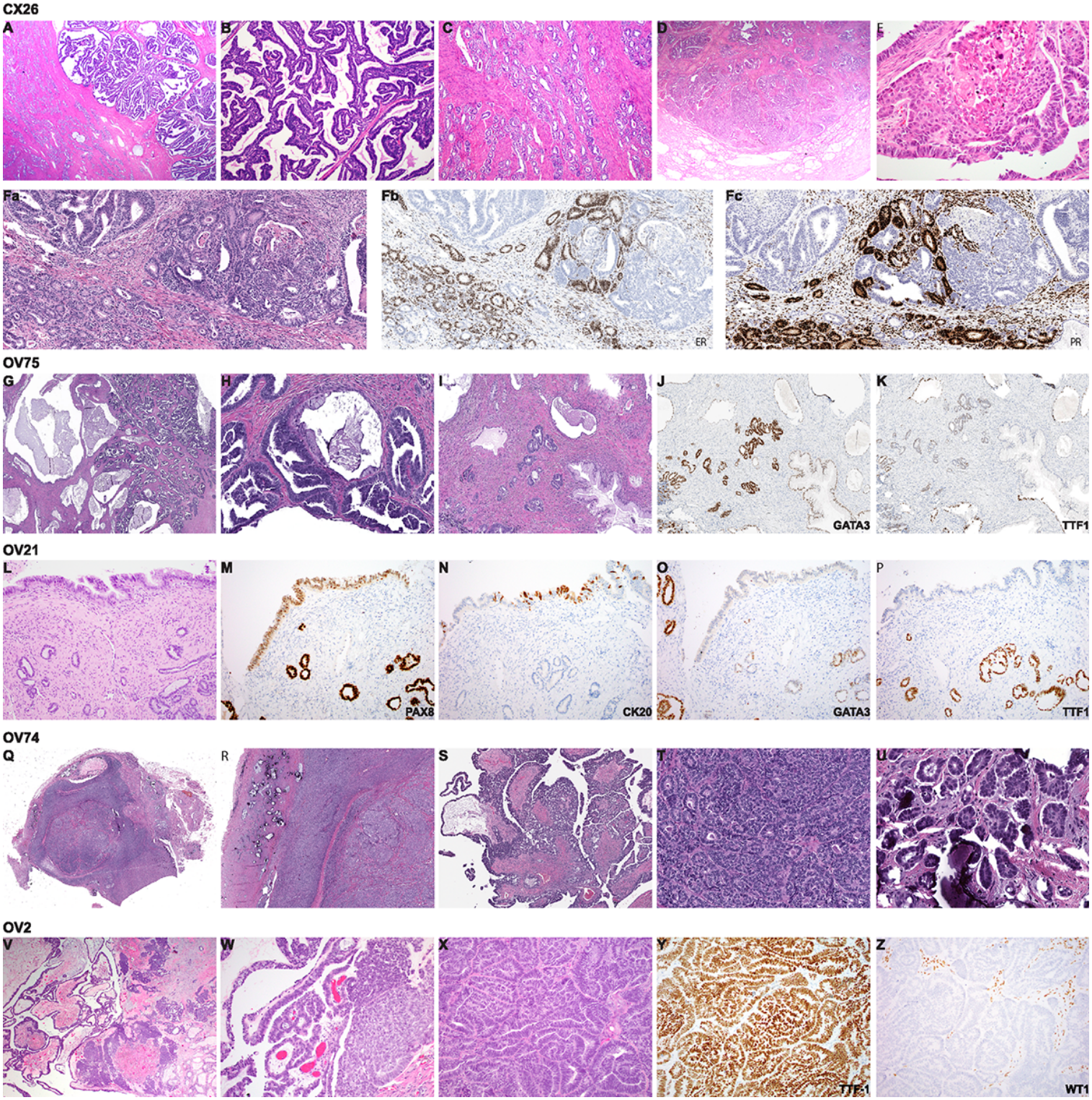
Supplementary Figure S1



Supplementary Figure S1: Morphologic patterns of cervical mesonephric and ovarian mesonephric-like carcinomas with mixed histology and matched metastasis.

