Supplementary Table 4

Rearrangement	Representative Accession	Coordinates			Repeat Element at Breakpoint (BP)		Species with identical BP ✧ in available sequence	State of element at breakpoint: Crossing or Truncated		Original (vs. Derived) State	Rearrangement Type	Size ✧✧ (bp)	Inferred Mechanism
		Left	Right		Left	Right							
1	PAB_AC188481.3	120780	124140	3360	L1M1	L1M1	PAB, GGO	C	C	O			
	MMU_AC150715.2	33597			L1M1/L1M1*		MMU	T/T			Deletion	3360	NHEJ
2	PAB_AC188481.3	128077			L1M5		PAB, GGO	C		O			
	MMU_AC150715.2	36948	42414	5466	L1M5	L1M5	MMU	T	T		Insertion	5466	LINE RT
3	HSA_HG18	100212678			L1M3		HSA, PTR 15q	C		O			
	MMU_AC148535.2	36394	42556	6162	L1M3	L1M3	MMU	T	T		Insertion	6162	LINE RT
4	HSA_HG18	100213018	100222547	9529	LOR1-int	L2	HSA, PTR 15q	C	C	O			
	MMU_AC150715.2	134811			LOR1-int /L2		MMU	T/T			Deletion	9531	NHEJ
5	HSA_HG18	100239257	100242320	3063	L1PA7	L1PA7	HSA, PTR 15q, PTR 4q	C	C	O			
	MMU_AC148535.2	61701			L1PA7/L1PA7**		MMU	T/T			Deletion	3063	NHEJ
6	HSA_HG18	100242452	100245066	2614	L1PA7	***	HSA, PTR 15q, PTR 4q	C	(C)	O			
	MMU_AC148535.2	61885			L1PA7/THEID-int		MMU	T/T			Deletion	≥2614	NHEJ
7	HSA_HG18	100253145	100258937	5792	-	L1P4	HSA, PTR 4q	-	C	O			
	MMU_AC148535.2	67351			- /L1P4		MMU	-/T			Deletion	≥5792	NHEJ
8	PAB_AC183330.3	29985			L2C		PAB, HSA, PTR 4q	C		O			
	MMU_AC148535.2	70211	74131	3920	L2C	L2C	MMU	T	T		Insertion	3920	LINE RT
9	PTR 4q_AC183669.3	63535	68394	4859	L2	L1PA3	PTR 4q	C	C	O			
	MMU_AC148535.2	145306			L2/L1PA3		MMU	T/T			Deletion	4859	NHEJ
10	PAB_AC183330.3	165419	169603	4184	-	-	PAB				Indel		
	MMU_AC148620.2	73570			-/-		MMU					4184	NHEJ
11	PAB_AC183330.3	176355	181239	4884	-	L1P4	PAB		C	O			
	MMU_AC148620.2	81628			-/L1P4		MMU	-/T			Deletion	4884	NHEJ
12	MMU_AC150715.2	52580	55392	2812	-	Tigger3	MMU		C	O			
	PAB_AC188481.3	137368			- /Tigger3		PAB, GGO	-/T			Deletion	2812	NHEJ
13	HSA_HG18	100200440	100213692	13252	L1M1	LTR57-int	HSA, PTR 15q, PTR 4q	C	C	O			
	PAB_AC183330.3	13624			L1M1/LTR57-int		PAB	T/T			Deletion	13252	NHEJ
14	HSA_HG18	100219570	100245066	25496	MLTH1	***	HSA, PTR 15q, PTR 4q	C	(C)	O			
	PAB_AC183330.3	18965			MLTH1/THEID-int		PAB	T/T			Deletion	≥25496	NHEJ
15	MMU_AC148535.2	67051			AluY		MMU	C		O			
	HSA_HG18	100248092	100252855	4763	AluY	AluY	HSA, PAB†, PTR 15q, PTR 4q	T	T		Insertion	4763	LINE RT
16	HSA_HG18	100256905	100260556	3651	L1MA8	L1ME3B	HSA, PTR 4q	C	C	O			
	PAB_AC183330.3	28542			L1MA8/L1ME3B		PAB	T/T			Deletion	3651	NHEJ
17	MMU_AC149242.2	36929	57410	20481	L1M4C	-	MMU, HSA , PTR 4q	C		O			
	PAB_AC183330.3	33511			L1M4C/-		PAB	T/-			Deletion	20480	NHEJ
18	Inferred				L1M4C ††		Inferred	C		O			
	PAB_AC183330.3	33511	39774	6263	L1M4C	-	PAB	T			Insertion	6263	LINE RT
19	PTR4q_AC183669.3	62153	72625	10472	-	AluSq	PTR4q, MMU		C	O			
	PAB_AC183330.3	88155			-/AluSq		PAB	-/T			Deletion	10472	NHEJ
20	MMU_AC148620.2	52576	58771	6195	L1MC1	-	MMU	C		O			
	PAB_AC183330.3	149153			L1MC1/-		PAB, PTR 4q	T/-			Deletion	6195	NHEJ
21	MMU_AC150715.2	16098	68983	52885	-	-	MMU, PAB, GGO			O			
	HSA_HG18	100155612			-/-		HSA, PTR 15q				Deletion	52885	NHEJ
22	MMU_AC148535.2	†††	64830		-	-	MMU, PAB			O			
	HSA_HG18	100245068			-/-		HSA, PTR 15q, PTR 4q				Deletion	≥2995	NHEJ
23	MMU_AC149242.2	42064	50763	8699	-	L1PB	MMU		C	O			
	HSA_HG18	100269229			-/L1PB		HSA	-/T			Deletion	8700	NHEJ
24	MMU_AC148535.2	94830			L1MC4A		MMU	C		O			
	HSA_HG18	100273152	100276019	2867	L1MC4A	L1MC4A	HSA, PTR4q	T	T		Insertion	2867	LINE RT
25	MMU_AC148535.2	127784	††††		LTR16C	AluSq/x	MMU, PAB 15q, PTR 4q	C	C	O			
	HSA_HG18	100307958			LTR16C/AluSq/x		HSA	T/T			Translocation-Mediated Deletion	~160000	NHEJ
26	HSA_HG18	100258107			AT-rich		HSA			O			
	PTR4q_AC150448.2	94792	98005	3213	AT-rich	AT-rich	PTR4Q				Insertion	3213	LINE RT
27	MMU_AC148535.2	83068	89013	5945	-	L1PA5	MMU		C	O			
	PTR4q_AC183669.3	1661			-/L1PA5		PTR4q	-/T			Deletion	5945	NHEJ
28	PAB_AC183330.3	104672			-		MMU, PAB			O			
	PTR4q_AC183669.3	89614	92759	3145	-	-	PTR4q				Insertion	3145	LINE RT
29	MMU_AC148620.2	33295	33296		-/-		MMU, PAB			O			
	PTR 4q_AC183669.3	112843	117305	4462	-		PTR4q				Insertion	4462	SUZ12 RT

