Supplementary Table S2. Non-synonymous somatic mutations identified in mucinous ovarian cancers by whole-exome sequencing or targeted massively parallel sequencing (MSK-IMPACT).

Whole-exome sequencing															
ID	Chrom	Position	Reference Allele	Alternate Allele	Gene	Amino Acid Change	Mutation Type	HOTSPOT	Tumor MAF	Normal MAF	Tumor Depth (x)	Normal Depth (x)	Cancer Cell Fraction	Clonal/Subclonal	Pathogenicity
MOC10T	1	42922310	G	C	PPCS	p.R25P	Missense_Mutation	FALSE	0.095238095	0.015384615	63	65	0.26	Subclonal	passenger
MOC10T	1	198509776	G	T	ATP6V1G3	p.T2K	Missense_Mutation	FALSE	0.113636364	0.016666667	44	60	0.31	Subclonal	passenger
MOC10T	13	21562482	C	CGGGGCG	LATS2	p.P479_A480dup	In_Frame_Ins	FALSE	0.125	0	16	17	0.34	Subclonal	passenger
MOC10T	1	907758	A	G	PLEKHN1	p.E319G	Missense_Mutation	FALSE	0.206896552	0	29	36	0.57	Subclonal	passenger
MOC10T	1	103380295	C	T	COL11A1	p.G1297R	Missense_Mutation	FALSE	0.210526316	0	19	48	0.58	Subclonal	likely_pathogenic
MOC10T	11	89891348	G	T	NAALAD2	p.G278*	Nonsense_Mutation	FALSE	0.288135593	0	118	136	0.79	Subclonal	passenger
MOC10T	12	115112379	C	T	TBX3	p.R454H	Missense_Mutation	FALSE	0.298245614	0	57	61	0.82	Clonal	likely_pathogenic
MOC10T	14	60212707	A	G	RTN1	p.V245A	Missense_Mutation	FALSE	0.299270073	0	137	216	0.82	Clonal	passenger
MOC10T	7	53103647	G	A	POM121L12	p.E95K	Missense_Mutation	FALSE	0.3	0	70	89	0.82	Clonal	passenger
MOC10T	12	113515459	C	T	DTX1	p.R164C	Missense_Mutation	FALSE	0.306451613	0	124	181	0.84	Clonal	passenger
MOC10T	22	18301240	C	G	MICAL3	p.G1396A	Missense_Mutation	FALSE	0.307692308	0	39	78	0.84	Clonal	passenger
MOC10T	23	84363724	C	T	SATL1	p.R84K	Missense_Mutation	FALSE	0.311827957	0	186	241	0.85	Clonal	passenger
MOC10T	3	142522976	A	G	TRPC1	p.K639E	Missense_Mutation	FALSE	0.327868852	0	61	94	0.9	Clonal	likely_pathogenic
MOC10T	15	44091203	C	T	SERINC4	p.V138I	Missense_Mutation	FALSE	0.328571429	0	70	112	0.9	Clonal	passenger
MOC10T	22	37334389	G	A	CSF2RB	p.E847K	Missense_Mutation	FALSE	0.333333333	0	153	239	0.91	Clonal	passenger
MOC10T	23	70613166	C	G	TAF1	p.R1043G	Missense_Mutation	FALSE	0.333333333	0	45	51	0.91	Clonal	likely_pathogenic
MOC10T	1	209948727	C	A	TRAF3IP3	p.L270M	Missense_Mutation	FALSE	0.352	0	125	201	0.96	Clonal	passenger
MOC10T	12	25398284	C	T	KRAS	p.G12D	Missense_Mutation	TRUE	0.35483871	0	31	62	0.97	Clonal	likely_pathogenic
MOC10T	10	71128357	A	T	HK1	p.K191N	Missense_Mutation	FALSE	0.356435644	0	101	135	0.98	Clonal	likely_pathogenic
MOC10T	20	37555101	G	C	FAM83D	p.E36Q	Missense_Mutation	FALSE	0.364583333	0	96	143	1	Clonal	passenger
MOC10T	6	30297321	G	A	TRIM39	p.R76H	Missense_Mutation	FALSE	0.367088608	0	158	210	1	Clonal	passenger
MOC10T	6	90461177	C	G	MDN1	p.R1067T	Missense_Mutation	FALSE	0.375	0	64	127	1	Clonal	passenger
MOC10T	18	32825301	C	A	ZNF397	p.S211*	Nonsense_Mutation	FALSE	0.38	0	50	96	1	Clonal	passenger
MOC10T	10	89720793	A	ATC	PTEN	p.V317*	Frame_Shift_Ins	FALSE	0.387755102	0	49	79	1	Clonal	likely_pathogenic
MOC10T	15	92459493	G	A	SLCO3A1	p.A151T	Missense_Mutation	FALSE	0.39047619	0	105	204	1	Clonal	passenger
MOC10T	1	27106426	A	T	ARID1A	p.K2013*	Nonsense_Mutation	FALSE	0.4	0	130	209	1	Clonal	likely_pathogenic
MOC10T	1	236925816	A	G	ACTN2	p.Y861C	Missense_Mutation	FALSE	0.421052632	0.014285714	57	70	1	Clonal	likely_pathogenic
MOC10T	8	103573033	A	G	ODF1	p.N225S	Missense_Mutation	FALSE	0.445652174	0.009174312	92	109	1	Clonal	passenger
MOC10T	1	12640646	C	T	DHRS3	p.E82K	Missense_Mutation	FALSE	0.487804878	0	82	130	1	Clonal	likely_pathogenic
MOC10T	20	34302145	G	A	RBM39	p.T353I	Missense_Mutation	TRUE	0.5	0	10	11	1	Clonal	likely_pathogenic
MOC10T	10	89653843	G	T	PTEN	p.R47S	Missense_Mutation	FALSE	0.518518519	0	81	122	1	Clonal	likely_pathogenic
MOC10T	12	57556182	G	C	LRP1	p.S762T	Missense_Mutation	FALSE	0.634615385	0	52	66	1	Clonal	likely_pathogenic
MOC01T	19	56423213	C	T	NLRP13	p.R657H	Missense_Mutation	FALSE	0.035460993	0	141	92	0.11	Subclonal	passenger
MOC01T	19	36339923	C	T	NPHS1	p.V323M	Missense_Mutation	FALSE	0.038167939	0	131	70	0.12	Subclonal	likely_pathogenic
MOC01T	7	82584756	G	A	PCLO	p.P1838L	Missense_Mutation	FALSE	0.077319588	0	194	126	0.24	Subclonal	passenger
MOC01T	1	42922310	G	C	PPCS	p.R25P	Missense_Mutation	FALSE	0.078947368	0	76	34	0.24	Subclonal	passenger
MOC01T	19	54299243	G	A	NLRP12	p.L990F	Missense_Mutation	FALSE	0.083333333	0	84	83	0.26	Subclonal	passenger
MOC01T	9	80537095	G	T	GNAQ	p.Y101*	Nonsense_Mutation	FALSE	0.09375	0	32	42	0.19	Subclonal	likely_pathogenic
MOC01T	23	142718111	C	T	SLITRK4	p.V272M	Missense_Mutation	FALSE	0.093959732	0	149	105	0.29	Subclonal	passenger
MOC01T	12	123470830	C	T	PITPNM2	p.R1265H	Missense_Mutation	FALSE	0.1	0	70	38	0.31	Subclonal	passenger
MOC01T	8	131964235	C	G	ADCY8	p.V374L	Missense_Mutation	FALSE	0.108695652	0	46	25	0.33	Subclonal	passenger
MOC01T	7	45123065	G	A	NACAD	p.P905L	Missense_Mutation	FALSE	0.12	0	25	21	0.37	Subclonal	passenger
MOC01T	9	80537112	T	A	GNAQ	p.T96S	Missense_Mutation	TRUE	0.125	0	40	45	0.26	Subclonal	likely_pathogenic
MOC01T	15	27725869	G	C	GABRG3	p.W216C	Missense_Mutation	FALSE	0.131944444	0	144	109	0.4	Subclonal	passenger
MOC01T	5	129520003	G	T	CHSY3	p.A390S	Missense_Mutation	FALSE	0.140625	0	128	86	0.43	Subclonal	passenger
MOC01T	19	58640035	C	A	ZNF329	p.R279I	Missense_Mutation	FALSE	0.152542373	0	118	78	0.47	Subclonal	passenger
MOC01T	1	202736100	G	A	KDM5B	p.S222L	Missense_Mutation	FALSE	0.160493827	0	81	41	0.49	Subclonal	passenger
MOC01T	4	123145791	G	T	KIAA1109	p.V918L	Missense_Mutation	FALSE	0.185185185	0	81	65	0.57	Subclonal	passenger
MOC01T	3	169485372	C	T	ACTRT3	p.A323T	Missense_Mutation	FALSE	0.190839695	0.013333333	131	75	0.58	Subclonal	passenger
MOC01T	2	74474313	C	T	SLC4A5	p.E637K	Missense_Mutation	FALSE	0.215686275	0	102	77	0.66	Subclonal	passenger
MOC01T	15	71272452	C	T	LRRC49	p.R317C	Missense_Mutation	FALSE	0.243243243	0	74	44	0.74	Subclonal	passenger
MOC01T	11	88300332	G	C	GRM5	p.S840C	Missense_Mutation	FALSE	0.243386243	0	189	136	0.74	Subclonal	likely_pathogenic
MOC01T	9	37537178	C	T	FBXO10	p.G450S	Missense_Mutation	FALSE	0.247524752	0	101	85	0.51	Subclonal	passenger
MOC01T	2	102490553	C	T	MAP4K4	p.S882F	Missense_Mutation	FALSE	0.259259259	0	81	45	0.79	Subclonal	passenger
MOC01T	19	42873738	G	A	MEGF8	p.V2166M	Missense_Mutation	FALSE	0.263157895	0	57	35	0.81	Subclonal	passenger
MOC01T	1	203141105	G	A	MYBPH	p.T191M	Missense_Mutation	FALSE	0.268292683	0	123	64	0.82	Subclonal	passenger
MOC01T	23	48823361	C	T	KCND1	p.R425Q	Missense_Mutation	FALSE	0.28125	0	192	105	0.86	Subclonal	passenger
MOC01T	5	172196125	C	G	DUSP1	p.K248N	Missense_Mutation	FALSE	0.281690141	0	71	36	0.86	Subclonal	passenger
MOC01T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.306122449	0	49	44	0.94	Clonal	likely_pathogenic
MOC01T	7	72892053	A	G	BAZ1B	p.Y580H	Missense_Mutation	FALSE	0.309090909	0.008474576	165	118	0.95	Clonal	passenger
MOC01T	3	196094927	C	T	UBXN7	p.S269N	Missense_Mutation	FALSE	0.31496063	0	127	69	0.96	Clonal	passenger
MOC01T	9	21971110	T	C	CDKN2A	p.H83R	Missense_Mutation	TRUE	0.315789474	0	95	60	0.65	Subclonal	likely_pathogenic
MOC01T	1	90398721	G	C	LRRC8D	p.A32P	Missense_Mutation	FALSE	0.319248826	0	213	133	0.98	Clonal	passenger
MOC01T	11	64756756	C	T	BATF2	p.D224N	Missense_Mutation	FALSE	0.32183908	0	87	55	0.98	Clonal	passenger
MOC01T	1	39845111	A	C	MACF1	p.N2443H	Missense_Mutation	FALSE	0.351351351	0	37	24	1	Clonal	passenger
MOC01T	14	77493761	TTGCTGC	T	IRF2BPL	p.Q126_Q127del	In_Frame_Del	FALSE	0.441860465	0.037037037	43	27	1	Clonal	passenger
MOC01T	17	7578212	G	A	TP53	p.R213*	Nonsense_Mutation	TRUE	0.491803279	0	61	35	1	Clonal	likely_pathogenic
MOC30T	11	66949321	C	T	KDM2A	p.P89S	Missense_Mutation	FALSE	0.036809816	0.004926108	163	203	0.1	Subclonal	likely_pathogenic
