

SW	perc	perc	perc	query	position	in query	matching	repeat	position	in repeat	ID
score	div.	del.	ins.	sequence	begin	end	repeat	class/family	begin	end	(left)
375	26.8	2.6	6.2	scaffold143.3_240,578-3,261,249	7	157	(20515)	C LTR118_Ame	(331)	146	1
373	33.3	0.0	0.0	scaffold143.3_240,578-3,261,249	158	298	(20374)	C LTR77-int_T5	(0)	5551	5411
826	15.7	11.6	5.5	scaffold143.3_240,578-3,261,249	2025	2213	(18459)	C SINEC1_Ame	(0)	201	2
329	23.3	15.8	0.0	scaffold143.3_240,578-3,261,249	2652	2771	(17901)	C LIMS	(1354)	4792	4654
13	16.9	0.0	5.7	scaffold143.3_240,578-3,261,249	2915	2951	(17721)	+ (TTTC)n	1	35	(0)
413	15.2	1.3	0.0	scaffold143.3_240,578-3,261,249	3229	3307	(17365)	C MLT1E2	(0)	627	548
845	21.0	25.6	6.5	scaffold143.3_240,578-3,261,249	3306	3671	(17001)	C MLT1E2	(191)	436	1
2778	11.5	1.9	2.7	scaffold143.3_240,578-3,261,249	3711	4163	(16509)	+ CorLTR7	LTR/ERV1	1	433
1491	4.7	3.1	0.5	scaffold143.3_240,578-3,261,249	4164	4357	(16315)	C SINEC1_Ame	(0)	201	3
1032	7.7	0.1	20.2	scaffold143.3_240,578-3,261,249	4358	4441	(16231)	+ CorLTR7	LTR/ERV1	415	483
1395	22.1	5.1	4.9	scaffold143.3_240,578-3,261,249	4444	4498	(16174)	+ Charlie4a	DNA/hAT-Charlie	60	116
2286	15.5	6.3	4.7	scaffold143.3_240,578-3,261,249	4951	4958	(15714)	C MER101B_CF	LTR/ERV1	(0)	467
1395	22.1	5.1	4.9	scaffold143.3_240,578-3,261,249	4959	5350	(15322)	+ Charlie4a	DNA/hAT-Charlie	117	588
473	27.5	11.2	0.0	scaffold143.3_240,578-3,261,249	5465	5624	(15048)	C MLT1	LTR/ERV1-MaLR	(315)	197
315	14.7	7.9	1.2	scaffold143.3_240,578-3,261,249	5745	5820	(14852)	C SINEC_c2	SINE/rRNA	(0)	212
480	21.6	11.7	0.0	scaffold143.3_240,578-3,261,249	5822	5932	(14740)	C SINEC2_Ame	SINE/rRNA	(9)	124
646	7.8	50.0	1.0	scaffold143.3_240,578-3,261,249	6217	6346	(14326)	+ SINEC_b2	SINE/rRNA	1	193
512	26.5	5.3	1.9	scaffold143.3_240,578-3,261,249	6448	6597	(14075)	C LTR86C	LTR/ERV1	(2)	619
354	29.9	4.7	0.0	scaffold143.3_240,578-3,261,249	7338	7444	(13228)	C MIR	SINE/MIR	(104)	158
379	22.4	3.9	14.1	scaffold143.3_240,578-3,261,249	7512	7667	(13005)	+ MER92D	LTR/ERV1	179	320
616	28.4	1.8	0.0	scaffold143.3_240,578-3,261,249	7708	7876	(12796)	+ MER5A	DNA/hAT-Charlie	18	189
285	32.1	7.1	0.0	scaffold143.3_240,578-3,261,249	9845	9956	(10716)	C PlatSat2A	Satellite	(671)	362
465	22.1	3.7	2.0	scaffold143.3_240,578-3,261,249	10044	10220	(10452)	C LTR154	LTR/ERV1	(45)	462
1463	7.8	3.1	0.0	scaffold143.3_240,578-3,261,249	10942	11134	(9538)	C SINEC1_Ame	SINE/rRNA	(2)	199
221	7.6	0.7	0.0	scaffold143.3_240,578-3,261,249	11329	11460	(9212)	+ SINEC1B_Ame	SINE/rRNA	1	141
370	28.7	8.4	4.5	scaffold143.3_240,578-3,261,249	12118	12332	(8340)	C MLT1K	LTR/ERV1-MaLR	(63)	532
1250	19.7	4.6	5.8	scaffold143.3_240,578-3,261,249	12440	12612	(8060)	C L1MB8	LINE/L1	(0)	6178
2449	14.9	6.8	0.9	scaffold143.3_240,578-3,261,249	12613	13053	(7619)	C MER101B_CF	LTR/ERV1	(0)	467
1250	19.7	4.6	5.8	scaffold143.3_240,578-3,261,249	13054	13245	(7427)	C L1MB8	LINE/L1	(164)	6014
259	32.2	9.1	2.9	scaffold143.3_240,578-3,261,249	13246	13475	(7107)	+ Cor-L_T5y	Satellite	(316)	2930
268	18.1	5.0	11.7	scaffold143.3_240,578-3,261,249	13477	13576	(7096)	C L1M3	LINE/L1	(2430)	5565
1832	24.4	7.3	5.3	scaffold143.3_240,578-3,261,249	13554	14007	(6665)	C L1M4	LINE/L1	(1485)	4661
1496	7.6	1.5	0.0	scaffold143.3_240,578-3,261,249	14008	14205	(6467)	C SINEC1_Ame	SINE/rRNA	(0)	201
2408	22.1	3.4	4.7	scaffold143.3_240,578-3,261,249	14206	14233	(6439)	C L1M4	LINE/L1	(1668)	4478
605	15.7	3.7	0.0	scaffold143.3_240,578-3,261,249	14234	14341	(6331)	C SINEC_old	SINE/rRNA	(0)	112
2408	16.2	4.6	1.9	scaffold143.3_240,578-3,261,249	14342	14967	(5757)	C L1M4	LINE/L1	(1841)	4594
1487	6.2	3.1	0.0	scaffold143.3_240,578-3,261,249	14968	15162	(5510)	C SINEC1_Ame	SINE/rRNA	(0)	201
1965	20.0	5.1	9.5	scaffold143.3_240,578-3,261,249	15163	15241	(5431)	C L1M4	LINE/L1	(2299)	3847
1496	7.5	1.0	1.0	scaffold143.3_240,578-3,261,249	15242	15442	(5230)	C SINEC1_Ame	SINE/rRNA	(0)	201
1965	20.0	5.1	9.5	scaffold143.3_240,578-3,261,249	15443	15601	(5071)	C L1M4	LINE/L1	(2368)	3778
1617	6.5	1.0	0.0	scaffold143.3_240,578-3,261,249	15602	15800	(4872)	+ SINEC1_Ame	SINE/rRNA	1	201
1965	20.0	5.1	9.5	scaffold143.3_240,578-3,261,249	15801	16016	(4656)	C L1M4	LINE/L1	(2521)	3625
4514	20.5	2.3	0.0	scaffold143.3_240,578-3,261,249	16017	16928	(3744)	C LTR21B2_EC	LTR/ERV1	(0)	913
963	15.7	10.8	0.0	scaffold143.3_240,578-3,261,249	16929	17151	(3521)	C L1M4	LINE/L1	(2740)	3406
307	18.3	4.0	4.0	scaffold143.3_240,578-3,261,249	17315	17388	(3284)	C Charlie1b	DNA/hAT-Charlie	(19)	504
293	21.7	5.7	5.7	scaffold143.3_240,578-3,261,249	18714	18801	(1871)	+ MER70-int	LTR/ERV1	4578	4665
