.01%	100.00%	100%	Clonal			
MTC17	OR4C3	p.Leu169Phe	missense_variant	11	48346997	C	T	7.42%	310	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8116	59.40%	100.00%	93%	Clonal			
MTC17	OR8J3	p.Val208Phe	missense_variant	11	55904573	C	A	6.64%	226	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7180	48.85%	98.73%	83%	Clonal			
MTC17	SLC22A9	p.Asp112Asp	synonymous_variant	11	63137864	C	T	4.77%	419	.	.	.		.	.	.			.	0.1217	38.64%	89.05%	60%	Subclonal			
MTC17	SPTBN2	p.Gly1760Arg	missense_variant	11	66459042	C	G	11.30%	354	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8717	81.21%	100.00%	100%	Clonal			
MTC17	SSH3	p.Pro69Pro	synonymous_variant	11	67072346	G	A	4.89%	184	.	.	.		.	.	.			.	0.4171	32.03%	95.86%	61%	Subclonal			
MTC17	FOLH1B	p.Pro160Pro	synonymous_variant	11	89413808	A	G	16.85%	89	.	.	.		.	.	.			.	0.9428	71.47%	100.00%	100%	Clonal			
MTC17	USP5	p.Gly387Arg	missense_variant	12	6969343	G	A	6.53%	337	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5655	49.42%	97.61%	75%	Clonal			
MTC17	HDAC7	p.Ala292Thr	missense_variant	12	48189721	C	T	10.81%	74	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.8443	49.51%	100.00%	100%	Clonal			
MTC17	NCKAP5L	p.Gly279Glu	missense_variant	12	50190807	C	T	16.44%	292	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9689	87.62%	100.00%	100%	Clonal			
MTC17	KRT75	p.Pro114Ser	missense_variant	12	52827749	G	A	13.49%	289	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8975	82.70%	100.00%	100%	Clonal			
MTC17	APOF	p.Gly252Glu	missense_variant	12	56755235	C	T	8.08%	421	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8299	64.75%	100.00%	93%	Clonal			
MTC17	R3HDM2	p.Gln670Gln	synonymous_variant	12	57660593	T	C	6.33%	158	.	.	.		.	.	.			.	0.6109	38.78%	97.95%	73%	Clonal			
MTC17	GLI1	p.Asp871His	missense_variant	12	57865134	G	C	22.04%	304	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.7891	92.34%	100.00%	100%	Clonal			
MTC17	PLXNC1	p.Arg689Trp	missense_variant	12	94631524	C	T	18.18%	198	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9621	85.33%	100.00%	100%	Clonal			
MTC17	CCDC42B	p.Phe167Leu	missense_variant	12	113592251	C	G	10.43%	115	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8402	54.66%	100.00%	100%	Clonal			
MTC17	DDX51	p.Gly594Arg	missense_variant	12	132624465	C	T	6.60%	303	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.4242	44.94%	96.06%	70%	Subclonal			
MTC17	GOLGA3	p.Arg1207Cys	missense_variant	12	133354355	G	A	24.89%	237	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.7467	91.61%	100.00%	100%	Clonal			
MTC17	SAP18	p.Pro71Arg	missense_variant	13	21715107	C	G	38.51%	444	D	.	Passenger		.	.	.			Indeterminate	0.2376	97.41%	100.00%	100%	Clonal			
MTC17	NBEA	p.Ser621Phe	missense_variant	13	35684975	C	T	6.11%	229	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.7612	50.19%	98.99%	89%	Clonal			
MTC17	PROSER1	p.Ser405Ser	synonymous_variant	13	39588174	G	A	5.13%	234	.	.	.		.	.	.			.	0.6172	41.71%	98.03%	75%	Clonal			
MTC17	PCDH17	p.Tyr1018His	missense_variant	13	58299000	T	C	4.44%	450	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2623	41.68%	93.48%	65%	Subclonal			
MTC17	OR4M1	p.Arg139His	missense_variant	14	20248897	G	A	24.47%	331	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9208	93.33%	100.00%	100%	Clonal			
MTC17	TEP1	p.Arg605Cys	missense_variant	14	20863724	G	A	5.81%	172	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.6078	38.67%	97.94%	73%	Clonal			
MTC17	MYH6	p.Leu774Leu	synonymous_variant	14	23865602	G	A	6.49%	231	.	.	.		.	.	.		TRUE	.	0.6987	48.01%	98.61%	82%	Clonal			
MTC17	RABGGTA	p.Arg476Gln	missense_variant	14	24736022	C	T	16.56%	163	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9575	81.33%	100.00%	100%	Clonal			
MTC17	NIN	p.Arg2095*	stop_gained	14	51190300	G	A	23.20%	181	D	.	.		true	.	.		TRUE	Likely pathogenic	0.7936	88.69%	100.00%	100%	Clonal			
MTC17	CCDC88C	p.Gly1780Gly	synonymous_variant	14	91739716	G	T	5.65%	248	.	.	.		.	.	.		TRUE	.	0.6350	44.62%	98.17%	77%	Clonal			
MTC17	TCL1A	p.Glu29Glu	synonymous_variant	14	96180317	C	T	6.67%	630	.	.	.		true	.	.		TRUE	.	0.8044	65.52%	100.00%	90%	Clonal			
MTC17	CA12	p.Gly137Arg	missense_variant	15	63637696	C	T	6.67%	210	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5264	41.53%	97.16%	70%	Clonal			
MTC17	TBC1D2B	p.Arg920Gln	missense_variant	15	78290635	C	T	6.16%	146	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.4954	33.83%	96.79%	65%	Subclonal			
MTC17	ABHD17C	p.Thr217Thr	synonymous_variant	15	81041914	G	C	14.62%	253	.	.	.		.	.	.			.	0.8963	81.97%	100.00%	100%	Clonal			
MTC17	VIMP	p.Gly171Gly	synonymous_variant	15	101813033	G	A	6.43%	171	.	.	.		.	.	.			.	0.3668	34.20%	94.98%	61%	Subclonal			
MTC17	NPRL3	p.Arg536His	missense_variant	16	136804	C	T	4.76%	147	D	.	Passenger		.	.	.			Indeterminate	0.5846	32.49%	97.75%	69%	Clonal			

MTC17	*FAM173A*	p.Pro100Leu	missense_variant	16	771832	C	T	17.65%	425	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7421	93.05%	100.00%	100%	Clonal			
MTC17	*ZNF597*	p.Leu72Arg	missense_variant	16	3487484	A	C	6.25%	224	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7737	50.99%	100.00%	91%	Clonal			
MTC17	*BRD7*	p.Ser462Arg	missense_variant	16	50357557	T	G	18.92%	74	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8692	72.49%	100.00%	100%	Clonal			
MTC17	*PSKH1*	p.Arg407Trp	missense_variant	16	67961489	C	T	3.64%	275	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0456	24.66%	81.07%	46%	Subclonal			
MTC17	*CHST5*	p.Arg287Arg	synonymous_variant	16	75563422	G	A	12.70%	378	.	.	.		.	.	.	.	.			.	0.8951	85.48%	100.00%	100%	Clonal			
MTC17	*ADAMTS18*	p.Gly630Cys	missense_variant	16	77359907	C	A	5.19%	154	D	PASSENGER/OTHER	Driver		.	.	.	.	.			Likely pathogenic	0.5136	32.49%	97.05%	65%	Clonal			
MTC17	*ADAMTS18*	p.Cys395Trp	missense_variant	16	77396033	A	C	5.32%	94	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.5798	27.38%	97.67%	67%	Clonal			
MTC17	*SPG7*	p.Ala35Ala	synonymous_variant	16	89574930	C	A	10.26%	78	.	.	.		.	.	.	.	.			.	0.8502	50.05%	100.00%	100%	Clonal			
MTC17	*HIC1*	p.Gly224Ser	missense_variant	17	1960597	G	A	33.33%	213	D	PASSENGER/OTHER	Passenger		.	.	.	.	.	TRUE	TRUE	Indeterminate	0.5153	94.03%	100.00%	100%	Clonal			
MTC17	*CLUH*	p.Arg1163Gln	missense_variant	17	2595347	C	T	4.83%	207	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.3719	32.72%	95.19%	61%	Subclonal			
MTC17	*OR3A2*	p.Val285Gly	missense_variant	17	3181376	A	C	7.14%	210	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.7704	51.62%	100.00%	90%	Clonal			