MOC30T	3	38592495	C	T	SCN5A	p.D1790N	Missense_Mutation	FALSE	0.037209302	0	215	260	0.1	Subclonal	likely_pathogenic
MOC30T	1	169696940	A	G	SELE	p.S470P	Missense_Mutation	FALSE	0.042372881	0	236	259	0.12	Subclonal	passenger
MOC30T	4	166243184	G	T	KLHL2	p.G589V	Missense_Mutation	FALSE	0.053435115	0	131	180	0.15	Subclonal	likely_pathogenic
MOC30T	8	1616573	C	T	DLGAP2	p.T550M	Missense_Mutation	FALSE	0.06122449	0	196	176	0.17	Subclonal	passenger
MOC30T	19	40520421	G	A	ZNF546	p.C415Y	Missense_Mutation	FALSE	0.072289157	0	83	100	0.2	Subclonal	likely_pathogenic
MOC30T	22	38483198	G	A	BAIAP2L2	p.P398S	Missense_Mutation	FALSE	0.072916667	0	96	105	0.2	Subclonal	passenger
MOC30T	4	48592682	C	T	FRYL	p.V501I	Missense_Mutation	FALSE	0.075	0	80	105	0.2	Subclonal	passenger
MOC30T	12	121868234	TGAA	T	KDM2B	p.F1289del	In_Frame_Del	FALSE	0.086206897	0	174	178	0.23	Subclonal	passenger
MOC30T	14	60591201	A	G	PCNXL4	p.Y537C	Missense_Mutation	FALSE	0.096774194	0	155	214	0.26	Subclonal	passenger
MOC30T	4	88903915	G	A	SPP1	p.R271H	Missense_Mutation	FALSE	0.115606936	0	173	207	0.31	Subclonal	passenger
MOC30T	7	88962863	C	A	ZNF804B	p.H189Q	Missense_Mutation	FALSE	0.126984127	0	189	254	0.34	Subclonal	passenger
MOC30T	5	140552690	C	T	PCDHB7	p.R92*	Nonsense_Mutation	FALSE	0.135483871	0	155	159	0.37	Subclonal	passenger
MOC30T	23	67940201	G	C	STARD8	p.G662A	Missense_Mutation	FALSE	0.135802469	0.019230769	81	104	0.37	Subclonal	passenger
MOC30T	7	100244378	C	T	ACTL6B	p.R338H	Missense_Mutation	FALSE	0.158333333	0	120	134	0.43	Subclonal	likely_pathogenic
MOC30T	16	72845642	G	A	ZFHX3	p.A1233V	Missense_Mutation	FALSE	0.16	0	150	168	0.43	Subclonal	passenger
MOC30T	6	144167217	G	T	LTV1	p.Q55H	Missense_Mutation	FALSE	0.223776224	0	143	169	0.61	Subclonal	passenger
MOC30T	2	166771813	T	G	TTC21B	p.N679T	Missense_Mutation	FALSE	0.259615385	0	104	145	0.7	Subclonal	passenger
MOC30T	2	179430642	T	G	TTN	p.K26739N	Missense_Mutation	FALSE	0.263803681	0	163	235	0.72	Subclonal	passenger
MOC30T	11	47436368	G	A	SLC39A13	p.R276Q	Missense_Mutation	FALSE	0.278195489	0	133	131	0.75	Subclonal	passenger
MOC30T	12	120214571	G	A	CIT	p.R581W	Missense_Mutation	FALSE	0.292682927	0	123	115	0.79	Subclonal	passenger
MOC30T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.303571429	0	56	55	0.82	Subclonal	likely_pathogenic
MOC30T	7	140481417	C	A	BRAF	p.G464V	Missense_Mutation	FALSE	0.30347826	0	92	145	0.83	Subclonal	likely_pathogenic
MOC30T	6	24582533	TG	T	KIAA0319	p.T379Qfs*7	Frame_Shift_Del	FALSE	0.307692308	0	156	178	0.84	Subclonal	passenger
MOC30T	4	177116623	G	A	SPATA4	p.P31S	Missense_Mutation	FALSE	0.325581395	0	215	256	0.88	Subclonal	passenger
MOC30T	19	7687701	C	T	XAB2	p.G440R	Missense_Mutation	FALSE	0.327868852	0	122	131	0.89	Clonal	passenger
MOC30T	19	18391251	T	G	JUND	p.*348Cext*211	FRAME_SHIFT	FALSE	0.357142857	0	70	90	0.97	Clonal	passenger
MOC30T	5	26885831	C	T	CDH9	p.D592N	Missense_Mutation	FALSE	0.37037037	0	162	222	1	Clonal	passenger
MOC30T	8	103573033	A	G	ODF1	p.N225S	Missense_Mutation	FALSE	0.398601399	0	143	146	1	Clonal	passenger
MOC30T	16	30621223	C	T	ZNF689	p.R47Q	Missense_Mutation	FALSE	0.406976744	0	86	110	1	Clonal	passenger
MOC30T	16	55907760	G	T	CES5A	p.T117N	Missense_Mutation	FALSE	0.410526316	0	95	108	1	Clonal	passenger
MOC30T	19	53572372	T	G	ZNF160	p.Q472P	Missense_Mutation	FALSE	0.425	0	40	47	1	Clonal	passenger
MOC32T	8	123965161	C	T	ZHX2	p.R471W	Missense_Mutation	FALSE	0.034843206	0	287	168	0.12	Subclonal	likely_pathogenic
MOC32T	11	6662745	CCAG	C	DCHS1	p.L33del	In_Frame_Del	FALSE	0.057377049	0	122	92	0.13	Subclonal	passenger
MOC32T	9	14307033	C	T	NFIB	p.V173I	Missense_Mutation	FALSE	0.066666667	0	45	81	0.09	Subclonal	passenger
MOC32T	17	4060227	C	T	CYB5D2	p.R216C	Missense_Mutation	FALSE	0.121212121	0	66	112	0.16	Subclonal	likely_pathogenic
MOC32T	22	28194894	CTGCTGT	C	MN1	p.Q549_Q550del	In_Frame_Del	FALSE	0.204545455	0.025641026	44	39	0.47	Subclonal	passenger
MOC32T	1	161736200	C	T	ATF6	p.P17L	Missense_Mutation	FALSE	0.261904762	0	84	51	1	Clonal	passenger
MOC32T	17	38251914	T	G	NR1D1	p.N344T	Missense_Mutation	FALSE	0.347222222	0	72	79	0.8	Subclonal	likely_pathogenic
MOC32T	23	12725012	G	A	FRMPD4	p.R422H	Missense_Mutation	FALSE	0.352	0	125	82	0.81	Subclonal	passenger
MOC32T	16	88664729	C	G	ZC3H18	p.P278A	Missense_Mutation	FALSE	0.36	0	75	51	0.83	Clonal	passenger
MOC32T	11	27078766	G	A	BBOX1	p.D80N	Missense_Mutation	FALSE	0.36875	0	160	150	0.85	Clonal	passenger
MOC32T	3	38798523	G	A	SCN10A	p.R360C	Missense_Mutation	FALSE	0.384615385	0	156	103	0.89	Clonal	likely_pathogenic
MOC32T	2	167151151	C	T	SCN9A	p.G308E	Missense_Mutation	FALSE	0.387931034	0	116	120	0.89	Clonal	likely_pathogenic
MOC32T	17	72943010	G	A	OTOP3	p.V354I	Missense_Mutation	FALSE	0.388157895	0	152	152	0.89	Clonal	passenger
MOC32T	10	69281706	A	T	CTNNA3	p.F158Y	Missense_Mutation	FALSE	0.388888889	0	108	96	0.9	Clonal	passenger
MOC32T	3	96962864	C	A	EPHA6	p.P447T	Missense_Mutation	FALSE	0.408333333	0	120	80	0.94	Clonal	passenger
MOC32T	9	112686051	G	T	PALM2	p.E98D	Missense_Mutation	FALSE	0.41	0	100	82	0.94	Clonal	passenger
MOC32T	2	226378271	C	T	NYAP2	p.R136W	Missense_Mutation	FALSE	0.413043478	0	138	121	0.95	Clonal	passenger
MOC32T	19	45165007	C	A	PVR	p.H395N	Missense_Mutation	FALSE	0.414285714	0	70	37	0.95	Clonal	passenger
MOC32T	12	25398284	C	T	KRAS	p.G12D	Missense_Mutation	TRUE	0.41509434	0	53	51	0.96	Clonal	likely_pathogenic

MOC32T	13	80911034	G	T	SPRY2	p.Y269*	Nonsense_Mutation	FALSE	0.419642857	0	224	189	0.97	Clonal	passenger
MOC32T	6	36982671	C	T	FGD2	p.R296W	Missense_Mutation	FALSE	0.424242424	0	33	24	0.98	Clonal	passenger
MOC32T	11	1078269	G	A	MUC2	p.V186M	Missense_Mutation	FALSE	0.424390244	0	205	143	0.98	Clonal	passenger
MOC32T	17	41143435	G	A	RUNDC1	p.S515N	Missense_Mutation	FALSE	0.448888889	0	225	147	1	Clonal	passenger
MOC32T	8	103573033	A	G	ODF1	p.N225S	Missense_Mutation	FALSE	0.451086957	0.011363636	184	88	1	Clonal	passenger
MOC32T	23	123227992	T	G	STAG2	p.L1235V	Missense_Mutation	FALSE	0.45323741	0	139	105	1	Clonal	passenger
MOC32T	8	75263563	C	G	GDAP1	p.L58V	Missense_Mutation	FALSE	0.469565217	0	115	109	1	Clonal	passenger
MOC32T	19	11303675	C	T	KANK2	p.G361S	Missense_Mutation	FALSE	0.470588235	0	102	67	1	Clonal	passenger
MOC32T	19	17476307	G	T	PLVAP	p.Q323K	Missense_Mutation	FALSE	0.473958333	0	192	179	1	Clonal	passenger
MOC32T	1	45984630	A	G	PRDX1	p.I29T	Missense_Mutation	FALSE	0.47826087	0	46	41	1	Clonal	passenger
MOC32T	8	38184340	C	T	WHSC1L1	p.G539E	Missense_Mutation	FALSE	0.490566038	0	53	37	1	Clonal	passenger
MOC32T	5	80409424	C	T	RASGRF2	p.P719S	Missense_Mutation	FALSE	0.494845361	0	194	178	1	Clonal	passenger
MOC32T	15	75047256	G	A	CYP1A2	p.G460R	Missense_Mutation	FALSE	0.507936508	0	126	96	1	Clonal	likely_pathogenic
MOC32T	17	37879658	G	A	ERBB2	p.R678Q	Missense_Mutation	TRUE	0.50877193	0	114	118	1	Clonal	likely_pathogenic
MOC32T	1	160915073	C	T	ITLN2	p.G279S	Missense_Mutation	FALSE	0.685714286	0	105	56	1	Clonal	passenger
MOC32T	17	7577539	G	A	TP53	p.R248W	Missense_Mutation	TRUE	0.735294118	0	34	52	0.96	Clonal	likely_pathogenic
MOC32T	12	90049525	G	A	ATP2B1	p.R47*	Nonsense_Mutation	FALSE	0.813333333	0	75	97	1	Clonal	likely_pathogenic
MOC37T	8	52733164	G	C	PCMTD1	p.P274R	Missense_Mutation	FALSE	0.065934066	0.011904762	91	84	0.17	Subclonal	passenger
MOC37T	3	30691871	GA	G	TGFBR2	p.K153Sfs*35	Frame_Shift_Del	FALSE	0.074626866	0	134	78	0.19	Subclonal	likely_pathogenic
MOC37T	3	10128939	G	A	FANCD2	p.E1153K	Missense_Mutation	FALSE	0.085365854	0.016949153	82	59	0.21	Subclonal	passenger
MOC37T	3	47044269	C	A	NBEAL2	p.S1812R	Missense_Mutation	FALSE	0.121212121	0	33	27	0.3	Subclonal	passenger
MOC37T	19	12917895	T	G	RNASEH2A	p.X67_splice	Splice_Site	FALSE	0.161290323	0	31	24	0.4	Subclonal	passenger