479	29.2	4.1	0.7	scaffold143.3_240,578-3,261,249	19106	19250	(1422)	+ LTR75B	LTR/ERV1	1	150
267	22.2	7.5	5.9	scaffold143.3_240,578-3,261,249	19313	19379	(1232)	C LTR75B	LTR/ERV1	262	229
218	32.1	3.7	0.0	scaffold143.3_240,578-3,261,249	19572	19582	(1080)	C MIRb	SINE/MIR	177	260
748	15.2	17.6	3.0	scaffold143.3_240,578-3,261,249	19879	20054	(618)	C SINEC1_Ame	SINE/rRNA	(0)	201
18	17.9	0.0	0.0	scaffold143.3_240,578-3,261,249	20206	20244	(428)	+ (CT)n	Simple_repeat	1	39
188	16.7	18.8	0.0	scaffold143.3_240,578-3,261,249	20439	20486	(186)	C L2a	LINE/L2	(1)	3425
258	28.0	10.9	0.9	scaffold143.3_240,578-3,261,249	20503	20603	(69)	+ MER94	DNA/hAT-Blackjack	23	133
1980	17.5	5.6	0.0	scaffold155.1_113,688-1,134,337	2	361	(20209)	C CorLTR2	LTR/ERV1	(198)	380
427	16.7	0.0	4.2	scaffold155.1_113,688-1,134,337	362	436	(20214)	C MER68-int	LTR/ERV1	(2656)	334
515	25.8	2.7	2.1	scaffold155.1_113,688-1,134,337	545	730	(19920)	C MER68-int	LTR/ERV1	(2795)	195
338	8.9	0.0	2.2	scaffold155.1_113,688-1,134,337	777	822	(19828)	+ LTR31_Ame	LTR/ERV1	1	45
666	19.3	11.4	4.1	scaffold155.1_113,688-1,134,337	823	1006	(19644)	+ SINEC1_Ame	SINE/rRNA	1	197
948	14.2	8.3	4.5	scaffold155.1_113,688-1,134,337	1035	1226	(19424)	C SINEC1_Ame	SINE/rRNA	(2)	199
1608	6.0	0.0	1.0	scaffold155.1_113,688-1,134,337	1211	1513	(19137)	+ SINEC1_Ame	SINE/rRNA	1	201
781	18.9	3.4	7.1	scaffold155.1_113,688-1,134,337	1781	1985	(18665)	+ SINEC1_Ame	SINE/rRNA	2	199
918	12.9	12.5	3.0	scaffold155.1_113,688-1,134,337	1989	2172	(18478)	+ SINEC1_Ame	SINE/rRNA	1	201
833	13.1	7.7	5.6	scaffold155.1_113,688-1,134,337	2190	2383	(18267)	C SINEC1_Ame	SINE/rRNA	(3)	198
2685	9.6	0.7	3.2	scaffold155.1_113,688-1,134,337	2390	2799	(17851)	C L1_Carn3	LINE/L1	(8)	6429
1116	32.5	2.9	1.8	scaffold155.1_113,688-1,134,337	2992	3483	(17167)	+ L1MED	LINE/L1	416	912
572	21.4	4.3	8.5	scaffold155.1_113,688-1,134,337	3484	3692	(16958)	+ SINEC1_Ame	SINE/rRNA	1	201
1575	7.0	0.0	0.0	scaffold155.1_113,688-1,134,337	4153	4351	(16299)	+ SINEC1_Ame	SINE/rRNA	1	199
877	11.9	20.6	0.0	scaffold155.1_113,688-1,134,337	4724	4883	(15767)	C SINEC_c1	SINE/rRNA	(16)	193
265	21.9	1.0	3.1	scaffold155.1_113,688-1,134,337	4884	4973	(15677)	+ L1MED	LINE/L1	882	970
518	16.5	7.7	0.0	scaffold155.1_113,688-1,134,337	4974	5064	(15586)	+ SINEC_old	SINE/rRNA	1	98
1365	13.1	0.0	0.0	scaffold155.1_113,688-1,134,337	5074	5271	(15379)	+ SINEC1_Ame	SINE/rRNA	1	198
1049	12.5	5.9	3.0	scaffold155.1_113,688-1,134,337	5281	5470	(15180)	+ SINEC1_Ame	SINE/rRNA	1	201
1037	19.9	4.4	1.1	scaffold155.1_113,688-1,134,337	5495	5811	(14593)	+ L1MED	LINE/L1	947	1297
1851	21.8	1.8	9.0	scaffold155.1_113,688-1,134,337	5812	5880	(14770)	C MLT1C	LTR/ERV1-MaLR	(0)	467
765	15.9	4.9	7.5	scaffold155.1_113,688-1,134,337	5881	6084	(14566)	C SINEC1_Ame	SINE/rRNA	(2)	199
1851	21.8	1.8	9.0	scaffold155.1_113,688-1,134,337	6085	6391	(14259)	C MLT1C	LTR/ERV1-MaLR	(59)	408
4214	7.7	0.8	3.1	scaffold155.1_113,688-1,134,337	6392	6981	(13669)	C CorLTR1B1	LTR/ERV1	(0)	579
1851	18.8	1.8	0.0	scaffold155.1_113,688-1,134,337	6982	7181	(13547)	C MLT1C	LTR/ERV1-MaLR	(361)	186
486	21.7	5.9	9.3	scaffold155.1_113,688-1,134,337	7185	7172	(13478)	+ L1MED	LINE/L1	1257	1350
1563	7.5	0.0	0.0	scaffold155.1_113,688-1,134,337	7173	7373	(13277)	+ SINEC1_Ame	SINE/rRNA	1	201
486	21.7	5.8	9.3	scaffold155.1_113,688-1,134,337	7374	7527	(13123)	+ L1MED	LINE/L1	1316	1477
523	20.2	1.8	0.9	scaffold155.1_113,688-1,134,337	7528	7637	(13013)	+ SINEC_old	SINE/rRNA	1	111
810	19.1	8.2	3.4	scaffold155.1_113,688-1,134,337	7638	7832	(12818)	+ SINEC_c1	SINE/rRNA	6	209
748	5.0	3.2	4.8	scaffold155.1_113,688-1,134,337	7782	7834	(12816)	+ B2_5	SINE/B4	164	216
961	14.9	6.7	2.5	scaffold155.1_113,688-1,134,337	7835	8027	(12623)	+ SINEC1_Ame	SINE/rRNA	1	201
444	20.6	14.1	2.4	scaffold155.1_113,688-1,134,337	8037	8185	(12465)	+ L1MED	LINE/L1	1450	1615
289	27.4	0.0	0.0	scaffold155.1_113,688-1,134,337	8222	8294	(12356)	+ MARNA	DNA/TcMar-Mariner	316	388
1531	4.7	4.2	0.0	scaffold155.1_113,688-1,134,337	8337	8529	(12121)	C SINEC1_Ame	SINE/rRNA	(0)	201
302	18.8	12.5	0.0	scaffold155.1_113,688-1,134,337	8567	8630	(12020)	+ tRNA-Lys-AAG	tRNA	2	73
824	10.2	18.0	9.5	scaffold155.1_113,688-1,134,337	8738	8943	(11707)	+ SINEC1B_Ame	SINE/rRNA	1	222
441	25.8	3.9	5.0	scaffold155.1_113,688-1,134,337	8949	8991	(11659)	+ L1MED	LINE/L1	4990	5025
959	9.3	18.6	0.0	scaffold155.1_113,688-1,134,337	8992	9152	(11498)	+ SINEC_b1	SINE/rRNA	2	192
441	25.8	3.9	5.0	scaffold155.1_113,688-1,134,337	9153	9312	(11338)	+ L1MED	LINE/L1	5026	5190
825	6.8	0.0	15.7	scaffold155.1_113,688-1,134,337	9296	9374	(11276)	+ L1_Canid_	LINE/L1	5254	5316
1003	11.3	0.0	0.8	scaffold155.1_113,688-1,134,337	9375	9508	(11142)				