MTC17	*ATP2A3*	p.Leu180Leu	synonymous_variant	17	3853993	G	A	4.40%	182	.	.	.		.	.	.	.	.		TRUE	.	0.3045	27.83%	93.81%	55%	Subclonal			
MTC17	*POLR2A*	p.Thr511Thr	synonymous_variant	17	7402672	G	A	7.16%	349	.	.	.		.	.	.	.	.		TRUE	.	0.7039	55.21%	98.63%	83%	Clonal			
MTC17	*MYH8*	p.Arg1679Cys	missense_variant	17	10297697	G	A	6.61%	121	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.6561	37.09%	98.30%	76%	Clonal			
MTC17	*FZD2*	p.Ala473Thr	missense_variant	17	42636473	G	A	16.35%	532	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.9746	92.54%	100.00%	100%	Clonal	TRUE	CCGCATCCGCACCATCAT	CACGGGATGGCCAGGCTCTT
MTC17	*EFTUD2*	p.Leu898Leu	synonymous_variant	17	42929800	G	A	7.82%	179	.	.	.		.	.	.	.	.		TRUE	.	0.7735	50.91%	100.00%	90%	Clonal			
MTC17	*MYOM1*	p.Pro432Pro	synonymous_variant	18	3168858	A	G	12.27%	163	.	.	.		.	.	.	.	.		TRUE	.	0.9218	72.14%	100.00%	100%	Clonal			
MTC17	*LAMA1*	p.Ile2434Ile	synonymous_variant	18	6964696	A	T	5.21%	307	.	.	.		.	.	.	.	.		TRUE	.	0.3612	40.08%	95.17%	65%	Subclonal			
MTC17	*PTPRM*	p.Ala672Ser	missense_variant	18	8113641	G	T	8.25%	291	N	CANCER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.8630	64.29%	100.00%	100%	Clonal			
MTC17	*ASXL3*	p.Pro1429Thr	missense_variant	18	31324097	C	A	5.69%	404	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.4402	47.39%	96.37%	71%	Subclonal			
MTC17	*TBXA2R*	p.Ala160Val	missense_variant	19	3600154	G	A	10.06%	318	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8994	77.15%	100.00%	100%	Clonal			
MTC17	*MRI1*	p.Gly183Ser	missense_variant	19	13876943	G	A	6.98%	258	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8073	56.34%	100.00%	95%	Clonal			
MTC17	*DCAF15*	p.Ser307Phe	missense_variant	19	14069992	C	T	5.25%	457	N	.	Passenger		.	.	.	.	.			Likely passenger	0.4186	47.59%	96.12%	71%	Subclonal			
MTC17	*TECR*	p.Leu104Leu	synonymous_variant	19	14674838	C	T	6.45%	465	.	.	.		.	.	.	.	.			.	0.7657	59.96%	100.00%	87%	Clonal			
MTC17	*TECR*	p.Phe105Phe	synonymous_variant	19	14674841	C	T	6.20%	468	.	.	.		.	.	.	.	.			.	0.7163	57.56%	98.73%	84%	Clonal			
MTC17	*TECR*	p.Ile139Ile	synonymous_variant	19	14675027	C	T	7.11%	436	.	.	.		.	.	.	.	.			.	0.8448	64.95%	100.00%	96%	Clonal			
MTC17	*CYP4F11*	p.Ala472Ala	synonymous_variant	19	16024701	C	T	7.19%	153	D	PASSENGER/OTHER	.		.	.	.	.	.			.	0.7922	49.29%	100.00%	97%	Clonal			
MTC17	*FAM129C*	p.Ala167Val	missense_variant	19	17644490	C	T	6.28%	191	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7298	46.36%	98.81%	85%	Clonal			
MTC17	*ZNF676*	p.Ser50Pro	missense_variant	19	22364371	A	G	6.76%	74	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.7033	32.42%	98.61%	85%	Clonal			
MTC17	*ZNF260*	p.Asn41Ile	missense_variant	19	37006019	T	A	6.36%	173	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.6837	42.94%	98.51%	80%	Clonal			
MTC17	*SERTAD3*	p.Asp144Asp	synonymous_variant	19	40947556	G	A	12.96%	216	.	.	.		.	.	.	.	.		TRUE	.	0.9350	78.67%	100.00%	100%	Clonal			
MTC17	*LTBP4*	p.Arg1622Gln	missense_variant	19	41135448	G	A	8.33%	132	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.8167	51.42%	100.00%	100%	Clonal			
MTC17	*IRF2BP1*	p.Pro187Ser	missense_variant	19	46388474	G	A	16.03%	443	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.9745	91.48%	100.00%	100%	Clonal			
MTC17	*KIZ*	p.Arg259His	missense_variant	20	21142882	G	A	7.83%	345	.	.	Passenger		.	.	.	.	.			Indeterminate	0.8488	63.94%	100.00%	98%	Clonal			
MTC17	*LPIN3*	p.Ser262Ser	synonymous_variant	20	39978721	C	T	7.58%	343	.	.	.		.	.	.	.	.			.	0.8642	65.14%	100.00%	100%	Clonal			
MTC17	*PTPRT*	p.Ala68Ala	synonymous_variant	20	41514457	T	C	12.35%	81	.	.	.		.	.	.	.	.			.	0.9151	59.56%	100.00%	100%	Clonal			
MTC17	*UCKL1*	p.Pro433Pro	synonymous_variant	20	62571950	G	A	22.38%	411	.	.	.		.	.	.	.	.			.	0.5878	94.67%	100.00%	100%	Clonal			
MTC17	*KRTAP13-1*	p.Cys76Phe	missense_variant	21	31768631	G	T	6.13%	375	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.4199	47.05%	96.09%	71%	Subclonal			
MTC17	*DSCAM*	p.Val1278Val	synonymous_variant	21	41465664	G	C	15.15%	66	.	.	.		.	.	.	.	.		TRUE	.	0.9231	60.46%	100.00%	100%	Clonal			
MTC17	*TRPM2*	p.Phe864Ser	missense_variant	21	45825077	T	C	3.81%	341	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0081	25.54%	73.51%	44%	Subclonal			
MTC17	*TTC28*	p.Trp1249*	stop_gained	22	28492198	C	T	11.40%	193	A	.	.		.	.	.	.	.			Indeterminate	0.9223	73.77%	100.00%	100%	Clonal			
MTC17	*RAC2*	p.Pro69Pro	synonymous_variant	22	37628859	C	T	25.36%	138	.	.	.		.	.	.	.	.			.	0.5254	87.81%	100.00%	100%	Clonal			
MTC17	*PLXNB2*	c.5261+1G>A	splice_donor_variant	22	50715270	C	T	4.11%	146	D	.	.		.	.	.	.	.			Indeterminate	0.3946	25.30%	95.46%	56%	Subclonal			
MTC17	*USP9X*	p.Gln51*	stop_gained	X	40988307	C	T	18.52%	216	A	.	.		.	true	.	true	.			Likely pathogenic	0.9614	86.72%	100.00%	100%	Clonal			
MTC17	*GATA1*	p.Arg253Trp	missense_variant	X	48651591	C	T	16.13%	310	D	CANCER	Passenger		true	.	.	.	.			Likely pathogenic	0.9678	87.87%	100.00%	100%	Clonal			
MTC17	*FAM104B*	p.Gly13Asp	missense_variant	X	55185644	C	T	5.32%	94	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.5202	25.62%	97.06%	61%	Clonal			
MTC17	*NLGN3*	p.Arg847Trp	missense_variant	X	70389939	C	T	17.24%	261	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9690	87.38%	100.00%	100%	Clonal			
MTC17	*DDX26B*	p.Asp398Gly	missense_variant	X	134703262	A	G	12.40%	121	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8862	63.46%	100.00%	100%	Clonal			
MTC17	*GPR112*	p.Thr1605Ile	missense_variant	X	135430679	C	T	8.04%	199	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7383	50.58%	98.82%	85%	Clonal			
MTC17	*UBE2NL*	p.Ser30Asn	missense_variant	X	142967291	G	A	4.59%	196	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.1108	25.42%	86.60%	48%	Subclonal			
MTC18	*NTNG1*	p.Gly323Ala	missense_variant	1	107937856	G	C	25.38%	130	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8730	75.06%	100.00%	100%	Clonal			
MTC18	*KIF26B*	p.Thr1093Thr	synonymous_variant	1	245849564	C	A	10.07%	298	.	.	.		.	.	.	.	.		TRUE	.	0.0025	39.42%	77.72%	56%	Subclonal			
MTC18	*REV1*	p.Pro1123Ser	missense_variant	2	100019369	G	A	19.81%	106	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7051	58.38%	100.00%	91%	Clonal			
MTC18	*CCDC148*	p.Asp436Asn	missense_variant	2	159077171	C	T	37.78%	45	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8491	69.63%	100.00%	100%	Clonal			
MTC18	*TOPBP1*	p.Pro1222Ser	missense_variant	3	133336099	G	A	29.01%	131	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.9613	85.85%	100.00%	100%	Clonal			