Representative hematoxylin and eosin-stained (H&E) sections and immunohistochemistry of the histologically distinct components of cervical mixed mesonephric and endometrioid carcinoma CX26 (**A-F**), including the intramural and exophytic components of mesonephric carcinoma (**A**), exophytic mesonephric component with slender villoglandular-like architecture (**B**), intramural mesonephric component with tubules containing eosinophilic luminal secretions (**C**), endometrioid (top) component juxtaposed to mesonephric (bottom) component (**D**) and endometrioid component with squamous differentiation (**E**), H&E showing the endometrioid component on high power with focal squamous differentiation on right (**Fa**), ER (**Fb**) and PR (**Fc**); Mixed mesonephric-like carcinoma and mucinous borderline tumor OV75 (**G-K**), showing mesonephric carcinoma (right) and mucinous neoplasm (left) (**G**), higher power showing intimate association of the two components (**H**), H&E of mixed components corresponding to immunohistochemistry (**I**), GATA3 expressed in both mesonephric-like and mucinous tumors (**J**) and TTF-1 expressed only in mesonephric-like component (**K**); Mesonephric-like carcinoma and mucinous borderline tumor OV21 (**L-P**), H&E showing gastrointestinal type mucinous component lining cyst wall (top) with mesonephric-like component within stroma (**L**), immunohistochemistry shows diffuse PAX8 expression in both components (**M**), focal CK20 expression in the mucinous component only (**N**); GATA3 (**O**) and TTF-1 (**P**) expression in mesonephric component only; Mesonephric-like and low-grade serous carcinoma (LSGC) OV74 (**Q-U**), whole slide image of ovary with central nodule of mesonephric-like carcinoma and LGSC along ovarian surface (**Q**), intermediate power of mesonephric-like carcinoma (right) and LGSC with psammoma bodies (left) (**R**), serous borderline tumor (SBT) with micropapillary/microcystic appearance (**S**), high power of mesonephric-like carcinoma (**T**) and LGSC (**U**); Ovarian mesonephric-like carcinoma with serous borderline tumor (OV2) with matched pelvic recurrence (**V-Z**), SBT (left) mixed with mesonephric-like carcinoma (right) (**V-W**) and pelvic recurrence comprised of mesonephric-like carcinoma only (**X**), which was diffusely TTF-1 positive (**Y**) and WT1 negative (**Z**).

Supplementary Table S1: List of non-synonymous somatic mutations identified in mesonephric and mesonephric-like carcinomas by targeted massively parallel sequencing (MSK-IMPACT).

Sample_ID	Chromosome	Position	REF	ALT	Gene Symbol	Variant	AA change	Tumor MAF	Normal MAF	Tumor Depth	Normal Depth	Loss of Heterozygosity	Pathogenicity	Hotspot mutation	Cancer Gene Census	Kandoth et al	Lawrence et al	Cancer Cell Fraction	Clonal Status
EM1T	10	89692948	AT	A	PTEN	Frame_Shift_Del	p.L146*	0.212837838	0.003267974	296	306		likely_pathogenic	YES	YES	YES	YES	0.55	Subclonal
EM1T	10	89692791	A	G	PTEN	Missense_Mutation	p.D92G	0.197278912	0.003937008	294	254		likely_pathogenic	YES	YES	YES	YES	0.51	Subclonal
EM1T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.376106195	0	226	261		likely_pathogenic	YES	YES	YES	YES	0.97	Clonal
EM1T	12	25398285	C	A	KRAS	Missense_Mutation	p.G12C	0.385964912	0	228	256		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM1T	23	123020318	T	C	XIAP	Missense_Mutation	p.I269T	0.241666667	0	240	182		passenger		NO	NO	NO	0.62	Subclonal
EM1T	12	49418395	G	A	KMT2D	Nonsense_Mutation	p.R5340*	0.185185185	0	297	344		likely_pathogenic		YES	YES	YES	0.48	Subclonal
OV2M	1	115256529	T	C	NRAS	Missense_Mutation	p.Q61R	0.65085639	0	759	499		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV2M	3	142212011	G	A	ATR	Missense_Mutation	p.A2014V	0.275167785	0	298	435		likely_pathogenic		YES	YES	NO	0.9	Clonal
OV2M	6	138202430	T	A	TNFAIP3	Missense_Mutation	p.F783I	0.233716475	0	522	558		passenger		YES	NO	NO	0.76	Subclonal
