

S3 Table: Mapping of the sites of *Trypanosoma cruzi* kDNA integration into the chromosome of humans.

Case	Access	kDNA	Human	Intermediate recombinatin site	Sites of integration		E-value
					Chromosome	Locus	
1	AL732374.14	167-577	7-170	GGTT	X	LINE-1	5e-29
	AL121780.11	177-536	1-191	TTAGTCTTGGGAGGG	20	(LINE-1	6e-15
	AL355595.10	15-80/ 146-367	62-154	TCCTGGTTTAGTCTTGGGA/ TTGGGAGGG	13	INE-1	4e-21
2	AC012596.4	135-551	35-153	CTCCGGTCTACAGCTCCCA	7	LINE-1	1e-49
	AC012596.4	20-318	307-425	CCCAATCGAACC	7	LINE-1/ PRIMA41	4e-47
3	NG_011441.1	4-356	342-386	ACCCCTCCCAAGAC	4	LINE-1	9e-11
4	AL732374.14	451- 745	367-460	CCCTCCCAAGAC/ AAACCAGGAA	X	LINE-1	6e-30
	AL163872.2	1-387	366-809	CCCTCCCAAGACTAAACCAGGA	14	LINE-1	1e-12
	AC090337.5	1-115	102-689	CCCAATGGAACCTG	18	LINE-1	0.0
	AC129713.1	1-381	378-567	CCCT	5	(INE-1	3e-75
	NG012005.1	523-840	7-531	AGGTTCCAT	8	LINE-1	0.0
	AC012596.4	1-394/ 483-917	383-501	CCCAATCGAACC/ CTCCGGTCTACAGCTCCCA	7	LINE-1 / PRIMA41	8e-48
5	AC093747.2	1-504/ 580-905	501-609	AACC/ ACATACACCCTCCCAAGACTAAACCAGGAA	4	LINE-1	5e-44
	NG_031854.1	7-200	197-250	CCAA	12	LINE-1	1e-14
	NG_012005.1	1-106/ 132-394	99-144/ 387-421	TTGGTGTA/ TTAGTCTTGGGAG/ TTGGTGTA	8	LINE-1	4e-10
6	FN397831.1	1-121/ 347-595	114-372	TTGGTGTA/ ACTTCTCCTGGTTTAGTCTTGGGAG	Not determined	LINE-1	5e-67
7	NM_015288.4	179-454	6-203	CCCCTTCTCACTGACCTAAACGCC	Not determined	PHF15 gene	6e-90
	AC006213.1	1-539	524-726	AACCCCAATCGAACCC	Not determined	L1PA13	1e-88
	AL137181.8	16-320/ 579-698	306-593	AACCCCAATCGAACCC/ GCTCCGGTGTACAGC	6	LINE-1 / PRIMA41	2e-135
	AC012596.4 AL732374.14	5-298/ 381-517	282-399/ 514-672	CCAATCGAACCTAAAA/ CTCCGGTGTACAGCTCCCA/ AACC	7 X	PRIMA41 LINE-1	1e-44 6e-16

7	AC129028.3	1-420	404-484	TGGGAGCTGTACACCGG	12	Family GTTTG-n	2e-27
	AL732374.14	3-462	459-622	AACC	X	LINE-1	1e-18
12	AL355595.10	6-360	346-400	CCCTCCCAAGACTAA	13	LINE-1	8e-18
	CR381572.5	20-553	545-652	AACCACCAT	21	LINE-1	1e-44
13	AC129713.1	5-359	342-453	ACCCCTCCCAAGACTAA	5	LINE-1	1e-41
	AL732374.14	1-360/ 419-650	346-439	CCCTCCCAAGACTAA/ CTCCCAAGACTAAACCAGGAA	X	LINE-1	3e-33
	AL050403.16	126-443	1-146	TCAGCCCCGACACTCTCCGGT	20	Not determined	2e-57
14	AL732374.14	221-369/ 474-777	9-267/ 364-480	CCCTCCCAAGACTAAACCAGGATGAAGTTGAACCCCTGA ATACACCA/ CCCTCC/ TACACCA	X	LINE-1	1e-77
	AC138473.1	6-293/ 699-961	276-728	CCAACCCCAATCGAACCAGCC/ GATACTCTCCGGTGTACAGCTCCCATCTCC	19	ACRO1- Acromeric Satellite	0.0
15	AC129713.1	1-170/ 381-487	157-384	TCAGAGCCTGTTAT/ AGGG	5	LINE-1)	2e-104
	AC129713.1	318-541	1-328	GGTGTATGTGT	5	LINE-1	2e-83
16	AL513128.11	1-159/ 232-561	155-262	AACCA/ ACACATATAGCCTCCCAAGACTAAACCAGGA	10	LINE-1	2e-46
	AL354711.24	1-210/ 330-777	208-348	TGG/ GTGTGGTTTCGATTGGGGTT	9	LINE-1	1e-58
	NG_029859.1	95-470	1-102	TGGGGTTC	12	Not determined	1e-41
	AC012596.4	1-187/ 301-636	184-302	TGGG/ GG	7	LINE-1 / PRIMA41	6e-48
17	AL732374.14	5-480	462-550	CTCCCAAGACTAAACCAGG	X	LINE-1	6e-28
	AC018647.5	1-96/ 144-811	66-161	TCCTGGTTTAGTCTTGGGAGAGTGTATGTGT/ TTAGTCTTGGGAGGGGGT	7	LINE-1	1e-20
	AL732374.14	1-379/ 427-612	367-458	CTCCCAAGACTAA/ ACACATACACTCTCCCAAGACTAAACCAGGAA	X	LINE-1	1e-30
	NG_031854.1	1-51/ 76-522	44-97	CACCGGAG/ ACAGGAGGAGAGGTTTCGATTGG	12	Not determined	2e-14
22	AC129713.1	136-504	1-192	TTGGTGTATTCAAGATTCAACTTCTTCTGGTTTAGTCTT GGGAGGGTGTATGTGT	5	LINE-1	4e-48
	AC037476.10	262-643	7-279/ 596-688	AATAACGGGCTCTGATAC/ CCCTCCCAAGACTAAACCA GGAGGAAGTTGAGTCTCTGAATAGACCAA	18	LINE-1	1e-63
	AC113165.1	139-796	14-147	ATACACCAA	5	LINE-1	5e-56