759 23.5 9.5 1.8 scaffold155.1,113,688-1,134,337 16625 16826 (3824) + ERV54-EC_I-int LTR/ERV1 3094 3303 (3960) 91

2648 11.1 1.3 0.2 scaffold155.1,113,688-1,134,337 17416 17804 (2846) + LTR31_Ame LTR/ERV1 1 393 (131) 92

305 13.7 1.9 1.9 scaffold155.1,113,688-1,134,337 17804 17804 (2795) SINEC_old SINE/ERNA (58) 54 3 93 *

12 13.9 0.0 0.0 scaffold155.1,113,688-1,134,337 17856 17879 (2771) + (ACC)n Simple_repeat 1 24 (0) 94

1367 18.8 5.0 1.4 scaffold155.1,113,688-1,134,337 17923 18263 (2387) + ERV54-EC_I-int LTR/ERV1 3704 4056 (3207) 91

161 15.2 2.0 0.0 scaffold155.1,113,688-1,134,337 18289 18387 (2263) + SINEC_old SINE/ERNA 9 109 (3) 95

351 23.8 0.0 5.0 scaffold155.1,113,688-1,134,337 18396 18501 (2149) + MER34-int LTR/ERV1 3187 3287 (2903) 86 *

484 18.3 0.0 0.0 scaffold155.1,113,688-1,134,337 18408 18505 (2145) + ERV1-5N-EC_I-int LTR/ERV1 2272 2357 (3254) 96

486 12.2 21.4 0.8 scaffold155.1,113,688-1,134,337 18508 18607 (2043) C SINEC_b1 SINE/ERNA (125) 103 1 97

1592 23.5 9.7 10.1 scaffold155.1,113,688-1,134,337 18628 19792 (858) + MER34-int LTR/ERV1 4243 5403 (1860) 86

332 17.2 5.2 0.0 scaffold155.1,113,688-1,134,337 19808 19865 (785) + SINEC_old SINE/ERNA 34 94 (18) 98

1103 19.0 9.9 6.8 scaffold155.1,113,688-1,134,337 19867 20090 (560) + MER34-int LTR/ERV1 5398 5638 (1625) 86

1633 7.5 0.0 0.0 scaffold155.1,113,688-1,134,337 20091 20291 (359) C SINEC1_Ame SINE/ERNA (0) 201 1 99

1103 19.3 10.7 7.1 scaffold155.1,113,688-1,134,337 20292 20498 (152) + MER34-int LTR/ERV1 5639 5791 (1472) 86

241 27.9 3.6 9.2 scaffold155.1,113,688-1,134,337 20499 20636 (14) + HAL1-10_Tbe1 LTR/ERV1 1785 1915 (615) 100

2352 6.4 0.0 0.0 scaffold162.1-18,384_(reversed) 1 295 (18089) + LSU-rRNA_Hsa rRNA 2420 2714 (2321) 101

313 15.9 8.8 10.0 scaffold162.1-18,384_(reversed) 296 386 (17998) C ERV3-1_S5c-LTR LTR/ERV1 (312) 137 48 102

1371 0.0 0.0 1.2 scaffold162.1-18,384_(reversed) 387 558 (17826) + LSU-rRNA_Hsa rRNA 2806 2975 (2060) 103

12353 3.9 1.2 0.8 scaffold162.1-18,384_(reversed) 765 2291 (16093) + LSU-rRNA_Hsa rRNA 3502 5035 (0) 103

38 4.7 0.0 0.0 scaffold162.1-18,384_(reversed) 3012 3055 (15329) + (GTG)n Simple_repeat 1 44 (0) 104

313 20.0 2.8 1.4 scaffold162.1-18,384_(reversed) 3070 3140 (15244) C rRNA-Lys-AAG rRNA (3) 73 2 105

253 17.8 0.0 2.2 scaffold162.1-18,384_(reversed) 3827 3872 (14512) C CorLTR2-int LTR/ERV1 (543) 4844 4800 106 *

266 12.2 0.0 0.0 scaffold162.1-18,384_(reversed) 3871 3911 (14473) C CorLTR1-int LTR/ERV1 (765) 4622 4582 106

69 6.9 1.7 4.3 scaffold162.1-18,384_(reversed) 3923 4040 (14344) + (TCTT)n Simple_repeat 1 115 (0) 107

492 18.0 3.0 1.0 scaffold162.1-18,384_(reversed) 4041 4141 (14243) C CorLTR1-int LTR/ERV1 (2683) 3932 3830 106

612 9.9 0.0 0.0 scaffold162.1-18,384_(reversed) 4143 4223 (14161) C L1_Conid.L LINE/L1 (1120) 5331 5251 108

483 29.1 2.2 9.7 scaffold162.1-18,384_(reversed) 4225 4580 (16193) C Sor-1_T5y Satellite LINE/L1 (1186) 2130 1791 109

2686 22.4 2.9 3.4 scaffold162.1-18,384_(reversed) 4646 4298 (13086) + ERV1-4N-EC_I-int LTR/ERV1 5486 6135 (174) 110

672 10.6 1.1 0.0 scaffold162.1-18,384_(reversed) 5381 5474 (12910) + SINEC_old SINE/ERNA 1 95 (17) 111

503 22.5 3.7 4.0 scaffold162.1-18,384_(reversed) 7462 7643 (10741) + LTRIS4 LTR/ERV1 309 465 (42) 112

713 31.9 0.7 1.7 scaffold162.1-18,384_(reversed) 8196 8485 (9899) + KORV_I-int LTR/ERV1 457 743 (6681) 113

2610 27.4 3.9 2.8 scaffold162.1-18,384_(reversed) 8736 10001 (8383) + KORV_I-int LTR/ERV1 1024 2334 (5090) 113

12163 31.2 5.3 6.8 scaffold162.1-18,384_(reversed) 11487 13001 (5338) + KORV_I-int LTR/ERV1 4189 5682 (1742) 113

360 35.2 0.0 0.0 scaffold162.1-18,384_(reversed) 13060 13201 (5183) + KORV_I-int LTR/ERV1 5813 5954 (1470) 113

291 28.4 0.0 0.0 scaffold162.1-18,384_(reversed) 13240 13313 (5071) + KORV_I-int LTR/ERV1 6023 6096 (1328) 113

891 33.4 3.0 2.6 scaffold162.1-18,384_(reversed) 13361 13821 (4563) + KORV_I-int LTR/ERV1 6962 7424 (0) 113

503 22.3 4.7 3.4 scaffold162.1-18,384_(reversed) 14243 14448 (3936) + LTRIS4 LTR/ERV1 205 465 (42) 114

1001 9.7 5.8 0.0 scaffold162.1-18,384_(reversed) 14887 15144 (3240) C L1-1_Ame LINE/L1 (4) 6843 6571 115

1233 29.7 6.2 2.7 scaffold182.1,642,082-1,661,437 5142 5156 (18200) + L1MS LINE/L1 4413 5182 (964) 116

295 30.7 8.9 2.7 scaffold182.1,642,082-1,661,437 1138 1445 (17911) L1MS LINE/L1 5254 5516 (607) 116

289 17.7 3.2 1.6 scaffold182.1,642,082-1,661,437 1461 1523 (17833) + L1MS LINE/L1 5573 5636 (487) 116

1242 18.8 4.4 1.9 scaffold182.1,642,082-1,661,437 1583 1856 (17500) + LTR22_FC LTR/ERV1 229 489 (0) 117

287 25.1 14.4 1.8 scaffold182.1,642,082-1,661,437 1867 2012 (17344) + L1ME3E LINE/L1 5780 5943 (299) 118

421 32.8 5.0 4.7 scaffold182.1,642,082-1,661,437 2232 2589 (16767) + ERVL-E-int LTR/ERVL 2725 3083 (2584) 119

1114 30.3 5.9 2.8 scaffold182.1,642,082-1,661,437 2759 3253 (16183) + ERVL-E-int LTR/ERVL 3307 3816 (1815) 119

273 31.5 1.6 4.9 scaffold182.1,642,082-1,661,437 3452 5578 (15757) + ERVL-E-int LTR/ERVL 4169 4291 (1470) 119

20 26.5 3.5 5.4 scaffold182.1,642,082-1,661,437 3631 3744 (15612) + A-rich Low_complexity 1 112 (0) 120

266 8.3 10.4 0.0 scaffold182.1,642,082-1,661,437 4050 4097 (15259) C MLT281 LTR/ERVL (3) 564 512 121

234 28.1 1.8 0.0 scaffold182.1,642,082-1,661,437 4138 4194 (15162) C HAL1-3A_ME LINE/L1 (835) 2023 1966 122

530 12.3 0.0 0.0 scaffold182.1,642,082-1,661,437 4457 4537 (14819) C L1_Carn5 LINE/L1 (8) 6501 6421 123

11 24.3 0.0 0.0 scaffold182.1,642,082-1,661,437 4546 4579 (14717) + TTTTAT)n Simple_repeat 1 34 (0) 124

383 25.7 0.2 9.9 scaffold182.1,642,082-1,661,437 4589 4696 (14660) + MLT3 LTR/ERVL-MLR 1 509 (440) 125

1174 14.0 0.0 5.5 scaffold182.1,642,082-1,661,437 5380 5591 (13765) C SINEC1_Ame SINE/ERNA (0) 201 1 126

1550 20.0 0.3 8.0 scaffold182.1,642,082-1,661,437 5596 6003 (13353) C L1MB3_EC LINE/L1 (624) 5590 5220 127

1479 24.2 2.7 2.7 scaffold182.1,642,082-1,661,437 6004 6445 (12911) + L1ME1 LINE/L1 5505 5946 (233) 128

366 27.0 2.7 0.0 scaffold182.1,642,082-1,661,437 6475 6585 (12771) + L1ME1 LINE/L1 6044 6157 (22) 128

