

## SUPPLEMENTARY INFORMATION

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

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**Supplementary Table 5. Variant regions of each sample**

	Case No.				
	1	2	3	4	5
Missense	143	1,335	259	608	151
Synonymous	234	1,038	304	532	220
Intron	317	787	341	528	258
Splice region & intron	33	102	42	68	31
Frameshift	26	14	14	10	10
Stop gained	1	87	6	37	3
Missense & splice region	1	30	2	12	2
Intragenic	203	568	228	363	176
5 prime UTR	11	30	19	27	6
Splice region & synonymous	2	20	5	15	2
3 prime UTR	17	39	20	25	10
Splice donor & intron	0	14	1	12	2
Splice acceptor & intron	0	11	1	2	0
In-frame insertion	2	1	1	1	1
Disruptive in-frame deletion	0	0	0	1	0
Splice donor & missense & splice region & intron	0	0	0	2	0
Stop gained & splice region	0	3	0	3	0
Noncoding exon	3	5	3	5	4
In-frame deletion	2	1	1	1	0
5 prime UTR premature start codon gain	0	8	3	1	2
Disruptive in-frame insertion	1	2	2	0	1
Stop retained	0	0	1	0	1
Frameshift variant & splice region	0	1	1	0	0
Unclassified	2	3	2	3	1
Total variants	998	4,099	1,256	2,256	881