OV2T	1	115256529	T	C	NRAS	Missense_Mutation	p.Q61R	0.590604027	0.004484305	298	223		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX8T-Met	1	27100985	CCTCAGCAAGAT	C	ARID1A	Frame_Shift_Del	p.P1423Rfs*18	0.292134831	0	178	308		likely_pathogenic		YES	YES	YES	0.64	Subclonal
CX8T-Met	1	11272485	T	C	MTOR	Missense_Mutation	p.T1149A	0.4375	0	160	179		passenger		YES	YES	YES	0.95	Clonal
CX8T-Met	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.642105263	0	285	284		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX8T-Met	15	91333927	G	A	BLM	Missense_Mutation	p.V958M	0.458333333	0.004081633	216	245		passenger		YES	NO	NO	1	Clonal
CX8T-Met	16	23619333	C	T	PALB2	Missense_Mutation	p.G1068R	0.06870229	0	131	132		passenger		YES	NO	NO	0.15	Subclonal
CX8T-Met	2	46605215	A	T	EPAS1	Missense_Mutation	p.S478C	0.048	0	125	94		passenger		YES	NO	NO	0.15	Subclonal
CX8T-Met	2	198267484	G	A	SF3B1	Missense_Mutation	p.R625C	0.285714286	0	161	144		likely_pathogenic	YES	YES	YES	YES	0.91	Clonal
CX8T-Met	3	178916876	G	A	PIK3CA	Missense_Mutation	p.R88Q	0.438247012	0	251	404		likely_pathogenic	YES	YES	YES	YES	0.96	Clonal
CX8T-Met	7	2946447	T	C	CARD11	Missense_Mutation	p.E1097G	0.065902579	0	349	315		passenger		YES	NO	YES	0.14	Subclonal
CX8T-Met	1	27100818	A	C	ARID1A	Splice_Site	p.X1368_splice	0.353535354	0	99	124		likely_pathogenic		YES	YES	YES	0.77	Subclonal
CX8T-Prim	1	27100985	CCTCAGCAAGAT	C	ARID1A	Frame_Shift_Del	p.P1423Rfs*18	0.21875	0	448	308		likely_pathogenic		YES	YES	YES	0.57	Subclonal
CX8T-Prim	1	11272485	T	C	MTOR	Missense_Mutation	p.T1149A	0.294326241	0	282	179		passenger		YES	YES	YES	0.76	Subclonal
CX8T-Prim	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.442196532	0	346	284		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX8T-Prim	15	88420197	G	C	NTRK3	Missense_Mutation	p.A830G	0.059055118	0	254	128		passenger		YES	NO	NO	0.15	Subclonal
CX8T-Prim	15	91333927	G	A	BLM	Missense_Mutation	p.V958M	0.306049822	0.004081633	281	245		passenger		YES	NO	NO	0.79	Subclonal
CX8T-Prim	16	9862892	T	A	GRIN2A	Missense_Mutation	p.K804M	0.051873199	0	347	199		passenger		YES	NO	NO	0.13	Subclonal
CX8T-Prim	19	45868372	G	T	ERCC2	Missense_Mutation	p.H135Q	0.038235294	0	680	395		passenger		YES	YES	YES	0.1	Subclonal
CX8T-Prim	3	178916876	G	A	PIK3CA	Missense_Mutation	p.R88Q	0.236311239	0	347	404		likely_pathogenic	YES	YES	YES	YES	0.61	Subclonal
CX8T-Prim	1	27100818	A	C	ARID1A	Splice_Site	p.X1368_splice	0.300847458	0	236	124		likely_pathogenic		YES	YES	YES	0.78	Subclonal
CX17T	15	42041080	TCTAATACCCAGCC	T	MGA	Frame_Shift_Del	p.N1821Tfs*13	0.07398568	0	419	245		likely_pathogenic		NO	NO	YES	0.24	Subclonal
CX17T	19	42791371	CAG	C	CIC	Frame_Shift_Del	p.S146*	0.141666667	0	840	378		likely_pathogenic		YES	NO	NO	0.46	Subclonal
CX17T	12	25398285	C	A	KRAS	Missense_Mutation	p.G12C	0.092348285	0	379	196		likely_pathogenic	YES	YES	YES	YES	0.3	Subclonal
CX17T	5	86685313	G	T	RASA1	Missense_Mutation	p.R1010L	0.138686131	0	137	64		likely_pathogenic		NO	NO	YES	0.45	Subclonal
OV19T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.567204301	0.028985507	372	276		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV19T	13	73340177	G	A	DIS3	Missense_Mutation	p.P635S	0.055555556	0.007936508	144	126		passenger		NO	NO	YES	0.15	Subclonal
OV19T	16	81965151	G	C	PLCG2	Missense_Mutation	p.E877D	0.033386328	0.003636364	629	275		passenger		NO	NO	NO	0.09	Subclonal
OV19T	16	89877386	G	C	FANCA	Missense_Mutation	p.T126R	0.043348281	0	669	281		passenger		YES	NO	NO	0.12	Subclonal
OV19T	19	15291576	C	G	NOTCH3	Missense_Mutation	p.A1020P	0.031413613	0	764	671		passenger		NO	NO	NO	0.08	Subclonal
OV19T	20	57429447	C	T	GNAS	Missense_Mutation	p.P376L	0.033766234	0	770	349		likely_pathogenic		NO	NO	NO	0.12	Subclonal
OV19T	11	108141874	G	A	ATM	Splice_Site	p.X974_splice	0.425641026	0.016853933	195	178	YES	likely_pathogenic		YES	YES	YES	1	Clonal
OV21T1	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.528911565	0	588	218		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV21T1	14	105246551	C	T	AKT1	Missense_Mutation	p.E17K	0.1037182	0	511	325		likely_pathogenic	YES	YES	YES	YES	0.28	Subclonal
