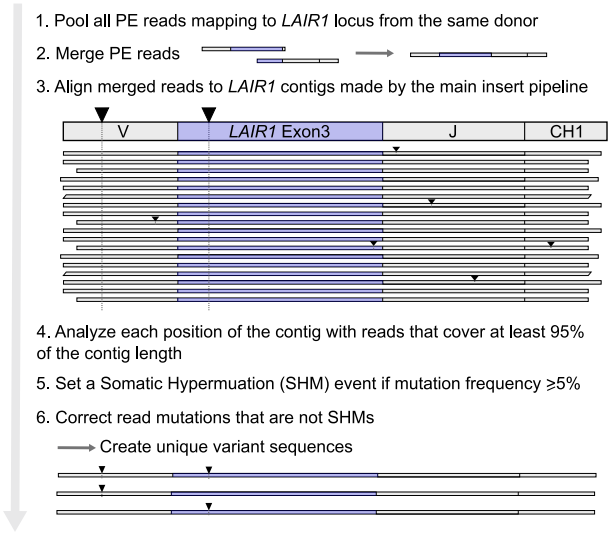
A



B

		Reads covering 95% of the *LAIR1* contig	Contig nucleotide variants	Contig amino acid variants	*LAIR1* nucleotide variants	*LAIR1* amino acid variants
Polyclonals	070	300'390	175	103	16	16
	215	2'164	73	54	56	43
Monoclonals	MMJ5	355'852	2	2	2	2
	MGO3	159'378	1	1	1	1

C

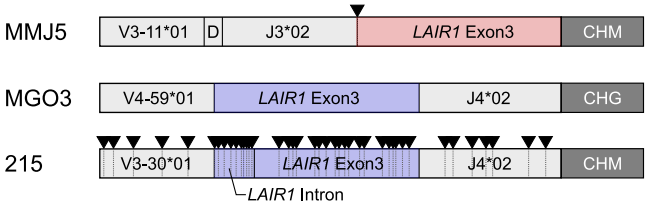


Fig. S3. Nucleotide and amino acid variant analysis of LAIR1-containing transcripts. (*A*) Outline of data processing. Paired-end reads mapping to *LAIR1* locus were extracted from samples and merged. Resulting reads were aligned to the consensus contig created by the main pipeline. Somatic hypermutations were assigned if a mismatch was present in more than 5% of reads. (*B*) Variants of *LAIR1* transcripts profiled for two donors of which one displayed LAIR1-containing antibodies in the serum, and another donor identified by suppression PCR (215). Two monoclonal cell lines (MMJ5, MGO3) expressing LAIR1-containing antibodies were used as controls. (*C*) Schematic representation of transcripts derived from monoclonal cell lines and donor 215. Black arrows indicate positions of nucleotide exchanges. The arrow in MMJ5 indicates a splice variant.