	AL732374.14	64-331	7-119	ACACATACACTCTCCCAAGACTAAACCAGGACGAAGTTTA ATCTCTGAATACACCA	X	LINE-1	9e-36
	AC023850.10	1-70	68-181	TTG	11	L1PA7	3e-06
23	AL732374.14	112-540	1-159	TTGGTCTATTCAGAGATTCAACTTCTTCTGGTTTAGTCTT GGGAGGG	X	LINE-1	5e-54
	AL732374.14	2-70/ 135-249/ 349-593	68-140/ 238- 355	CCC/ TACACC/ CCCTCCCAAGAC/ ACACCA	X	LINE-1	1e-43
	AC079052.4	1-192	183-338	GGGGCGTTCA	18	Not determined	3e-67
	AC093329.6	417-768	9-436	TGAACGCCCTCCCAAACC	8	L1ME4A	0.0
24	BC137023.1	1-288	276-329	CCCCAATGGAACC	Not determined	OR1-17 gene	2e-12
	FN397831.1	71-304	13-95	CTCCCAAGACTAAACCAGGAATAAG	Not determined	LINE-1	9e-29
	AC087600.21	7-629	619-736	GGGGGAGATGC	12	AluJb	2e-47
	FN397831.1	1-343	324-473	TCCTGGTTTAGTCTTGGGAG	Not determined	LINE-1	1e-61
	CR788268.5	6-167/ 233-378	153-245	GTCTACAGTCCCAT/ CCCCTCCCAAAC	9	Not determined	3e-29
26	AL732374.14	20-110	104-211	CTCCCAA	X	LINE-1	8e-40
	AL732374.14	301-430	11-308/ 424- 541	TGGGAGGG/ TGGTGTA	X	LINE-1	1e-67
	AC245096.1	622-709/ 811-905	11-628/ 701- 819	CCCGTAC/ TTGGTGTAT/ TTGGGAGGG	X	LINE-1	0.0
	NG_027782.1	1-129/ 229-522	118-236	CTCTCCCAAGAC/ TACACCAA	15	LINE-1	3e-18
	AC234834.5	108-290	5-122	TTAGTCTTGGGAGAG	10	LINE-1	1e-13
	AL356270.11	117-296	11-128	GTCTTGGGAGAG	1	LINE-1	1e-14
27	NG_030016.1	1-105/ 211-380/ 411-580/ 621-780/ 960-1093	100-218/ 374- 420/ 576-622/ 777- 966	TTGGTG/ TGGGAGAG/ TGGTGTA/ TGGGAGGG/ TGGTG/ GG/ TTGG/ GGAGAG	7	LINE-1	8e-24
	AL732374.14	1-166/ 263-460/ 557-797	160-277/ 454- 569	TGGTGTA/ TTAGTCTTGGGAGGG/ TGGTGTA/ TTAGTCTTGGGAG	X	LINE-1	7e-42
	AC008769.7	24-533	531-749	TCA	5	LINE-1	2e-106

	AL591602.7	20-771	764-847	GTACATTA	1	LINE-1	3e-33
	AC005018.2	19-89/ 132-437	87-134	CCTT/ CAA	7	LINE-1	3e-11
28	NG_027782.1	1-58/ 243-429	53-253/ 426-584	AACCCT/ TACAGCTCCCA/ AACC	15	L1P_MA2	6e-41
29	NG_028929.1	1-375	361-422	ACCCCCTCCCAAGAC	1	LINE-1	7e-19
	NG_030016.1	35-130	123-179	CCCTCCCA	7	LINE-1	1e-17
	AL732374.14	76-261	2-120	CTCCCAAGACTAAACCATGACGAAGTTTGATCTCTGAATACACCA	X	LINE-1	4e-39
	AC110583.3	1-47/ 182-330	40-227	TTGGTGTA/ TTGGTCTATTCAGAGACTCAACTTCCTCTGGTTTAGTCTTGGGAG	18	L1PA6	2e-13
	AL732374.14	1-170/ 226-365	144-273	CTCTCAAGACTAAACCAGGAGGAAGTT/ AAACCAGGAA GAAGTTGGATCTCTAAATAGACCAATAACAGGCTCTGA	X	LINE-1	1e-47
	AL732374.14	1-130/ 206-454	122-253	CCCTCCCAA/ AAACCAGGAAGAAGTTGGATCTCTAAATAGACCAATAACAGGCTCTGA	X	LINE-1	1e-48
29	AC010723.3	1-29/ 197-676	22-212	TTGGTGTA/ TTAGTCTTGGGAGTGG	Y	LINE-1	2e-10
30	AL732374.14	1-120/ 361-593	110-370/ 586-749	TTGGTGATTC/ CTTGGGAGAG/ TGGTGTAT	X	LINE-1	5e-56
	NG_029532.1	51-121	21-58	TAGACCAA	7	LINE-1	4e-09
	AC090092.9	4-360	553-739	ACATTATT	11	Family CA-n	2e-86
31	NG_029225.1	20-190/ 228-754	183-248	ACAGTCCC/ ATAATGTACGGGGGAGATGCA	3	Not determined	7e-16
32	CR788268.5	1-91/ 164-602	85-177	GTCTACA/ CCCCTCCCAAAAC	9	Not determined	2e-27
	CR788268.5	1-135	121-202	GTCTACAGTCCCAT	9	Not determined	5e-29
	CR788268.5	72-200/ 271-471/ 546-603	1-74/ 188-280/ 465-555	GAC/ GTTTTGGGAGGGG/ GACTGTAGAC/ TTTGGGA/ GACTGTAGAC	9	Not determined	4e-24
33	AL732374.14	101-236	1-113/ 229-417	AGTCTTGGGAGGG/ TGGTGTAT	X	LINE-1	9e-50
	AL732374.14	121-250	7-124/ 242-410	ACCA/ CTCCCAAGA	X	LINE-1	1e-47
34	AL732374.14	1-603	599-755	AACCA	X	LINE-1	6e-17
	AC104006.6	5-263	260-336	AACC	8	L1P	2e-24

	AL732374.14	1-157/ 298-394	149-312	AACCAACAT/ TTAGTCTTGGGAAGG	X	LINE-1	7e-19
	AC104006.6	6-600	597-673	AACC	8	L1P	5e-24
	AL136983.11	1-186/ 350-679	170-357	CTCCGGTCTACAGTCCC/ TTTGAAGC	1	Not determined	9e-84
35	FN397831.1	1-180	158-393	CTTATTCTGGTTTAGTCTTGGG	Not determined	LINE-1	9e-30
	BC137023.1	1-430	421-483	CCCCAATCGA	Not determined	OR1-17 gene	9e-19
	AL732374.14	2-640	636-730	CTTAT	X	LINE-1	9e-27
	AL591768.2	1-146	129-750	ACCAACCCCAATGGAACC	14	L1P_MA2	0.0
37	AC025040.7	514-972	26-527	GACCGCCCCCTCCA	15	L1M2_5	0.0
	AC105133.6	1-247/ 327-416	242-335	GAGGGG/ TGGGGACTG	15	Family L2	3e-36
37	AC100835.2	205-756	3-218	CTGAACGCCCTCC	15	Not determined	3e-103
38	FN397831.1	1-431	468-557	TCCTGGTTTAGTCTTGGGA	Not determined	LINE-1	3e-31
	BC137023.1	15-434	420-483	CCCCAGTGGAAACCC	Not determined	OR1-17 gene	4e-11
	AC138951.2	6-277/ 374-525	266-378	CTACAGTCCCCA/ TTGAC	5	LINE-1	2e-47
	FN397831.1	119-228	1-140	CCCTCCCAAGACTAAACCAGGA	Not determined	LINE-1	2e-61
40	AL732374.14	98-196	1-112	TTAGTCTTGGGAGGG	X	LINE-1	1e-43
	AC129713.1	1-400	384-609	TCAGAGCCTGTTATTGG	5	L1P_MA2	1e-99
	FN397831.1	202-728	1-214	TAGTCTTGGGAGG	Not determined	LINE-1	6e-55
41	AL732374.14	20-499	486-611	CCCTCCCAAGACTA	X	LINE-1	4e-49
	AC129713.1	18-76/ 382-861	76-385	T/ GTTT	5	Not determined	5e-88
	FN397831.1	1-523	510-741	GCCCCCTCCCAAAAC	Not determined	LINE-1	1e-70
	AL353744.18	218-472	1-220	TGA	X	LINE-1	2e-104
	NG_008042.1	301-581	2-312	CCCCTCCCAAAA	8	LINE-1	2e-149
42	AL023583.25	20-617/ 720-852	601-741	CAACCCCAATGGAACCA/ CCTCCCAAGACTAAACCAGGAT	6	Not determined	2e-55
	AL358253.16 NG_016598.1	1-190/ 291-510/ 732-1213	188-296/ 508-749	CCC/ GCTCCC/ CAA/ TCCGGTGTACAGCTCCCA	1 16	PLA2G2E gene L1M2_5	3e-38 4e-34