OV21T1	17	47696598	A	G	SPOP	Missense_Mutation	p.M117T	0.408268734	0	387	227		passenger		YES	YES	YES	1	Clonal
OV21T1	3	41266098	A	T	CTNNB1	Missense_Mutation	p.D32V	0.174528302	0	212	134		likely_pathogenic	YES	YES	YES	YES	0.47	Subclonal
OV21T1	3	41266124	A	G	CTNNB1	Missense_Mutation	p.T41A	0.05106383	0	235	133		likely_pathogenic	YES	YES	YES	YES	0.14	Subclonal
OV21T2	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.314285714	0	350	218		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV21T2	17	47696598	A	G	SPOP	Missense_Mutation	p.M117T	0.207885305	0	279	227		passenger		YES	YES	YES	0.66	Subclonal
OV21T2	19	15288759	A	G	NOTCH3	Missense_Mutation	p.F1327S	0.039473684	0.002785515	380	359		passenger		NO	NO	NO	0.13	Subclonal
CX26T-EndoSq	20	31021670	ACCGAAAAG	A	ASXL1	Frame_Shift_Del	p.E558Tfs*4	0.248120301	0	133	122		likely_pathogenic		YES	YES	YES	0.73	Subclonal
CX26T-EndoSq	16	23646890	G	A	PALB2	Missense_Mutation	p.S326L	0.338983051	0.011673152	118	257		passenger		YES	NO	NO	1	Clonal
CX26T-EndoSq	3	41266103	G	A	CTNNB1	Missense_Mutation	p.G34R	0.283783784	0	74	82		likely_pathogenic	YES	YES	YES	YES	0.84	Clonal
CX26T-EndoSq	1	27087417	C	G	ARID1A	Nonsense_Mutation	p.S664*	0.356862745	0.004	255	250		likely_pathogenic		YES	YES	YES	1	Clonal
CX26T-MesoExo	20	31021670	ACCGAAAAG	A	ASXL1	Frame_Shift_Del	p.E558Tfs*4	0.32735426	0	223	122		likely_pathogenic		YES	YES	YES	0.74	Subclonal
CX26T-MesoExo	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.483333333	0	180	152		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX26T-MesoExo	16	23646890	G	A	PALB2	Missense_Mutation	p.S326L	0.631268437	0.011673152	339	257		passenger		YES	NO	NO	1	Clonal
CX26T-MesoExo	7	151945145	G	A	KMT2C	Missense_Mutation	p.P792S	0.040618956	0.001355014	517	738		likely_pathogenic		YES	YES	YES	0.09	Subclonal
CX26T-MesoExo	1	27087417	C	G	ARID1A	Nonsense_Mutation	p.S664*	0.424947146	0.004	473	250		likely_pathogenic		YES	YES	YES	0.96	Clonal
CX26T1-Meso	20	31021670	ACCGAAAAG	A	ASXL1	Frame_Shift_Del	p.E558Tfs*4	0.343915344	0	189	122		likely_pathogenic		YES	YES	YES	0.72	Subclonal
CX26T1-Meso	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.390374332	0	187	152		likely_pathogenic	YES	YES	YES	YES	0.81	Subclonal
CX26T1-Meso	16	23646890	G	A	PALB2	Missense_Mutation	p.S326L	0.62628866	0.011673152	388	257		passenger		YES	NO	NO	1	Clonal
CX26T1-Meso	4	55575594	G	A	KIT	Missense_Mutation	p.V374I	0.057142857	0	105	72		passenger		YES	YES	YES	0.12	Subclonal
CX26T1-Meso	7	151945145	G	A	KMT2C	Missense_Mutation	p.P792S	0.053648069	0.001355014	466	738		likely_pathogenic		YES	YES	YES	0.11	Subclonal
CX26T1-Meso	9	139566486	C	A	EGFL7	Missense_Mutation	p.R249S	0.1296	0	625	501		likely_pathogenic		NO	NO	NO	0.27	Subclonal
CX26T1-Meso	1	27087417	C	G	ARID1A	Nonsense_Mutation	p.S664*	0.487695749	0.004	447	250		likely_pathogenic		YES	YES	YES	1	Clonal
CX33T	11	118354997	G	T	KMT2A	Missense_Mutation	p.D1396Y	0.359550562	0.005617978	178	178		likely_pathogenic		YES	NO	YES	0.98	Clonal
CX33T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.841059603	0	302	255	YES	likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV34T	4	187628616	GT	G	FAT1	Frame_Shift_Del	p.T789Pfs*2	0.33970276	0.002493766	471	401				YES	NO	YES	0.68	Subclonal
OV34T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.657894737	0.009259259	494	216		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV34T	3	178916936	G	A	PIK3CA	Missense_Mutation	p.R108H	0.525679758	0.004901961	331	204		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV34T	4	187630158	A	T	FAT1	Missense_Mutation	p.I275N	0.076726343	0	391	285		passenger		YES	NO	YES	0.15	Subclonal
OV34T	1	16202911	G	T	SPEN	Nonsense_Mutation	p.E207*	0.325657895	0	304	269		likely_pathogenic		YES	NO	YES	0.65	Subclonal
EM36T	12	25398281	C	T	KRAS	Missense_Mutation	p.G13D	0.820945946	0	296	105	YES	likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM36T	14	105241460	G	C	AKT1	Missense_Mutation	p.R174G	0.390532544	0	676	219		passenger		YES	YES	YES	1	Clonal