MTC18	*STAG1*	p.Trp318Leu	missense_variant	3	136196204	C	A	25.93%	27	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8612	52.92%	100.00%	100%	Clonal			
MTC18	*PIK3CA*	p.His1047Arg	missense_variant	3	178952085	A	G	43.04%	79	D	CANCER	Driver		true	true	true	true	true			Likely pathogenic	0.6098	87.47%	100.00%	100%	Clonal	TRUE	ATCTCTTCATAAATCTTTTCTCAAT	ACAGTGCAGTGTGGAATCCA
MTC18	*ANKRD17*	p.Gly157Asp	missense_variant	4	74043174	C	T	43.48%	23	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.9286	64.66%	100.00%	100%	Clonal			
MTC18	*FAT4*	p.Thr3531Ile	missense_variant	4	126372757	C	T	4.76%	126	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0002	12.04%	55.33%	27%	Subclonal			
MTC18	*LRBA*	p.Cys343Arg	missense_variant	4	151835481	A	G	33.33%	24	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8970	57.80%	100.00%	100%	Clonal			
MTC18	*TNS3*	p.His77His	synonymous_variant	7	47474973	G	A	14.02%	107	.	.	.		.	.	.	.	.			.	0.2056	39.29%	94.06%	64%	Subclonal			
MTC18	*ZNF713*	p.Gln292*	stop_gained	7	56007280	C	T	15.12%	86	D	.	.		.	.	.	.	.			Indeterminate	0.3632	40.73%	96.76%	69%	Subclonal			
MTC18	*KCNU1*	p.Leu155Leu	synonymous_variant	8	36662800	G	A	5.14%	311	.	.	.		.	.	.	.	.			.	0.7834	60.87%	100.00%	100%	Clonal			
MTC18	*LRP12*	p.Glu562Lys	missense_variant	8	105507334	C	T	70.21%	94	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.2566	94.17%	100.00%	100%	Clonal			
MTC18	*EPPK1*	p.Leu1757Val	missense_variant	8	144942153	G	C	3.36%	238	N	PASSENGER/OTHER	Passenger		.	true	.	true	.			Likely passenger	0.0000	10.93%	42.22%	22%	Subclonal			
MTC18	*CUBN*	p.Ala3056Thr	missense_variant	10	16916443	C	T	54.00%	50	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.3340	86.15%	100.00%	100%	Clonal			
MTC18	*MUC6*	p.Pro1634Thr	missense_variant	11	1017901	G	T	6.98%	86	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0022	14.59%	65.49%	32%	Subclonal			
MTC18	*PIK3C2A*	p.Gln372Lys	missense_variant	11	17177128	G	T	10.71%	56	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.1391	22.68%	91.01%	49%	Subclonal			
MTC18	*USP5*	p.Val143Phe	missense_variant	12	6965303	G	T	49.61%	127	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9328	92.41%	100.00%	100%	Clonal			
MTC18	*CAPRIN2*	p.Arg877Trp	missense_variant	12	30867914	G	A	13.95%	43	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.3908	29.13%	97.00%	64%	Subclonal			
MTC18	*BTBD11*	p.Leu928Leu	synonymous_variant	12	108034134	G	T	41.82%	55	.	.	.		.	.	.	.	.			.	0.9569	80.06%	100.00%	100%	Clonal			
MTC18	*CKAP2*	p.Leu297Ile	missense_variant	13	53035847	T	A	74.42%	129	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0826	95.83%	100.00%	100%	Clonal			
MTC18	*CASC5*	p.Ser530Leu	missense_variant	15	40913973	C	T	36.11%	36	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.8266	63.34%	100.00%	100%	Clonal			
MTC18	*CHD9*	p.Ile2452Val	missense_variant	16	53348774	A	G	32.14%	28	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.7661	52.78%	100.00%	100%	Clonal			
MTC18	*TP53*	c.672+1G>T	splice_donor_variant	17	7578176	C	A	100.00%	6	D	.	Passenger		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.5169	58.83%	100.00%	100%	Clonal	TRUE	GACAACCACCCTTAACCCCTC	CTGGTTGCCCAGGGTCCC
MTC18	*KRT28*	p.Arg197Gln	missense_variant	17	38954587	C	T	40.86%	93	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9368	87.68%	100.00%	100%	Clonal			
MTC18	*KRTAP4-1*	p.Cys107Cys	synonymous_variant	17	39340729	G	A	5.49%	91	.	.	.		.	.	.	.	.			.	0.0047	13.07%	67.64%	31%	Subclonal			
MTC18	*DNAH17*	p.Val2097Val	synonymous_variant	17	76490235	C	T	11.88%	101	.	.	.		.	.	.	.	.			.	0.3211	38.04%	96.21%	66%	Subclonal			
MTC18	*ZIK1*	p.Arg286Gln	missense_variant	19	58102036	G	A	10.62%	113	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0180	27.97%	80.11%	49%	Subclonal			
MTC18	*BMP2*	p.Arg289Arg	synonymous_variant	20	6759412	G	A	26.14%	153	.	.	.		.	.	.	.	.			.	0.8885	78.65%	100.00%	100%	Clonal			
MTC18	*JAG1*	p.Gly47Arg	missense_variant	20	10653597	C	G	45.16%	279	D	PASSENGER/OTHER	Passenger		.	.	.	.	.	TRUE		Indeterminate	0.9782	95.69%	100.00%	100%	Clonal			
MTC18	*PBDC1*	p.Leu87Trp	missense_variant	X	75395411	T	G	14.91%	114	D	.	Passenger		.	.	.	.	.			Indeterminate	0.6047	51.32%	98.71%	83%	Clonal			
MTC18	*TMEM35*	p.Arg133Cys	missense_variant	X	100349838	C	T	19.25%	239	D	.	Passenger		.	.	.	.	.			Indeterminate	0.8702	76.01%	100.00%	100%	Clonal			
MTC18	*ALG13*	p.Pro841Pro	synonymous_variant	X	110978344	C	G	14.91%	114	.	.	.		.	.	.	.	.			.	0.6047	51.32%	98.71%	83%	Clonal			
MTC18	*LRCH2*	p.Val746Phe	missense_variant	X	114347841	C	A	6.45%	155	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0005	19.42%	63.55%	36%	Subclonal			
MTC18	*MAGEA5*	p.Thr32Ala	missense_variant	X	151283919	T	C	20.26%	227	.	.	Passenger		.	.	.	.	.			Indeterminate	0.8858	78.02%	100.00%	100%	Clonal			
MTC19	*INADL*	p.Thr504fs	frameshift_variant	1	62267402	AC	A	30.32%	221	A	.	.		.	.	.	.	.			Indeterminate	0.4817	70.74%	98.85%	88%	Subclonal			
MTC19	*PSRC1*	p.Arg200Gln	missense_variant	1	109823794	C	T	5.28%	720	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	18.46%	34.67%	26%	Subclonal			
MTC19	*TRIM33*	p.Gln517His	missense_variant	1	114968215	C	G	5.16%	213	D	PASSENGER/OTHER	Passenger		true	.	.	.	.			Likely pathogenic	0.0000	8.03%	25.71%	15%	Subclonal			
MTC19	*UBAP2L*	p.Asn318Lys	missense_variant	1	154218791	T	A	5.42%	295	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	12.68%	33.22%	21%	Subclonal			
MTC19	*SPTA1*	p.Arg137Cys	missense_variant	1	158651439	G	A	56.76%	222	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.9061	96.11%	100.00%	100%	Clonal			
MTC19	*PAPPA2*	p.Asn539Lys	missense_variant	1	176564357	C	A	25.91%	386	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8164	82.08%	100.00%	100%	Clonal			
MTC19	*PUM2*	p.Gln913*	stop_gained	2	20454988	G	A	44.00%	175	A	.	.		.	.	.	.	.			Indeterminate	0.7149	89.15%	100.00%	100%	Clonal			
MTC19	*TTN*	p.Tyr32078Tyr	synonymous_variant	2	179408637	G	A	7.26%	441	.	.	.		.	.	.	.	.			.	0.0000	14.55%	28.78%	21%	Subclonal			
MTC19	*TTN*	p.Val10895Leu	missense_variant	2	179549096	C	G	40.23%	256	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8790	89.23%	100.00%	100%	Clonal			
MTC19	*SPATA3*	p.Thr27Asn	missense_variant	2	231861028	C	A	30.90%	424	N	.	Passenger		.	.	.	.	.			Likely passenger	0.4654	76.90%	98.80%	90%	Subclonal			
MTC19	*ITGA9*	p.Arg601Cys	missense_variant	3	37670789	C	T	13.62%	235	D	PASSENGER/OTHER	Driver		.	.	.	.	.			Likely pathogenic	0.0000	28.06%	53.57%	40%	Subclonal			