	AC231759.3	582-905	11-600	CTCCGGGTGTACAGCTCCCA	X	L1P_MA2	0.0
	AC078793.13	433-1264	15-454	ACACTCTCCGGTGTACAGCTCC	3	Not determined	0.0
43	AC005394.1	134-597	11-149	CTCCGGGTGTACAGCTC	19	MER5B	2e-58
	AC002383.1	448-578	6-455	CTCCGGTG	7	ERV46I	0.0
44	AC002383.1	448-686	6-470	CTCCGGGTGTACAGCTCCAACTCC	7	HERV46I	0.0
45	AC002383.1	448-843	6-455	CTCCGGTG	7	HERV46I	0.0
46	AL031681.16	1-151	144-310	CACCGGAG	20	Not determined	2e-74
	NG_029859.1	4-283/ 365-925	276-376	GAACCCCA/ CTCCGGTGTACA	12	Not determined	4e-39
	AC002383.1	430-1110	6-440	CCAACCCCGAC	7	HERV46I	0.0
46	AC025287.8	1-309	304-390	GGAGAG	16	Not determined	2e-12
	AL356962.8	2-295	283-410	CCCCAATCGAACC	6	L1M2_5	3e-23
47	AL732374.14	1-370	366-460	CCCTC	X	LINE-1	5e-34
	AC129713.1	1-579	569-797	ACACATACACC	5	LINE-1	8e-104
	AC023926.6	1-296	279-691	ACCAACCCCAATGGAACC	8	L1PA13	2e-40
	AL732374.14	1-370	366-460	CCCTC	X	LINE-1	5e-34
	AL732374.14	57-444	1-70	TGGTCTTGGGAGGG	X	LINE-	4e-16
	AC023926.6	1-571	551-892	ACCACCCCAATGGAACCAGA	8	L1PA1	4e-166
	FN397831.1	1-396	373-609	GCCCCTCCCAAGACTAAACCAGGA	Not determined	LINE-1	1e-69
48	FN397831.1	1-375	357-446	TCCTGGTTTAGTCTTGGGA	Not determined	LINE-1	3e-31
	BC137023.1 AL732374.14	1-405	393-455/ 437-531	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 7e-27
	AL732374.14 BC137023.1	1-650	644-706/ 688-783	CCCCAAT/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	6e-17 4e-26
	BC137023.1 AL732374.14	6-710	709-775/ 756-855	CC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-13 8e-16

	BC137023.1 AL732374.14	5-726	712-774/ 756- 850	CCCCAATCGAACCAC/ CTTATTCCTGGTTAGTCT	Indeterminado X	OR1-17 gene LINE-1	7e-17 3e-28
	BC137023.1 AL732374.14	1-410	409-471/ 453- 547	CC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 3e-31
	NG_027527.1	1-718	750-844	CTTATTCCTGG	18	LINE-1)	2e-17
	AL358253.16	1-220/ 320-393	216-324	CCCCA/ CTCCC	1	PLA2G2E gene	8e-37
49	BC137023.1	1-420	417-479	CCCC	Not determined	OR1-17 gene	4e-17
	AP002533.1	1-730	726-788	CCCCA	1	Not determined	6e-17
49	BC137023.1 AL732374.14	1-348	336-398/ 380- 474	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	8e-19 1e-29
	AL513533.15	1-584	576-721	ATGGAACCC	10	L1PB2c	1e-50
	NG_023332.1	2-545	531-764	ACCCCAATGGAACCC	8	L1PB2c	2e-62
51	AC004865.1	1-288	275-823	CCCAATGGAACCCA	1	L1M4B	0.0
	AC008865.3	1-287	277-837	CAATGGAACCC	5	AluS	0.0
	FP700059.5	1-180/ 242-638	171-263	GTCTACAGTC/ ATTTGAAGCCCCCTCCAAAAC	9	Not determined	5e-30
	NG_012343.1	1-598	586-670	CTACAGTCCCAT	12	L1MA7	3e-32
	NG_023038.1	114-797	22-119	TGAACC	2	Not determined	3e-34
52	NG_012005.1	1-787	778-1317	ATGGAACCTG	8	(LINE-1	0.0
	AC091940.3	1-168	151-398	ACCAACCCCAATGGAACC	5	L1M2_5)	5e-109
	AC002383.1	1-146/ 557-951	129-567	AAGGCCCTCCAAAACC/ CCAACCCCGAC	7	HERV46I	0.0
53	AC091940.3	1-201/ 414-473	184-430	ACCAACCCCAATGGAACC/ CTCCGGTGTACAGCTCC	5	L1M2_5	2e-110
	AL358253.16	1-294/ 372-630	281-389	CCCCAATGGAACCC/ CTCCGGTGTACAGCTCCC	1	PLA2G2E gene	3e-38
	AC245054.3	1-436/ 567-602	421-580	CAACCCCAATGGAACC/ CTCCGGTGTACAGC	22	L1PB2c	1e-68
	AC104069.3	1-130/ 188-381	122-206	AATGGAACC/ CTCCGGTGTACAGCTCCA	2	L1MA7	2e-32
	AC078793.13	1-333	312-569	GGAGCTGTACACCGGAGGGTGT	3	Not determined	6e-123

54	AL732374.14	22-286/ 347-550	283-400	CCCT/ ACATACACCCTCCAAGACTAAACCAGGAAGA AGTTGAATCTCTGAATACACCA	X	LINE-1	9e-45
	AL732374.14	1-135/ 232-324	121-238	CCCTCCCAAGACTAA/ TACACCA	X	LINE-1	5e-45
	AC002383.1	433-518	2-455	ACCCCAACCATGAGACTCCGGTG	7	HERV46I	0.0
	AC002383.1 AC091940.3 AC012596.4	448-641/ 855-949	6-455/ 624-871/ 938-1055	CTCCGGTG/ ACCAACCCCAATGGAACC/ CTCCGGTGTACAGCTCC/ CCCAATCGAACC	7 5 7	HERV46I L1M2_5 LINE-1 / PRIMA41	0.0 4e-110 4e-46
55	AL732374.14	2-580	564-658	CTTATTC	X	LINE-1	4e-31
	AL358253.16	1-178	165-273	CCCCAATGGAACCC	1	PLA2G2E gene	1e-38
	AC091940.3	1-95/ 310-663	78-326	ACCAACCCCAATGGAACC/ CTCCGGTGTACAGCTCC	5	L1M2_5	3e-115
	AC104069.3	1-288/ 346-683	280-364	AATGGAACC/ CTCCGGTGTACAGCTCCCA	2	L1MA7	4e-31
	AC091940.3	1-171/ 386-684	154-402	ACCAACCCCAATGGAACC/ CTCCGGTGTACAGCTCC	5	L1M2_5	2e-112
	AL031681.16	164-500	6-172	CCTCCGGTG	20	Not determined	5e-73
55	NG_029859.1	1-128/ 211-461	121-222	GAACCCCA/ CTCCGGTGTACA	12	LINE-1	7e-39
56	AP006197.1	147-420	1-165	CTCCGGTCTACAGCTCCCA	6	L1M2C_5	2e-77
57	NG_012566.2	168-442	20-173	AGCTCCCA	X	L1PA16	3e-30
58	FN397831.1	184-267	1-200	TTAGTCTTGGGAGGGGC	Not determined	LINE-1	2e-35
	AL732374.14	1-137	133-323	AACCT	X	LINE-1	3e-66
	AC091930.3	136-281	32-154	GGTTCCATTGGGGTTGGTG	5	LINE-1	8e-48
	Z96050.1	20-180/ 396-725	173-414	TTTGGGAG/ TGGGGACTGTAGACCGGAG	1	LINE-1	3e-108
59	AL732374.14	112-380	7-119	ATACACCA	X	LINE-1	1e-35
60	AC104237.2	81-167	7-93	TCTACAGCTCCCA	11	L1PA2	3e-30
	AL732374.14	2-118/ 189-281	111-228	TTCAGAGATTCAACTTCTCCTGGTTTAGTCTTGGGAGG	X	LINE-1	2e-42
	AL137181.8	297-476	23-310	CTCCGGTGTACAGC	6	Not determined	7e-134
	AC012596.4	1-82/ 171-452	71-189	CCCAATCGAACC/ CTCCGGTGTACAGCTCCCA	7	LINE-1 / PRIMA41	4e-48

