

S3 Table. Mapping of whole genome sequencing data

Patient ID		Raw reads	QC-passed reads	Mapped reads	Mapping rate (%)	Mean depth	% bases above 15
3	Blood	93,808,395,257	648,625,793	647,468,246	99.82	32.38	94.8
	Tumor	79,306,355,539	550,315,503	548,538,660	99.68	27.37	91.5
5	Blood	117,758,278,543	815,680,480	814,366,936	99.84	40.64	96.3
	Tumor	98,839,843,029	682,827,458	681,313,846	99.78	34.11	95.9
6	Blood	100,862,806,540	697,063,601	695,825,615	99.82	34.81	95.7
	Tumor	84,717,205,430	591,372,627	587,035,964	99.27	29.24	92.3
8	Blood	84,764,356,765	585,350,683	584,282,987	99.82	29.26	93.9
	Tumor	156,603,515,114	1102,038,663	1089,192,351	98.83	54.05	96.9
9	Blood	112,274,059,584	774,105,980	772,791,060	99.83	38.75	96.3
	Tumor	119,614,311,138	843,076,436	830,889,832	98.55	41.28	96.1
15	Blood	97,110,697,807	672,315,971	671,018,050	99.81	33.52	96.1
	Tumor	74,420,439,040	523,413,451	518,450,921	99.05	25.69	93.2
16	Blood	89,719,760,468	625,607,247	624,393,052	99.81	30.97	95.4
	Tumor	74,840,261,095	529,261,838	523,047,271	98.83	25.83	90.5
18	Blood	89,163,851,887	618,812,757	617,707,088	99.82	30.77	96.0
	Tumor	71,652,480,606	504,976,793	500,098,229	99.03	24.73	90.3
19	Blood	89,919,123,699	628,226,830	627,021,514	99.81	31.04	95.5
	Tumor	77,434,101,197	538,505,816	535,839,735	99.50	26.73	92.3
11	Tumor	62,176,883,953	446,766,432	419,323,878	97.88	21.46	81.9
13	Tumor	69,294,228,929	487,593,143	469,253,922	98.09	23.92	84.3

Mapping summary report was obtained by the BWA-mem in GATK pipeline. QC, quality control.