

Supplementary Table S4. New insertions identified using LoRTE v1.2 in nanopore reads of Horezu_LaPeri genome.

RepBaseID#Type/Family	Coverage	Genomic coordinates	Genomic region	Percentage of covered NT	Percentage of polymorph	Number of deletion
DM176_LTR#LTR/Gypsy	10	2R:7,606,220.. 7,606,623	CG1358 intron	99.95	2.93	568
M4DM#DNA/CMC- Transib	13	2L:20,969,629..20,970,029	CG42238 intron			
TRANSIB2#DNA/CMC- Transib	7	3R:14,049,171..14,049,575	noncoding region			
LINEJ1_DM#LINE/Jockey	1	2L:15,257,737..15,258,141	<i>yuri</i> exon			
LINEJ1_DM#LINE/Jockey	1	3R:22,199,769..22,200,183	<i>SKIP</i> intron and <i>lncRNA:CR45224</i>			
M4DM#DNA/CMC- Transib	4	X:18,356,645..18,357,047	INE-1{}4916			
Jockey- 4_DAn#LINE/Jockey	1	3R:31,536,097..31,536,508	noncoding region			