	AL162424.20	1-302/ 511-545	276-529	ACCAACCCCAATCGAACCTTACACAAG/ CTCCGGGTGTACAGTTCCCA	9	Not determined	8e-115
61	AC236396.2	1-148	140-376	AATGGAACC	Not determined	L1MED_5	6e-114
	AP000620.4	1-36/ 243-290	32-247	GAACC/ TCCCA	11	L1PB2c	3e-98
62	AC092198.5	1-307	294-781	ACCCCAATGGAACC	X	CHARLIE8A	0.0
64	AL732374.14	1-130/ 326-535	123-340	AACCACCA/ AATAACGGGCTCTGA	X	LINE-1	4e-87
	NG_031854.1	115-315	1-125	CAGGAGGAGAGGTTTCGATTGG	12	Not determined	1e-14
	AC012596.4	1-250/ 349-501	243-361	TGGGAGC/ GGGTTCGATTGGG	7	LINE-1 / (PRIMA41	5e-47
66	AL359999.11	1-164	146-482	TGGGAGCTGTAGACCGGAG	11	L1P_MA	4e-169
	AC087600.21	1-201	191-678	GGGGGAGATGC	12	AluJb	0.0
67	FN397831.1	1-396	373-522	GCCCCTCCAAGACTAAACCAGGA	Not determined	LINE-1	9e-57
	AL355595.10	46-163	1-60/ 156-198	TTAGTCTTGGGAGGG/ TTGGTGTGA	13	LINE-1	8e-21
68	AC020783.8	1-130/ 248-314	118-251	TTGGTGTATTTCAG/ GGTT	8	L1PA6	1e-52
	AL732374.14	1-149/ 289-419	135-333	CCATCAGAGAATACT/ CTCCCAAGACTAAACCAGGAA GAAGTTGAATCCCTGAATACACCA	X	LINE-1	3e-75
	AL450108.12	1-490	470-1109	ACCAACCCCAATCGAACCACA	X	LINE-1	0.0
	AC096768.3	14-100	90-290	TGGGAGCTGTGA	4	HERVH48I	5e-89
68	AC236396.2	246-417	18-249	GGTT	Not determined	LINE-1 / PRIMA41	3e-112
	AL049875.2	1-437/ 646-729	429-664	AATCGAACC/ CTCCGGGTGTACAGCTTCCA	14	L1P_MA2	2e-110
69	FN397831.1	61-125	1-65	ACACC	Not determined	LINE-1	4e-22
70	AL732374.14	74-185/ 245-346	7-79/ 178-250	TACACC/ CCCTCCCA/ TACACC	X	LINE-1	3e-23
	AC021133.5	31-325/ 426-729	320-427	AACCAC/ GA	6	INE-1	4e-44
	FP700059.5	22-117/ 183-372	103-195	GTCTACAGTCCCAT/ CCCCTCCCAAAC	9	Not determined	3e-30
71	AL732374.14	2-70/ 179-378	68-185	CCC/ TACACCA	X	LINE-1	7e-44
	AL732374.14	5-72/ 132-336	70-185	CTC/ ACATACACTCTCCCGAGACTAAGCCAGGAGGAA GTTGAATCTCTGAATACACCA	X	LINE-1	2e-37
	AC105242.4	161-364	1-177	GTTTAGTCTTGGGAGGG	8	L1PA3	2e-26

	NG_011441.1	2-90/ 195-494	88-207	TTG/ GTCTTGGGAGGGG	4	LINE-1	2e-21
	AL732374.14	1-100/ 193-281	98-215	CCC/ AAGCTGAATCTCTGAATACACCA	X	LINE-1	2e-42
	AL732374.14	10-193/ 267-340/ 440-520	189-260/ 329- 446	CCCTC/ TACAC/ CCCTCCCAAGAC/ TACACCA	X	LINE-1	4e-42
	NG_031854.1	1-292/ 328-363	282-334	CCAATCGAACC/ CTCCGGT	12	Not determined	5e-14
72	NG_011880.1	7-164	157-328	TTGGTGTA	13	MER5A	3e-61
	AL732374.14	310-835	1-365	ACACATACACCCTCCCAAGACTAAACCAGGATGAAGTTTG ATCTCTGAATACACCA	X	LINE-1	5e-56
	AC233279.2	215-478	7-261	CTCTCCCAAGACTAAACCAGGAAGAAGTTGAATCCCTGA ATATACCA	X	LINE-1	3e-44
	AC126474.6	95-290/ 372-550/ 620-694	1-151/ 288-406/ 547-678	ACACATACAACCTCCCAAGACTAAACCAGGAAGAAGTTG AATCCCTGAATACACCAA/ CCC/ AAACCAGGAGGAA GTTTGATCTCTGAATACACCAA/ CTCCCAAGACTAAAC CAGGAGGAAGTTTGATCTCTGAATACACCAACCCCNNGC TCTGA	12	L1PA6	1e-31
	AL732374.14	1-86/ 245-450	84-267/ 404- 681	TGG/ ACTTCCTCCTGGTTTTGGGAGGG/ TGGTATATT CAGGGATTCAACTTCTTCTTGGTTTAGTCTTGGGAGGG	X	LINE-1	9e-84
	AL049875.2	1-174	166-344	AATCGAACC	14	L1P_MA2	2e-82
73	AL732374.14	1-386/ 458-586	377-464/ 583- 674	CTCCCAAGAC/ TACACCA/ CCCT	X	LINE-1	2e-27
	AL732374.14	51-248/	1-62/ 220-378	GTTTTGGGAGGG/ GGTGTATGTGTACCAGAGCCCGTTATTGG	X	LINE-1	6e-58
	AC244605.2	1-330	326-570	AATCG	16	Pseudogene/ tRNA-Asp- GAY	9e-121
75	AC079052.4	159-531	5-163	CCCC	18	(INE-1)	5e-67
	AL732374.14	6-80/ 295-424	69-298	CCCTCCCAAAAC/ GGTT	X	LINE-1	5e-46
76	AL512603.26	11-808	805-892	CCAA	10	Not determined	1e-26
	AL137181.8	1-76/ 335-546	73-349	AACC/ GCTCCGGTGTACAGC	6	(LINE-1)	3e-132
	AC012596.4	124-321	18-136	GGGTTTCGATTGGG	7	LINE-1 / PRIMA41	3e-48
	AL353996.3	1-110	100-166	CCAATGGAACC	17	Not determined	2e-20