MOC37T	6	39838131	C	T	DAAM2	p.R297C	Missense_Mutation	FALSE	0.165137615	0	218	140	0.41	Subclonal	likely_pathogenic
MOC37T	17	35297730	A	G	LHX1	p.Y105C	Missense_Mutation	FALSE	0.248826291	0	213	133	0.87	Clonal	likely_pathogenic
MOC37T	18	8379193	G	A	PTPRM	p.R1214Q	Missense_Mutation	FALSE	0.316666667	0	120	99	0.79	Subclonal	passenger
MOC37T	12	25380275	T	G	KRAS	p.Q61H	Missense_Mutation	TRUE	0.333333333	0	27	23	0.84	Clonal	likely_pathogenic
MOC37T	19	12981902	G	A	MAST1	p.R1060H	Missense_Mutation	FALSE	0.36440678	0	118	100	0.91	Clonal	passenger
MOC37T	17	37866386	C	G	ERBB2	p.L231V	Missense_Mutation	FALSE	0.372093023	0	86	40	1	Clonal	passenger
MOC37T	2	48915444	C	T	LHCGR	p.A498T	Missense_Mutation	FALSE	0.380952381	0	189	128	0.96	Clonal	passenger
MOC37T	5	76128713	G	A	F2RL1	p.G94D	Missense_Mutation	FALSE	0.38410596	0	151	103	0.96	Clonal	passenger
MOC37T	8	145058891	C	A	PARP10	p.A427S	Missense_Mutation	FALSE	0.384180791	0	177	104	0.96	Clonal	passenger
MOC37T	20	35060613	G	A	DLGAP4	p.G165S	Missense_Mutation	FALSE	0.391534392	0	189	124	0.98	Clonal	passenger
MOC37T	10	105139776	G	C	TAF5	p.Q471H	Missense_Mutation	FALSE	0.396396396	0	111	71	0.99	Clonal	passenger
MOC37T	1	54417905	G	A	LRRC42	p.R78Q	Missense_Mutation	FALSE	0.415178571	0	224	183	1	Clonal	passenger
MOC37T	13	113748908	T	A	MCF2L	p.S1012T	Missense_Mutation	FALSE	0.428571429	0	28	16	1	Clonal	passenger
MOC37T	10	82369271	G	A	SH2D4B	p.E317K	Missense_Mutation	FALSE	0.433333333	0	90	71	1	Clonal	passenger
MOC37T	19	36365512	G	A	APLP1	p.R388H	Missense_Mutation	FALSE	0.526315789	0	114	87	1	Clonal	likely_pathogenic
MOC37T	17	7577106	G	A	TP53	p.P278S	Missense_Mutation	TRUE	0.528571429	0	70	58	0.8	Subclonal	likely_pathogenic
MOC37T	23	36057104	G	A	CHDC2	p.R23H	Missense_Mutation	FALSE	0.588235294	0	153	92	1	Clonal	passenger
MOC37T	7	6548738	G	A	GRID2IP	p.R660C	Missense_Mutation	FALSE	0.714285714	0	21	13	1	Clonal	passenger
MOC59T	11	48327992	C	G	OR4S1	p.S73C	Missense_Mutation	FALSE	0.03626943	0	386	275	0.24	Subclonal	passenger
MOC59T	12	31944836	C	T	H3F3C	p.V89I	Missense_Mutation	FALSE	0.043636364	0.003508772	275	285	0.2	Subclonal	passenger
MOC59T	14	59113076	G	A	DACT1	p.V579M	Missense_Mutation	FALSE	0.048076923	0	104	122	0.22	Subclonal	passenger
MOC59T	9	37349426	G	A	ZCCHC7	p.A354T	Missense_Mutation	FALSE	0.051351351	0	370	221	0.44	Subclonal	passenger
MOC59T	23	134707988	G	A	DDX26B	p.X544_splice	Splice_Site	FALSE	0.0625	0	64	84	0.23	Subclonal	passenger
MOC59T	6	33371739	G	A	KIFC1	p.A197T	Missense_Mutation	FALSE	0.071428571	0	98	108	0.33	Subclonal	passenger
MOC59T	22	29885580	A	AAGGCCAAGTCCCCTGAGA	NEFH	p.A652_K657dup	In_Frame_Ins	FALSE	0.108108108	0	37	53	0.39	Subclonal	passenger
MOC59T	2	163253447	C	G	KCNH7	p.D806H	Missense_Mutation	FALSE	0.138888889	0	36	73	0.5	Subclonal	likely_pathogenic
MOC59T	19	49858454	G	T	TEAD2	p.L164I	Missense_Mutation	FALSE	0.156424581	0	179	134	1	Clonal	passenger
MOC59T	14	21552928	A	G	ARHGEF40	p.Q1269R	Missense_Mutation	FALSE	0.179487179	0	39	37	0.83	Clonal	passenger
MOC59T	2	36744573	TA	T	CRIM1	p.T699Lfs*83	Frame_Shift_Del	FALSE	0.180327869	0	61	100	0.65	Subclonal	passenger
MOC59T	19	54926844	T	A	TTYH1	p.Y40N	Missense_Mutation	FALSE	0.194444444	0	36	30	1	Clonal	passenger
MOC59T	1	247588590	A	C	NLRP3	p.K615N	Missense_Mutation	FALSE	0.198198198	0	111	110	0.91	Clonal	passenger
MOC59T	12	56825358	C	T	TIMELESS	p.G240R	Missense_Mutation	FALSE	0.203539823	0	113	100	0.73	Subclonal	passenger
MOC59T	7	128505224	G	A	ATP6V1F	p.R70H	Missense_Mutation	FALSE	0.225	0.005649718	160	177	1	Clonal	passenger
MOC59T	10	99661339	C	T	CRTAC1	p.D352N	Missense_Mutation	FALSE	0.225806452	0	31	48	0.81	Clonal	passenger
MOC59T	8	131861901	C	T	ADCY8	p.V787I	Missense_Mutation	FALSE	0.234042553	0.011235955	94	89	1	Clonal	passenger
MOC59T	7	113519083	T	A	PPP1R3A	p.K688N	Missense_Mutation	FALSE	0.248648649	0	185	210	1	Clonal	passenger
MOC59T	1	201750222	A	T	NAV1	p.K483I	Missense_Mutation	FALSE	0.252336449	0	107	137	1	Clonal	passenger
MOC59T	2	220421191	G	A	OBSL1	p.R1441W	Missense_Mutation	FALSE	0.258474576	0	236	218	1	Clonal	passenger
MOC59T	1	33402759	G	C	RNF19B	p.A616G	Missense_Mutation	FALSE	0.260869565	0	138	163	1	Clonal	passenger
MOC59T	9	100616700	AGCCGCC	A	FOXE1	p.A178_A179del	In_Frame_Del	FALSE	0.266666667	0.029411765	30	34	0.96	Clonal	passenger
MOC59T	16	67859094	C	T	TSNAXIP1	p.R191*	Nonsense_Mutation	FALSE	0.266666667	0	60	109	0.96	Clonal	passenger
MOC59T	2	164466592	C	A	FIGN	p.V584F	Missense_Mutation	FALSE	0.270588235	0	85	131	0.98	Clonal	likely_pathogenic
MOC59T	9	140062281	G	C	GRIN1	p.S940T	Missense_Mutation	FALSE	0.272151899	0	158	161	1	Clonal	passenger
MOC59T	15	75687179	G	A	SIN3A	p.R707*	Nonsense_Mutation	FALSE	0.272727273	0	55	60	0.98	Clonal	likely_pathogenic
MOC59T	3	13441275	C	T	NUP210	p.R85H	Missense_Mutation	FALSE	0.291044776	0	134	129	1	Clonal	passenger
MOC59T	15	99434814	G	A	IGF1R	p.G301S	Missense_Mutation	FALSE	0.291139241	0	79	116	1	Clonal	likely_pathogenic
MOC59T	2	186665672	T	G	FSIP2	p.I3969R	Missense_Mutation	FALSE	0.294117647	0	102	133	1	Clonal	passenger
MOC59T	19	31770542	C	T	TSHZ3	p.A53T	Missense_Mutation	FALSE	0.298780488	0	164	148	1	Clonal	passenger
MOC59T	2	186665661	A	C	FSIP2	p.R3965S	Missense_Mutation	FALSE	0.308411215	0	107	135	1	Clonal	passenger
MOC59T	2	51254673	G	A	NRXN1	p.R247*	Nonsense_Mutation	FALSE	0.310344828	0	58	84	1	Clonal	passenger
MOC59T	10	81903991	A	G	PLAC9	p.T59A	Missense_Mutation	FALSE	0.315789474	0	95	147	1	Clonal	passenger
MOC59T	20	20349585	C	A	INSM1	p.A225D	Missense_Mutation	FALSE	0.338983051	0	59	72	1	Clonal	passenger
MOC59T	5	160721254	C	T	GABRB2	p.R458Q	Missense_Mutation	FALSE	0.352941176	0	136	201	1	Clonal	passenger
MOC59T	4	138451498	C	T	PCDH18	p.R582H	Missense_Mutation	FALSE	0.37	0.006578947	100	152	1	Clonal	passenger
MOC59T	10	131640457	G	A	EBF3	p.T423M	Missense_Mutation	FALSE	0.389380531	0	113	184	1	Clonal	passenger
MOC59T	12	57918748	G	C	MBD6	p.D77H	Missense_Mutation	FALSE	0.405797101	0	138	112	1	Clonal	likely_pathogenic
MOC59T	15	100252709	CCAG	C	MEF2A	p.Q422del	In_Frame_Del	FALSE	0.418604651	0.222222222	86	108	1	Clonal	passenger
MOC59T	12	57918871	G	A	MBD6	p.E118K	Missense_Mutation	FALSE	0.425531915	0	141	108	1	Clonal	passenger
MOC59T	3	48452385	T	A	PLXNB1	p.K1770*	Nonsense_Mutation	FALSE	0.4375	0	32	69	1	Clonal	passenger
MOC59T	8	10466466	G	T	RP1L1	p.H1714Q	Missense_Mutation	FALSE	0.444444444	0	63	141	1	Clonal	passenger
MOC59T	22	24837306	T	G	ADORA2A	p.L363R	Missense_Mutation	FALSE	0.456521739	0	46	52	1	Clonal	passenger
MOC59T	6	33374436	C	T	KIFC1	p.A632V	Missense_Mutation	FALSE	0.509090909	0	110	103	1	Clonal	passenger
MOC59T	17	7577094	G	A	TP53	p.R282W	Missense_Mutation	TRUE	0.573529412	0	68	89	1	Clonal	likely_pathogenic
MOC59T	17	17039561	CCAGCAG	C	MPRIP	p.S188_S189del	In_Frame_Del	FALSE	0.772727273	0.45	22	20	1	Clonal	passenger
MOC05T	18	76757113	G	A	SALL3	p.V1232I	Missense_Mutation	FALSE	0.04	0	250	282	0.11	Subclonal	passenger
MOC05T	1	154961217	G	T	FLAD1	p.E337*	Nonsense_Mutation	FALSE	0.048387097	0	124	121	0.13	Subclonal	passenger
MOC05T	16	5037571	G	A	SEC14L5	p.R26H	Missense_Mutation	FALSE	0.085526316	0	152	176	0.23	Subclonal	passenger
MOC05T	11	1018390	C	T	MUC6	p.A1471T	Missense_Mutation	FALSE	0.176470588	0.029850746	34	67	0.47	Subclonal	passenger
MOC05T	19	9090635	C	A	MUC16	p.G394C	Missense_Mutation	FALSE	0.257641921	0	229	157	0.94	Clonal	passenger
MOC05T	15	89864001	G	A	POLG	p.R993C	Missense_Mutation	FALSE	0.3125	0.034482759	32	29	0.83	Clonal	likely_pathogenic
MOC05T	22	33264982	C	T	SYN3	p.V198I	Missense_Mutation	FALSE	0.338983051	0	59	67	0.9	Clonal	passenger
MOC05T	20	55746035	G	A	BMP7	p.R426W	Missense_Mutation	FALSE	0.357142857	0	98	107	0.95	Clonal	likely_pathogenic