EM36T	2	190682829	A	G	PMS1	Missense_Mutation	p.I169V	0.537671233	0	292	74		passenger		NO	NO	NO	1	Clonal
EM36T	2	242794499	C	T	PDCD1	Missense_Mutation	p.R148K	0.357534247	0	730	212		passenger		NO	NO	NO	1	Clonal
EM36T	3	41266104	G	A	CTNNB1	Missense_Mutation	p.G34E	0.388888889	0	126	68		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX44T	16	3900385	G	GCTGCT	CREBBP	Frame_Shift_Ins	p.S237Rfs*9	0.297161937	0.004444444	599	675		likely_pathogenic		YES	NO	YES	0.7	Subclonal
CX44T	1	46726436	G	A	RAD54L	Missense_Mutation	p.R172H	0.063694268	0	157	394	YES	likely_pathogenic		NO	NO	NO	0.09	Subclonal
CX44T	11	64127964	G	A	RPS6KA4	Missense_Mutation	p.G121E	0.07615894	0.001371742	604	729	YES	passenger		NO	NO	NO	0.18	Subclonal
CX44T	11	64135976	C	T	RPS6KA4	Missense_Mutation	p.R413W	0.06920904	0	708	759	YES	passenger		NO	NO	NO	0.16	Subclonal
CX44T	3	178952117	A	T	PIK3CA	Missense_Mutation	p.I1058F	0.065384615	0	260	222		likely_pathogenic		YES	YES	YES	0.15	Subclonal
CX44T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.430740038	0	527	465		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX44T	9	137309155	G	A	RXRA	Missense_Mutation	p.M254I	0.124694377	0.004010695	409	748	YES	passenger		NO	NO	YES	0.17	Subclonal
OV50T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.69740634	0	347	147		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV50T	22	29091782	G	A	CHEK2	Missense_Mutation	p.A392V	0.261154856	0.007633588	762	655		passenger		YES	YES	NO	0.78	Subclonal
OV50T	1	27023307	C	G	ARID1A	Nonsense_Mutation	p.S138*	0.471590909	0.002475248	528	404		likely_pathogenic		YES	YES	YES	0.94	Clonal
EM52T1	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.204903678	0	571	166		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM52T2	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.488372093	0	344	166		likely_pathogenic	YES	YES	YES	YES	0.98	Clonal
OV57T	1	46726236	G	T	RAD54L	Missense_Mutation	p.V144F	0.320939335	0	511	254		likely_pathogenic		NO	NO	NO	1	Clonal
OV57T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.631379962	0.003344482	529	299		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV57T	12	57488484	G	T	NAB2	Missense_Mutation	p.A520S	0.176470588	0	595	328		passenger		YES	NO	NO	1	Clonal
OV57T	12	111856127	G	A	SH2B3	Missense_Mutation	p.A60T	0.028023599	0.002645503	678	378		passenger		YES	NO	NO	0.18	Subclonal
OV57T	3	178927980	T	C	PIK3CA	Missense_Mutation	p.C420R	0.498245614	0	285	145		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV57T	23	53223390	C	A	KDM5C	Missense_Mutation	p.E1323D	0.409967846	0.002169197	622	461	YES	passenger		YES	YES	YES	1	Clonal
OV57T	23	123220555	G	A	STAG2	Missense_Mutation	p.R1071Q	0.22	0	500	362	YES	passenger		YES	YES	YES	0.96	Clonal
CX58T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.67037037	0	270	275		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX58T	19	15272408	C	T	NOTCH3	Missense_Mutation	p.V2011I	0.1625	0.003448276	80	290		passenger		NO	NO	NO	0.37	Subclonal
CX58T	19	15281176	G	A	NOTCH3	Missense_Mutation	p.R1694W	0.045454545	0	88	308		likely_pathogenic		NO	NO	NO	0.1	Subclonal
EM59T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.550505051	0	396	394		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM59T	15	66774153	G	A	MAP2K1	Missense_Mutation	p.G210E	0.268258427	0.001492537	712	670		likely_pathogenic		YES	NO	YES	1	Clonal
EM59T	21	42870110	A	G	TMPRSS2	Missense_Mutation	p.I21T	0.328897338	0	526	452		passenger		NO	NO	NO	1	Clonal
EM59T	3	178917478	G	A	PIK3CA	Missense_Mutation	p.G118D	0.030701754	0	228	212		likely_pathogenic	YES	YES	YES	YES	0.11	Subclonal
EM59T	4	153247289	G	A	FBXW7	Missense_Mutation	p.R505C	0.08203125	0	512	356		likely_pathogenic	YES	YES	YES	YES	0.31	Subclonal
EM59T	6	157527491	A	T	ARID1B	Missense_Mutation	p.D1739V	0.213151927	0	441	385		passenger		YES	NO	NO	0.8	Subclonal