77	AC079052.4	160-550	4-163	CCCC	18	LINE-1	7e-65
	AC079052.4	155-528	4-163	GAACGCCCC	18	LINE-1	2e-66
	AL732374.14	245-560	9-247/ 549-639	CAA/ CTCTCCCAAGAC	X	LINE-1	2e-41
	AC027807.6	6-129/ 476-654	128-525	CC/ ACACATACAACCTCCCAAGACTAAACCAGGATGA AGTTTGATCTCTGAAT	15	L1PA6	9e-46
	AL732374.14	1-61/ 158-470/ 582-700/ 756-1091	55-172/ 465- 596/ 688-767	TGGTGTA/ TTAGTCTTGGGAAGG/ TCAGAG/ TTAGTCTT GGGAGGG/ TTGGGTTGGTGTA/ GTTTTGGGAGGG	X	LINE-1	4e-46
	NG_023312.1	1-730/ 831-1023	724-842	TTGGTGT/ GTTTTGGGAGGG	1	LINE-1	7e-18
78	AC012596.4	1-80/ 151-413/ 501-551	74-192/ 401- 519	CCCAATC/ CCAAGATGGCCAAATAGGAACAGCTCCGG TGTACAGCTCCCA/ CCCAATCGAACCC/ CTCCGGTGTA CAGCTCCC	7	LINE-1 / (PRIMA41	5e-48
	NG_029495.1	1-164/ 425-787	147-453	CCAACCCCAATCGAACCA/ CCAACCCTCTCCGGTGTACAGCTCCCAAC	2	LINE-1 / PRIMA41	2e-142
	AC092995.7	75-480	10-87	GGTTCGATTGGGG	3	HERV9	2e-27
79	AC020783.8	125-533	1-128	TCTT	8	L1PA2	5e-16
	AL732374.14	94-220	7-100	CCAGGAA	X	LINE-1	2e-29
	NG_030414.1	1-174	171-235	AACC	4	LINE-1	5e-18
	AL732374.14	10-146/ 191-296	129-196	CCCTCCCAAAACCAGGAA/ TACACC	X	LINE-1	6e-18
92	BC137023.1 AL732374.14	1-401	389-451/ 433- 526	CCCCAATGGAACC/ CTTATTCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	4e-17 2e-27
	AC233279.2	74-372	1-80/ 358-416	TACACCA/ CTCTCCCAAGACTAA	X	LINE-1	3e-24
	AL732374.14	1-403	389-507	CCCTCCCAAGACTAA	X	LINE-1	2e-45
	NG_011441.1	53-169	4-60/ 153-213	TACACCAA/ CCCCTCCCAAGACTAA	4	LINE-1	9e-14
	AC129713.1	194-370/ 421-540/ 651-750/ 1001- 1122	1-197/ 364-424/ 534-652/ 747- 1009	CTGA/ CCCTCCC/ CTGA/ CCCTCCC/ AA/ CCCT/ ATACACCAA	5	LINE-1	2e-83
92	AL732374.14	1-130/ 227-342/ 396-591	124-241/ 338- 410/ 587-659	TGGTGTA/ TTAGTCTTGGGAGGG/ GGTGT/ TTAGTCTTGGGAGGG/ GGTGT	X	LINE-1	1e-43

	AC129713.1	186-536/ 572-737	19-246/ 526-586	CCCTCCCAAGACTAAACCAGGAAGAAGTTGAATCTCTGA ATAGACCAATAACAGGCTCTGA/ CCCTCCCAAGA/ AA TAACAGGCTCTGA	5	LINE-1	1e-100
	AL732374.14	85-489	14-132/ 449-520	TTGGTCTATTCAGAGATCCAAC TTCTCTGGTTTAGTCTT GGGAGGG/ GGTGTTTGTGTATCAGAGCCTGTTATTG GTCTATTCAGAGA	X	LINE-1	2e-45
95	BC137023.1	1-300	289-351	CCCCAATCGAAC	Not determined	gene OR1-17	6e-19
	BC137023.1	56-656	6-68	GGTTCGATTGGGG	Not determined	gene OR1-17	1e-18
	AL732374.14	284-475/ 691-827	1-295/ 471-702/ 822-910	GTCTTGGGAGGG/ TGGTG/ GTCTTGGGAGGG/ TTCCTG	X	LINE-1	3e-15
	AL732374.14	106-218	1-120/ 212-288	GTCTTGGGAGGGGGT/ TGGTGTA	X	LINE-1	2e-43
96	BC137023.1	56-512	6-68	GGTTCATTGGGG	Not determined	OR1-17 gene	5e-16
	AL732374.14	113-240/ 289-376/ 402-550/ 585-701/ 798-914	7-119/ 237-289/ 364-409/ 544-591/ 687-804	TACACCA/ CTCC/ G/ CTCCCAAGACTAA/ TAGACCAA/ CTCTCCC/ ACACCAA/ CCCTCCCAAGACTAA/ TACACCA	X	LINE-1	2e-43
	AL732374.14	221-349/ 592-720/ 761-884	1-226/ 342-601/ 716-763/ 878- 918	GGAGGG/ TGGTGTAT/ CTTGGGAGAG/ TTGGT/ GGG/ TTGGTGT	X	LINE-1	5e-31
	AL732374.14	69-199/ 296-427/ 529-625	187-302/ 420- 535	CTCCCAAGACTAA/ TACACCA/ CTCCCAAG/ TACACCA	X	LINE-1	1e-43
97	AL732374.14	8-357/ 503-756	339-506	ACACCCTTCCCAAGACTAA/ GGTT	X	LINE-1	1e-13
	AC104006.6	1-510/ 578-611	505-581	CCAGGA/ GGTT	8	L1P	2e-21
	AL732374.14	5-263	260-420	AACC	X	LINE-1	7e-19
	AC104006.6	5-268	260-420	AACCAACAT	8	L1P	3e-24
	AC010104.3	5-263	260-420	AACC	Y	LINE-1	3e-24
	BC137023.1	1-265	251-313	CCCCAATGGAACCAC	Not determined	OR1-17 gene	2e-17
97	NG_029861.1	5-268	260-336	AACCAACAT	1	LINE-1	1e-22
	AC241994.3	5-263	260-336	AACC	3	LINE-1	1e-22
	AC104006.6	5-337	331-409	CAAACCA	8	L1P	2e-25