16 13.7 2.9 2.9 scaffold182.1,642,082-1,661,437 7203 7236 (12120) + (CTA)n Simple_repeat 1 34 (0) 129

481 21.1 3.9 2.2 scaffold182.1,642,082-1,661,437 9787 9972 (9384) + LTRIS4 LTR/ERV1 144 462 (45) 130

299 24.7 9.4 0.6 scaffold182.1,642,082-1,661,437 9996 10147 (9209) C MIR_Mars SINE/MIR (13) 261 96 131

608 21.1 0.8 0.0 scaffold182.1,642,082-1,661,437 10637 10764 (8592) + L1-1_Ame LINE/L1 6700 6828 (19) 132

1366 8.6 0.5 0.0 scaffold182.1,642,082-1,661,437 10771 10957 (8399) + SINEC1_Ame SINE/ERNA 1 188 (13) 133

47 0.0 0.0 0.0 scaffold182.1,642,082-1,661,437 10961 11003 (8353) + (AAAT)n Simple_repeat 1 43 (0) 134

234 19.5 0.0 6.0 scaffold182.1,642,082-1,661,437 11062 11322 (8224) + LTR1A2_ML LTR/ERV1 510 576 (191) 135

326 31.4 8.8 1.4 scaffold182.1,642,082-1,661,437 11452 11793 (7363) + L1ME3F LINE/L1 4303 4669 (1477) 136

544 23.7 2.5 8.8 scaffold182.1,642,082-1,661,437 12150 12390 (6966) C SINEC1B_Ame SINE/ERNA (0) 228 2 137

265 26.2 3.9 3.4 scaffold182.1,642,082-1,661,437 12565 12742 (6614) + L1ME3F LINE/L1 5264 5442 (801) 136 *

293 27.0 1.2 2.4 scaffold182.1,642,082-1,661,437 12629 12771 (6585) + L1P5 LINE/L1 5329 5453 (701) 138 *

1147 24.8 9.6 2.4 scaffold182.1,642,082-1,661,437 12770 13206 (6150) + L1ME3F LINE/L1 5494 5961 (282) 136

564 22.9 3.4 0.0 scaffold182.1,642,082-1,661,437 14452 14569 (6177) + SINEC2_Ame SINE/ERNA 1 122 (11) 139

338 8.7 14.5 0.0 scaffold182.1,642,082-1,661,437 14574 14642 (4714) + SINEC_c2 SINE/ERNA 132 210 (2) 140

16 21.6 2.3 0.0 scaffold182.1,642,082-1,661,437 14714 14756 (4600) + A-rich Low_complexity 1 44 (0) 141

243 36.5 3.3 2.2 scaffold182.1,642,082-1,661,437 15286 15467 (3889) + L2-2_ME LINE/L2 1655 1838 (703) 142

23 24.5 1.4 1.4 scaffold182.1,642,082-1,661,437 16631 16700 (2656) + GA-rich Low_complexity 1 70 (0) 143

694 20.8 1.3 0.7 scaffold182.1,642,082-1,661,437 17549 17698 (1658) C L1_Conid.L LINE/L1 (0) 6451 6301 144

533 23.2 6.3 9.6 scaffold182.1,642,082-1,661,437 18645 18849 (609) + SINEC1_Ame SINE/ERNA 1 199 (2) 145

24 19.8 1.3 3.0 scaffold182.1,642,082-1,661,437 19197 19264 (392) C (ATAGAT)n Simple_repeat 1 66 (0) 146

1553 7.1 0.5 0.0 scaffold1_66,687,907-66,667,100_(reversed) 67 262 (20546) + SINEC1_Ame SINE/ERNA 1 197 (4) 147

592 29.5 1.7 7.5 scaffold1_66,687,907-66,667,100_(reversed) 1100 1188 (19620) + L1MC1 LINE/L1 4142 4529 (1905) 148

1784 18.4 0.0 0.6 scaffold1_66,687,907-66,667,100_(reversed) 1189 1506 (19302) + L1MC LINE/L1 3984 4299 (1847) 149

812 12.3 28.4 0.0 scaffold1_66,687,907-66,667,100_(reversed) 1507 1661 (19147) + SINEC_c1 SINE/ERNA 1 199 (10) 150

592 29.5 1.7 7.5 scaffold1_66,687,907-66,667,100_(reversed) 1662 1675 (19133) + L1MC LINE/L1 4530 4540 (1894) 149

3465 22.0 4.2 4.5 scaffold1_66,687,907-66,667,100_(reversed) 1688 1859 (17949) + L1MC1 LINE/L1 4288 6277 (723) 148 *

425 15.6 0.9 2.5 scaffold1_66,687,907-66,667,100_(reversed) 2075 2826 (17949) + L1MC1_EC LINE/L1 4674 5448 (889) 151

823 13.5 0.8 0.0 scaffold1_66,687,907-66,667,100_(reversed) 2869 2994 (17814) + SINEC_b1 SINE/ERNA 1 127 (67) 152

29 0.0 0.0 0.0 scaffold1_66,687,907-66,667,100_(reversed) 2995 3019 (17789) + (TC)n Simple_repeat 1 25 (0) 153

4560 18.5 3.9 0.0 scaffold1_66,687,907-66,667,100_(reversed) 3056 3932 (16876) + L1MC1 LINE/L1 5423 6333 (0) 148

433 30.9 2.1 4.9 scaffold1_66,687,907-66,667,100_(reversed) 4808 5832 (15776) C MonGyLTR3 LTR/Gypsy (18) 963 711 154

269 33.7 2.4 0.0 scaffold1_66,687,907-66,667,100_(reversed) 5347 5512 (15296) C MonGyLTR3 LTR/Gypsy (609) 285 66 154

531 27.7 10.8 0.9 scaffold1_66,687,907-66,667,100_(reversed) 5842 5943 (14865) C MIR3_Mars8 SINE/MIR (71) 144 33 155

213 21.7 4.7 3.4 scaffold1_66,687,907-66,667,100_(reversed) 6386 6591 (14217) + LTRIS4 LTR/ERV1 205 465 (42) 156

253 28.4 0.0 1.1 scaffold1_66,687,907-66,667,100_(reversed) 6842 6930 (13878) + KORV_I-int LTR/ERV1 198 285 (7297) 157

13 20.6 2.4 2.4 scaffold1_66,687,907-66,667,100_(reversed) 7071 7111 (13697) + TGTTT)n Simple_repeat 1 41 (0) 158

754 30.9 0.7 1.7 scaffold1_66,687,907-66,667,100_(reversed) 7143 7432 (13376) + KORV_I-int LTR/ERV1 457 743 (6681) 157

6139 29.3 2.8 2.5 scaffold1_66,687,907-66,667,100_(reversed) 7683 10804 (10004) + KORV_I-int LTR/ERV1 1024 4183 (320) 157

269 33.7 2.4 0.0 scaffold1_66,687,907-66,667,100_(reversed) 12340 12505 (8303) C MonGyLTR3 LTR/Gypsy (609) 285 66 159

231 27.7 10.8 0.9 scaffold1_66,687,907-66,667,100_(reversed) 12835 12936 (7872) C MIR3_Mars8 SINE/MIR (71) 144 33 160

513 21.7 4.7 3.4 scaffold1_66,687,907-66,667,100_(reversed) 13379 13584 (7224) + LTRIS4 LTR/ERV1 205 465 (42) 161

238 26.9 1.0 5.3 scaffold1_66,687,907-66,667,100_(reversed) 13628 13725 (7083) C Mon1f4 SINE/MIR (120) 147 54 162

220 29.4 2.6 3.9 scaffold1_66,687,907-66,667,100_(reversed) 14406 14483 (6325) C MIR0 SINE/MIR (26) 242 166 163

234 31.2 1.1 0.0 scaffold1_66,687,907-66,667,100_(reversed) 14860 14955 (5853) + MIR3 SINE/MIR 111 208 (0) 164

32 23.4 0.0 0.0 scaffold1_66,687,907-66,667,100_(reversed) 16909 16978 (3830) + A-rich Low_complexity 1 70 (0) 165

31 19.6 4.8 1.2 scaffold1_66,687,907-66,667,100_(reversed) 17536 17618 (3190) + (AT)n Simple_repeat 1 86 (0) 166

217 27.7 14.7 0.6 scaffold1_66,687,907-66,667,100_(reversed) 17665 17820 (2988) C MIRc SINE/MIR (27) 241 64 167