MTC19	*MYRIP*	p.Glu34del	inframe_deletion	3	39942398	AAAG	A	26.67%	180	D	.	.	Deleterious	.	.	.	.	.			Indeterminate	0.1317	59.74%	95.27%	77%	Subclonal			
MTC19	*SLC9A9*	p.Leu150Val	missense_variant	3	143515676	G	C	31.52%	165	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6088	70.97%	100.00%	92%	Clonal			
MTC19	*VWA5B2*	p.Arg745His	missense_variant	3	183957213	G	A	39.72%	282	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8881	89.47%	100.00%	100%	Clonal			
MTC19	*GABRP*	p.Lys50Gln	missense_variant	5	170216227	A	C	6.03%	365	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	11.17%	25.57%	18%	Subclonal			
MTC19	*CAGE1*	p.Val418Ala	missense_variant	6	7373799	A	G	5.10%	431	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	9.34%	21.65%	15%	Subclonal			
MTC19	*TRIM10*	p.Phe64Val	missense_variant	6	30128446	A	C	10.13%	464	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	21.91%	37.90%	29%	Subclonal			
MTC19	*TNXB*	p.Gly1157Gly	synonymous_variant	6	32050078	C	T	38.40%	125	.	.	.		.	.	.	.	.	TRUE		.	0.8313	80.16%	100.00%	100%	Clonal			
MTC19	*GIMAP6*	p.Gly127Gly	synonymous_variant	7	150325515	T	G	34.11%	513	.	.	.		.	.	.	.	.			.	0.8351	85.79%	100.00%	99%	Clonal			
MTC19	*KMT2C*	p.Met3827Ile	missense_variant	7	151856137	C	A	7.11%	197	D	PASSENGER/OTHER	Passenger		true	true	true	true	true			Likely pathogenic	0.0000	12.02%	33.15%	21%	Subclonal			
MTC19	*MYOM2*	p.Tyr1301His	missense_variant	8	2088746	T	C	35.71%	182	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8155	80.28%	100.00%	100%	Clonal			
MTC19	*RIMS2*	p.Ser968Ser	synonymous_variant	8	104987711	A	G	43.01%	193	.	.	.		.	.	.	.	.			.	0.7776	89.25%	100.00%	100%	Clonal			
MTC19	*OGDHL*	p.Val406Met	missense_variant	10	50954876	C	T	20.16%	903	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8056	92.15%	100.00%	100%	Clonal			
MTC19	*CTNNA3*	p.Asn477Thr	missense_variant	10	68280476	T	G	16.50%	800	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7703	81.38%	100.00%	97%	Clonal			
MTC19	*MUC6*	p.Leu2052Leu	synonymous_variant	11	1016645	G	C	6.25%	96	.	.	.		.	.	.	.	.		TRUE	.	0.0000	5.12%	24.25%	12%	Subclonal			
MTC19	*KRTAP5-2*	p.Ser20Gly	missense_variant	11	1619423	T	C	15.79%	76	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	17.23%	48.39%	30%	Subclonal			
MTC19	*LRRC55*	p.Pro82Pro	synonymous_variant	11	56949613	C	A	33.22%	569	.	.	.		.	.	.	.	.			.	0.0366	94.43%	100.00%	100%	Clonal			
MTC19	*DAK*	p.Val200Ile	missense_variant	11	61109327	G	A	3.20%	406	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	5.03%	15.21%	9%	Subclonal			
MTC19	*DIXDC1*	p.Pro401Arg	missense_variant	11	111887496	C	G	34.03%	191	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.0000	52.25%	77.70%	65%	Subclonal	TRUE	AGTCTCTTTCTGATTGTAGAGTTGCC	CATGTGGGCAGTAACTAATGAGG
MTC19	*VPS11*	p.Cys824Cys	synonymous_variant	11	118951838	T	C	3.93%	280	.	.	.		.	.	.	.	.		TRUE	.	0.0000	3.67%	12.69%	7%	Subclonal			
MTC19	*PARP11*	p.His269Gln	missense_variant	12	3921499	A	T	5.87%	341	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	10.61%	25.36%	17%	Subclonal			
MTC19	*PZP*	p.Gly1271Arg	missense_variant	12	9305903	C	T	38.21%	123	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8272	79.71%	100.00%	100%	Clonal			
MTC19	*SOX5*	p.Asp172His	missense_variant	12	23908626	C	G	3.70%	216	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.0000	5.07%	20.25%	11%	Subclonal			
MTC19	*KMT2D*	p.Glu748*	stop_gained	12	49445224	C	A	19.67%	305	A	.	.		true	true	true	true	true		TRUE	Likely pathogenic	0.0000	29.22%	46.23%	37%	Subclonal			
MTC19	*TMTC2*	p.Gly111Val	missense_variant	12	83251037	G	T	68.13%	364	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	97.05%	100.00%	100%	Clonal			
MTC19	*FAM124A*	p.His375Gln	missense_variant	13	51854768	C	G	8.50%	459	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	11.40%	21.28%	16%	Subclonal			
MTC19	*PRKD1*	p.Gln689Lys	missense_variant	14	30068864	G	T	43.46%	214	D	CANCER	Driver		.	.	.	.	.			Likely pathogenic	0.6833	90.38%	100.00%	100%	Clonal			
MTC19	*CCDC78*	p.Arg393Gln	missense_variant	16	773117	C	T	4.51%	244	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	6.94%	22.46%	13%	Subclonal			
MTC19	*GLYR1*	c.1283-1G>A	splice_acceptor_variant	16	4861804	C	T	4.55%	264	D	.	.		.	.	.	.	.			Indeterminate	0.0000	7.15%	22.10%	13%	Subclonal			
MTC19	*VAT1L*	p.Arg370Pro	missense_variant	16	78005778	G	C	3.08%	357	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	2.78%	9.87%	6%	Subclonal			
MTC19	*EIF4A1*	p.Arg368His	missense_variant	17	7481686	G	A	11.96%	92	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	12.52%	37.96%	23%	Subclonal			
MTC19	*TP53*	p.Trp146*	stop_gained	17	7578493	C	T	55.30%	132	A	.	.		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.9022	84.55%	100.00%	100%	Clonal	TRUE	CTGGGCAACCAGCCCTGT	TGTTCACTTGTGCCCTGACTT
MTC19	*MGAT5B*	p.Leu30Pro	missense_variant	17	74868920	T	C	4.00%	375	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	6.56%	18.41%	12%	Subclonal			
MTC19	*ADNP2*	p.Ter1132Lysext*?	stop_lost	18	77896690	T	A	13.33%	45	N	.	.		.	.	.	.	.		TRUE	Indeterminate	0.0000	11.57%	49.56%	25%	Subclonal			
MTC19	*LILRB1*	p.Tyr298Tyr	synonymous_variant	19	55144147	C	T	7.14%	84	.	.	.		.	.	.	.	.			.	0.0000	9.29%	42.33%	21%	Subclonal			
MTC19	*RFPL4AL1*	p.Thr205Ile	missense_variant	19	56284295	C	T	23.08%	52	.	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.1814	39.23%	95.78%	67%	Subclonal			
MTC19	*STAU1*	p.Arg196Gln	missense_variant	20	47752392	C	T	25.95%	185	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.0792	58.09%	93.61%	75%	Subclonal			
MTC19	*UFD1L*	p.Ser3Tyr	missense_variant	22	19463121	G	T	8.72%	218	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	10.26%	24.72%	17%	Subclonal			
MTC19	*FHL1*	p.Asp309Glu	missense_variant	X	135292068	C	G	8.46%	130	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	8.66%	27.20%	16%	Subclonal			
MTC20	*TTC34*	p.Leu517Pro	missense_variant	1	2572958	A	G	22.64%	159	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8473	74.83%	100.00%	100%	Clonal			
MTC20	*KLHL21*	p.Pro15Ser	missense_variant	1	6662835	G	A	24.39%	246	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8891	83.65%	100.00%	100%	Clonal			
MTC20	*ARHGEF10L*	p.Val366Met	missense_variant	1	17949566	G	A	20.00%	240	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8019	73.14%	100.00%	99%	Clonal			
MTC20	*FAM110D*	p.Ala181Ala	synonymous_variant	1	26488325	A	G	3.85%	182	.	.	.		.	.	.	.	.			.	0.0000	8.97%	37.84%	19%	Subclonal			
