

Supplementary Information 1. QC metrics of whole-exome sequencing and RNA sequencing for Patients 1-1

a. Whole exome sequencing

		Pt1		Pt2		Pt3		Pt4	
		T	N	T	N	T	N	T	N
Tissue source		CS	PBMC	CS	PBMC	CS	PBMC	FFPE	PBMC
Exome									
Coverage	Target coverage(mean)	222	252	337	342	315	346	285	244
	% targets with >= 20x	94.37	94.95	94.42	94.98	93.59	94.64	95.9	96.47
	% targets without coverage	1.19	1.15	1.3	1.22	1.25	1.19	1.67	1.52
Quality	% contamination	0.3	0.3	0.1	0.1	0.1	0.1	0.1	0.1
	% Indel Rate	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
	% Purity	23		52		0.93		43	
	Ploidy	1.91		1.85		1.99		1.86	

*T: tumor

*N: germline

*CS: tumor cell-suspension

*PBMC: peripheral blood mononuclear cell

*FFPE: formalin-fixed paraffine-embedded

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Pt5		Pt6		Pt7		Pt8		Pt9		Pt10	
T	N	T	N	T	N	T	N	T	N	T	N
CS	PBMC	FFPE	PBMC	CS	PBMC	FFPE	PBMC	CS	PBMC	FFPE	PBMC
234	307	313	280	243	218	313	280	269	185	233	274
95.9	96.59	96.32	96.47	93.64	93.35	96.32	96.47	94.61	93.04	95.98	96.86
1.74	1.68	1.66	1.6	1.27	1.28	1.66	1.6	1.16	1.3	1.69	1.57
0.1	0.1	0.1	0.1	0.2	0.2	0.1	0.1	0.2	0.1	0.1	0.1
0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
78		45		19		45		70		71	
1.86		3.37		2.05		3.37		2		1.94	