100	AC104006.6	31-385	1-41/ 377-469	ACCCCAATGGA/ AACCAACAT	8	L1P	3e-24
	AC010104.3	5-336	331-408	AAACCA	Y	LINE-1	8e-25
	AL732374.14	5-268	260-420	AACCAACAT	X	LINE-1	7e-19
	AL732374.14	18-198	174-268	CTTATTCTGGTTTAGTCTTGGGAG	X	LINE-1	1e-31
101	AL732374.14	81-502	7-99	TCCCAAGACTAAACCAGGA	X	LINE-1	2e-27
	AC087600.21	6-459	449-933	GGGTGAGATGC	12	AluJb	0.0
	BC137023.1	1-431	419-481	CCCCAATGGAAC C	Not determined	gene OR1-17	4e-17
	AL732374.14	6-895	887-1048	AACCAACAT	X	LINE-1	2e-18
	AC104006.6	5-268	260-336	AACCAACAT	8	L1P	2e-24
	AC020783.8	5-263	260-291	AACC	8	L1PA6	2e-05
	AF315553.1	5-263	260-336	AACC	Y	PRKY gene	2e-24
	AL732374.14	6-359	345-413	CCCTCCCAAGACTAA	X	(LINE-1)	6e-20
	NG_011635.1	1-458	428-562	ACACATACACCCTCCCGAGACTAAACCAGGA	10	(gene MYO3A)	4e-24
	AL732374.14	1-137/ 331-606	129-333	TGGTGTATT/ GTT	X	LINE-1	3e-77
102	BC137023.1	1-407	395-457	CCCCAATCGGACC	Not determined	OR1-17 gene	3e-17
	AL732374.14	1-336	330-420	TTCCTGG	X	LINE-1	4e-29
	AC233279.2	1-850	827-920	CTTATTCTGGTTTAGTCTTGGGA	X	LINE-1	1e-25
	AL732374.14	117-469	7-124	AATACACC	X	LINE-1	2e-39
	AL732374.14	7-202	190-315	CTCCCAAGACTAA	X	LINE-1	2e-49
103	AL732374.14	5-49/ 121-430	39-136	CCCTCCCAAGA/ CTAAACCGGAATAAG	X	LINE-1	2e-31
	AL732374.14	1-694	691-851	AACC	X	LINE-1	2e-18
	AL732374.14	5-263/ 409-791	260-421	AACC/ TTAGTCTTGGGAG	X	LINE-1	1e-18
103	AC104006.6	6-263/ 326-426	260-331	AACC/ TACATT	8	L1P	1e-21
	AC104006.6	7-264	261-337	AACC	8	L1P	2e-24
	AL732374.14	99-444	20-111	TTAGTCTTGGGAG	X	LINE-1	2e-32

	AC125629.1	5-210	203-872	AACCAAAC	12	L1P	0.0
104	BC137023.1 AL732374.14	10-289	277-339/ 321-415	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	7e-19 1e-29
	AL732374.14	4-590	581-675	CTTATTCCTG	X	LINE-1	2e-29
	AC010104.3	17-319/ 387-644	313-390	ACCAGGA/ TGGT	Y	LINE-1	6e-22
	AC104006.6	15-245	240-316	CCAGGA	8	L1P	2e-24
	AL732374.14	1-100/ 226-290 BC137023.1	89-183/ 165-227	TCCAAGACTAA/ AGACTAAACCAGGAATAAG/ GG	Not determined	LINE-1 OR1-17 gene	7e-30 6e-18
	NG_029111.1	5-262	259-335	AACC	3	LINE-1	1e-21
	NG_030039.1	5-340/ 392-516	333-397	TCAGAGCC/ TGTATA	1	LINE-1	2e-20
105	NG_029111.1 AL732374.14	1-263/ 321-650	259-335/ 641-735	AACCA/ TGGATACATTCCTGG/ CTTATTCCTG	3 X	LINE-1 LINE-1	1e-19 2e-29
	BC137023.1 AL732374.14	4-263	251-300/ 295-387	CCCCAATCGAACC/ CTTATT	Not determined X	OR1-17 gene LINE-1	3e-15 1e-27
	AL732374.14	17-378/ 461-528	373-467	CTCCCA/ GGAATAA	X	LINE-1	1e-29
	BC137023.1	1-690	682-744	CCCCAATCG	Not determined	OR1-17 gene	1e-18
	AC010104.3 AL732374.14	4-260	259-335/ 329-488	AA/ AATGGAT	Y X	LINE-1 LINE-1	2e-24 7e-33
	NG_015812.1	4-262	259-335	AACC	4	LINE-1	1e-21
	BC137023.1 AL732374.14	4-400	394-440/ 438-532	CCCCAAT/ CTT	Not determined X	OR1-17 gene LINE-1	9e-12 2e-27
	AC006979.2 AL732374.14	4-267/ 414-935	265-335/ 329-420	CAT/ TTCCTGG/ TTGGGAG	7 X	LINE-1 LINE-1	1e-21 2e-30
BC137023.1	1-264/ 311-574	250-312/ 562-624	CCCCAATCGAACCAC/ CT/ CCCCCAATCGAACC	Not determined	OR1-17 gene	1e-17	
105	NG_030414.1	6-268	260-423	AACCAACAT	4	LINE-1	2e-20
	AL445464.9	5-410	399-562	TCGAACCAACAT	1	LINE-1	2e-16

106	AL132825.35	5-405/ 551-645	381-563	ATATTACACCAACCCCAATCGAACC/ TTAGTCTTGGGAG	20	LINE-1	8e-21
	BC137023.1 AL732374.14	13-420	415-477/ 459-553	CCCCAA/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 2e-28
	AC104006.6	5-406	403-479	AACC	8	L1P	3e-24
	AC011996.8	344-694	1-389/ 649-776	CTCCCAAGACTAAACCAGGAAGAAGTTTAAATCTCTGAATA CACCAA/ CTCCCAAGACTAAACCAGGAGGAAGTTG AGTCTCTGAATAGACCAA	2	LINE-1	1e-57
	AL732374.14	96-640	7-129	AAACCAGGAGGAAGTTTAAATCTCTGAATACACCA	X	LINE-1	1e-25
	CU639415.7 AL356270.11	1-58/ 114-436	54-116/ 427-528	CACCA/ ATA	21 1	Not determined LINE-1	4.5 4e-24
	AC203609.3	6-390	380-436	CTCTCCAAGA	17	(INE-1)	3e-17
109	BC137023.1 AL732374.14	1-542	530-592/ 574-668	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	5e-17 2e-29
	BC137023.1 AL732374.14	1-600	597-659/ 641-735	CCCC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 5e-30
	BC137023.1 AL732374.14	1-636	624-686/ 668-762	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 5e-31
	BC137023.1 AL732374.14	1-49/ 175-734	37-99/ 722-784 81-175/ 766-860	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT/ A/ ACCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	2e-18 4e-26
	AL732374.14	1-390	366-460	CTTATTCCTGGTTTAGTCTTGGGAG	X	LINE-1	3e-31
110	BC137023.1 AL732374.14	4-714	711-757/ 755-849	CCCC/ CTT	Not determined X	OR1-17 gene LINE-1	4e-13 3e-28
	BC137023.1 AL732374.14	1-624	610-672/ 654-748	CCCCAATCGAACCAC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 4e-31
	BC137023.1 AL732374.14	1-583	571-633/ 615-709	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 2e-29
	BC137023.1 AL732374.14	1-487	475-537/ 519-613	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 4e-31