485 24.5 0.0 0.9 scaffold1_66,687,907-66,667,100_(reversed) 17910 18020 (2789) + ORSL DNA/HAT-Tip100 1 110 (165) 168 *

607 14.5 10.3 2.9 scaffold1_66,687,907-66,667,100_(reversed) 18015 18146 (2662) + SINEC_c2 SINE/ERNA 75 219 (0) 169

23 22.7 2.7 2.7 scaffold1_66,687,907-66,667,100_(reversed) 18216 18288 (2520) + G-rich Low_complexity 1 73 (0) 170

271 27.5 0.0 0.0 scaffold1_66,687,907-66,667,100_(reversed) 18340 18408 (2400) + L2c LINE/L2 3091 3159 (228) 171

1634 20.4 5.8 1.2 scaffold1_66,687,907-66,667,100_(reversed) 19129 19271 (1537) C L1MA9 LINE/L1 (0) 6312 6167 172

36 0.0 0.0 0.0 scaffold1_66,687,907-66,667,100_(reversed) 19272 19302 (1506) + (GT)n Simple_repeat 1 31 (0) 173

1634 20.4 5.8 1.2 scaffold1_66,687,907-66,667,100_(reversed) 19303 19540 (1268) C L1MA9 LINE/L1 (146) 6166 5915 172

25 10.0 2.3 0.0 scaffold1_66,687,907-66,667,100_(reversed) 20157 20199 (609) + TTTTGT)n Simple_repeat 1 44 (0) 174

55 1.7 3.3 0.0 scaffold1_66,687,907-66,667,100_(reversed) 20513 20573 (235) C TTTAT)n Simple_repeat 1 63 (0) 175

264 16.3 2.6 3.4 scaffold1200.144,464-153,663 6 79 (9121) + L1_Mur2 LINE/L1 2903 2958 (2919) 176

159 29.6 10.2 3.2 scaffold200.144,464-153,663 120 590 (8610) + ERVL-E-int LTR/ERVL 1262 1790 (3924) 177

503 22.3 4.7 3.4 scaffold200.144,464-153,663 1021 1226 (7974) + LTRIS4 LTR/ERV1 205 465 (42) 178

743 31.2 0.7 1.7 scaffold200.144,464-153,663 1378 1667 (7533) + KORV_I-int LTR/ERV1 457 743 (6681) 179

6735 29.6 3.1 3.4 scaffold200.144,464-153,663 1918 6560 (2640) + KORV_I-int LTR/ERV1 1024 5682 (1742) 179

240 35.0 0.0 0.0 scaffold200.144,464-153,663 6658 6760 (2440) + KORV_I-int LTR/ERV1 5958 5852 5954 (1470) 179

276 22.6 0.0 0.0 scaffold200.144,464-153,663 6820 6872 (2328) + KORV_I-int LTR/ERV1 6044 6096 (1328) 179

383 36.2 2.5 2.1 scaffold200.144,464-153,663 7056 7292 (1908) + KORV_I-int LTR/ERV1 6300 6537 (887) 179

1293 33.3 3.6 4.2 scaffold200.144,464-153,663 7412 8217 (983) + KORV_I-int LTR/ERV1 6624 7424 (0) 179

476 22.4 6.5 2.3 scaffold200.144,464-153,663 8654 8833 (367) + LTRIS4 LTR/ERV1 205 465 (42) 180