MOC05T	17	36876711	G	T	MLLT6	p.E748*	Nonsense_Mutation	FALSE	0.368525896	0	502	56	1	Clonal	passenger
MOC05T	18	72914164	C	G	ZADH2	p.R114T	Missense_Mutation	FALSE	0.377777778	0	135	136	1	Clonal	passenger
MOC05T	15	42980913	G	C	STARD9	p.E2379D	Missense_Mutation	FALSE	0.383928571	0	224	246	1	Clonal	passenger
MOC05T	8	37729132	T	C	RAB11FIP1	p.D1063G	Missense_Mutation	FALSE	0.396396396	0	222	256	1	Clonal	passenger
MOC05T	2	11780569	C	T	GREB1	p.R1947*	Nonsense_Mutation	FALSE	0.404145078	0	193	229	1	Clonal	passenger
MOC05T	9	139649747	T	A	LCN8	p.K124*	Nonsense_Mutation	FALSE	0.410958904	0	146	171	1	Clonal	passenger
MOC05T	23	153041471	G	A	PLXNB3	p.V1534M	Missense_Mutation	FALSE	0.412371134	0	97	100	1	Clonal	passenger
MOC05T	11	105967469	G	A	AASDHPPT	p.X256_splice	Splice_Site	FALSE	0.41314554	0	213	235	1	Clonal	passenger
MOC05T	23	36303830	T	C	CXorf30	p.C5R	Missense_Mutation	FALSE	0.413793103	0	203	215	1	Clonal	passenger
MOC05T	18	32920476	C	A	ZNF24	p.D47Y	Missense_Mutation	FALSE	0.423076923	0	182	145	1	Clonal	passenger
MOC05T	16	601526	G	A	CAPN15	p.R736Q	Missense_Mutation	FALSE	0.431506849	0	146	146	1	Clonal	likely_pathogenic
MOC05T	12	46231201	G	A	ARID2	p.X374_splice	Splice_Site	FALSE	0.444444444	0	117	110	1	Clonal	likely_pathogenic
MOC05T	16	2326713	C	T	ABCA3	p.A1693T	Missense_Mutation	FALSE	0.456410256	0	195	173	1	Clonal	likely_pathogenic
MOC05T	1	6509022	C	T	ESPN	p.P596S	Missense_Mutation	FALSE	0.461538462	0	26	31	1	Clonal	likely_pathogenic
MOC05T	4	54362522	C	T	LNX1	p.A340T	Missense_Mutation	FALSE	0.466165414	0	133	110	1	Clonal	passenger
MOC05T	1	43203960	G	A	CLDN19	p.S138L	Missense_Mutation	FALSE	0.467948718	0	156	152	1	Clonal	likely_pathogenic
MOC05T	22	20073776	G	A	DGCR8	p.R97H	Missense_Mutation	FALSE	0.476190476	0	231	241	1	Clonal	passenger
MOC05T	19	51363282	T	C	KLK3	p.W229R	Missense_Mutation	FALSE	0.66	0	50	131	1	Clonal	likely_pathogenic
MOC05T	17	7577568	C	A	TP53	p.C238F	Missense_Mutation	TRUE	0.675	0	40	95	1	Clonal	likely_pathogenic
MOC73T	7	100334940	C	T	ZAN	p.A194V	Missense_Mutation	FALSE	0.043478261	0	92	105	0.37	Subclonal	passenger
MOC73T	4	88535277	G	A	DSPP	p.R488Q	Missense_Mutation	FALSE	0.048484848	0	165	245	0.41	Subclonal	passenger
MOC73T	11	110035345	A	T	ZC3H12C	p.K512I	Missense_Mutation	FALSE	0.049079755	0.005813953	163	172	0.41	Subclonal	likely_pathogenic
MOC73T	8	8235359	G	C	SGK223	p.A187G	Missense_Mutation	FALSE	0.051612903	0	155	234	0.43	Subclonal	passenger
MOC73T	2	131130796	A	C	PTPN18	p.*461Sext*2	FRAME_SHIFT	FALSE	0.060606061	0	99	161	0.51	Subclonal	passenger
MOC73T	12	25398284	C	T	KRAS	p.G12D	Missense_Mutation	TRUE	0.065217391	0	46	50	0.55	Subclonal	likely_pathogenic
MOC73T	23	15574209	G	A	BMX	p.R656H	Missense_Mutation	FALSE	0.065217391	0	92	151	0.55	Subclonal	likely_pathogenic
MOC73T	5	158139228	C	T	EBF1	p.A495T	Missense_Mutation	FALSE	0.06779661	0	118	153	0.57	Subclonal	passenger
MOC73T	1	46471917	C	T	MAST2	p.S251L	Missense_Mutation	FALSE	0.068965517	0	174	255	0.58	Subclonal	passenger
MOC73T	5	140594149	A	G	PCDHB13	p.T152A	Missense_Mutation	FALSE	0.074074074	0.013333333	54	75	0.62	Subclonal	passenger

MOC73T	4	123192580	G	A	KIAA1109	p.R2634K	Missense_Mutation	FALSE	0.076923077	0	104	185	0.65	Subclonal	passenger
MOC73T	3	123033122	G	C	ADCY5	p.T801S	Missense_Mutation	FALSE	0.079545455	0	88	107	0.67	Subclonal	passenger
MOC73T	10	26998680	T	G	PDSS1	p.I150M	Missense_Mutation	FALSE	0.081632653	0	147	181	0.69	Subclonal	passenger
MOC73T	2	73467642	G	A	CCT7	p.V80I	Missense_Mutation	FALSE	0.086538462	0	104	140	0.73	Subclonal	passenger
MOC73T	18	48593406	G	T	SMAD4	p.G386V	Missense_Mutation	TRUE	0.095238095	0.006329114	84	158	0.8	Subclonal	likely_pathogenic
MOC73T	17	9480058	C	CT	WDR16	p.D17*	Frame_Shift_Ins	FALSE	0.104166667	0	48	87	0.87	Subclonal	passenger
MOC73T	1	19525421	T	G	UBR4	p.K127T	Missense_Mutation	FALSE	0.105263158	0.016393443	76	122	0.88	Clonal	passenger
MOC73T	17	7578190	T	C	TP53	p.Y220C	Missense_Mutation	TRUE	0.12195122	0	41	64	1	Clonal	likely_pathogenic
MOC09T	14	64066236	A	C	WDR89	p.L142W	Missense_Mutation	FALSE	0.03875969	0.007575758	129	132	0.1	Subclonal	passenger
MOC09T	19	11977406	A	G	ZNF439	p.N77S	Missense_Mutation	FALSE	0.046511628	0	86	86	0.12	Subclonal	passenger
MOC09T	13	109792621	G	A	MYO16	p.R1332Q	Missense_Mutation	FALSE	0.053763441	0	93	120	0.14	Subclonal	passenger
MOC09T	11	124767005	C	T	ROBO4	p.V75M	Missense_Mutation	FALSE	0.148148148	0	27	50	0.23	Subclonal	passenger
MOC09T	12	55641351	G	A	OR6C74	p.D94N	Missense_Mutation	FALSE	0.201612903	0	124	148	0.51	Subclonal	passenger
MOC09T	22	36123161	A	C	APOL5	p.H349P	Missense_Mutation	FALSE	0.235294118	0.024390244	34	41	0.59	Subclonal	passenger
MOC09T	7	4801940	A	C	FOXK1	p.T683P	Missense_Mutation	FALSE	0.236842105	0.034482759	38	29	0.6	Subclonal	passenger
MOC09T	1	87033162	CTG	C	CLCA4	p.V338*	Frame_Shift_Del	FALSE	0.272727273	0	88	97	0.69	Subclonal	passenger
MOC09T	11	57571240	G	A	CTNND1	p.W523*	Nonsense_Mutation	FALSE	0.290322581	0	31	41	0.44	Subclonal	passenger
MOC09T	23	75649309	G	T	MAGEE1	p.S329I	Missense_Mutation	FALSE	0.315533981	0	206	197	0.8	Subclonal	passenger
MOC09T	9	140850188	G	A	CACNA1B	p.R370H	Missense_Mutation	FALSE	0.371428571	0	35	61	0.57	Subclonal	likely_pathogenic
MOC09T	10	55582498	C	A	PCDH15	p.C1665F	Missense_Mutation	FALSE	0.387283237	0	173	198	0.98	Clonal	passenger
MOC09T	19	58084835	T	A	ZNF416	p.E146V	Missense_Mutation	FALSE	0.397321429	0	224	184	1	Clonal	passenger
MOC09T	20	61510839	G	A	DIDO1	p.R2157C	Missense_Mutation	FALSE	0.398907104	0	183	175	1	Clonal	passenger
MOC09T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.428571429	0	35	59	1	Clonal	likely_pathogenic
MOC09T	13	103710635	C	T	SLC10A2	p.V159I	Missense_Mutation	FALSE	0.436619718	0	71	61	1	Clonal	passenger
MOC09T	23	67417041	T	C	OPHN1	p.D364G	Missense_Mutation	FALSE	0.4375	0	32	43	1	Clonal	passenger
MOC09T	4	5735137	C	T	EVC	p.T226M	Missense_Mutation	FALSE	0.451612903	0	62	57	1	Clonal	passenger
MOC09T	4	113530576	C	T	C4orf21	p.E893K	Missense_Mutation	FALSE	0.490196078	0	51	52	1	Clonal	passenger
MOC09T	1	190129797	C	A	BRINP3	p.X395_splice	Splice_Site	FALSE	0.513888889	0	72	66	1	Clonal	passenger
MOC09T	11	118344803	G	A	KMT2A	p.G977S	Missense_Mutation	FALSE	0.538116592	0	223	242	0.82	Subclonal	passenger
MOC09T	6	26388361	A	T	BTN2A2	p.E188V	Missense_Mutation	FALSE	0.660465116	0	215	120	1	Clonal	passenger
MOC09T	17	7578406	C	T	TP53	p.R175H	Missense_Mutation	TRUE	0.745762712	0	59	131	1	Clonal	likely_pathogenic

Targeted sequencing (MSK-IMPACT)															
ID	Chrom	Position	Reference Allele	Alternate Allele	Gene	Amino Acid Change	Mutation Type	HOTSPOT	Tumor MAF	Normal MAF	Tumor Depth	Normal Depth	Cancer Cell Fraction	Clonal/Subclonal	Pathogenicity
MOC17T	3	178952085	A	G	PIK3CA	p.H1047R	Missense_Mutation	TRUE	0.279352227	0	247	214	0.87	Clonal	likely_pathogenic
MOC17T	19	42794669	AC	A	CIC	p.P584fs	Frame_Shift_Del	FALSE	0.395348837	0	215	278	1	Clonal	likely_pathogenic
MOC17T	1	162737093	C	A	DDR2	p.L413M	Missense_Mutation	FALSE	0.258258258	0	333	190	1	Clonal	passenger
MOC17T	11	532738	G	C	HRAS	p.F156L	Missense_Mutation	FALSE	0.286407767	0	206	303	0.89	Clonal	likely_pathogenic
MOC17T	20	9561268	C	T	PAK5	p.V172I	Missense_Mutation	FALSE	0.033195021	0	241	171	0.1	Subclonal	passenger
MOC17T	4	55958840	G	C	KDR	p.L1005V	Missense_Mutation	FALSE	0.300813008	0	246	225	0.93	Clonal	likely_pathogenic
MOC17T	6	26056176	G	A	HIST1H1C	p.P161S	Missense_Mutation	FALSE	0.304832714	0.00308642	269	648	0.95	Clonal	passenger
MOC17T	7	151874194	C	G	KMT2C	p.D2782H	Missense_Mutation	FALSE	0.229166667	0	192	224	0.71	Subclonal	passenger
MOC19T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.6	0	25	236	1	Clonal	likely_pathogenic
MOC19T	21	44524456	G	A	U2AF1L5|U2AF1	p.S34F	Missense_Mutation	TRUE	0.147058824	0	34	248	0.69	Subclonal	likely_pathogenic