111	AB045360.1	17-338/ 375-411	326-388	CCCCAATCGAACC/ TCCTGGTTTAGTCT	1	Not determined	7e-19
	AL732374.14	1-470	462-556	CTTATTCCT	X	LINE-1	3e-31
	AC114982.2	162-649	7-185	GGTTCGATTGGGGTTGGTGTGATA	5	LINE-1	3e-07
	AL732374.14	1-470	467-561	CTTA	X	LINE-1	3e-31
	AL390844.12	5-754	749-848	CTTATT	9	LINE-1	9e-22
	AC233279.2	1-470	462-625	CTTATTCCT	X	LINE-1	4e-43
	AC093689.4	8-250/ 596-831	238-641	CTCTCCCAAGACT/ CTCCCAAGACTAAACCAGGAAGAA ATTGAATCTCTGAATACACCAA	4	LINE-1	5e-18
	AL732374.14	15-170/ 275-506 610-890/ 994-1161	166-281/ 477-665 861-1049	CTCCC/ TACACCA/ CCCTCCCAAGACTAAACCAGGAAG ANTTG/ ACACATACACCCTCCCAAGACTAAACCAGGAA GAAGTTTAATCTCTGAATACACCA/ CCCTCCCAAGACTA AACCAGGAAGAAGTTG/ ACACATACACCCTCCCAAGAC TAAACCAGGAAGAAGTTTAATCTCTGAATACACCA	X	LINE-1	2e-43
	AF104455.1	1-260/ 461-643	257-517/ 632- 868	CTCC/ ACACACACACCCTCCCAAGACTAAACCAGGAGG AAATTGAATCTCTGAATACACCAA/ CCCTCCCAAGAC	7	LINE-1	4e-14
	AC016819.8	113-349	15-120	TACACCAA	10	LINE-1	2e-11
	AL607022.11	113-250/ 347-485	7-120/ 236-354	TACACCAA/ CCCTCCCAAGACTAA/ TACACCAA	10	LINE-1	4e-10
Z84475.1	7-280/ 545-727	269-600/ 716- 804	CCCTCCCAAGAC/ ACACATACACCCTCCCAAGACTAAA CCAGGAAGAAGTTTAATCTCTGAATACACCA/ CCCTCC CAAGAC	6	LINE-1	3e-15	
112	AL732374.14	1-450	442-532	TTCCTGGTT	X	LINE-1	4e-30
	BC137023.1 AL732374.14	1-287	275-337/ 319- 413	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	7e-19 2e-31
	BC137023.1	1-540/ 600-681	538-600	CCC/ T	Not determined	OR1-17 gene	7e-16
	BC137023.1 AL732374.14	7-576	564-626/ 608- 705	CCCCAATCGAACC/ CTTATTCCTGGTTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 3e-27
	BC137023.1 AL732374.14	1-617/ 697-808	603-665/ 647- 741	CCCCAATCGAACCAC/ CTTATTCCTGGTTTAGTCT/ TTG GTCTATTTCAGAGACTCAACTTCTCCTGGTTTAGTCTTGG GA	Not determined X	OR1-17 gene (LINE-1)	2e-18 5e-31
	AC010982.5	5-431	423-513	AACCACCAT	2	LINE-1	1e-35

112	AP003551.2	5-394	390-644	AATCG	8	L1PA2	2e-124
	AL355595.10	5-330	317-409	CCCTCCAAGACTA	13	LINE-1	5e-21
113	AL732374.14	155-358	16-160/ 323-437	CAACTT/ CTTATTCCTGGTTAGTCTTGGGCGGGTGTATGTGT	X	LINE-1	2e-32
	AL356416.8	6-170	161-382	CTTATTCCTG	13	LINE-1	3e-24
	AL732374.14	119-332/ 425-764	21-165/ 327-471	TGTATGTGTATCAGAGCCTGTTATTGGTCTATTCAGAGAC TCAACTT/ CTTATT/ TGTATGTGTATCAGAGCCTGTTA TTGGTCTATTCAGAGACTCAACTT	X	LINE-1	4e-38
	AC090146.5	6-280	275-394	AATCGA	8	L1PA6	2e-50
	AC025427.11	1-450	443-550	AACCACCA	10	LINE-1	2e-46
	AC193086.1	54-525	1-61	CACACCAA	12	LINE-1	3e-07
114	AL732374.14	135-636	7-170	ACACATGCACCCTCCAAGACTAAACAGGAATAAG	X	LINE-1	2e-40
	AL357507.9	4-910	895-1060	CTTATTCCTGGTTTAG	6	LINE-1	3e-23
	BC137023.1	7-430	418-480	CCCCAATCGAACC	Not determined	OR1-17 gene	9e-19
	BC137023.1 AL732374.14	1-432	420-482/ 464-561	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 6e-28
	BC137023.1 AL732374.14	18-189	177-239/ 221-315	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	5e-19 8e-30
	AL355103.3	1-410/ 481-571	404-512	AACCACC/ ACACATACAACCTCCAAGACTAAACCAGGAA	14	LINE-1	3e-45
	AC010232.10	1-270	266-610	ACCAA	5	LINE-1	1e-88
	AC025218.8	141-311	9-172	ACACATACACTCTCCAAGACTAAACCAGGAA	8	L1PA2	2e-43
115	AL732374.14	1-338	331-425	CTTATTCC	X	LINE-1	1e-29
	AC104006.6	1-263/ 407-673	260-420	AACC/ GTTTGTCTTGGGAG	8	L1P	5e-24
	AC091930.3	7-330/ 364-436	323-371	CCCCTCCC/ TACACCAA	5	LINE-1	7e-13
	NG_011487.1	1-447/ 592-783	445-601	ACC/ AATACACCAA	7	LINE-1	2e-67
	AL732374.14	1-230	221-327	CTCCAAGAC	X	LINE-1	1e-40

116	AL732374.14	1-142/ 221-242	134-222	GTTTAGTCT/ GT	X	LINE-1	2e-28
	AL355595.10	1-80/ 131-186	72-132	TCAGAGCCT/ GG	13	(INE-1	2e-21
116	FN397831.1	1-90/ 154-181	83-175	TCCTGGTT/ TCCTGGTTTAGTCTTGGGAGGG	Not determined	LINE-1	1e-30
117	BC137023.1 AL732374.14	1-265	251-313/ 295-389	CCCCAATCGAACCAC/ TTCCCTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	7e-19 1e-29
	AC104006.6	5-694	689-767	CAAACC	8	L1P	4e-25
	AC084033.33	1-60/ 95-340	60-102	TGGGAAGCCC/ TAGACCAA	12	L1PA7	8e-04
	AL732374.14	1-378	364-457	CCCTCCCAAGACTAA	X	LINE-1	8e-32
118	AC104006.6	6-263	260-336	AACC	8	L1P	2e-24
	AC244606.2	3- 150/ 200-343	148-208	TCA/ TTGGGAGAG	6	(INE-1	6e-13
	AL732374.14	1-115/ 198-343	111-206	TTAT/ TCTTGGGAG	X	LINE-1	3e-29
	AC203609.3	170-516	1-188	TCCCAAGACTAAACCAGGA	17	LINE-1	3e-24
	AF315553.1	5-263	260-336	AACC	Y	LINE-1	2e-24
	AC010104.3	6-268	260-336	AACCAACAT	Y	LINE-1	2e-24
	AL732374.14	5-263	260-420	AACC	X	LINE-1	3e-17
	BC137023.1 AL732374.14	1-693	681-743/ 725-820	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	2e-17 7e-29
NG_029111.1	4-261	258-416	AACC	3	LINE-1	1e-21	
120	BC137023.1 AL732374.14	1-511	499-561/ 543-637	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-18 4e-31
	AL355595.10	19-182/ 261-701	182-273	C/ TTAGTCTTGGGAG	13	LINE-1	1e-19
	AC226149.2	1-357	346-391	CCCTCCCAAGAC	Not determined	LINE-1	6e-13
	AL732374.14	21-215/ 263-701	185-275	TCCTGGTTTAGTCTTGGGAGAGTGTATGTGT/ TTAGTCTTGGGAG	X	LINE-1	5e-30
	AC018647.5	1-397	388-448	CTCCCAAGAC	7	LINE-1	1e-15
121	AC129713.1	165-325	7-195	ACACATACACCCTCCCAAGACTAAACCAGGA	5	LINE-1	6e-88