341	30.6	13.4	1.2	scaffold200_144,464-153,663	8956	9104	(96) + MER3A	DNA/HAT-Blackjack	7	173	(37)	181	
31	2.5	2.4	2.4	scaffold200_144,464-153,663	9137	9178	(22) + (TCCT)n	Simple_repeat					
1687	11.0	2.5	0.0	scaffold211.1,354,903-1,360,362	235	470	(4900) + CorLTR1-int	LTR/ERV1	1310	1560	(5655)	183	
311	9.8	0.0	0.0	scaffold211.1,354,903-1,360,362	473	513	(4947) + ERV5A-EC_I-int	LTR/ERV1	4000	4040	(3223)	184 *	
726	7.5	33.3	1.1	scaffold211.1,354,903-1,360,362	497	688	(4772) + CorLTR1-int	LTR/ERV1	1993	2248	(4367)	183	
581	6.7	0.0	0.0	scaffold211.1,354,903-1,360,362	688	762	(4698) + HUERS-P3-int	LTR/ERV1	2007	2081	(4534)	185 *	
1855	33.5	4.4	2.5	scaffold211.1,354,903-1,360,362	915	1953	(3507) + HUERS-P3-int	LTR/ERV1	2634	3691	(5228)	185	
374	32.9	8.2	2.9	scaffold211.1,354,903-1,360,362	1954	2247	(3213) + HUERS-P3-int	LTR/ERV1	2746	3054	(4370)	186	
755	34.3	0.4	0.0	scaffold211.1,354,903-1,360,362	2251	2515	(2945) + HUERS-P3-int	LTR/ERV1	3977	4242	(2849)	186	
3401	32.2	2.8	1.7	scaffold211.1,354,903-1,360,362	2530	3910	(1550) + HUERS-P3-int	LTR/ERV1	4367	5762	(3157)	186	
481	33.9	5.6	3.4	scaffold211.1,354,903-1,360,362	3916	4288	(1172) + KORV_I-int	LTR/ERV1	4741	5121	(2303)	187	
375	30.0	2.4	2.4	scaffold211.1,354,903-1,360,362	4405	4568	(892) + HUERS-P3-int	LTR/ERV1	6652	6815	(1811)	186	
679	27.2	4.6	4.6	scaffold211.1,354,903-1,360,362	4673	4888	(572) + LTR77-int_TS	LTR/ERV1	5336	5551	(0)	188	
1071	20.4	2.9	7.1	scaffold211.1,354,903-1,360,362	5009	5287	(173) + CorLTR9	LTR/ERV1	296	563	(0)	189	
641	23.7	3.5	0.0	scaffold211.1,354,903-1,360,362	5288	5460	(0) + L1MBB_EC	LINE/L1	(186)	6788	6610	190	
784	19.0	7.1	2.1	scaffold217_224,999-245,612	1	183	(204313) + SINEC_c2	SINE/rRNA	21	212	(0)	191	
723	17.1	10.6	3.5	scaffold217_224,999-245,612	214	401	(20213) + SINEC1_Ame	SINE/rRNA	(0)	201	1	192	
17	29.7	0.0	0.0	scaffold217_224,999-245,612	2257	2305	(18309) + (AC)n	Simple_repeat	1	49	(0)	193	
1008	8.8	16.7	8.4	scaffold217_224,999-245,612	2325	2534	(18080) + SINEC1B_Ame	SINE/rRNA	1	226	(2)	194	
225	11.8	0.0	0.0	scaffold217_224,999-245,612	2659	2692	(17922) + CORRIAS-int	LTR/ERV1-MaLR	(11)	1952	1919	195	
189	29.2	5.6	1.1	scaffold217_224,999-245,612	2804	2893	(17721) + MIR	SINE/MIR	166	259	(3)	196	
40	0.0	0.0	0.0	scaffold217_224,999-245,612	3324	3357	(17257) + (CA)n	Simple_repeat	1	34	(0)	197	
222	23.1	18.2	0.0	scaffold217_224,999-245,612	4112	4254	(16360) + C MIR	SINE/MIR	(53)	215	40	198	
269	27.1	1.0	2.1	scaffold217_224,999-245,612	4350	4447	(16167) + C WALLS14	SINE/rRNA-Core-RTE	(108)	141	45	199 *	
281	26.9	4.0	4.1	scaffold217_224,999-245,612	4360	4460	(16154) + C MonIg3	SINE/MIR	(153)	134	38	200	
196	26.1	0.0	7.8	scaffold217_224,999-245,612	5340	5422	(15192) + L2d	LINE/L2	3018	3094	(370)	201	
21	18.4	0.0	9.0	scaffold217_224,999-245,612	7660	7732	(12882) + (CTCTAGAA)n	Simple_repeat	1	67	(0)	202	
283	27.4	2.4	1.2	scaffold217_224,999-245,612	7989	8073	(12543) + C MIRb	SINE/MIR	(68)	200	115	203	
315	29.4	6.5	0.9	scaffold217_224,999-245,612	9252	9450	(11164) + MIR	SINE/MIR	12	221	(41)	204	
367	26.3	2.1	9.0	scaffold217_224,999-245,612	9728	9869	(10745) + C PlatSat2A	Satellite	(642)	391	259	205	
502	21.9	14.6	3.8	scaffold217_224,999-245,612	10045	10221	(10393) + C LTRIS4	LTR/ERV1	(39)	468	309	206	
199	26.1	0.0	0.0	scaffold217_224,999-245,612	10726	10771	(9843) + C MIR3	SINE/MIR	(61)	147	102	207	
28	21.0	1.6	0.0	scaffold217_224,999-245,612	11496	11556	(9865) + (CT)n	Simple_repeat	1	62	(0)	208	
15	15.5	2.8	0.0	scaffold217_224,999-245,612	11623	11658	(8956) + (CTCTCTC)n	Simple_repeat	1	37	(0)	209	
15	13.2	4.4	4.4	scaffold217_224,999-245,612	11823	11867	(8747) + (TCCTCAC)n	Simple_repeat	1	45	(0)	210	
348	27.9	7.2	4.4	scaffold217_224,999-245,612	13194	13635	(6979) + L2b	LINE/L2	2921	3374	(1)	211	
255	22.9	0.0	1.4	scaffold217_224,999-245,612	14017	14087	(6527) + MSR1	Satellite	10	79	(32)	212	
36	17.5	0.0	1.4	scaffold217_224,999-245,612	14332	14405	(6209) + G-rich	Low_complexity	1	73	(0)	213	
325	27.9	4.2	1.0	scaffold217_224,999-245,612	14572	14761	(5830) + L1	LINE/L1	5476	5859	(335)	214	
443	19.8	3.8	4.8	scaffold217_224,999-245,612	14913	15018	(55967) + C MER77	LTR/ERV1	(0)	604	580	215	
1399	24.0	5.9	4.6	scaffold217_224,999-245,612	15039	15462	(5152) + C MER77	LTR/ERV1	(72)	532	105	215	
259	15.4	0.0	0.0	scaffold217_224,999-245,612	15484	15522	(5092) + C L2B_ME	LINE/L2	(18)	3429	3391	216	
13	4.7	0.0	4.3	scaffold217_224,999-245,612	15705	15728	(4886) + (GAGC)n	Simple_repeat	1	23	(0)	217	
606	31.6	7.4	0.9	scaffold217_224,999-245,612	15800	16421	(4193) + L1M5	LINE/L1	5254	5703	(491)	218	
1424	12.0	0.5	0.0	scaffold217_224,999-245,612	16565	16764	(3850) + SINEC1_Ame	SINE/rRNA	1	201	(0)	219	