MOC19T	22	30051641	AC	A	NF2	p.Y192fs	Frame_Shift_Del	FALSE	0.128205128	0	39	180	0.48	Subclonal	likely_pathogenic
MOC19T	11	85979520	C	T	EED	p.H295Y	Missense_Mutation	FALSE	0.108108108	0	37	186	0.4	Subclonal	likely_pathogenic
MOC19T	13	32905080	C	T	BRCA2	p.H236Y	Missense_Mutation	FALSE	0.148148148	0	27	124	0.55	Subclonal	passenger
MOC19T	17	29663662	A	T	NF1	p.R2053W	Missense_Mutation	FALSE	0.166666667	0	24	178	0.62	Subclonal	likely_pathogenic
MOC19T	2	48018254	C	T	MSH6	p.P150L	Missense_Mutation	FALSE	0.147058824	0	34	110	0.55	Subclonal	passenger
MOC19T	20	57429207	C	T	GNAS	p.T296M	Missense_Mutation	FALSE	0.3	0.011235955	10	89	1	Clonal	passenger
MOC19T	3	178916944	A	G	PIK3CA	p.K111E	Missense_Mutation	FALSE	0.242424242	0.006329114	33	158	0.9	Clonal	likely_pathogenic
MOC19T	6	157099193	G	A	ARID1B	p.A44T	Missense_Mutation	FALSE	0.166666667	0	24	208	0.62	Subclonal	passenger
MOC19T	19	10270597	GTC	G	DNMT1	p.D348fs	Splice_Site	FALSE	0.19047619	0	21	122	0.71	Subclonal	likely_pathogenic
MOC19T	1	27106069	C	T	ARID1A	p.Q1894*	Nonsense_Mutation	FALSE	0.153846154	0.007692308	26	130	0.57	Subclonal	likely_pathogenic
MOC19T	3	47059211	G	A	SETD2	p.Q2484*	Nonsense_Mutation	FALSE	0.192307692	0	26	176	0.72	Subclonal	likely_pathogenic
MOC19T	23	70361740	G	A	MED12	p.R2139H	Missense_Mutation	FALSE	0.148148148	0	27	151	0.55	Subclonal	passenger
MOC21T	12	25380275	T	A	KRAS	p.Q61H	Missense_Mutation	TRUE	0.39628483	0	323	350	0.79	Subclonal	likely_pathogenic
MOC21T	17	7577130	A	G	TP53	p.F270L	Missense_Mutation	TRUE	0.441734417	0	369	334	0.88	Subclonal	likely_pathogenic
MOC21T	14	36986875	T	TGCCCCCGCC	NKX2-1	p.240_241insGGG	In_Frame_Ins	FALSE	0.17826087	0	230	113	0.36	Subclonal	passenger
MOC21T	1	176175819	A	C	RFWD2	p.V99G	Missense_Mutation	FALSE	0.547263682	0	201	248	1	Clonal	passenger
MOC21T	11	108124761	T	C	ATM	p.S707P	Missense_Mutation	FALSE	0.405286344	0	227	190	0.81	Subclonal	passenger
MOC21T	16	23635370	C	T	PALB2	p.V932M	Missense_Mutation	FALSE	0.453089245	0	437	322	0.91	Clonal	passenger
MOC21T	17	37686920	C	T	CDK12	p.P1275L	Missense_Mutation	FALSE	0.502083333	0	480	275	1	Clonal	likely_pathogenic
MOC21T	19	18280096	G	A	PIK3R2	p.A727T	Missense_Mutation	FALSE	0.457627119	0	177	73	0.92	Clonal	passenger
MOC21T	3	72897459	A	C	SHQ1	p.D11E	Missense_Mutation	FALSE	0.513944223	0	251	272	1	Clonal	passenger
MOC21T	3	142284987	G	A	ATR	p.H90Y	Missense_Mutation	FALSE	0.5086313	0	377	297	1	Clonal	passenger
MOC21T	4	106157698	T	C	TET2	p.Y867H	Missense_Mutation	FALSE	0.46097561	0	410	346	0.92	Clonal	likely_pathogenic
MOC21T	4	106196834	C	T	TET2	p.P1723S	Missense_Mutation	FALSE	0.461538462	0	286	315	0.92	Clonal	likely_pathogenic
MOC21T	4	143191898	G	A	INPP4B	p.T178I	Missense_Mutation	FALSE	0.360294118	0	408	306	0.72	Subclonal	passenger
MOC21T	4	143235890	T	C	INPP4B	p.H133R	Missense_Mutation	FALSE	0.5	0	316	284	1	Clonal	passenger
MOC25T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.419475655	0	534	231	1	Clonal	likely_pathogenic
MOC25T	17	7578446	TGGCCATGGCGCGGACGCGG	T	TP53	p.TRVRAMA155fs	Frame_Shift_Del	FALSE	0.281690141	0	355	166	0.64	Subclonal	likely_pathogenic
MOC25T	13	32932035	G	A	BRCA2	p.D2592N	Missense_Mutation	FALSE	0.274760383	0.008064516	313	124	0.9	Clonal	passenger
MOC25T	20	57429086	G	A	GNAS	p.A256T	Missense_Mutation	FALSE	0.339130435	0.007936508	460	126	1	Clonal	passenger
MOC31T	12	25398285	C	T	KRAS	p.G12S	Missense_Mutation	TRUE	0.421171171	0.004115226	444	486	1	Clonal	likely_pathogenic
MOC31T	12	56492683	G	A	ERBB3	p.V945I	Missense_Mutation	FALSE	0.808290155	0	193	79	1	Clonal	likely_pathogenic
MOC31T	17	7990712	C	T	ALOX12B	p.G17R	Missense_Mutation	FALSE	0.056074766	0.009174312	107	109	0.11	Subclonal	passenger
MOC31T	6	161969968	C	T	PARK2	p.R334H	Missense_Mutation	FALSE	0.363057325	0.004291845	157	233	1	Clonal	passenger
MOC31T	17	7576865	A	T	TP53	p.Y327*	Nonsense_Mutation	FALSE	0.550458716	0	109	223	1	Clonal	likely_pathogenic
MOC38T	17	7577121	G	A	TP53	p.R273C	Missense_Mutation	TRUE	0.428571429	0.003575685	21	839	0.94	Clonal	likely_pathogenic
MOC38T	3	178936082	G	A	PIK3CA	p.E542K	Missense_Mutation	TRUE	0.384615385	0	26	203	0.85	Clonal	likely_pathogenic
MOC38T	1	27105963	CT	C	ARID1A	p.F1859Sfs*24	Frame_Shift_Del	FALSE	0.785714286	0.003355705	14	596	0.94	Clonal	likely_pathogenic
MOC38T	12	49443666	AC	A	KMT2D	p.G1235Vfs*95	Frame_Shift_Del	FALSE	0.4	0.008574491	25	933	0.88	Clonal	likely_pathogenic
MOC38T	12	49444249	TG	T	KMT2D	p.Q1041Sfs*15	Frame_Shift_Del	FALSE	0.423076923	0.000980392	26	1020	0.93	Clonal	likely_pathogenic
MOC38T	12	121432114	CG	C	HNF1A	p.P291Qfs*51	Frame_Shift_Del	FALSE	0.4	0.002164502	30	924	0.88	Clonal	likely_pathogenic
MOC38T	13	28611369	TC	T	FLT3	p.E421Kfs*13	Frame_Shift_Del	FALSE	0.095238095	0	21	718	0.21	Subclonal	likely_pathogenic
MOC38T	2	215593634	GC	G	BARD1	p.G700Afs*14	Frame_Shift_Del	FALSE	0.307692308	0.003067485	13	652	0.68	Subclonal	passenger
MOC38T	20	31022441	AG	A	ASXL1	p.G645Vfs*58	Frame_Shift_Del	FALSE	0.304347826	0.018421053	23	380	0.67	Subclonal	likely_pathogenic
MOC38T	7	151874187	TTA	T	KMT2C	p.D2783Efs*4	Frame_Shift_Del	FALSE	0.297297297	0	37	591	0.65	Subclonal	likely_pathogenic
MOC38T	1	193117012	A	AT	CDC73	p.A251Cfs*16	Frame_Shift_Ins	FALSE	0.272727273	0.001040583	22	961	0.6	Subclonal	likely_pathogenic
MOC38T	3	89391023	T	TA	EPHA3	p.C366Mfs*9	Frame_Shift_Ins	FALSE	0.181818182	0.001663894	11	601	0.4	Subclonal	likely_pathogenic
MOC38T	3	52621442	ACTT	A	PBRM1	p.E991del	In_Frame_Del	FALSE	0.46875	0.001278772	32	782	0.56	Subclonal	likely_pathogenic
MOC38T	12	463288	G	A	KDM5A	p.P328L	Missense_Mutation	FALSE	0.102040816	0	49	829	0.22	Subclonal	passenger
MOC38T	12	56494873	G	A	ERBB3	p.R1077Q	Missense_Mutation	FALSE	0.084745763	0	59	835	0.19	Subclonal	passenger
MOC38T	12	121434146	C	T	HNF1A	p.T346I	Missense_Mutation	FALSE	0.785714286	0.001233046	14	811	1	Clonal	passenger
MOC38T	12	133226270	G	A	POLE	p.T1263I	Missense_Mutation	FALSE	0.3125	0.001262626	16	792	0.69	Subclonal	passenger
MOC38T	2	61145544	G	A	REL	p.R219H	Missense_Mutation	FALSE	0.208333333	0.003649635	24	548	0.46	Subclonal	likely_pathogenic
MOC38T	2	190656560	G	A	PMS1	p.V9I	Missense_Mutation	FALSE	0.125	0	32	665	0.28	Subclonal	likely_pathogenic
MOC38T	2	190719037	G	C	PMS1	p.E347Q	Missense_Mutation	FALSE	0.411764706	0	17	320	0.91	Clonal	likely_pathogenic
MOC38T	3	52442080	G	A	BAP1	p.S90F	Missense_Mutation	FALSE	0.615384615	0.001694915	13	590	0.74	Subclonal	passenger
MOC38T	5	223646	A	T	SDHA	p.D38V	Missense_Mutation	FALSE	0.592592593	0.046931408	27	831	1	Clonal	passenger
MOC38T	6	157099858	G	C	ARID1B	p.M265I	Missense_Mutation	FALSE	0.142857143	0.001222494	28	818	0.31	Subclonal	passenger
MOC38T	7	116340262	A	G	MET	p.N375S	Missense_Mutation	FALSE	0.7	0	30	490	1	Clonal	likely_pathogenic
MOC38T	23	47030588	G	T	RBM10	p.E121D	Missense_Mutation	FALSE	0.137931034	0.003442341	29	581	0.3	Subclonal	passenger
MOC38T	12	49432651	G	A	KMT2D	p.R2830*	Nonsense_Mutation	FALSE	0.272727273	0.001201923	11	832	0.6	Subclonal	likely_pathogenic
MOC38T	7	106509300	C	T	PIK3CG	p.Q432*	Nonsense_Mutation	FALSE	0.416666667	0	12	795	0.92	Clonal	likely_pathogenic
MOC38T	12	416111	C	T	KDM5A	p.X1358_splice	Splice_Site	FALSE	0.142857143	0.004076087	42	736	0.31	Subclonal	likely_pathogenic
MOC04T	17	7578394	T	A	TP53	p.H179L	Missense_Mutation	TRUE	0.453781513	0	119	180	1	Clonal	likely_pathogenic
MOC46T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.566909976	0	411	179	1	Clonal	likely_pathogenic
MOC46T	3	41266136	T	C	CTNNB1	p.S45P	Missense_Mutation	TRUE	0.540880503	0	318	88	1	Clonal	likely_pathogenic
MOC46T	3	41266133	C	G	CTNNB1	p.P44A	Missense_Mutation	FALSE	0.541538462	0	325	91	1	Clonal	likely_pathogenic
MOC48T	12	25398284	C	A	KRAS	p.G12V	Missense_Mutation	TRUE	0.781767956	0	362	31	1	Clonal	likely_pathogenic
