

**Table S2 Parameters estimated by GIANT on replicate SNP arrays**

Sample <sup>*</sup>	ACN <sup>#</sup>	Tumor <sup>&amp;</sup> (%)	GC coefficient	Baseline Shift	BAF SD <sup>^</sup>	LRR SD <sup>^</sup>
N1+T1	2.21	10.0	-0.08	-0.02	0.04	0.22
N1+T2	2.22	10.0	-0.05	-0.01	0.04	0.19
N2+T1	2.22	10.0	-0.08	-0.02	0.04	0.22
N2+T2	2.22	10.0	-0.05	-0.01	0.04	0.19

<sup>\*</sup>: N1: Normal replicate 1, N2: Normal replicate 2, T1: Tumor replicate 1, T2: Tumor replicate 2; <sup>#</sup>: ACN=Average Copy Number; <sup>&</sup>: Estimated cancer cell proportion; <sup>^</sup>: SD= Standard Deviation