13	27.7	4.9	0.0	scaffold217_224,999-245,612	17301	17361	(3253) + (CTCTGT)n	Simple_repeat	1	64	(0)	220	
1386	18.6	7.9	4.3	scaffold217_224,999-245,612	17616	18020	(2594) + C L1MC	LINE/L1	(1117)	5029	4611	221	
2237	17.4	2.7	2.3	scaffold217_224,999-245,612	18099	18459	(2155) + C L1MC	LINE/L1	(1489)	4657	4291	221	
2268	16.0	4.5	3.1	scaffold217_224,999-245,612	18460	18905	(1709) + CorERV4o_LTR	LTR/ERV1	5	456	(0)	222	
2237	17.4	2.7	2.3	scaffold217_224,999-245,612	18906	19018	(1596) + C L1MC	LINE/L1	(1856)	4290	4181	221	
1580	7.0	0.0	1.0	scaffold217_224,999-245,612	19024	19226	(1388) + SINEC1_Ame	SINE/rRNA	(0)	201	(0)	223	
727	23.0	2.1	8.7	scaffold217_224,999-245,612	19231	19463	(1151) + C L1MCL_EC	LINE/L1	(2144)	4201	3983	224	
300	30.4	8.4	3.3	scaffold217_224,999-245,612	19470	19612	(1002) + C LTR40a	LTR/ERV1	(219)	300	151	225	
989	12.8	6.4	7.0	scaffold217_224,999-245,612	20102	20303	(311) + SINEC1_Ame	SINE/rRNA	1	201	(0)	226	
218	25.3	11.4	0.0	scaffold30_5,823,614-5,844,139	348	426	(20100) + C L2d	LINE/L2	(86)	3339	3252	227	
424	28.1	7.1	6.7	scaffold30_5,823,614-5,844,139	747	998	(19528) + C MonRep605	LTR?	210	462	(387)	228	
773	25.9	1.6	3.2	scaffold30_5,823,614-5,844,139	1130	1384	(19142) + C MIR	SINE/MIR	(18)	201	252	229	
325	23.9	2.0	0.0	scaffold30_5,823,614-5,844,139	1863	1962	(18564) + L1_Conid_	LINE/L1	6364	6451	(0)	230	
297	31.5	8.1	10.3	scaffold30_5,823,614-5,844,139	3135	3481	(17045) + L1M6	LINE/L1	682	1021	(5475)	231	
404	30.6	9.8	0.4	scaffold30_5,823,614-5,844,139	3648	3893	(16633) + L1M6	LINE/L1	1251	1519	(4977)	231	
244	24.4	0.0	1.9	scaffold30_5,823,614-5,844,139	4133	4222	(16304) + L1M6	LINE/L1	1813	1988	(688)	231	
1061	8.7	2.0	0.0	scaffold30_5,823,614-5,844,139	4770	4918	(15608) + L1_Corn3	LINE/L1	6285	6436	(1)	232	
49	13.7	2.5	0.0	scaffold30_5,823,614-5,844,139	4935	4974	(15552) + A-rich	Low_complexity	1	41	(0)	233	
361	23.5	16.9	3.6	scaffold30_5,823,614-5,844,139	5941	6212	(15314) + C SINEC1_Ame	SINE/rRNA	(7)	194	1	234	
1606	5.5	1.0	0.0	scaffold30_5,823,614-5,844,139	5427	5625	(14901) + C SINEC1_Ame	SINE/rRNA	(0)	201	1	235	
24	20.9	0.0	0.0	scaffold30_5,823,614-5,844,139	5850	5904	(14622) + (AATC)n	Simple_repeat	1	55	(0)	236	
12	20.2	2.9	0.0	scaffold30_5,823,614-5,844,139	6136	6169	(14357) + (ATATA)n	Simple_repeat	1	35	(0)	237	
488	25.8	0.8	0.0	scaffold30_5,823,614-5,844,139	6220	6339	(14187) + SINEC2_Ame	SINE/rRNA	4	124	(9)	238	
356	13.9	15.1	1.0	scaffold30_5,823,614-5,844,139	6340	6425	(14101) + SINEC_Fc3	SINE/rRNA	642	6418	226	(1)	239
387	33.9	1.6	0.0	scaffold30_5,823,614-5,844,139	7383	7509	(13017) + MIRb	SINE/MIR	44	172	(96)	240	
565	20.3	0.8	0.0	scaffold30_5,823,614-5,844,139	8747	8869	(11657) + SINEC2_Ame	SINE/rRNA	1	124	(9)	241	
242	19.5	6.4	1.2	scaffold30_5,823,614-5,844,139	8871	8948	(11578) + SINEC_c1	SINE/rRNA	126	207	(2)	242	
303	36.0	7.5	1.9	scaffold30_5,823,614-5,844,139	9735	9989	(10537) + C L2c	LINE/L2	(85)	3302	3034	243	
513	22.1	4.1	4.0	scaffold30_5,823,614-5,844,139	10010	10215	(10311) + C LTRIS4	LTR/ERV1	(42)	465	205	244	
378	18.5	18.4	0.8	scaffold30_5,823,614-5,844,139	10678	10806	(9720) + MER68	DNA/HAT-Tip100	49	176	(241)	245	
53	1.9	0.0	0.0	scaffold30_5,823,614-5,844,139	10934	11045	(9483) + (CTA)n	Simple_repeat	1	52	(0)	246	
489	14.6	7.7	2.3	scaffold30_5,823,614-5,844,139	11095	11257	(9269) + SINEC_a2	SINE/rRNA	1	179	(0)	247	
12	8.9	4.2	0.0	scaffold30_5,823,614-5,844,139	11269	11292	(9234) + (TTTA)n	Simple_repeat	1	25	(0)	248	
658	16.5	26.7	2.0	scaffold30_5,823,614-5,844,139	11297	11457	(9069) + C SINEC_c1	SINE/rRNA	(9)	200	1	249	
240	30.3	9.0	9.0	scaffold30_5,823,614-5,844,139	11545	11722	(8804) + MIRc	SINE/MIR	51	231	(37)	250	
782	18.5	11.9	3.5	scaffold30_5,823,614-5,844,139	12219	12403	(8123) + SINEC1_Ame	SINE/rRNA	2	203	(0)	251	
14	4.3	4.2	0.0	scaffold30_5,823,614-5,844,139	12894	12917	(7099) + (CATT)n	Simple_repeat	1	25	(0)	252	
442	8.5	0.2	1.3	scaffold30_5,823,614-5,844,139	13517	13598	(6928) + L1-L1_Ame	LINE/L1	6162	6216	(631)	253	
1393	8.6	0.0	0.5	scaffold30_5,823,614-5,844,139	13861	14058	(6468) + L1-L1_Ame	LINE/L1	6651	6847	(0)	253	
62	0.0	4.5	0.0	scaffold30_5,823,614-5,844,139	14941	15006	(5520) + (TTTTT)n	Simple_repeat	1	69	(0)	254	
15	21.1	0.0	0.0	scaffold30_5,823,614-5,844,139	15036	15064	(5462) + G4-rich	Low_complexity	1	29	(0)	255	
532	21.9	0.8	0.0	scaffold30_5,823,614-5,844,139	15070	15188	(5338) + SINEC2_Ame	SINE/rRNA	(13)	120	1	256	
447	27.6	10.1	1.9	scaffold30_5,823,614-5,844,139	16110	16356	(4170) + LTR37b	LTR/ERV1	197	463	(5)	257	
325	31.4	4.7	1.5	scaffold30_5,823,614-5,844,139	16398	16555	(3971) + C MIR	SINE/MIR	(0)	274	105	258	
781	21.1	7.3	2.1	scaffold30_5,823,614-5,844,139	16814	16							