MTC20	*ARID1A*	p.Gly1269Arg	missense_variant	1	27099926	G	C	5.57%	305	D	PASSENGER/OTHER	Passenger		true	true	true	true	true			Likely pathogenic	0.0000	17.00%	42.92%	28%	Subclonal			
MTC20	*ZC3H12A*	p.Glu129*	stop_gained	1	37941482	G	T	7.73%	427	A	.	.		.	.	.	.	.			Indeterminate	0.0004	38.24%	73.73%	54%	Subclonal			
MTC20	*TTC39A*	p.Arg310Pro	missense_variant	1	51768188	C	G	10.88%	524	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7866	73.25%	100.00%	98%	Clonal			
MTC20	*BRINP3*	p.Leu303Val	missense_variant	1	190195266	G	C	40.93%	193	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7177	93.79%	100.00%	100%	Clonal			
MTC20	*LHX9*	p.Ala205Ala	synonymous_variant	1	197890671	G	A	2.86%	490	.	.	.		.	.	.	.	.			.	0.0000	13.18%	37.25%	23%	Subclonal			
MTC20	*NFASC*	p.Ala614fs	frameshift_variant	1	204946815	AG	A	46.52%	632	A	.	.		.	.	.	.	.			Indeterminate	0.1015	98.23%	100.00%	100%	Clonal			
MTC20	*KCNK2*	p.Leu117His	missense_variant	1	215260014	T	A	17.11%	374	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8901	83.23%	100.00%	100%	Clonal			
MTC20	*PCNXL2*	p.Pro758Leu	missense_variant	1	233372676	G	A	4.35%	299	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0003	22.56%	64.90%	39%	Subclonal			
MTC20	*ADSS*	p.Gly291*	stop_gained	1	244582136	C	A	13.33%	315	A	.	.		.	.	.	.	.			Indeterminate	0.8623	77.88%	100.00%	100%	Clonal			
MTC20	*FKBP1B*	p.Gly70Arg	missense_variant	2	24285943	G	A	8.67%	392	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.0073	43.23%	82.17%	60%	Subclonal			
MTC20	*THSD7B*	p.Arg599Lys	missense_variant	2	137988779	G	A	34.72%	288	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9666	94.36%	100.00%	100%	Clonal			
MTC20	*SLC38A11*	p.His336Tyr	missense_variant	2	165755162	G	A	26.93%	349	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9603	93.36%	100.00%	100%	Clonal			
MTC20	*B3GALT1*	p.Ser237Leu	missense_variant	2	168726259	C	T	15.56%	360	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8625	78.29%	100.00%	100%	Clonal			
MTC20	*IL17RE*	p.Arg112*	stop_gained	3	9945781	C	T	24.83%	596	A	.	.		.	.	.	.	.			Indeterminate	0.9188	96.10%	100.00%	100%	Clonal			
MTC20	*ACKR2*	p.Ala243Thr	missense_variant	3	42906721	G	A	5.21%	307	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	12.34%	32.43%	21%	Subclonal			
MTC20	*FBXO40*	p.Ser240Ser	synonymous_variant	3	121340996	C	T	29.41%	595	.	.	.		.	.	.	.	.			.	0.6763	96.82%	100.00%	100%	Clonal			
MTC20	*CLDN11*	p.Ala145Thr	missense_variant	3	170150353	G	A	25.00%	332	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9095	92.07%	100.00%	100%	Clonal			
MTC20	*PCDH7*	p.Ala265Val	missense_variant	4	30723838	C	T	39.49%	157	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.9643	91.28%	100.00%	100%	Clonal			
MTC20	*ARAP2*	p.Ser169Cys	missense_variant	4	36230603	G	C	15.44%	259	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.2673	56.77%	96.34%	77%	Subclonal			
MTC20	*DTHD1*	p.Glu758Glu	synonymous_variant	4	36345374	A	G	13.14%	449	.	.	.		.	.	.	.	.		TRUE	.	0.0017	50.78%	81.83%	65%	Subclonal			
MTC20	*WDFY3*	p.Phe489Tyr	missense_variant	4	85742362	A	T	5.66%	265	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	16.74%	44.83%	28%	Subclonal			
MTC20	*SYNPO2*	p.Asp452Asp	synonymous_variant	4	119951286	C	T	7.71%	506	.	.	.		.	.	.	.	.		TRUE	.	0.0000	33.45%	61.34%	46%	Subclonal			
MTC20	*ZNF608*	p.Leu124Phe	missense_variant	5	124080311	C	G	11.78%	416	D	CANCER	Passenger		.	.	.	.	.			Likely pathogenic	0.0001	44.32%	75.14%	58%	Subclonal			
MTC20	*LRRTM2*	p.Leu297_Asn298del	disruptive_inframe_deletion	5	138209354	GAGTTTA	G	5.03%	537	D	.	.	Deleterious	.	.	.	.	.			Indeterminate	0.0000	16.79%	35.36%	25%	Subclonal			
MTC20	*PCDHB2*	p.Asp127Glu	missense_variant	5	140474755	C	A	8.48%	342	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	29.17%	58.67%	42%	Subclonal			
MTC20	*PCDHB15*	p.His735Tyr	missense_variant	5	140627349	C	T	6.09%	115	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0003	14.49%	59.27%	30%	Subclonal			
MTC20	*ATAT1*	p.His158His	synonymous_variant	6	30596180	C	T	19.86%	277	.	.	.		.	.	.	.	.			.	0.8844	81.59%	100.00%	100%	Clonal			
MTC20	*MICB*	p.Thr238Ser	missense_variant	6	31474898	C	G	13.04%	46	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.4994	33.89%	98.37%	78%	Subclonal			
MTC20	*MICB*	p.Asn249Asp	missense_variant	6	31474930	A	G	8.11%	74	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.1164	22.26%	90.96%	48%	Subclonal			
MTC20	*BTBD9*	p.Ala590Val	missense_variant	6	38142831	G	A	22.19%	329	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7643	87.51%	100.00%	100%	Clonal			
MTC20	*GABRR2*	p.Cys365Tyr	missense_variant	6	89967693	C	T	7.54%	504	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	38.14%	70.43%	53%	Subclonal			
MTC20	*MDN1*	p.Asp4281Asn	missense_variant	6	90384229	C	T	25.84%	89	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9300	78.06%	100.00%	100%	Clonal			
MTC20	*TCF21*	p.Arg91Cys	missense_variant	6	134210806	C	T	20.00%	595	D	CANCER	Driver		.	.	.	.	.			Likely pathogenic	0.0979	92.11%	100.00%	100%	Clonal			
MTC20	*RAPGEF5*	p.Ile454Thr	missense_variant	7	22190089	A	G	9.92%	262	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.1697	47.29%	94.28%	69%	Subclonal			
MTC20	*PPP1R9A*	p.Glu630Lys	missense_variant	7	94827794	G	A	50.45%	111	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.6872	91.93%	100.00%	100%	Clonal			
MTC20	*SSBP1*	p.Arg28*	stop_gained	7	141442026	A	T	4.66%	279	A	.	.		.	.	.	.	.			Indeterminate	0.0000	18.71%	53.88%	32%	Subclonal			
MTC20	*CSMD1*	p.Val3194Phe	missense_variant	8	2820036	C	A	27.86%	262	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.9238	83.16%	100.00%	100%	Clonal			
MTC20	*ZFHX4*	p.Gly2460Arg	missense_variant	8	77766535	G	A	4.00%	575	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	12.83%	28.94%	20%	Subclonal			
MTC20	*RMDN1*	p.Tyr224Cys	missense_variant	8	87491210	T	C	34.30%	172	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.9600	90.92%	100.00%	100%	Clonal			
MTC20	*KIAA1429*	p.Arg1276His	missense_variant	8	95521968	C	T	4.41%	272	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	14.75%	44.56%	26%	Subclonal			
MTC20	*NUDT2*	p.Ile10Phe	missense_variant	9	34339065	A	T	47.37%	228	D	.	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.7578	95.37%	100.00%	100%	Clonal			
MTC20	*CYLC2*	p.Lys261Asn	missense_variant	9	105767696	G	C	11.14%	449	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	41.98%	70.91%	55%	Subclonal			
MTC20	*COL5A1*	p.Glu1124Lys	missense_variant	9	137701032	G	A	23.76%	202	D	PASSENGER/OTHER	Passenger		.	.	true	.	true	TRUE	TRUE	Likely pathogenic	0.8790	80.26%	100.00%	100%	Clonal			