✧Chromosome locations are MMU 7q, PAB 15q, HSA 15q, and GGO 15q unless denoted otherwise.

✧✧ When a deletion size is ≥ a value, this deletion encompasses or overlaps deletion(s) in all genomes and its true size cannot be determined.

* These two Line elements are joined at nonhomologous sites

** Deletion is internal to L1PA7.

*** THEID-int is truncated or missing from all genomes analyzed, but it can be inferred to have crossed the righthand breakpoint. It is missing from HSA due to rearrangement #22.

† Repeat masker incorrectly identifies the portion of the AluY to the right of this insertion as an AluSq. PAB lacks a portion of the insertion and the AluY sequence to the right of the breakpoint due to a sequencing gap.

†† Insertion is at the right edge of the truncated L1M4C created by rearrangement #17; or, alternatively, rearrangement #17 occurred subsequent to this insertion and deleted part of it.

††† MMU & PAB are missing sequence for the lefthand breakpoint due to additional deletions (rearrangements 6 & 14).

†††† Several human subtelomeres and the 2q fusion site retain block 2 sequence an an intact Alu element crossing the other translocation breakpoint healed by NHEJ to create this join (Linardopoulou et al., 2005).
There is ~160 kb from the breakpoint of HSA15q and MMU7 sequence homology to the fission site.