

Supplementary Table S3. The total number of P-element insertions having both ends (TIRs) and intact TSDs identified in the Horezu_LaPeri genome using GA_v2.

Assembly_contig ID	Chromosome	Genomic coordinate	Hit/Nearby Genes/NTs	NT Orientation	TSD
Canu_491	3L	21,347,168	<i>ebd2</i> , CG32436 intronic	+	GTTCCGCT
Canu_869	X	10,547,695	<i>pri</i> intronic	+	GGAGAGCC
Canu_1601	3L	3,250,477	<i>lncRNA:</i> CR43626	-	GCTCAAAT
Canu_1937	3L	959,438	<i>Glut1</i> intronic	+	CTTGGAAC
Canu_1938	3L	1,688,826	CG7991 exonic	-	CGCCGTCC
Canu_2082	2L	21,697,891	<i>nolo</i> intronic	+	ACTCGGGG
Canu_2967	3R	19,180,631	close to CG5555, CG31475	-	GTTTGGAT
Canu_3114	X	11,201,707	gipsy5{}103	-	CGCCAGTG
CanuAlt_3182	3L	14,410,404	<i>lncRNA:</i> CR45233	+	GTCTGGCA
CanuAlt_3419	2R	12,188,531	<i>Cyp6g2</i> exonic	-	GTCTAGAC
FlyeAlt_1148	2R	23,635,173	<i>retn</i> intronic	-	GTCCATGG
FlyeAlt_1188	X	15,552,365	<i>Ac13E</i> intronic	+	GTATGAGC
FlyeAlt_1736	3L	13,477,235	close to <i>stv</i>	-	GTCTGATG
FlyeAlt_1795	X	17,562,651	close to CG43658	-	CGCCAGCT
FlyeAlt_2153	X	13,641,922	<i>NFAT</i> intronic	-	GGCCACGC