MOC48T	17	7578190	T	C	TP53	p.Y220C	Missense_Mutation	TRUE	0.74	0	100	28	1	Clonal	likely_pathogenic
MOC48T	12	49433093	T	A	KMT2D	p.I2760F	Missense_Mutation	FALSE	0.243902439	0	82	42	0.63	Subclonal	passenger
MOC48T	17	16068412	C	T	NCOR1	p.D167N	Missense_Mutation	FALSE	0.057377049	0	122	42	0.15	Subclonal	passenger
MOC51T	12	25398285	C	G	KRAS	p.G12R	Missense_Mutation	TRUE	0.241666667	0	240	193	1	Clonal	likely_pathogenic
MOC51T	1	156843578	C	T	NTRK1	p.P335L	Missense_Mutation	FALSE	0.213836478	0.008695652	159	115	0.92	Clonal	passenger
MOC51T	17	7577046	C	A	TP53	p.E298*	Nonsense_Mutation	FALSE	0.295652174	0	115	82	0.98	Clonal	likely_pathogenic
MOC52T	12	25398285	C	G	KRAS	p.G12R	Missense_Mutation	TRUE	0.376146789	0	109	217	0.99	Clonal	likely_pathogenic
MOC52T	17	7577082	C	T	TP53	p.E286K	Missense_Mutation	TRUE	0.352941176	0	102	94	0.93	Clonal	likely_pathogenic
MOC52T	3	47147573	C	T	SETD2	p.D1585N	Missense_Mutation	FALSE	0.058139535	0	86	57	0.21	Subclonal	passenger
MOC60T	12	25380275	T	G	KRAS	p.Q61H	Missense_Mutation	TRUE	0.592920354	0	113	157	1	Clonal	likely_pathogenic

MOC60T	17	7579313	G	A	TP53	p.T125M	Missense_Mutation	TRUE	0.543209877	0	81	124	1	Clonal	likely_pathogenic
MOC60T	20	31022441	A	AG	ASXL1	p.G643fs	Frame_Shift_Ins	FALSE	0.223214286	0.027210884	112	147	0.74	Subclonal	likely_pathogenic
MOC62T	10	89692905	G	A	PTEN	p.R130Q	Missense_Mutation	TRUE	0.039513678	0.004237288	329	236	0.33	Subclonal	likely_pathogenic
MOC62T	2	61719472	C	T	XPO1	p.E571K	Missense_Mutation	TRUE	0.053191489	0	188	137	0.44	Subclonal	likely_pathogenic
MOC62T	3	41268766	A	C	CTNNB1	p.K335T	Missense_Mutation	TRUE	0.032019704	0	406	283	0.27	Subclonal	likely_pathogenic
MOC62T	3	178952074	G	T	PIK3CA	p.M1043I	Missense_Mutation	TRUE	0.02994012	0	334	199	0.25	Subclonal	likely_pathogenic
MOC62T	5	112174631	C	T	APC	p.R1114*	Nonsense_Mutation	TRUE	0.041916168	0	334	230	0.35	Subclonal	likely_pathogenic
MOC62T	3	178952018	A	G	PIK3CA	p.T1025A	Missense_Mutation	FALSE	0.031496063	0	381	248	0.26	Subclonal	likely_pathogenic
MOC62T	3	189586470	C	T	TP63	p.S365L	Missense_Mutation	FALSE	0.06185567	0	194	101	0.52	Subclonal	likely_pathogenic
MOC62T	9	101900288	C	T	TGFBR1	p.S241L	Missense_Mutation	FALSE	0.039506173	0	405	250	0.33	Subclonal	likely_pathogenic
MOC62T	1	27087469	C	A	ARID1A	p.F681L	Missense_Mutation	FALSE	0.034722222	0	432	230	0.29	Subclonal	passenger
MOC62T	1	65305439	C	T	JAK1	p.E897K	Missense_Mutation	FALSE	0.04887218	0	266	113	0.41	Subclonal	likely_pathogenic
MOC62T	1	162735844	A	C	DDR2	p.T385P	Missense_Mutation	FALSE	0.042979943	0	349	236	0.36	Subclonal	likely_pathogenic
MOC62T	1	162745566	G	T	DDR2	p.D661Y	Missense_Mutation	FALSE	0.062686567	0.00462963	335	216	0.52	Subclonal	likely_pathogenic
MOC62T	1	176104165	C	T	RFWD2	p.A317T	Missense_Mutation	FALSE	0.040322581	0	248	205	0.34	Subclonal	passenger
MOC62T	10	43596047	C	A	RET	p.L72I	Missense_Mutation	FALSE	0.059859155	0	284	108	0.5	Subclonal	passenger
MOC62T	10	70406295	C	T	TET1	p.T1270M	Missense_Mutation	FALSE	0.042253521	0.004291845	355	233	0.35	Subclonal	passenger
MOC62T	10	70406692	C	A	TET1	p.F1402L	Missense_Mutation	FALSE	0.032520325	0	369	266	0.27	Subclonal	passenger
MOC62T	10	70426835	C	A	TET1	p.L1499I	Missense_Mutation	FALSE	0.043918919	0	296	188	0.37	Subclonal	passenger
MOC62T	10	88659602	T	G	BMPR1A	p.L129V	Missense_Mutation	FALSE	0.0302267	0	397	319	0.25	Subclonal	passenger
MOC62T	10	104375092	C	T	SUFU	p.R364W	Missense_Mutation	FALSE	0.054755043	0.006622517	347	151	0.46	Subclonal	passenger
MOC62T	11	17741416	C	A	MYOD1	p.F29L	Missense_Mutation	FALSE	0.043583535	0.007936508	413	126	0.36	Subclonal	passenger
MOC62T	11	64575382	T	G	MEN1	p.N217T	Missense_Mutation	FALSE	0.048034934	0	229	127	0.4	Subclonal	passenger
MOC62T	11	77047314	G	T	PAK1	p.F410L	Missense_Mutation	FALSE	0.03021978	0	364	184	0.25	Subclonal	passenger
MOC62T	11	94180598	T	G	MRE11A	p.T524P	Missense_Mutation	FALSE	0.028806584	0	243	139	0.24	Subclonal	likely_pathogenic
MOC62T	11	108139242	C	A	ATM	p.T915N	Missense_Mutation	FALSE	0.040123457	0	324	211	0.33	Subclonal	passenger
MOC62T	11	108183219	T	G	ATM	p.S2000R	Missense_Mutation	FALSE	0.056179775	0	89	72	0.47	Subclonal	likely_pathogenic
MOC62T	11	118373267	T	G	KMT2A	p.N2217K	Missense_Mutation	FALSE	0.039772727	0	352	176	0.33	Subclonal	passenger
MOC62T	11	119155929	C	A	CBL	p.P532T	Missense_Mutation	FALSE	0.035175879	0	597	275	0.29	Subclonal	likely_pathogenic
MOC62T	12	402132	C	A	KDM5A	p.K1553N	Missense_Mutation	FALSE	0.047191011	0	445	259	0.39	Subclonal	passenger
MOC62T	12	18435088	C	A	PIK3C2G	p.L25I	Missense_Mutation	FALSE	0.036585366	0	246	189	0.3	Subclonal	passenger
MOC62T	12	46230632	G	T	ARID2	p.R294I	Missense_Mutation	FALSE	0.031914894	0	376	234	0.27	Subclonal	likely_pathogenic
MOC62T	12	46243954	G	T	ARID2	p.R683I	Missense_Mutation	FALSE	0.03877551	0	490	257	0.32	Subclonal	passenger
MOC62T	12	56490608	A	T	ERBB3	p.Q751L	Missense_Mutation	FALSE	0.047058824	0	255	110	0.39	Subclonal	likely_pathogenic
MOC62T	12	69203067	A	C	MDM2	p.T26P	Missense_Mutation	FALSE	0.034375	0	320	196	0.29	Subclonal	passenger
MOC62T	12	102813307	C	T	IGF1	p.D128N	Missense_Mutation	FALSE	0.049382716	0	324	186	0.41	Subclonal	passenger
MOC62T	12	115117340	G	T	TBX3	p.F278L	Missense_Mutation	FALSE	0.03180212	0	283	270	0.26	Subclonal	passenger
MOC62T	12	133219468	G	A	POLE	p.R1556W	Missense_Mutation	FALSE	0.055452865	0	541	156	0.46	Subclonal	passenger
MOC62T	12	133249857	C	G	POLE	p.A456P	Missense_Mutation	FALSE	0.043478261	0	138	58	0.36	Subclonal	passenger
MOC62T	13	28891696	A	C	FLT1	p.F1109V	Missense_Mutation	FALSE	0.048338369	0	331	138	0.4	Subclonal	likely_pathogenic
MOC62T	13	28931790	A	C	FLT1	p.F717V	Missense_Mutation	FALSE	0.039906103	0	426	213	0.33	Subclonal	passenger
MOC62T	13	48951156	G	A	RB1	p.E440K	Missense_Mutation	FALSE	0.038793103	0.005681818	232	176	0.32	Subclonal	likely_pathogenic
MOC62T	15	88476338	C	A	NTRK3	p.E598D	Missense_Mutation	FALSE	0.057324841	0	314	135	0.48	Subclonal	likely_pathogenic
MOC62T	15	90628243	C	A	IDH2	p.D390Y	Missense_Mutation	FALSE	0.039634146	0	328	97	0.33	Subclonal	likely_pathogenic
MOC62T	15	91292829	T	G	BLM	p.F111V	Missense_Mutation	FALSE	0.043046358	0	302	105	0.36	Subclonal	passenger
MOC62T	15	91358483	C	A	BLM	p.L1410I	Missense_Mutation	FALSE	0.031496063	0	381	169	0.26	Subclonal	passenger
MOC62T	16	9984955	A	C	GRIN2A	p.F337C	Missense_Mutation	FALSE	0.035326087	0	368	150	0.29	Subclonal	passenger
MOC62T	16	23647413	T	C	PALB2	p.K152E	Missense_Mutation	FALSE	0.038123167	0	341	192	0.32	Subclonal	passenger
MOC62T	17	15978910	T	C	NCOR1	p.E1203G	Missense_Mutation	FALSE	0.031662269	0	379	258	0.26	Subclonal	likely_pathogenic
MOC62T	17	29684332	C	A	NF1	p.L2639I	Missense_Mutation	FALSE	0.055944056	0	286	180	0.47	Subclonal	passenger
MOC62T	17	47696386	G	A	SPOP	p.A146V	Missense_Mutation	FALSE	0.039145907	0	281	183	0.33	Subclonal	passenger
MOC62T	17	59761049	C	A	BRIP1	p.D1120Y	Missense_Mutation	FALSE	0.038004751	0	421	229	0.32	Subclonal	passenger
MOC62T	17	59926512	C	T	BRIP1	p.R162Q	Missense_Mutation	FALSE	0.0425	0.003937008	400	254	0.35	Subclonal	passenger
MOC62T	17	66526547	G	A	PRKAR1A	p.R368Q	Missense_Mutation	FALSE	0.036474164	0	329	206	0.3	Subclonal	passenger
MOC62T	18	739801	T	G	YES1	p.L357F	Missense_Mutation	FALSE	0.063037249	0	349	217	0.53	Subclonal	likely_pathogenic
MOC62T	18	745794	T	G	YES1	p.K213T	Missense_Mutation	FALSE	0.04	0	300	202	0.33	Subclonal	likely_pathogenic
MOC62T	18	60795942	G	T	BCL2	p.F212L	Missense_Mutation	FALSE	0.045283019	0.008130081	265	123	0.38	Subclonal	passenger
MOC62T	19	15271637	C	T	NOTCH3	p.E2268K	Missense_Mutation	FALSE	0.054263566	0	387	136	0.45	Subclonal	passenger
MOC62T	19	15278123	C	T	NOTCH3	p.A1767T	Missense_Mutation	FALSE	0.039130435	0	460	186	0.33	Subclonal	passenger
