

Table S3

Retroviral map intervals that potentially overlap between species*.

Summary of potential orthologous PTERV1 insertion sites by species

Human Coordinates (Build34 assembly)				Summary of potential orthologous PTERV1 insertion sites by species				
BACID	Chrom	begin	end	% Identity	Chimp	Gorilla	Baboon	Macaque
*RP41_31a20TJ.836	chr1	119530260	119530321 +	95.2%	X	X	X	X
*CH250_168c7TJ.825	chr1	119664263	119664347 +	96.5%		1 X	X	X
*RP41_31a20TV.880	chr1	119690678	119690520 -	98.1%			2 X	X
RP41_0065D07.g1.705	chr1	119703847	119703734 -	94.7%		3	0	5 X
*CH250_168c7TV.892	chr1	119808674	119808161 -	97.3%				
*RP41_0082H03.g1.753	chr10	63369779	63369930 +	96.1%				
*CH250_82f19TV.838	chr10	63402978	63403544 +	94.5%				
*CH250_61n13TV.711	chr10	63514427	63514236 -	95.3%				
*RP41_0082H03.b1.725	chr10	63523433	63523327 -	94.4%				
*RP43_0002J22.g1.634	chr12	31775357	31775588 +	98.7%				
*CH250_21m16TJ.537	chr12	31793783	31793876 +	94.7%				
*RP43_0088A08.b1.682	chr12	31889282	31889015 -	96.6%				
*CH250_92e23TV.880	chr12	31987590	31987363 -	94.3%				
*CH250_172c10TJ.846	chr13	95686016	95686249 +	97.0%				
*RP41_0050D04.g1.751	chr13	95732167	95732440 +	94.5%				
*RP41_0068D04.b1.774	chr13	95754130	95754255 +	93.7%				
*CH250_23a7TJ.466	chr13	95821229	95821075 -	96.1%				
CH250_172c10TV.888	chr13	95843921	95843847 -	97.3%				
*RP41_0050D04.b1.776	chr13	95888828	95888775 -	94.4%				
*RP43_0161K06.g1.620	chr14	18946695	18947124 +	97.0%				
*RP41_10g5TJ.750	chr14	19098959	19099313 +	94.1%				
*RP41_0072B21.g1.699	chr14	19110956	19110864 -	94.6%				
*RP43_0161K06.b1.717	chr14	19116461	19115950 -	98.4%				
*CH255_12i11TV.399	chr18	49704814	49705208 +	97.7%				
*RP41_0061O18.b1.788	chr18	49789665	49789840 +	96.0%				
*CH255_12i11TJ.302	chr18	49884393	49884123 -	98.2%				
*RP41_18k21TJ.852	chr18	49965079	49965026 -	96.3%				

*CH250_148j3TV.691	chr2	4209530	4209765	+	91.9%
*RP41_0161O24.g1.688	chr2	4247027	4247105	+	94.9%
*CH250_148j3TJ.728	chr2	4367524	4367292	-	94.4%
*RP41_0053H13.g1.693	chr2	4378320	4377828	-	94.3%
*CH250_12d8TJ.810	chr2	142195969	142196106	+	97.8%
*RP43_0151J13.b1.721	chr2	142199448	142199733	+	97.9%
*CH250_86e17TJ.850	chr2	142337324	142337220	-	100.0%
CH250_63j16TJ.736	chr2	142348857	142348765	-	96.8%
CH250_9j16TV.534	chr2	142348857	142348765	-	96.8%
*RP43_0070B15.g1.633	chr2	142355976	142355468	-	97.6%
*CH250_92j13TJ.838	chr2	143662193	143662258	+	98.5%
*RP43_114h16TJ.777	chr2	143684971	143685693	+	99.3%
*CH250_172e2TV.874	chr2	143762549	143762472	-	100.0%
CH250_92j13TV.809	chr2	143811041	143810959	-	95.2%
*RP43_114h16TV.760	chr2	143880427	143880367	-	96.7%
*CH255_202k13TV.579	chr7	39874303	39874716	+	100.0%
*RP41_0088E12.g1.723	chr7	39945430	39945544	+	91.3%
*CH255_202k13TJ.566	chr7	40092429	40092285	-	99.3%
*RP41_0088E12.b1.746	chr7	40105977	40105865	-	98.2%
*RP41_18d7TJ.837	chr9	88209117	88209380	+	94.3%
*CH250_150f13TJ.843	chr9	88246399	88246482	+	96.4%
*RP41_18d7TV.767	chr9	88419834	88419654	-	95.6%
*CH250_170p12TJ.842	chr9	88525961	88525860	-	98.0%
*CH255_205h24TJ.681	chrY	13544028	13544129	+	94.1%
*RP43_0040H16.g1.631	chrY	13585498	13585866	+	98.6%
*RP43_98i4TJ.863	chrY	13625083	13624871	-	99.1%
*CH255_254i8TV.626	chrY	13718331	13718237	-	96.8%

*Each BAC was T7 and SP6 end-sequenced. Sequences were mapped to the human genome assembly (orientation is indicated +/-)