

SUPPLEMENTARY INFORMATION

Mutational Analysis of Extranodal NK/T-Cell Lymphoma Using Targeted Sequencing with a Comprehensive Cancer Panel

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Supplementary Table 4. Statistics of sequencing data

	Case No.				
	1	2	3	4	5
No. of mapped reads	30011197	20141112	26154647	19948919	19604624
Percent reads on target	99.15	96.08	98.91	97.46	99.09
Total aligned base reads	3221573610	2152419889	2859551662	2155768494	2168519003
Total base reads on target	3121683146	2038239169	2766357049	2061669592	2101677011
Bases in target regions	1688650	1688650	1688650	1688650	1688650
Percent base reads on target	96.90	94.70	96.74	95.64	96.92
Average base coverage depth	1,849	1,207	1,638	1,221	1,245
Uniformity of base coverage (%)	47.72	38.39	42.22	39.27	37.25
Target base coverage at $\times 1$ (%)	93.48	87.87	90.71	88.08	85.93
Target base coverage at $\times 20$ (%)	72.48	57.81	64.53	58.87	56.86
Target base coverage at $\times 100$ (%)	59.51	45.32	51.74	46.62	44.33
Target base coverage at $\times 500$ (%)	44.73	32.11	38.59	33.06	31.67
Target bases with no strand bias (%)	92.68	92.76	92.97	92.61	93.20