EM59T	23	63412095	G	A	AMER1	Nonsense_Mutation	p.R358*	0.033274956	0	571	661		likely_pathogenic		YES	NO	NO	0.12	Subclonal
EM59T	12	133219316	C	T	POLE	Splice_Site	p.X1577_splice	0.037634409	0	372	323		likely_pathogenic		YES	NO	YES	0.14	Subclonal
EM59T	8	90949304	C	T	NBN	Splice_Site	p.X729_splice	0.240740741	0	216	182		likely_pathogenic		YES	NO	NO	0.9	Clonal
EM61T1	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.716783217	0.003745318	286	267		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM61T2	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.820454545	0	440	333	YES	likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM61T2	16	30128056	T	A	MAPK3	Missense_Mutation	p.E358V	0.042179262	0	569	353		passenger		NO	NO	NO	0.1	Subclonal
EM61T2	3	185146667	G	A	MAP3K13	Missense_Mutation	p.G100R	0.197860963	0	561	319		passenger		YES	NO	NO	0.48	Subclonal
EM61T2	7	116423360	T	G	MET	Missense_Mutation	p.L1212R	0.16	0	450	160		likely_pathogenic		YES	NO	YES	0.55	Subclonal
CX62T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.587275693	0	613	503		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX62T	22	30069456	G	T	NF2	Missense_Mutation	p.A441S	0.403914591	0	562	348		likely_pathogenic		YES	NO	NO	0.98	Clonal
CX62T	5	176721492	C	A	NSD1	Missense_Mutation	p.L2375M	0.418879056	0.002352941	678	425		passenger		YES	YES	YES	1	Clonal
EM63T	16	3779600	GCAGCC	G	CREBBP	Frame_Shift_Del	p.G1815Pfs*149	0.358925144	0	521	324		.		YES	NO	YES	1	Clonal
EM63T	10	89692792	C	A	PTEN	Missense_Mutation	p.D92E	0.275324675	0	385	259		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM63T	12	25398284	C	G	KRAS	Missense_Mutation	p.G12A	0.637826962	0	497	313		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM63T	3	178947827	G	T	PIK3CA	Missense_Mutation	p.C901F	0.429885057	0	435	366		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM63T	8	55370985	C	G	SOX17	Missense_Mutation	p.A96G	0.484949833	0.003676471	299	272		likely_pathogenic		NO	YES	YES	1	Clonal
EM64T	10	89685308	A	G	PTEN	Missense_Mutation	p.Y68C	0.074733096	0	281	215		likely_pathogenic		YES	YES	YES	0.41	Subclonal
EM64T	10	89692904	C	G	PTEN	Missense_Mutation	p.R130G	0.302977233	0	571	389		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM64T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.20703125	0	512	370		likely_pathogenic	YES	YES	YES	YES	0.94	Clonal
EM64T	12	49420229	G	A	KMT2D	Missense_Mutation	p.R5174W	0.228989038	0.002331002	821	429		passenger		YES	YES	YES	1	Clonal
EM64T	16	2226132	C	T	TRAF7	Missense_Mutation	p.T610M	0.143340858	0	886	476		passenger		YES	NO	NO	0.65	Subclonal
EM64T	16	89836984	G	A	FANCA	Missense_Mutation	p.A737V	0.103694875	0	839	426		passenger		YES	NO	NO	0.47	Subclonal
EM64T	2	212566890	C	T	ERBB4	Missense_Mutation	p.G431S	0.114206128	0	359	250		passenger		YES	YES	NO	0.52	Subclonal
EM65T	3	89156955	C	CG	EPHA3	Frame_Shift_Ins	p.E21Gfs*9	0.342052314	0	497	437		.		NO	YES	NO	1	Clonal
EM65T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.567528736	0	696	422		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM65T	19	18272232	G	A	PIK3R2	Missense_Mutation	p.A248T	0.166666667	0	12	9		passenger		NO	NO	NO	0.49	Subclonal
EM65T	3	178916636	G	A	PIK3CA	Missense_Mutation	p.G8D	0.161290323	0	341	332		passenger		YES	YES	YES	0.47	Subclonal
OV66T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.6859375	0	640	297		likely_pathogenic	YES	YES	YES	YES	1	Clonal
CX67T	19	2210417	CG	C	DOT1L	Frame_Shift_Del	p.R343Afs*44	0.127906977	0	688	300		.		NO	NO	NO	0.33	Subclonal
CX67T	12	25398278	A	ACGC	KRAS	In_Frame_Ins	p.G13dup	0.321917808	0	292	292		.		YES	YES	YES	0.84	Subclonal
CX67T	12	49415904	A	C	KMT2D	Missense_Mutation	p.C5481W	0.04842615	0	413	402		likely_pathogenic		YES	YES	YES	0.13	Subclonal
CX67T	2	47702391	A	T	MSH2	Missense_Mutation	p.M663L	0.042654028	0	211	235		likely_pathogenic		YES	NO	NO	0.11	Subclonal
CX67T	5	112177010	G	A	APC	Missense_Mutation	p.A1907T	0.275609756	0	410	445		likely_pathogenic		YES	YES	YES	0.72	Subclonal