MOC62T	2	16082433	C	T	MYCN	p.L83F	Missense_Mutation	FALSE	0.04950495	0	202	83	0.41	Subclonal	passenger
MOC62T	2	25964983	A	C	ASXL2	p.I1408S	Missense_Mutation	FALSE	0.045576408	0	373	134	0.38	Subclonal	likely_pathogenic
MOC62T	2	25965013	G	A	ASXL2	p.S1398L	Missense_Mutation	FALSE	0.056300268	0	373	164	0.47	Subclonal	likely_pathogenic
MOC62T	2	25982446	T	G	ASXL2	p.N282H	Missense_Mutation	FALSE	0.035326087	0	368	213	0.29	Subclonal	passenger
MOC62T	2	61121563	G	A	REL	p.R62K	Missense_Mutation	FALSE	0.03652968	0	219	131	0.3	Subclonal	passenger
MOC62T	2	178096050	C	A	NFE2L2	p.E427D	Missense_Mutation	FALSE	0.0375	0	240	96	0.31	Subclonal	passenger
MOC62T	2	178096354	T	G	NFE2L2	p.K326T	Missense_Mutation	FALSE	0.03125	0	384	220	0.26	Subclonal	passenger
MOC62T	2	198269854	T	G	SF3B1	p.R495S	Missense_Mutation	FALSE	0.032352941	0	340	193	0.27	Subclonal	likely_pathogenic
MOC62T	2	212248565	C	A	ERBB4	p.K1234N	Missense_Mutation	FALSE	0.04587156	0	436	201	0.38	Subclonal	likely_pathogenic
MOC62T	2	212285292	G	T	ERBB4	p.F1003L	Missense_Mutation	FALSE	0.048	0	375	228	0.4	Subclonal	likely_pathogenic
MOC62T	2	212568865	G	T	ERBB4	p.S418Y	Missense_Mutation	FALSE	0.033222591	0	301	183	0.28	Subclonal	passenger
MOC62T	2	212812164	T	G	ERBB4	p.N138H	Missense_Mutation	FALSE	0.032786885	0	244	162	0.27	Subclonal	passenger
MOC62T	20	9624884	C	A	PAK5	p.K31N	Missense_Mutation	FALSE	0.032200358	0	559	271	0.3	Subclonal	likely_pathogenic
MOC62T	20	39726974	A	C	TOP1	p.K324N	Missense_Mutation	FALSE	0.056603774	0	212	122	0.53	Subclonal	likely_pathogenic
MOC62T	20	40757428	G	A	PTPRT	p.P938L	Missense_Mutation	FALSE	0.039170507	0.005586592	434	179	0.37	Subclonal	likely_pathogenic
MOC62T	20	57430328	G	A	GNAS	p.D670N	Missense_Mutation	FALSE	0.05019305	0	518	163	0.47	Subclonal	likely_pathogenic
MOC62T	21	42840334	C	T	TMPRSS2	p.D435N	Missense_Mutation	FALSE	0.053380783	0.009090909	281	110	0.44	Subclonal	passenger
MOC62T	22	30035159	G	T	NF2	p.E107D	Missense_Mutation	FALSE	0.04076087	0	368	188	0.34	Subclonal	likely_pathogenic
MOC62T	22	30057277	G	T	NF2	p.K253N	Missense_Mutation	FALSE	0.044854881	0	379	151	0.37	Subclonal	passenger
MOC62T	22	30074265	C	A	NF2	p.F509L	Missense_Mutation	FALSE	0.044217687	0	294	107	0.37	Subclonal	passenger
MOC62T	3	41266633	G	A	CTNNB1	p.D144N	Missense_Mutation	FALSE	0.042492918	0	353	223	0.35	Subclonal	likely_pathogenic
MOC62T	3	41279559	G	A	CTNNB1	p.R710H	Missense_Mutation	FALSE	0.050139276	0.003333333	359	300	0.42	Subclonal	passenger
MOC62T	3	47165023	C	T	SETD2	p.R368Q	Missense_Mutation	FALSE	0.061538462	0	260	134	0.51	Subclonal	passenger
MOC62T	3	47205371	A	G	SETD2	p.F15S	Missense_Mutation	FALSE	0.045070423	0	710	333	0.38	Subclonal	passenger
MOC62T	3	70005612	G	A	MITF	p.R321Q	Missense_Mutation	FALSE	0.038135593	0	236	175	0.32	Subclonal	likely_pathogenic
MOC62T	3	134885846	G	A	EPHB1	p.R586Q	Missense_Mutation	FALSE	0.049180328	0	183	60	0.41	Subclonal	passenger
MOC62T	3	134968206	A	G	EPHB1	p.I907V	Missense_Mutation	FALSE	0.046703297	0	364	142	0.39	Subclonal	likely_pathogenic
MOC62T	3	142269034	T	G	ATR	p.L972F	Missense_Mutation	FALSE	0.044871795	0	312	242	0.37	Subclonal	passenger
MOC62T	3	181430786	C	T	SOX2	p.S213L	Missense_Mutation	FALSE	0.053619303	0	373	173	0.45	Subclonal	passenger
MOC62T	3	182662953	G	A	DCUN1D1	p.P237S	Missense_Mutation	FALSE	0.038022814	0	263	153	0.32	Subclonal	passenger
MOC62T	3	185183566	C	T	MAP3K13	p.R474W	Missense_Mutation	FALSE	0.056338028	0	355	171	0.47	Subclonal	likely_pathogenic
MOC62T	4	55144623	G	T	PDGFRA	p.E699D	Missense_Mutation	FALSE	0.058103976	0.005263158	327	190	0.48	Subclonal	likely_pathogenic
MOC62T	4	55592106	C	A	KIT	p.S477Y	Missense_Mutation	FALSE	0.048991354	0	347	207	0.41	Subclonal	passenger
MOC62T	4	55976930	G	T	KDR	p.P328T	Missense_Mutation	FALSE	0.032653061	0	245	121	0.27	Subclonal	passenger
MOC62T	4	55981193	C	A	KDR	p.R169I	Missense_Mutation	FALSE	0.039215686	0	306	207	0.33	Subclonal	passenger
MOC62T	4	66230907	T	G	EPHA5	p.E688D	Missense_Mutation	FALSE	0.052631579	0	190	108	0.44	Subclonal	likely_pathogenic
MOC62T	4	106156703	A	G	TET2	p.N535S	Missense_Mutation	FALSE	0.051851852	0	270	126	0.43	Subclonal	passenger
MOC62T	4	143003314	G	A	INPP4B	p.R838C	Missense_Mutation	FALSE	0.045454545	0	286	183	0.38	Subclonal	passenger
MOC62T	4	187524969	C	T	FAT1	p.D3571N	Missense_Mutation	FALSE	0.056338028	0	284	133	0.47	Subclonal	passenger
MOC62T	5	1282603	C	A	TERT	p.K570N	Missense_Mutation	FALSE	0.036101083	0	277	87	0.3	Subclonal	passenger
MOC62T	5	35876352	C	A	IL7R	p.L382I	Missense_Mutation	FALSE	0.048	0	250	146	0.4	Subclonal	passenger
MOC62T	5	86649004	A	C	RASA1	p.K428N	Missense_Mutation	FALSE	0.052631579	0	228	154	0.44	Subclonal	likely_pathogenic
MOC62T	5	112102935	A	C	APC	p.K90N	Missense_Mutation	FALSE	0.053061224	0	245	184	0.44	Subclonal	likely_pathogenic
MOC62T	5	112175490	C	T	APC	p.S1400L	Missense_Mutation	FALSE	0.049180328	0	244	134	0.41	Subclonal	likely_pathogenic
MOC62T	5	176562918	A	C	NSD1	p.N272H	Missense_Mutation	FALSE	0.060728745	0	247	209	0.51	Subclonal	passenger
MOC62T	6	20480168	G	A	E2F3	p.R162Q	Missense_Mutation	FALSE	0.054054054	0	222	92	0.45	Subclonal	passenger
MOC62T	6	117609960	C	A	ROS1	p.D2247Y	Missense_Mutation	FALSE	0.035598706	0	309	179	0.3	Subclonal	likely_pathogenic
MOC62T	6	117679019	T	C	ROS1	p.I1268V	Missense_Mutation	FALSE	0.043902439	0	205	116	0.37	Subclonal	likely_pathogenic
MOC62T	6	117687344	T	G	ROS1	p.I903L	Missense_Mutation	FALSE	0.057057057	0	333	156	0.48	Subclonal	passenger
MOC62T	6	117715484	T	G	ROS1	p.Q335H	Missense_Mutation	FALSE	0.061643836	0	146	132	0.51	Subclonal	passenger
MOC62T	6	149997741	G	T	LATS1	p.S909Y	Missense_Mutation	FALSE	0.04290429	0	303	209	0.36	Subclonal	likely_pathogenic
MOC62T	6	152265489	G	T	ESR1	p.Q314H	Missense_Mutation	FALSE	0.031468531	0	286	215	0.26	Subclonal	passenger
MOC62T	6	152382178	G	A	ESR1	p.A430T	Missense_Mutation	FALSE	0.048109966	0	291	229	0.4	Subclonal	passenger
MOC62T	6	162864499	A	G	PARK2	p.V5A	Missense_Mutation	FALSE	0.045283019	0	265	102	0.38	Subclonal	passenger
MOC62T	7	2974166	G	A	CARD11	p.S480L	Missense_Mutation	FALSE	0.050955414	0	314	85	0.42	Subclonal	passenger
MOC62T	7	13935673	G	A	ETV1	p.P418S	Missense_Mutation	FALSE	0.044247788	0	226	122	0.37	Subclonal	passenger
MOC62T	7	81355310	C	T	HGF	p.R355Q	Missense_Mutation	FALSE	0.037288136	0	295	214	0.31	Subclonal	passenger
MOC62T	7	106513165	G	T	PIK3CG	p.R690I	Missense_Mutation	FALSE	0.042780749	0	187	83	0.36	Subclonal	likely_pathogenic
MOC62T	7	106523498	G	T	PIK3CG	p.D884Y	Missense_Mutation	FALSE	0.039344262	0	305	143	0.33	Subclonal	likely_pathogenic
MOC62T	7	116409706	A	G	MET	p.D882G	Missense_Mutation	FALSE	0.06626506	0	166	93	0.55	Subclonal	likely_pathogenic
MOC62T	7	148515021	C	A	EZH2	p.E391D	Missense_Mutation	FALSE	0.04009434	0	424	228	0.33	Subclonal	passenger
MOC62T	7	148525883	C	T	EZH2	p.D192N	Missense_Mutation	FALSE	0.035812672	0	363	191	0.3	Subclonal	likely_pathogenic
MOC62T	7	152008954	T	G	KMT2C	p.K223T	Missense_Mutation	FALSE	0.057736721	0	433	288	0.48	Subclonal	passenger
MOC62T	8	38283760	G	T	FGFR1	p.R118S	Missense_Mutation	FALSE	0.04	0	200	98	0.33	Subclonal	likely_pathogenic

MOC62T	9	5090747	G	T	JAK2	p.E965D	Missense_Mutation	FALSE	0.040540541	0	148	84	0.34	Subclonal	likely_pathogenic
MOC62T	9	8319898	C	A	PTPRD	p.G1868V	Missense_Mutation	FALSE	0.038461538	0	416	252	0.32	Subclonal	likely_pathogenic
MOC62T	9	8518276	C	A	PTPRD	p.G372V	Missense_Mutation	FALSE	0.039130435	0	230	114	0.33	Subclonal	passenger
MOC62T	9	8528662	A	T	PTPRD	p.I157N	Missense_Mutation	FALSE	0.043046358	0	302	164	0.36	Subclonal	likely_pathogenic
MOC62T	9	8633406	C	T	PTPRD	p.R88Q	Missense_Mutation	FALSE	0.0625	0	352	177	0.52	Subclonal	likely_pathogenic