	AL732374.14	1-420	413-484	CCCTCCCA	X	LINE-1	3e-24
	NG_012634.1	165-325	7-195	ACACATACACCCTCCCAAGACTAAACCAGGA	2	LINE-1	1e-46
122	AL732374.14	1-410/ 505-641	396-511/ 627-683	CTCCCAAGACTAAAC/ TACACCA/ CCCTCCCAAGACTAA	X	LINE-1	2e-42
	AL732374.14	128-264/ 361-498	17-134/ 250-367/ 484-542	TACACCA/ CCCTCCCAAGACTAA/ TACACCA/ CCCTCCCAAGACTAA	X	LINE-1	5e-41
122	AC233279.2	6-420	413-649	CCCTCCCA	X	LINE-1	7e-41
	AC012596.4	1-57/ 91-671	54-108	ATTT/ TTTTAGGGTTCCATTGGG	7	PRIMA41	8e-15
123	AC090809.9	1-283/ 357-483	280-388	AACC/ ACACATACACCCTCCCAAGACTAAACCAGGAA	8	L1P2	3e-44
	AL133325.20	1-286/ 367-781	281-389	ACCTAC/ CCCTCCCAAGACTAAACCAGGAA	20	LINE-1	4e-45
	AL732374.14	1-452	444-769	AACCACCAT	X	LINE-1	5e-69
	FP671131.2	5-283/ 366-629	280-388	AACC/ CCCTCCCAAGACTAAACCAGGAA	9	LINE-1	3e-45
124	BC137023.1 AL732374.14	1-367	355-417/ 399-493	CCCCAATCGAACC/ CTTATTCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	9e-19 6e-27
	AL359704.9	6-379/ 476-536	365-482	CCCTCCCAAGACTAA/ TACACCA	1	LINE-1	8e-20
	AL732374.14	6-379	365-469	CCCTCCCAAGACTAA	X	LINE-1	4e-35
	AL732374.14	1-360/ 457-876	346-463	CCCTCCCAAGACTAA/ TACACCA	X	LINE-1	1e-44
128	AL732374.14	1-130	125-200	TGGGAG	X	LINE-1	6e-16
	AL358253.16 AC078793.13	1-41/ 116-748	28-135/ 734-1103	CCCCAATCGAACCC/ CTCTCCGGGTGTACAGCTCCC/ ACCCAATCGAACCCCA	1 3	PLA2G2E gene Not determined	2e-31 4e-173
	AL358253.16 AC012596.4	74-353/ 450-806	1-91/ 350-468	CTCCGGGTGTACAGCTCCC/ CCCA/ CTCCGGGTGTACAGCTCCC	1 7	PLA2G2E gene (LINE-1) / PRIMA41	6e-32 4e-45
	AC012596.4	1-71/ 137-172	36-148	CTGTACACCGGAGCTGTTCTATTTGGCCATCTTGG/ GGTTCGATTGGG	7	(LINE-1 / PRIMA41	1e-41
	AC012596.4	122-517	22-140	CTCCGGGTGTACAGTCCCA	7	LINE-1 / PRIMA41	5e-48
	AC104069.3	1-173/ 230-606	164-248	ATTTTCGGGC/ AACTCTCCGGGGCATATA	2	Not determined	2e-32

131	BC137023.1 AL732374.14	1-270	258-320/ 302-379	CCCCAATCGAACC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	7e-19 4e-22
	BC137023.1 AL732374.14	1-229	215-277/ 259-351	CCCCAATCGGACCCC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-14 7e-25
	BC137023.1 AL732374.14	1-229	215-277/ 259-351	CCCCAATCGGACCCC/ CTTATTCCTGGTTAGTCT	Not determined X	OR1-17 gene LINE-1	1e-14 7e-25
	AL732374.14	170-357	1-182/ 326-434	TTAGTCTTGGGAG/ TTCCTGGTTAGTCTTGGGAGGGTGTATGTGT	X	LINE-1	2e-34
	AC234834.5	1-205/ 268-434	194-287	CTCTCCAAGAC/ TATCCAAGACTAAACCAGGAA	10	LINE-1	2e-19
131	AC117525.2	1-240/419-732	233-450	CTCTCCCA/ ACACATACTCTCCCAAGACTAAACCAGGAA	5	LINE-1	1e-44
	NG_032674.1	1-294/ 406-495	273-414	ACACCAACCCCAATCGAACCCC/ TCCTGGTTT	17	EFTUD2 gene	2e-59
132	AL732374.14 BC137023.1	127-178	1-95/ 77-139	AGACTAAACCAGGAATAAG/ GGTTCGATTGGGG	X Not determined	LINE-1 OR1-17 gene	4e-30 3e-19
	AL732374.14	1-108	84-176	CTTATTCCTGGTTAGTCTTGGGAG	X	LINE-1	1e-30
	BC137023.1	1-289	277-339	CCCCAATCGAACC	Not determined	OR1-17 gene	6e-19
	AC011996.8	216-299	1-236	AGTCTTGGAGAGTGTATGTGT	2	LINE-1	2e-44
	AC104006.6	1-107	104-264	AACC	8	L1P	2e-24
133	BC137023.1	30-315	1-42	GGTTCGATTGGGG	Not determined	OR1-17 gene	8e-11
	AL732374.14	1-184	181-273	TCCT	X	LINE-1	1e-27
	AL732374.14	1-189	186-346	AACC	X	LINE-1	3e-17
	NG_011441.1	1-108/ 173-360	98-218	CCCCCTCCCAA/ CTCCAAGACTAAACCAGGAAGAAGT TTAATCTCTGAATACACCA	4	LINE-1	3e-22
	AC114982.2	1-237	234-374	AACC	5	LINE-1	6e-51
	AC243972.3	6-366	363-441	AACC	14	LINE-1	2e-25
	FQ976904.3	1-144	142-186	ATT	9	LINE-1	1e-12

134	AL732374.14	5-263	260-423	AACC	X	LINE-1	8e-19
	AC233279.2	5-268	260-420	AACCAACAT	X	LINE-1	3e-17
	BC137023.1	6-269	251-313	CCCCAATCGAACCAACATT	Not determined	OR1-17 gene	2e-17
	AC104006.6	87-286	14-90/ 294-354	GGTT/ TCAGAG	8	(L1P)	1e-22
	AL355530.6	1-150	145-185	GTCTAT	10	LINE-1	1e-10
	AL732374.14	1-90	80-220	TCAGAGCCTGT	X	LINE-1	1e-30
135	NG_021366.1	113-270	7-120	TACACCAA	7	LINE-1	2e-11
137	AL732374.14	1-640	631-727	CTTATTCCTG	X	(INE-1)	4e-25
	AL732374.14	1-300	284-378	CTTATTCCTGGTTTAGT	X	LINE-1	2e-31
137	AL445684.8	2-309	283-449	TATATTACACCAACCCCAATGGAACCC	9	L1PB2c	7e-64
	AL157837.10	1-197	191-579	GAGATGC	1	LINE-1	8e-179
138	AL732374.14	53-189/ 243-379	1-67/ 185-255/ 375-448	TTGGTTTTGGGAGGG/ GGTGT/ TTAGTCTTGGGAG/ GGTGT	X	LINE-1	8e-19
	AC129713.1	1-740	728-954	TCAGGGCTTGTTA	5	LINE-1	1e-96
	AL732374.14	1-130/ 184-320/ 374-510	126-196/ 316- 388/ 506-577	GGTGT/ TTAGTCTTGGGAG/ GGTGT/ TTAGTCTTGGGAGGG/ GGTGT	X	LINE-1	6e-22
	AC004887.2	1-463/ 547-600	463-559	C/ CTCCGGTGTACAG	7	LINE-1	1e-36
	AC004887.2	1-116/ 200-687	108-212	AATCGAACCC/ CTCCGGTGTACAG	7	LINE-1	4e-38