MTC20	*ZNF365*	p.Ile437Ile	synonymous_variant	10	64429983	C	T	13.57%	221	.	.	.		.	.	.	.	.		TRUE	.	0.7174	64.32%	100.00%	95%	Clonal			
MTC20	*CDH23*	p.Leu65Leu	synonymous_variant	10	73269886	C	T	6.67%	375	.	.	.		.	.	.	.	.		TRUE	.	0.0001	31.29%	66.78%	46%	Subclonal			
MTC20	*ANXA7*	p.Ser36Cys	missense_variant	10	75158092	T	A	9.48%	401	D	PASSENGER/OTHER	Passenger		.	.	.	.	.	TRUE	TRUE	Indeterminate	0.0324	48.17%	87.89%	66%	Subclonal			
MTC20	*PTEN*	c.209+1_209+4delGTAA	splice_donor_variant	10	89685314	TGTAA	T	52.29%	153	.	.	.		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.1582	94.73%	100.00%	100%	Clonal	TRUE	CTCATTTTTGTTAATGGTGGC	CTCTACCTCACTCTAACAAGCAGA
MTC20	*HPSE2*	p.Ala273Ala	synonymous_variant	10	100481551	T	C	8.37%	203	.	.	.		.	.	.	.	.		TRUE	.	0.0607	36.46%	88.54%	58%	Subclonal			
MTC20	*HBG2*	p.Gly137Ala	missense_variant	11	5274541	C	G	7.53%	93	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0063	18.09%	72.51%	37%	Subclonal			
MTC20	*SLC17A6*	p.Met350Arg	missense_variant	11	22396308	T	G	14.35%	209	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.1731	50.33%	94.48%	71%	Subclonal			
MTC20	*PRDM11*	p.Pro440fs	frameshift_variant	11	45246339	GC	G	19.63%	489	D	.	.		.	.	.	.	.		TRUE	Likely pathogenic	0.8247	79.09%	100.00%	97%	Clonal			
MTC20	*SMTNL1*	p.Ser120Tyr	missense_variant	11	57310474	C	A	47.65%	170	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.8102	94.06%	100.00%	100%	Clonal			
MTC20	*INTS5*	p.Arg576Cys	missense_variant	11	62415826	G	A	13.10%	397	D	.	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0035	49.81%	82.78%	65%	Subclonal			
MTC20	*ARL2*	p.Asp40Gly	missense_variant	11	64785889	A	G	5.04%	119	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.0000	11.28%	51.95%	25%	Subclonal			
MTC20	*SNX32*	p.Arg222*	stop_gained	11	65618586	C	T	3.60%	555	A	.	.		.	.	.	.	.			Indeterminate	0.0000	15.88%	37.82%	25%	Subclonal			
MTC20	*PHOX2A*	p.Arg133Arg	synonymous_variant	11	71952152	G	A	26.57%	271	.	CANCER	.		.	.	.	.	.		TRUE	.	0.7651	87.66%	100.00%	100%	Clonal			
MTC20	*ARRB1*	p.Lys403Lys	synonymous_variant	11	74977255	C	T	4.08%	392	.	.	.		.	.	.	.	.		TRUE	.	0.0000	12.10%	31.91%	20%	Subclonal			
MTC20	*DYNC2H1*	p.Gln2689Lys	missense_variant	11	103070182	C	A	14.68%	252	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.1622	53.31%	94.38%	73%	Subclonal			
MTC20	*GRIA4*	p.Asn769Lys	missense_variant	11	105842653	C	A	20.99%	81	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.7452	60.47%	100.00%	100%	Clonal			
MTC20	*ACRV1*	p.Arg3Arg	synonymous_variant	11	125550667	C	T	9.84%	305	.	.	.		.	.	.	.	.		TRUE	.	0.0000	34.18%	67.53%	49%	Subclonal			
MTC20	*KCNA1*	p.Glu420Lys	missense_variant	12	5021802	G	A	6.88%	276	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	21.65%	51.66%	34%	Subclonal			
MTC20	*ADAMTS20*	p.Pro383Pro	synonymous_variant	12	43862477	A	G	19.70%	198	.	.	.		.	.	.	.	.			.	0.7733	69.90%	100.00%	98%	Clonal			
MTC20	*NTS*	p.Lys45Asn	missense_variant	12	86270479	G	C	20.32%	187	D	.	Passenger		.	.	.	.	.			Indeterminate	0.7971	71.07%	100.00%	100%	Clonal			
MTC20	*LHX5*	p.Glu367Asp	missense_variant	12	113901103	C	G	15.36%	280	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.2301	57.07%	95.82%	76%	Subclonal			
MTC20	*FANCM*	p.Ala1689Val	missense_variant	14	45658291	C	T	4.84%	351	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.0000	14.65%	37.35%	24%	Subclonal			
MTC20	*LMAN1L*	p.Arg76Gln	missense_variant	15	75108549	G	A	10.00%	90	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0541	26.25%	86.51%	50%	Subclonal			
MTC20	*FAM154B*	p.Gln271Glu	missense_variant	15	82575017	C	G	15.12%	291	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.1815	56.36%	94.94%	75%	Subclonal			
MTC20	*TMEM8A*	p.Gln369Gln	synonymous_variant	16	426253	C	T	28.06%	417	.	.	.		.	.	.	.	.			.	0.9705	94.77%	100.00%	100%	Clonal			
MTC20	*ABCC1*	p.Tyr710Tyr	synonymous_variant	16	16177237	T	C	27.15%	372	.	.	.		.	.	.	.	.			.	0.9632	93.86%	100.00%	100%	Clonal			
MTC20	*KIAA0556*	p.Tyr956Cys	missense_variant	16	27761148	A	G	16.41%	323	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.8752	79.68%	100.00%	100%	Clonal			
MTC20	*ZNF768*	p.Pro24Thr	missense_variant	16	30537665	G	T	15.19%	553	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8803	81.59%	100.00%	100%	Clonal			
MTC20	*PAPD5*	p.Phe366Ile	missense_variant	16	50256319	T	A	15.96%	520	D	PASSENGER/OTHER	Passenger		.	.	true	.	true			Likely pathogenic	0.8980	83.53%	100.00%	100%	Clonal			
MTC20	*PIEZO1*	p.Arg459Arg	synonymous_variant	16	88802736	G	C	11.48%	305	.	.	.		.	.	.	.	.			.	0.4263	57.48%	97.92%	80%	Subclonal			
MTC20	*CLUH*	p.Gln606Arg	missense_variant	17	2601220	T	C	16.13%	62	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.5216	42.56%	98.50%	80%	Clonal			
MTC20	*TP53*	p.Pro190fs	frameshift_variant	17	7578279	AG	A	40.45%	267	A	.	.		true	true	true	true	true	TRUE	TRUE	Likely pathogenic	0.9727	94.85%	100.00%	100%	Clonal	TRUE	GACAACCACCCTTAACCCCTC	CTGGTTGCCCAGGGTCCC
MTC20	*FNDC8*	p.Thr277Asn	missense_variant	17	33457308	C	A	18.63%	322	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.7235	71.64%	100.00%	93%	Clonal			
MTC20	*CNTNAP1*	p.Ala734Thr	missense_variant	17	40843295	G	A	24.78%	226	D	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Indeterminate	0.8832	83.34%	100.00%	100%	Clonal			
MTC20	*NACA2*	p.Pro2Pro	synonymous_variant	17	59668536	C	T	19.37%	351	.	.	.		.	.	.	.	.		TRUE	.	0.7892	75.15%	100.00%	96%	Clonal			
MTC20	*CCDC40*	p.Ser131Ile	missense_variant	17	78013909	G	T	3.48%	230	N	PASSENGER/OTHER	Passenger		.	.	.	.	.		TRUE	Likely passenger	0.0000	8.39%	32.82%	17%	Subclonal			
MTC20	*AATK*	p.Arg122Gln	missense_variant	17	79102319	C	T	23.97%	121	D	CANCER	Passenger		.	.	.	.	.		TRUE	Likely pathogenic	0.8432	73.67%	100.00%	100%	Clonal			
MTC20	*NOL4*	p.Leu623*	stop_gained	18	31432855	A	T	5.73%	314	D	.	.		.	.	.	.	.			Indeterminate	0.0000	25.06%	61.36%	40%	Subclonal			
MTC20	*DYM*	p.Ser83Pro	missense_variant	18	46906075	A	G	3.57%	224	D	.	Passenger		.	.	.	.	.			Indeterminate	0.0000	12.33%	47.47%	25%	Subclonal			
MTC20	*POLRMT*	p.Asp594Glu	missense_variant	19	622218	G	T	17.65%	51	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.6836	48.87%	100.00%	100%	Clonal			
MTC20	*ACER1*	p.Leu212Pro	missense_variant	19	6306885	A	G	21.50%	200	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.8624	80.91%	100.00%	100%	Clonal			
MTC20	*OR7A5*	p.Phe288Phe	synonymous_variant	19	14938190	A	G	5.75%	87	.	.	.		.	.	.	.	.			.	0.0136	14.65%	75.01%	34%	Subclonal			