CX67T	12	11905465	C	T	ETV6	Nonsense_Mutation	p.R39*	0.379816514	0	545	228		likely_pathogenic		YES	NO	NO	0.99	Clonal
CX67T	12	49433394	G	A	KMT2D	Nonsense_Mutation	p.R2685*	0.071111111	0	225	240		likely_pathogenic		YES	YES	YES	0.19	Subclonal
CX67T	12	50482421	G	T	SMARCD1	Splice_Site	p.X257_splice	0.327536232	0	345	361		likely_pathogenic		YES	NO	NO	0.85	Subclonal
EM68T	1	65316512	C	T	JAK1	Missense_Mutation	p.R577Q	0.059160305	0	524	241		passenger		YES	NO	NO	0.14	Subclonal
EM68T	12	25398285	C	A	KRAS	Missense_Mutation	p.G12C	0.619469027	0	339	269		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM68T	17	47696708	G	C	SPOP	Missense_Mutation	p.S80R	0.382899628	0.003322259	269	301		likely_pathogenic		YES	YES	YES	0.91	Clonal
EM68T	9	21971028	C	T	CDKN2A	Nonsense_Mutation	p.W110*	0.84375	0	576	151	YES	likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM68T	23	63412110	G	A	AMER1	Nonsense_Mutation	p.R353*	0.026755853	0	598	626		likely_pathogenic		YES	NO	NO	0.06	Subclonal
EM69T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.541538462	0.001872659	650	534		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM69T	12	57865657	C	A	GLI1	Missense_Mutation	p.T1045N	0.324074074	0	756	746		passenger		NO	NO	NO	1	Clonal
EM69T	3	41266113	C	T	CTNNB1	Missense_Mutation	p.S37F	0.344559585	0	386	416		likely_pathogenic	YES	YES	YES	YES	0.94	Clonal
OV70T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.596194503	0.002369668	473	422		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM71T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.911937378	0	511	625	YES	likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM71T	2	46605215	A	T	EPAS1	Missense_Mutation	p.S478C	0.040358744	0	223	273		passenger		YES	NO	NO	0.14	Subclonal
EM71T	3	89528647	G	A	EPHA3	Missense_Mutation	p.V983M	0.432748538	0	171	189		passenger		NO	YES	NO	1	Clonal
EM72T	11	14316390	T	A	RRAS2	Missense_Mutation	p.Q72L	0.419497784	0	677	568		likely_pathogenic	YES	NO	NO	NO	1	Clonal
EM72T	12	25398281	C	T	KRAS	Missense_Mutation	p.G13D	0.408250356	0	703	628		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM72T	17	7577520	A	T	TP53	Missense_Mutation	p.I254N	0.410609037	0	509	441		likely_pathogenic		YES	YES	YES	1	Clonal
EM72T	19	11121173	C	G	SMARCA4	Missense_Mutation	p.A747G	0.676844784	0	393	632	YES	passenger		YES	NO	YES	0.98	Clonal
OV73T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.918552036	0.002624672	663	381		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV73T	9	87285838	G	A	NTRK2	Missense_Mutation	p.E59K	0.368841545	0.001980198	751	505		likely_pathogenic		NO	NO	NO	1	Clonal
OV74T1	1	115256529	T	C	NRAS	Missense_Mutation	p.Q61R	0.642750374	0	669	473		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV74T1	6	27839787	C	T	HIST1H3I	Missense_Mutation	p.G103R	0.173361522	0.002386635	473	419		passenger		NO	NO	NO	0.6	Subclonal
OV74T2	1	115256529	T	C	NRAS	Missense_Mutation	p.Q61R	0.563953488	0	688	473		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV75T1	1	120465364	C	T	NOTCH2	Missense_Mutation	p.V1633I	0.458398744	0	637	350		passenger		YES	NO	NO	1	Clonal
OV75T1	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.128571429	0	560	328	YES	likely_pathogenic	YES	YES	YES	YES	0.28	Subclonal
OV75T1	12	123874031	C	T	SETD8	Missense_Mutation	p.A21V	0.086956522	0	46	20	YES	passenger		NO	NO	NO	0.19	Subclonal
OV75T1	19	42383644	C	A	CD79A	Missense_Mutation	p.T140N	0.466666667	0	570	395		passenger		YES	NO	NO	1	Clonal
OV75T1	19	50919042	A	C	POLD1	Missense_Mutation	p.I927L	0.443197756	0.002040816	713	490		passenger		NO	NO	NO	0.97	Clonal
OV75T1	3	178936074	C	G	PIK3CA	Missense_Mutation	p.P539R	0.062015504	0.001675042	645	597	YES	likely_pathogenic	YES	YES	YES	YES	0.14	Subclonal
OV75T2	1	120465364	C	T	NOTCH2	Missense_Mutation	p.V1633I	0.40960452	0	708	350		passenger		YES	NO	NO	0.92	Clonal
OV75T2	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.405529954	0	651	328		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV75T2	19	42383644	C	A	CD79A	Missense_Mutation	p.T140N	0.466562986	0	643	395		passenger		YES	NO	NO	1	Clonal
