

Attached document I:

1. Alignment of the LTRs of the full proviral sequences of human, orangutan and gorilla.

2. Images of the results of the lone LTR search in human, gorilla and orangutan.

Likely lone LTRs
signalled with red

Human BLAT Results

BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser_details	YourSeq	445	1	445	445	100.0%	6	-	67889061	67889505	445
browser_details	YourSeq	360	1	444	445	92.5%	6	-	67880988	67881434	447
browser_details	YourSeq	552	1	451	445	91.6%	8	-	134922609	134925123	455
browser_details	YourSeq	337	6	444	445	90.1%	6_GL000253v2_alt	+	246465	246927	463
browser_details	YourSeq	337	6	444	445	90.1%	6_GL000251v2_alt	+	467379	467841	463
browser_details	YourSeq	337	6	444	445	90.1%	6	+	28980905	28981367	463
browser_details	YourSeq	334	1	442	445	90.5%	X	-	114047514	114047963	450
browser_details	YourSeq	333	1	445	445	90.0%	9	+	92071666	92072132	467
browser_details	YourSeq	333	6	444	445	90.0%	6_GL000256v2_alt	+	290355	290817	463
browser_details	YourSeq	331	27	444	445	90.7%	4	-	79210069	79210506	438
browser_details	YourSeq	327	6	444	445	91.9%	6_GL000255v2_alt	+	246483	246945	463
browser_details	YourSeq	327	6	444	445	91.9%	6_GL000252v2_alt	+	246508	246970	463
browser_details	YourSeq	327	6	444	445	91.9%	6_GL000250v2_alt	+	246490	246952	463
browser_details	YourSeq	321	1	434	445	90.3%	8	-	97827677	97828118	442
browser_details	YourSeq	317	1	444	445	90.0%	19	-	56045276	56046021	746
browser_details	YourSeq	316	8	444	445	89.7%	3	+	162601108	162601567	460
browser_details	YourSeq	312	1	444	445	89.8%	4	+	20845141	20845612	472
browser_details	YourSeq	308	1	429	445	90.3%	13	-	82661030	82661483	454
browser_details	YourSeq	305	9	430	445	89.5%	1	-	247079356	247079792	437
browser_details	YourSeq	298	1	444	445	87.1%	14	-	27919141	27921579	2439
browser_details	YourSeq	292	1	444	445	90.9%	9	+	25994626	26000032	5407
browser_details	YourSeq	263	1	434	445	87.3%	8	+	15925900	15926355	456

Gorilla BLAT Results

BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser_details	AJ431197.1	424	1	446	446	97.1%	6	-	67564510	67564954	445
browser_details	AJ431197.1	363	1	446	446	91.4%	8	-	134851495	134851964	470
browser_details	AJ431197.1	359	1	446	446	92.7%	6	-	67556178	6755626	449
browser_details	AJ431197.1	327	29	446	446	90.2%	4	-	87975889	87976326	438
browser_details	AJ431197.1	324	42	446	446	91.4%	6	+	29884398	29884820	423
browser_details	AJ431197.1	317	1	436	446	89.6%	8	-	96888504	96888947	444
browser_details	AJ431197.1	312	1	445	446	89.4%	4	+	20878773	20879245	473
browser_details	AJ431197.1	306	1	431	446	89.8%	13	-	65525922	65526377	456
browser_details	AJ431197.1	301	1	432	446	90.0%	1	-	227726898	227727346	449
browser_details	AJ431197.1	298	10	446	446	89.3%	3	+	163433637	163434096	460
browser_details	AJ431197.1	293	1	446	446	89.1%	14	-	9024304	9026761	2458
browser_details	AJ431197.1	291	1	433	446	88.6%	X	-	111510023	111510433	411
browser_details	AJ431197.1	272	5	446	446	91.8%	19	-	53567139	53567882	744
browser_details	AJ431197.1	248	1	429	446	86.0%	2A	+	94979365	94979810	446

Orangutan BLAT Results

BLAT Search Results

ACTIONS	QUERY	SCORE	START	END	QSIZE	IDENTITY	CHRO	STRAND	START	END	SPAN
browser_details	YourSeq	410	1	445	445	95.3%	6	-	68202971	68203412	442
browser_details	YourSeq	349	1	444	445	91.1%	4	-	62023708	62024171	464
browser_details	YourSeq	348	1	438	445	91.0%	8	-	68108384	68108718	438
browser_details	YourSeq	336	1	434	445	91.7%	8	-	142996777	142997234	458
browser_details	YourSeq	335	1	431	445	91.3%	X	-	113074992	113075430	439
browser_details	YourSeq	335	1	444	445	90.1%	9	+	97758691	97759241	551
browser_details	YourSeq	317	1	431	445	89.1%	4	+	20877809	20878265	457
browser_details	YourSeq	311	1	444	445	87.9%	3	+	166020102	166020568	467
browser_details	YourSeq	307	1	444	445	87.4%	3	+	166015998	166016456	467
browser_details	YourSeq	304	4	429	445	89.0%	13	-	84188142	84188601	469
browser_details	YourSeq	298	1	434	445	89.7%	19	-	67979989	67980720	732
browser_details	YourSeq	295	9	434	445	90.0%	19_random	-	6030295	6031018	724
browser_details	YourSeq	287	1	444	445	87.9%	14	-	27385157	27394458	9302
browser_details	YourSeq	286	41	444	445	92.9%	6	+	29900762	29901188	427
browser_details	YourSeq	263	1	444	445	87.1%	9	+	35831839	35832268	430
browser_details	YourSeq	248	1	427	445	86.3%	2A	+	4189795	4190242	448
browser_details	YourSeq	240	1	316	445	91.7%	i_random	-	28179751	28179879	329
browser_details	YourSeq	232	1	444	445	87.0%	9	-	101666291	101666757	467
browser_details	YourSeq	232	1	444	445	84.3%	4	+	125108602	125109064	463
browser_details	YourSeq	230	33	431	445	86.9%	2B	+	119955318	119955732	417
browser_details	YourSeq	213	2	408	445	86.7%	Un	+	4568291	4568693	403
browser_details	YourSeq	208	1	425	445	87.5%	X	+	36061882	36062328	447
browser_details	YourSeq	207	1	408	445	88.2%	1	-	84773574	84774003	430
browser_details	YourSeq	202	1	423	445	86.9%	13	-	26287987	26288430	444