MTC20	*F2RL3*	p.Thr246Thr	synonymous_variant	19	17001012	C	T	4.85%	103	.	.	.		.	.	.	.	.			.	0.0020	12.29%	64.24%	29%	Subclonal			
MTC20	*MAST3*	p.Arg248Trp	missense_variant	19	18234944	C	T	9.55%	398	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0006	41.49%	76.06%	57%	Subclonal			
MTC20	*CILP2*	p.Gly815Gly	synonymous_variant	19	19655799	C	T	15.95%	301	.	.	.		.	.	.	.	.			.	0.7538	70.56%	100.00%	95%	Clonal			
MTC20	*FFAR1*	p.Phe248Leu	missense_variant	19	35843198	C	A	39.31%	954	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.2207	98.88%	100.00%	100%	Clonal			
MTC20	*RYR1*	p.Glu1564Gln	missense_variant	19	38973736	G	C	14.78%	690	D	PASSENGER/OTHER	Passenger		.	.	.	.	.	TRUE		Indeterminate	0.9064	87.25%	100.00%	100%	Clonal			
MTC20	*PNKP*	p.Pro16Pro	synonymous_variant	19	50370414	A	G	8.33%	132	.	.	.		.	.	.	.	.			.	0.0020	23.08%	70.55%	41%	Subclonal			
MTC20	*PNKP*	p.Glu13Gln	missense_variant	19	50370425	C	G	12.15%	107	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.1349	35.50%	92.59%	60%	Subclonal			
MTC20	*ZNF808*	p.Glu340Val	missense_variant	19	53057188	A	T	26.09%	23	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7248	45.54%	100.00%	100%	Clonal			
MTC20	*ZIK1*	p.Arg286Gln	missense_variant	19	58102036	G	A	18.88%	286	N	PASSENGER/OTHER	Passenger		.	.	.	.	.			Likely passenger	0.7420	71.34%	100.00%	94%	Clonal			
MTC20	*C20orf202*	p.Ala71Ala	synonymous_variant	20	1187590	G	A	19.05%	252	.	.	.		.	.	.	.	.			.	0.8693	78.54%	100.00%	100%	Clonal			
MTC20	*PLCB1*	p.Val375Val	synonymous_variant	20	8678388	C	T	7.43%	269	.	.	.		.	.	.	.	.			.	0.0001	28.58%	66.36%	44%	Subclonal			
MTC20	*SEL1L2*	p.Glu524Lys	missense_variant	20	13830875	C	T	12.57%	334	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.2038	55.77%	95.35%	75%	Subclonal			
MTC20	*NKX2-4*	p.Arg219His	missense_variant	20	21376958	C	T	2.76%	507	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.0000	9.37%	26.83%	16%	Subclonal			
MTC20	*CEP250*	p.Leu1692Leu	synonymous_variant	20	34091273	G	A	18.11%	381	.	.	.		.	.	.	.	.			.	0.8789	80.74%	100.00%	100%	Clonal			
MTC20	*RPN2*	p.Phe557Leu	missense_variant	20	35860788	C	A	14.96%	234	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.6528	63.57%	100.00%	89%	Clonal			
MTC20	*L3MBTL1*	p.His339His	synonymous_variant	20	42158950	C	T	15.07%	272	.	.	.		.	.	.	.	.			.	0.6668	65.77%	100.00%	90%	Clonal			
MTC20	*ZNF335*	p.Glu661Lys	missense_variant	20	44588886	C	T	15.43%	350	D	PASSENGER/OTHER	Passenger		.	.	.	.	.			Indeterminate	0.7106	70.02%	100.00%	92%	Clonal			

MTC20	*NCAM2*	p.Ter838Glnext*?	stop_lost	21	22910276	T	C	5.15%	427	N	.	.		.	.	.			Indeterminate	0.0000	16.52%	37.65%	26%	Subclonal				
MTC20	*KRTAP24-1*	p.Ser230Phe	missense_variant	21	31654562	G	A	3.05%	328	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0000	7.83%	26.90%	15%	Subclonal				
MTC20	*PAM47B*	p.Ile582Ile	synonymous_variant	X	34962694	T	A	7.77%	309	.	.	.		.	.	.				0.0001	31.04%	66.90%	46%	Subclonal				
MTC20	*MUM1L1*	p.Val574Ala	missense_variant	X	105451146	T	C	3.16%	475	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	11.04%	30.19%	19%	Subclonal				
MTC20	*SLITRK4*	p.Asn646His	missense_variant	X	142716989	T	G	23.15%	324	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5487	88.58%	100.00%	100%	Clonal				
MTC23	*TTC34*	p.Glu480Lys	missense_variant	1	2573070	C	T	11.56%	209	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0018	35.98%	74.96%	53%	Subclonal				
MTC23	*SPEN*	p.Asp1539Asn	missense_variant	1	16257390	G	A	26.90%	394	D	CANCER	Passenger		.	.	true		TRUE	Likely pathogenic	0.9296	88.79%	100.00%	100%	Clonal				
MTC23	*DOCK7*	c.1872-1G>C	splice_acceptor_variant	1	63044638	C	G	9.80%	102	D	.	.		.	.	.		TRUE	Likely pathogenic	0.0109	23.59%	75.09%	43%	Subclonal				
MTC23	*RHOC*	p.Glu169fs	frameshift_variant	1	113244235	ACCTC	A	44.97%	169	D	.	.		.	.	.		TRUE	Likely pathogenic	0.9787	93.04%	100.00%	100%	Clonal				
MTC23	*SPAG17*	p.Gln645Gln	synonymous_variant	1	118624093	C	T	13.04%	276	.	.	.		.	.	.		TRUE	.	0.0014	41.86%	77.01%	58%	Subclonal				
MTC23	*RPRD2*	p.Arg774Lys	missense_variant	1	150443745	G	A	11.21%	446	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.0000	37.56%	63.54%	50%	Subclonal				
MTC23	*C4BPA*	p.Gly514Cys	missense_variant	1	207317258	G	T	17.74%	124	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.5743	52.16%	98.00%	78%	Clonal				
MTC23	*CPSF3*	p.Pro560Leu	missense_variant	2	9597137	C	T	28.40%	162	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9119	81.94%	100.00%	100%	Clonal				
MTC23	*LTBP1*	p.Pro573Leu	missense_variant	2	33442635	C	T	11.24%	258	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.0001	34.64%	68.84%	50%	Subclonal				
MTC23	*EML4*	p.Ala264Val	missense_variant	2	42508113	C	T	28.97%	145	N	PASSENGER/OTHER	Passenger		true	.	.			Likely passenger	0.9046	81.33%	100.00%	100%	Clonal				
MTC23	*DYSF*	p.Pro828Ala	missense_variant	2	71791260	C	G	37.46%	299	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.6065	94.09%	100.00%	100%	Clonal				
MTC23	*DUSP11*	p.Ser22Phe	missense_variant	2	74007178	G	A	11.91%	655	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0000	42.16%	64.12%	53%	Subclonal				
MTC23	*CTNNA2*	p.Val988Met	missense_variant	2	79971696	G	A	16.49%	194	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.2926	52.22%	95.05%	73%	Subclonal				
MTC23	*HECW2*	c.400+1G>A	splice_donor_variant	2	197208380	C	T	21.84%	87	D	.	.		.	.	.			Indeterminate	0.8056	59.65%	100.00%	97%	Clonal				
MTC23	*MYRIP*	p.Ala205Val	missense_variant	3	40208400	C	T	29.73%	111	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.8719	70.70%	100.00%	100%	Clonal				
MTC23	*PLXNB1*	p.Val1290Phe	missense_variant	3	48456683	C	A	65.56%	302	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.7743	97.48%	100.00%	100%	Clonal				
MTC23	*PBRM1*	p.Arg835fs	frameshift_variant	3	52643391	AC	A	35.16%	128	A	.	.		true	true	true		TRUE	Likely pathogenic	0.7185	65.58%	98.45%	85%	Clonal				
MTC23	*PIK3CA*	p.Glu542Lys	missense_variant	3	178636062	G	A	25.62%	242	D	CANCER	Driver		true	true	true			Likely pathogenic	0.6985	87.08%	100.00%	100%	Clonal	TRUE	CTGTGAATCCAGAGGGGAAA	ACATGCTGAGATCAGCCAAA	
MTC23	*KIAA0232*	p.Ser722Leu	missense_variant	4	6864274	C	T	33.19%	458	D	.	Passenger		.	.	.			Indeterminate	0.9721	96.20%	100.00%	100%	Clonal				
MTC23	*CORIN*	p.Asp373Asp	synonymous_variant	4	47682171	G	A	48.76%	687	.	.	.		.	.	.			.	0.5997	98.34%	100.00%	100%	Clonal				
MTC23	*RRH*	p.Arg87Trp	missense_variant	4	110754357	C	T	45.45%	264	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9828	95.40%	100.00%	100%	Clonal				