OV75T2	19	50919042	A	C	POLD1	Missense_Mutation	p.I927L	0.422636103	0.002040816	698	490		passenger		NO	NO	NO	0.94	Clonal
OV75T2	3	178936074	C	G	PIK3CA	Missense_Mutation	p.P539R	0.245045045	0.001675042	555	597		likely_pathogenic	YES	YES	YES	YES	0.55	Subclonal
OV75T2	5	67589168	C	G	PIK3R1	Missense_Mutation	p.R386G	0.114695341	0.00462963	279	216		likely_pathogenic		YES	YES	YES	0.26	Subclonal
EM76T1	11	14316390	T	A	RRAS2	Missense_Mutation	p.Q72L	0.900497512	0	603	686		likely_pathogenic	YES	NO	NO	NO	1	Clonal
EM76T1	12	123874031	C	T	SETD8	Missense_Mutation	p.A21V	0.15	0.028571429	20	35		passenger		NO	NO	NO	0.33	Subclonal
EM76T1	3	41274911	T	A	CTNNB1	Missense_Mutation	p.N387K	0.433962264	0	583	597		likely_pathogenic	YES	YES	YES	YES	0.96	Clonal
EM76T1	7	140453193	T	C	BRAF	Missense_Mutation	p.N581S	0.383495146	0	412	451		likely_pathogenic	YES	YES	YES	YES	0.85	Subclonal
EM76T1	23	70338671	G	T	MED12	Missense_Mutation	p.D23Y	0.440677966	0	531	688		likely_pathogenic		YES	NO	YES	0.98	Clonal
EM76T2	11	14316390	T	A	RRAS2	Missense_Mutation	p.Q72L	0.726296959	0	559	686		likely_pathogenic	YES	NO	NO	NO	1	Clonal
EM76T2	17	62007499	C	T	CD79B	Missense_Mutation	p.C123Y	0.351493849	0.001402525	569	713		likely_pathogenic		YES	NO	YES	0.97	Clonal
EM76T2	19	18975056	C	A	UPF1	Missense_Mutation	p.S951R	0.376237624	0.002785515	303	359		likely_pathogenic		NO	NO	NO	1	Clonal
EM76T2	3	41278106	G	C	CTNNB1	Missense_Mutation	p.R661P	0.037783375	0	397	607		likely_pathogenic		YES	YES	YES	0.1	Subclonal
EM76T2	7	140453193	T	C	BRAF	Missense_Mutation	p.N581S	0.392105263	0	380	451		likely_pathogenic	YES	YES	YES	YES	1	Clonal
EM76T2	23	70338671	G	T	MED12	Missense_Mutation	p.D23Y	0.378892734	0	578	688		likely_pathogenic		YES	NO	YES	1	Clonal
OV77T	9	139412307	GC	G	NOTCH1	Frame_Shift_Del	p.G446Afs*185	0.42	0	400	482	YES	.		YES	YES	YES	1	Clonal
OV77T	12	25398284	C	T	KRAS	Missense_Mutation	p.G12D	0.51417004	0	494	344		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV77T	17	47696599	T	C	SPOP	Missense_Mutation	p.M117V	0.584355828	0	652	506		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV77T	3	178936082	G	A	PIK3CA	Missense_Mutation	p.E542K	0.863157895	0	380	319		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV77T	8	38274936	T	G	FGFR1	Splice_Site	p.X549_splice	0.281535649	0	547	442		likely_pathogenic		YES	NO	NO	1	Clonal
OV79T	20	31022383	AGGTCCGAGGG	A	ASXL1	Frame_Shift_Del	p.V624Rfs*76	0.346153846	0	130	261		.		YES	YES	YES	0.89	Clonal
OV79T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.49270073	0	274	487		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV79T	17	47699371	T	C	SPOP	Missense_Mutation	p.E46G	0.326797386	0	153	423		passenger		YES	YES	YES	0.84	Subclonal
OV79T	2	61719271	G	A	XPO1	Missense_Mutation	p.R596C	0.494023904	0	251	383		passenger		YES	NO	YES	1	Clonal
OV79T	4	153247295	C	T	FBXW7	Missense_Mutation	p.A503T	0.695402299	0.003401361	174	294	YES	likely_pathogenic		YES	YES	YES	1	Clonal
OV80T	16	3786727	TTGGGTATTTTTTGATCAGGTGGG	T	CREBBP	Frame_Shift_Del	p.H1487Qfs*24	0.071528752	0	713	491		.		YES	NO	YES	0.25	Subclonal
OV80T	6	30672748	AGG	A	MDC1	Frame_Shift_Del	p.P1404*	0.27919708	0.001757469	548	569		.		NO	NO	NO	0.71	Subclonal
OV80T	1	117699528	G	A	VTCN1	Missense_Mutation	p.T38I	0.376033058	0	242	254		passenger		NO	NO	NO	0.96	Clonal
OV80T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.553349876	0.002347418	403	426		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV80T	12	123874031	C	T	SETD8	Missense_Mutation	p.A21V	0.068965517	0	87	63		passenger		NO	NO	NO	0.24	Subclonal
OV80T	17	47696599	T	C	SPOP	Missense_Mutation	p.M117V	0.279012346	0	405	385		likely_pathogenic	YES	YES	YES	YES	0.99	Clonal
OV81T	12	25398284	C	A	KRAS	Missense_Mutation	p.G12V	0.502487562	0	402	304		likely_pathogenic	YES	YES	YES	YES	1	Clonal
OV81T	3	178916930	G	T	PIK3CA	Missense_Mutation	p.G106V	0.328828829	0	222	237		likely_pathogenic	YES	YES	YES	YES	0.96	Clonal