

Supplemental Table S2: Reasons for excluding previously detected

Genome position (cow)		Marker*	Presence	Reason for not detecting
chr1	96,558,839-96,559,927	N265	horse+ dog+	Miss-alignments in 2-ways
chr2	89,508,583-89,509,011	H/B901	bat+ dog+	Insertion is not a 3' region of LINE; old and probably inactive L1MEc
chr2	134,089,587-134,091,396	N283	horse+ cow+ dog+	L1MA9 overlap with flank by 12 nt
chr3	67,728,964-67,729,179	N382	horse+ bat+ dog+	Miss-alignments in 2-ways
chr6	58,805,911-58,806,784 58,805,806-58,806,230	N189 H8382	horse+ dog+ horse+ bat+ cow+	Miss-alignments in 2-ways (two parallel insertions without clear interpretation)
chr6	89,168,890-89,169,342	H/B1676	bat+ cow+ dog+	L1MC1 overlap with both flanks by 15 nt and 19 nt
chr7	14,744,403-14,744,892	H75125	horse+ dog+	Insertion is not the 3' region of LINE
chr8	53,779,449-53,779,900	H6017	horse+ bat+ dog+	Miss-alignments in 2-ways
chr14	62,827,384-62,827,877	H/B1522	horse+ bat+ cow+	Insertion is not the 3' region of LINE
chr16	3,212,980-3,213,408 3,212,964-3,213,491	H7214 H41443	bat+ cow + dog+	Short insertion not detected in 2-ways
chr21	28,973,565-28,974,082	N165	horse+ bat + dog+	Additional long sequence in cow (absence not clean)
chr21	57,424,882-57,425,208	H/B1060	horse+ bat+ dog+	Insertion is not a 3' region of LINE; old and probably inactive L1M5
chr23	32,856,614-32,856,993	H42785	horse+ dog+	L1MA9 cover less than 70% of gap
chr26	33,220,496-33,221,281 33,220,895-33,221,224	N391 H44900	horse+ bat+ dog+	Insertion is not a 3' region of LINE; old and probably inactive L1MEc

*markers labeled “H” were taken from the work of Hallström et al. (2011), and markers labeled “N” were taken from the work of Nishihara et al. (2006). Green letters denote markers that we detected under relaxed search criteria (see manuscript).