MOC62T	9	8733794	C	T	PTPRD	p.R17H	Missense_Mutation	FALSE	0.057432432	0	296	146	0.48	Subclonal	passenger
MOC62T	9	87325640	G	T	NTRK2	p.D173Y	Missense_Mutation	FALSE	0.054404145	0	386	220	0.45	Subclonal	likely_pathogenic
MOC62T	9	98270582	A	C	PTCH1	p.I21S	Missense_Mutation	FALSE	0.076271186	0	118	76	0.64	Subclonal	likely_pathogenic
MOC62T	23	1314969	T	G	CRLF2	p.K231T	Missense_Mutation	FALSE	0.041401274	0	314	89	0.39	Subclonal	passenger
MOC62T	23	39911509	G	T	BCOR	p.F1707L	Missense_Mutation	FALSE	0.051820728	0	714	323	0.48	Subclonal	likely_pathogenic
MOC62T	23	39922917	G	A	BCOR	p.A1264V	Missense_Mutation	FALSE	0.038356164	0	365	132	0.36	Subclonal	likely_pathogenic
MOC62T	23	39932617	G	A	BCOR	p.P661L	Missense_Mutation	FALSE	0.03125	0	320	115	0.29	Subclonal	passenger
MOC62T	23	39933942	C	A	BCOR	p.K219N	Missense_Mutation	FALSE	0.050880626	0	511	156	0.47	Subclonal	passenger
MOC62T	23	44894222	A	C	KDM6A	p.N204T	Missense_Mutation	FALSE	0.064981949	0	554	363	0.61	Subclonal	passenger
MOC62T	23	44949014	C	A	KDM6A	p.S1192Y	Missense_Mutation	FALSE	0.045918367	0	392	213	0.43	Subclonal	likely_pathogenic
MOC62T	23	44966727	T	G	KDM6A	p.I1317M	Missense_Mutation	FALSE	0.031428571	0	700	478	0.29	Subclonal	passenger
MOC62T	23	53239748	T	C	KDM5C	p.K532E	Missense_Mutation	FALSE	0.044176707	0	498	190	0.41	Subclonal	likely_pathogenic
MOC62T	23	53240825	C	T	KDM5C	p.E419K	Missense_Mutation	FALSE	0.044217687	0	588	216	0.41	Subclonal	passenger
MOC62T	23	63410667	G	T	AMER1	p.L834I	Missense_Mutation	FALSE	0.035947712	0	612	243	0.34	Subclonal	passenger
MOC62T	23	63411223	C	A	AMER1	p.E648D	Missense_Mutation	FALSE	0.041176471	0	340	105	0.38	Subclonal	passenger
MOC62T	23	63411863	C	A	AMER1	p.G435V	Missense_Mutation	FALSE	0.05112782	0	665	232	0.48	Subclonal	passenger
MOC62T	23	70341515	C	T	MED12	p.S317F	Missense_Mutation	FALSE	0.025673941	0	779	340	0.24	Subclonal	passenger
MOC62T	23	76763854	C	T	ATRX	p.G2485E	Missense_Mutation	FALSE	0.046413502	0	474	248	0.43	Subclonal	passenger
MOC62T	23	76764055	T	C	ATRX	p.Y2418C	Missense_Mutation	FALSE	0.027972028	0	715	373	0.26	Subclonal	passenger
MOC62T	23	76849266	C	A	ATRX	p.D2004Y	Missense_Mutation	FALSE	0.047854785	0	606	300	0.45	Subclonal	passenger
MOC62T	23	76937236	C	A	ATRX	p.R1171I	Missense_Mutation	FALSE	0.054054054	0	592	339	0.5	Subclonal	passenger
MOC62T	23	76937258	C	A	ATRX	p.D1164Y	Missense_Mutation	FALSE	0.041584158	0	505	289	0.39	Subclonal	passenger
MOC62T	23	76937356	C	A	ATRX	p.R1131I	Missense_Mutation	FALSE	0.044077135	0	363	204	0.41	Subclonal	likely_pathogenic
MOC62T	23	76938330	C	A	ATRX	p.K806N	Missense_Mutation	FALSE	0.045226131	0	398	213	0.42	Subclonal	likely_pathogenic
MOC62T	23	76944355	C	A	ATRX	p.D184Y	Missense_Mutation	FALSE	0.043405676	0	599	337	0.41	Subclonal	passenger
MOC62T	23	76949418	T	G	ATRX	p.I127L	Missense_Mutation	FALSE	0.045833333	0	480	273	0.43	Subclonal	passenger
MOC62T	23	76953080	C	T	ATRX	p.R78Q	Missense_Mutation	FALSE	0.038720539	0.005347594	594	374	0.36	Subclonal	passenger
MOC62T	23	100608323	T	G	BTK	p.E589D	Missense_Mutation	FALSE	0.037572254	0	346	124	0.35	Subclonal	likely_pathogenic
MOC62T	23	100615608	A	C	BTK	p.F242V	Missense_Mutation	FALSE	0.032307692	0	650	253	0.3	Subclonal	passenger
MOC62T	23	100630232	G	A	BTK	p.S14F	Missense_Mutation	FALSE	0.031007752	0	645	226	0.29	Subclonal	passenger
MOC62T	23	123164844	A	G	STAG2	p.K53E	Missense_Mutation	FALSE	0.040084388	0	474	248	0.37	Subclonal	passenger
MOC62T	23	123220413	A	C	STAG2	p.K1024Q	Missense_Mutation	FALSE	0.052752294	0	436	237	0.49	Subclonal	passenger
MOC62T	17	29677227	C	T	NF1	p.R2450*	Nonsense_Mutation	FALSE	0.044742729	0.003937008	447	254	0.37	Subclonal	likely_pathogenic
MOC62T	2	25976476	G	A	ASXL2	p.R357*	Nonsense_Mutation	FALSE	0.043280182	0	439	263	0.36	Subclonal	passenger
MOC62T	1	27059183	C	A	ARID1A	p.S607*	Nonsense_Mutation	FALSE	0.036613272	0	437	211	0.31	Subclonal	likely_pathogenic
MOC62T	11	94192696	C	A	MRE11A	p.E460*	Nonsense_Mutation	FALSE	0.046511628	0	387	233	0.39	Subclonal	passenger
MOC62T	11	108175475	C	A	ATM	p.S1857*	Nonsense_Mutation	FALSE	0.030487805	0	328	204	0.25	Subclonal	likely_pathogenic
MOC62T	11	118374582	C	T	KMT2A	p.R2656*	Nonsense_Mutation	FALSE	0.037463977	0	347	159	0.31	Subclonal	likely_pathogenic
MOC62T	12	46230538	G	T	ARID2	p.E263*	Nonsense_Mutation	FALSE	0.049792531	0	241	145	0.41	Subclonal	likely_pathogenic
MOC62T	16	2647666	T	G	PDPK1	p.Y523*	Nonsense_Mutation	FALSE	0.04076087	0	368	139	0.34	Subclonal	likely_pathogenic
MOC62T	16	67654661	T	A	CTCF	p.L383*	Nonsense_Mutation	FALSE	0.041564792	0.004694836	409	213	0.35	Subclonal	likely_pathogenic
MOC62T	17	29586092	G	T	NF1	p.E1459*	Nonsense_Mutation	FALSE	0.043352601	0.004032258	346	248	0.36	Subclonal	likely_pathogenic
MOC62T	17	37676232	T	G	CDK12	p.L996*	Nonsense_Mutation	FALSE	0.058295964	0	446	176	0.49	Subclonal	likely_pathogenic
MOC62T	19	5223247	C	T	PTPRS	p.W852*	Nonsense_Mutation	FALSE	0.056338028	0	142	33	0.47	Subclonal	passenger
MOC62T	2	26068357	C	A	ASXL2	p.E45*	Nonsense_Mutation	FALSE	0.048192771	0	166	134	0.4	Subclonal	passenger
MOC62T	3	52663032	C	A	PBRM1	p.E441*	Nonsense_Mutation	FALSE	0.05859375	0	256	189	0.49	Subclonal	likely_pathogenic
MOC62T	3	70008509	G	T	MITF	p.E373*	Nonsense_Mutation	FALSE	0.037617555	0	319	186	0.31	Subclonal	likely_pathogenic
MOC62T	3	142274944	C	A	ATR	p.E706*	Nonsense_Mutation	FALSE	0.035856574	0	251	120	0.3	Subclonal	likely_pathogenic
MOC62T	4	55146574	G	T	PDGFRA	p.E750*	Nonsense_Mutation	FALSE	0.063973064	0.004694836	297	213	0.53	Subclonal	likely_pathogenic
MOC62T	4	187584747	G	A	FAT1	p.R1096*	Nonsense_Mutation	FALSE	0.046511628	0	258	154	0.39	Subclonal	likely_pathogenic
MOC62T	5	86645108	G	T	RASA1	p.E394*	Nonsense_Mutation	FALSE	0.043010753	0	279	217	0.36	Subclonal	likely_pathogenic
MOC62T	5	86672371	G	T	RASA1	p.E725*	Nonsense_Mutation	FALSE	0.041237113	0	194	120	0.34	Subclonal	likely_pathogenic
MOC62T	7	128845577	G	T	SMO	p.E292*	Nonsense_Mutation	FALSE	0.038709677	0	310	130	0.32	Subclonal	likely_pathogenic
MOC62T	9	8521370	C	A	PTPRD	p.E290*	Nonsense_Mutation	FALSE	0.030674847	0	326	177	0.26	Subclonal	passenger
MOC62T	9	101909998	G	T	TGFBR1	p.E440*	Nonsense_Mutation	FALSE	0.03654485	0	301	197	0.3	Subclonal	passenger
MOC62T	23	48650491	C	A	GATA1	p.S154*	Nonsense_Mutation	FALSE	0.029411765	0	680	185	0.27	Subclonal	likely_pathogenic
MOC62T	23	76889056	C	A	ATRX	p.E1652*	Nonsense_Mutation	FALSE	0.046641791	0	536	340	0.44	Subclonal	likely_pathogenic
MOC62T	23	76939766	C	A	ATRX	p.E328*	Nonsense_Mutation	FALSE	0.040665434	0	541	292	0.38	Subclonal	likely_pathogenic
MOC62T	23	100611821	C	A	BTK	p.E434*	Nonsense_Mutation	FALSE	0.041884817	0	573	229	0.39	Subclonal	passenger
MOC62T	23	123211837	G	T	STAG2	p.E902*	Nonsense_Mutation	FALSE	0.034798535	0.005571031	546	359	0.32	Subclonal	likely_pathogenic
MOC62T	5	35857117	C	A	IL7R	p.S13Y	Missense_Mutation	FALSE	0.041884817	0	191	141	0.35	Subclonal	
MOC62T	11	64571891	G	A	MEN1	p.S588L	Missense_Mutation	FALSE	0.035487959	0	789	449	0.3	Subclonal	
MOC62T	23	123156522	G	T	STAG2	p.X15_splice	Splice_Site	FALSE	0.04048583	0	494	239	0.38	Subclonal	likely_pathogenic
MOC67T	9	21974726	GCCTCCAGCAGCGCCCGCA	G	CDKN2A	p.VRALLE28del	In_Frame_Del	FALSE	0.247706422	0	109	42	0.67	Subclonal	likely_pathogenic
MOC67T	17	7578542	G	C	TP53	p.L130V	Missense_Mutation	FALSE	0.571428571	0	63	43	1	Clonal	likely_pathogenic
MOC67T	19	10602493	C	T	KEAP1	p.R362Q	Missense_Mutation	FALSE	0.656862745	0	102	51	1	Clonal	passenger
MOC72T	12	25398281	C	T	KRAS	p.G13D	Missense_Mutation	TRUE	0.352791878	0	394	177	1	Clonal	likely_pathogenic
MOC72T	17	7579355	A	T	TP53	p.L111Q	Missense_Mutation	TRUE	0.189781022	0	137	86	0.54	Subclonal	likely_pathogenic
MOC72T	3	47158140	C	T	SETD2	p.C1520Y	Missense_Mutation	FALSE	0.1525	0	400	209	0.43	Subclonal	passenger

MAF, mutant allele fraction