MTC23	*STOX2*	p.Pro236Ser	missense_variant	4	184930697	C	T	48.71%	427	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9626	97.32%	100.00%	100%	Clonal				
MTC23	*MRCH2B*	p.Val210Ile	missense_variant	5	41056293	C	T	10.00%	130	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.0808	31.82%	86.83%	54%	Subclonal				
MTC23	*PCDHB6*	p.Leu268Leu	synonymous_variant	5	140530642	A	G	24.07%	565	.	.	.		.	.	.			.	0.9485	86.83%	100.00%	100%	Clonal				
MTC23	*TRIM41*	p.Val613fs	frameshift_variant	5	180661716	CGT	C	18.67%	375	D	.	.		.	.	.			Indeterminate	0.4741	65.95%	97.37%	83%	Subclonal				
MTC23	*C8orf132*	p.Pro1098Pro	synonymous_variant	6	42072362	G	A	45.88%	340	.	.	.		.	.	.			.	0.9844	96.39%	100.00%	100%	Clonal				
MTC23	*XPO5*	p.Ser1006Leu	missense_variant	6	43493626	G	A	25.27%	91	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8745	68.29%	100.00%	100%	Clonal				
MTC23	*NT5E*	p.Asp237Asp	synonymous_variant	6	86181103	C	T	23.68%	397	.	.	.		.	.	.	TRUE		.	0.9304	82.99%	100.00%	100%	Clonal				
MTC23	*SRRT*	p.Gln218Gln	synonymous_variant	7	100481757	A	G	10.43%	508	.	.	.		.	.	.			.	0.0000	43.24%	72.13%	57%	Subclonal				
MTC23	*PDIA4*	p.Tyr392Tyr	synonymous_variant	7	148703101	G	A	50.00%	150	.	.	.		.	.	.		TRUE	.	0.8645	92.40%	100.00%	100%	Clonal				
MTC23	*FOCAD*	p.Lys30*	stop_gained	9	20717823	A	T	55.46%	119	A	.	.		.	.	.		TRUE	Likely pathogenic	0.9760	92.32%	100.00%	100%	Clonal				
MTC23	*ZNF618*	p.Arg843Gln	missense_variant	9	116812389	G	A	24.09%	440	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.9402	84.84%	100.00%	100%	Clonal				
MTC23	*LSP20*	p.Ser389Ser	synonymous_variant	9	132631172	C	G	18.83%	308	.	.	.		.	.	.			.	0.5426	65.02%	97.98%	83%	Clonal				
MTC23	*RNF208*	p.Ser128Leu	missense_variant	9	140115282	G	A	25.38%	327	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9398	84.74%	100.00%	100%	Clonal				
MTC23	*ZNF239*	p.Gly287Ser	missense_variant	10	44052669	C	T	52.74%	483	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.5818	98.04%	100.00%	100%	Clonal				
MTC23	*STOX1*	p.Leu779Leu	synonymous_variant	10	70645889	G	C	7.56%	582	.	.	.		.	.	.			.	0.0000	36.02%	63.72%	49%	Subclonal				
MTC23	*TMPRSS13*	p.Gln83Arg	missense_variant	11	117789327	T	C	37.50%	24	P	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.8435	55.71%	100.00%	100%	Clonal				
MTC23	*OR6X1*	p.Gly81Glu	missense_variant	11	123624985	C	T	31.12%	376	N	PASSENGER/OTHER	Passenger		.	.	.			Likely passenger	0.9471	86.25%	100.00%	100%	Clonal				
MTC23	*OR8G5*	p.Ala191Val	missense_variant	11	124135294	C	T	29.84%	305	.	.	Passenger		.	.	.			Indeterminate	0.9228	82.07%	100.00%	100%	Clonal				
MTC23	*RPAP3*	p.Met565Val	missense_variant	12	48062719	T	C	34.72%	144	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9268	82.15%	100.00%	100%	Clonal				
MTC23	*MARS*	p.Glu887*	stop_gained	12	57910320	G	T	59.51%	247	D	.	.		.	.	.		TRUE	Likely pathogenic	0.9858	96.49%	100.00%	100%	Clonal				
MTC23	*PPFIA2*	p.Arg338Lys	missense_variant	12	81769690	C	T	65.00%	80	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.9549	91.57%	100.00%	100%	Clonal				
MTC23	*PRKAB1*	p.Glu56Gln	missense_variant	12	120110112	G	C	54.32%	81	D	.	Passenger		.	.	.			Indeterminate	0.8938	89.99%	100.00%	100%	Clonal				
MTC23	*DNAH10*	p.Tyr1268Tyr	synonymous_variant	12	124305284	C	T	45.54%	202	.	.	.		.	.	.			.	0.9804	94.18%	100.00%	100%	Clonal				
MTC23	*MTUS2*	p.Asn485Ser	missense_variant	13	29598948	A	G	70.99%	393	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5705	98.23%	100.00%	100%	Clonal				
MTC23	*ATP11A*	p.Ala1075Thr	missense_variant	13	113530151	G	A	80.39%	311	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.5016	98.21%	100.00%	100%	Clonal				
MTC23	*PTGDR*	p.Arg332Trp	missense_variant	14	52741596	C	T	13.73%	306	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	34.81%	61.22%	47%	Subclonal				
MTC23	*C15orf39*	p.Pro130Pro	synonymous_variant	15	75498779	C	G	56.41%	312	.	.	.		.	.	.		TRUE	.	0.9843	97.01%	100.00%	100%	Clonal				
MTC23	*RAB26*	c.591+1G>C	splice_donor_variant	16	2203047	G	C	42.43%	304	D	.	.		.	.	.			Indeterminate	0.9744	95.41%	100.00%	100%	Clonal				
MTC23	*FAQR4*	p.Glu226Lys	missense_variant	16	3021803	G	A	28.46%	376	D	PASSENGER/OTHER	Passenger		.	.	.			Indeterminate	0.8178	90.23%	100.00%	100%	Clonal				
MTC23	*CORO7*	p.Ala319Ala	synonymous_variant	16	4414863	C	T	32.65%	294	.	.	.		.	.	.			.	0.0603	91.77%	100.00%	100%	Clonal				
MTC23	*TMC5*	p.Ala670Ala	synonymous_variant	16	19485518	C	T	11.43%	350	.	.	.		.	.	.			.	0.0000	37.14%	66.69%	51%	Subclonal				
MTC23	*RBL2*	p.Ser425Gly	missense_variant	16	53493456	A	G	36.82%	201	D	CANCER	Passenger		.	.	.			Likely pathogenic	0.9767	92.52%	100.00%	100%	Clonal				
MTC23	*TP53*	c.994-1G>C	splice_acceptor_variant	17	7574034	C	G	80.91%	197	D	.	.		true	true	true	TRUE	TRUE	Likely pathogenic	0.9811	95.97%	100.00%	100%	Clonal	TRUE	GGGGAGTAGGGCCAGGAA	ACTGTGTATATACTTACTTCTCCCCC	
MTC23	*DKKL40*	p.Gln486Gln	synonymous_variant	17	57663568	A	G	3.33%	180	.	.	.		.	.	.			.	0.0000	8.02%	37.86%	18%	Subclonal				
MTC23	*EMR1*	p.Ser165Phe	missense_variant	19	6897538	C	T	59.59%	344	N	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Likely passenger	0.9876	97.37%	100.00%	100%	Clonal				
MTC23	*LRP3*	p.Arg53Gln	missense_variant	19	33693790	G	A	7.78%	90	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0000	12.73%	51.54%	27%	Subclonal				
MTC23	*ACSS1*	p.Val139Val	synonymous_variant	20	25028735	C	T	46.09%	243	.	.	.		.	.	.			.	0.9815	95.19%	100.00%	100%	Clonal				
MTC23	*PHF20*	p.Val346Val	synonymous_variant	20	34458992	A	G	37.28%	247	.	.	.		.	.	.			.	0.9787	93.98%	100.00%	100%	Clonal				
MTC23	*DSCAM*	p.Val1278Val	synonymous_variant	21	41465664	G	C	14.81%	54	.	.	.		.	.	.		TRUE	.	0.1119	26.03%	88.03%	51%	Subclonal				
MTC23	*C21orf2*	p.Thr46Met	missense_variant	21	45755647	G	A	17.19%	221	D	PASSENGER/OTHER	Passenger		.	.	.		TRUE	Indeterminate	0.0010	43.27%	77.26%	59%	Subclonal				
MTC23	*SEC14L4*	p.Phe37Phe	synonymous_variant	22	30899983	G	A	42.86%	217	.	PASSENGER/OTHER	.		.	.	.		TRUE	.	0.0194	92.30%	100.00%	100%	Clonal				
MTC23	*BCOR*	p.Pro457Thr	missense_variant	X	39933386	G	T	13.56%	450	N	PASSENGER/OTHER	Passenger		true	.	true			Likely passenger	0.0000	36.12%	57.78%	46%	Subclonal				
MTC23	*TAF1*	p.Met21Ile	missense_variant	X	70586227	G	A	50.82%	488	D	PASSENGER/OTHER	Passenger		.	true	.			Likely pathogenic	0.7855	97.92%	100.00%	100%	Clonal				
MTC23	*ZNF711*	p.Ile76Ile	synonymous_variant	X	84510413	C	T	49.64%	417	.	.	.		.	.	.		TRUE	.	0.1148	97.02%	100.00%	100%	Clonal				