

Supplementary Table 1. Sequence analysis summary of tumor and blood samples from four NKTCL cases

Sample ID	Sample	Bases in Target Region	Bases Sequenced	Bases mapped to hg19 genome	Filtered Bases Mapped to Target Region	Ave. Depth Per Targeted Base	% Targeted Bases with depth at least 1x	% Targeted Bases with depth at least 20x
7	Tumor	37806033	9,574,927,044	8,605,051,964	4,342,361,440	114.86	97.9%	85.0%
	Normal	37806033	9,771,429,826	8,880,589,854	4,329,726,976	114.52	97.8%	85.0%
31	Tumor	37806033	10,014,935,854	9,017,960,716	3,237,222,574	85.63	98.0%	80.0%
	Normal	37806033	9,928,610,266	8,853,623,884	4,396,483,338	116.29	97.9%	85.0%
27	Tumor	37806033	9,574,927,044	8,605,051,964	4,342,361,440	114.86	97.9%	85.0%
	Normal	37806033	9,771,429,826	8,880,589,854	4,329,726,976	114.52	97.8%	85.0%
10	Tumor	37806033	10,035,531,164	9,139,715,506	4,559,878,964	120.61	97.9%	84.0%
	Normal	37806033	8,979,384,442	8,042,878,922	4,107,375,550	108.64	98.0%	84.0%
	Average	37806033	9706396933	8753182833	4205642157	111.24	97.90%	84.13%