313	28.6	12.1	0.6	scaffold42_16,713,922-16,693,294	11941	12081	(8578)	C	MER91A	DNA/hAT-Tip100	(4)	192	36	290
255	17.1	0.0	0.5	scaffold42_16,713,922-16,693,294	12502	12565	(8094)	C	Charlie7b_Mars	DNA/hAT-Charlie	(148)	124	62	291
361	18.7	0.0	0.0	scaffold42_16,713,922-16,693,294	13052	13117	(75)	C	MIR3	SINE/MIR	124	189	(19)	292
122	28.4	11.9	0.0	scaffold42_16,713,922-16,693,294	13365	13431	(7228)	C	MIR3	SINE/MIR	90	164	(44)	293
1642	19.5	16.8	5.9	scaffold42_16,713,922-16,693,294	13600	14122	(6537)	C	CorLTR2	LTR/ERV1	2	578	(0)	294
398	23.2	16.1	0.7	scaffold42_16,713,922-16,693,294	14146	14275	(6384)	C	LTR33	LTR/ERV1	(2)	513	364	295
2480	17.6	4.8	0.0	scaffold42_16,713,922-16,693,294	14727	15057	(5602)	C	CorLTR2	LTR/ERV1	(0)	578	253	296
2725	13.6	1.4	0.2	scaffold42_16,713,922-16,693,294	15058	15486	(5173)	C	CorERV2b2_LTR	LTR/ERV1	(0)	434	1	297
2480	17.6	4.8	0.0	scaffold42_16,713,922-16,693,294	15487	15755	(4904)	C	CorLTR2	LTR/ERV1	(326)	252	1	296
198	33.8	1.3	0.0	scaffold42_16,713,922-16,693,294	15756	15832	(4827)	C	MIRb	SINE/MIR	113	190	(78)	298
259	30.8	0.0	0.0	scaffold42_16,713,922-16,693,294	16511	16575	(4084)	C	MIRb	SINE/MIR	122	186	(82)	299
30	0.0	0.0	0.0	scaffold42_16,713,922-16,693,294	16913	16938	(3721)	C	(AC)n	Simple_repeat	1	26	(0)	300
18	33.9	0.0	0.0	scaffold42_16,713,922-16,693,294	16940	16994	(3665)	C	(CA)n	Simple_repeat	1	55	(0)	301
399	27.5	1.1	0.0	scaffold42_16,713,922-16,693,294	17165	17255	(3404)	C	Mon1g1	SINE/MIR	59	150	(153)	302
915	25.4	3.8	2.8	scaffold42_16,713,922-16,693,294	17720	18006	(2653)	C	LIME3A	LINE/L1	5861	6150	(23)	303
270	21.0	7.4	0.0	scaffold42_16,713,922-16,693,294	18129	18209	(2450)	C	MIRb	SINE/MIR	(82)	186	100	304
1710	5.0	0.0	0.0	scaffold42_16,713,922-16,693,294	18300	18500	(2159)	C	SINEC1_Ame	SINE/rRNA	1	201	(0)	305
14	4.3	0.0	7.7	scaffold42_16,713,922-16,693,294	19251	19278	(1381)	C	(AAT)n	Simple_repeat	1	26	(0)	306
396	21.8	10.9	9.1	scaffold42_16,713,922-16,693,294	19833	20080	(579)	C	MamRep38	DNA/hAT	1	252	(43)	307
1990	21.1	4.7	0.5	scaffold42_16,713,922-16,693,294	20253	20653	(6)	C	LTR3_EC	LTR/ERV1	(8)	740	323	308
449	30.0	0.6	1.8	scaffold52_8,175,534-8,196,159	1	175	(20453)	C	L2z	LINE/L2	2445	2615	(804)	309
1140	10.8	15.3	0.9	scaffold52_8,175,534-8,196,159	181	376	(20250)	C	SINEC1B_Ame	SINE/rRNA	(4)	224	1	310
424	30.4	6.8	0.0	scaffold52_8,175,534-8,196,159	380	540	(20086)	C	L2z	LINE/L2	2605	2776	(643)	309
405	26.2	6.0	0.9	scaffold52_8,175,534-8,196,159	584	813	(19813)	C	L2z	LINE/L2	2868	3162	(264)	309
399	17.5	2.4	2.4	scaffold52_8,175,534-8,196,159	814	895	(19731)	C	MER34C_EC	LTR/ERV1	(20)	582	501	311
651	20.3	0.8	0.8	scaffold52_8,175,534-8,196,159	912	1035	(19591)	C	SINEC2_Ame	SINE/rRNA	1	124	(9)	312
302	13.0	14.5	0.5	scaffold52_8,175,534-8,196,159	1036	1124	(19502)	C	SINEC2_C2	SINE/rRNA	125	225	(0)	313
1197	20.2	13.0	0.3	scaffold52_8,175,534-8,196,159	1118	1451	(19173)	C	MER34C_EC	LTR/ERV1	(142)	379	1	311
379	25.8	10.8	3.1	scaffold52_8,175,534-8,196,159	1454	1615	(19011)	C	L2z	LINE/L2	3161	3339	(87)	309
33	0.0	0.0	0.0	scaffold52_8,175,534-8,196,159	1616	1646	(18980)	C	(T)n	Simple_repeat	1	31	(0)	314
379	22.0	8.8	1.9	scaffold52_8,175,534-8,196,159	1647	1716	(18910)	C	L2z	LINE/L2	3311	3388	(38)	309
422	30.6	3.5	2.5	scaffold52_8,175,534-8,196,159	2286	2483	(18143)	C	LIME4b	LINE/L1	5928	6127	(18)	315
16	15.5	0.0	2.7	scaffold52_8,175,534-8,196,159	3915	3991	(16620)	C	(TCATTC)n	Simple_repeat	1	20	(0)	316
260	38.0	0.6	4.4	scaffold52_8,175,534-8,196,159	4788	4952	(15674)	C	MIR	SINE/MIR	53	211	(53)	317
12	14.4	0.0	0.0	scaffold52_8,175,534-8,196,159	5589	5612	(15014)	C	(TAA)n	Simple_repeat	1	24	(0)	318
445	25.5	0.0	0.9	scaffold52_8,175,534-8,196,159	6322	6432	(14194)	C	MIR	SINE/MIR	61	170	(92)	319
207	16.7	0.0	0.0	scaffold52_8,175,534-8,196,159	6444	6479	(14147)	C	L2b	LINE/L2	3322	3357	(18)	320
218	17.5	0.0	2.5	scaffold52_8,175,534-8,196,159	6450	6490	(14136)	C	MIRb	SINE/MIR	225	264	(4)	321
183	16.1	0.0	0.0	scaffold52_8,175,534-8,196,159	7620	7650	(12925)	C	L2	LINE/L2	(1086)	234	2353	322
319	34.9	10.1	3.3	scaffold52_8,175,534-8,196,159	7955	7881	(12745)	C	MIR	SINE/MIR	(18)	249	8	323
396	33.8	5.6	2.6	scaffold52_8,175,534-8,196,159	8302	8605	(12021)	C	L2	LINE/L2	(1368)	2051	1739	322
314	32.4	2.5	5.3	scaffold52_8,175,534-8,196,159	8861	9066	(11560)	C	MIRb	SINE/MIR	(26)	242	45	324
14	0.0	0.0	0.0	scaffold52_8,175,534-8,196,159	9274	9291	(11335)	C	(GTT)n	Simple_repeat	1	18	(0)	325
446	23.2	4.3	5.4	scaffold52_8,175,534-8,196,159	9988	10196	(10430)	C	LTR154A	LTR/ERV1	(42)	432	205	326
194	30.4	11.1	0.7	scaffold52_8,175,534-8,196,159	11714	11839	(8787)	C	(CT)n	LINE/L2	3249	3387	(0)	327
19	14.5	0.0	0.0	scaffold52_8,175,534-8,196,159	11944	11974	(8652)	C	(T)n	Simple_repeat	1	31	(0)	328
18	4.3	0.0	4.0	scaffold52_8,175,534-8,196,159	12537	12562	(8064)	C	(CA)n	Simple_repeat	1	25	(0)	329
712	26.4	7.6	0.8	scaffold52_8,175,534-8,196,159	13041	13277	(7349)	C	MIR	SINE/MIR	(1)	261	9	330
257	30.0	3.3	0.0	scaffold52_8,175,534-8,196,159	13717	13806	(6820)	C	L2c	LINE/L2	3292	3384	(3)	331
1582	21.1	6.4	4.3	scaffold52_8,175,534-8,196,159	14339	14837	(5789)	C	MER34A	LTR/ERV1	(6)	501	2	332
855	13.0	17.2	1.7	scaffold52_8,175,534-8,196,159	15802	15178	(5449)	C	SINEC2_b1	SINE/rRNA	(11)	143	3	333
189	15.8	2.6	0.0	scaffold52_8,175,534-8,196,159	17561	17598	(3082)	C	MIR3	SINE/MIR	(87)	121	83	334
12	15.8	0.0	3.5	scaffold52_8,175,534-8,196,159	18154	18183	(2443)	C	(TGAT)n	Simple_repeat	1	29	(0)	335
184	26.1	8.7	0.0	scaffold52_8,175,534-8,196,159	18374	18442	(2184)	C	L2b	LINE/L2	3297	3371	(4)	336
589	13.6	0.9	1.9	scaffold52_8,175,534-8,196,159	19084	19188	(1438)	C	MLT1D	LTR/ERV1-MaLR	(0)	505	402	337
334	35.2	6.2	7.5	scaffold52_8,175,534-8,196,159	19228	19700	(936)	C	L2b	LINE/L2	2907	3372	(3)	338
230	14.7	0.0	0.0	scaffold52_13,107,950-13,128,518	208	223	(20336)	C	PlasSat2A	Satellite	263	296	(737)	339
510	17.2	4.2	1.6	scaffold52_13,107,950-13,128,518	640	757	(19812)	C	SINEC2_Ame	SINE/rRNA	2	122	(11)	340
14	8.8	0.0	0.0	scaffold52_13,107,950-13,128,518	805	828	(19741)	C	(AATT)n	Simple_repeat	1	24	(0)	341
245	33.6	6.2	0.0	scaffold52_13,107,950-13,128,518	1049	1161	(19408)	C	MIRb	SINE/MIR	41	160	(108)	342
440	28.2	7.8	3.6	scaffold52_13,107,950-13,128,518	1175	1417	(19152)	C	MamRep1527	LTR	(466)	503	251	343
2305	18.3	9.8	0.0	scaffold52_13,107,950-13,128,518	2220	2677	(17892)	C	MLT1D	LTR/ERV1-MaLR	(0)	505	3	344
167	29.6	0.0	0.0	scaffold52_13,107,950-13,128,518	2764	2817	(17752)	C	L2c	LINE/L2	(37)	3350	3297	345
494	28.5	9.4	0.9	scaffold52_13,107,950-13,128,518	2843	3044	(17525)	C	MIR	SINE/MIR	(18)	244	26	346
15	33.0	0.0	0.0	scaffold52_13,107,950-13,128,518	3170	3221	(17348)	C	(ATG)n	Simple_repeat	1	52	(0)	347
27	0.0	0.0	0.0	scaffold52_13,107,950-13,128,518	4694	4719	(15850)	C	(TTAT)n	Simple_repeat	1	26	(0)	348
1114	8.0	0.7	0.0	scaffold52_13,107,950-13,128,518	4728	4877	(15692)	C	L1-L1_Ame	LINE/L1	(18)	6829	6679	349
1506	22.4	7.2	7.0	scaffold52_13,107,950-13,128,518	4939	5437	(15132)	C	MLT1D	LTR/ERV1-MaLR	(3)	502	3	350
234	20.3	3.3	3.3	scaffold52_13,107,950-13,128,518	5538	5598	(14971)	C	L3	LINE/rRNA	3413	3473	(66)	351
205	28.4	5.6	7.0	scaffold52_13,107,950-13,128,518	5659	5802	(14767)	C	MIRb	SINE/MIR	(30)	338	97	352
16	3.2	8.8	2.8	scaffold52_13,107,950-13,128,518	5961	5994	(14575)	C	(AAC)n	Simple_repeat	1	36	(0)	353
941	28.2	5.7	2.9	scaffold52_13,107,950-13,128,518	6204	6605	(13964)	C	L2	LINE/L2	1597	2009	(1410)	354
387	27.3	1.1	0.0	scaffold52_13,107,950-13,128,518	6606	6693	(13876)	C	MER94	DNA/hAT-Blackjack	(0)	134	46	355
828	29.6	12.1	4.1	scaffold52_13,107,950-13,128,518	6733	7138	(1343)	C	LTR16	LTR/ERV1	(1)	437	1	356
533	32.2	2.1	0.4	scaffold52_13,107,950-13,128,518	7171	7404	(12165)	C	L2	LINE/L2	2012	2249	(1170)	354
822	26.2	0.9	0.0	scaffold52_13,107,950-13,128,518	7432	7641	(12028)	C	MER58A	DNA/hAT-Charlie	5	222	(2)	357
388	28.5	9.1	3.2	scaffold52_13,107,950-13,128,518	7679	7804	(12765)	C	L2a	LINE/L2	3107	3250	(176)	358
2164	18.4	0.9	6.8	scaffold52_13,107,950-13,128,518	7805	8242	(12327)	C	MLT2D	LTR/ERV1	(0)	414	1	359
383	27.6	8.8	4.4	scaffold52_13,107,950-13,128,518	8243	8413	(12156)	C	L2a	LINE/L2	3251	3426	(0)	358
458	26.2	1.4	0.6	scaffold52_13,107,950-13,128,518	8412	8575	(11994)	C	L2	LINE/L2	2305	2479	(940)	354
51	23.4	6.3	3.2	scaffold52_13,107,950-13,128,518	8767	8975	(11594)	C	LTR16B1	LTR/ERV1	191	409	(71)	360
947	15.0	11.2	2.7	scaffold52_13,107,950-13,128,518	10355	10560	(10000)	C	LTR154	LTR/ERV1	285	365	(42)	361
255	8.8	0.0	0.0	scaffold52_13,107,950-13,128,518	11982	12186	(8383)	C	SINEC1B_Ame	SINE/rRNA	1	222	(6)	362
311	31.2	2.8	5.8	scaffold52_13,107,950-13,128,518	12713	12746	(7823)	C	MARE8	DNA	148	181	(119)	363
728	16.4	4.3	5.3	scaffold52_13,107,950-13,128,518	13070	13246	(7323)	C	MERSA	DNA/hAT-Charlie	(0)			

274	13.0	1.5	9.5	scaffold7_30,636,998-30,609,301	10612	10679	(17019) + KORV_I-int	LTR/ERV1	1	63	(7500)	394
745	30.9	0.7	1.7	scaffold7_30,636,998-30,609,301	11111	11400	(16298) + KORV_I-int	LTR/ERV1	457	743	(6681)	394
6801	29.8	3.3	3.6	scaffold7_30,636,998-30,609,301	11653	16299	(11400) + KORV_I-int	LTR/ERV1	1824	5682	(1742)	394
360	35.2	0.0	0.0	scaffold7_30,636,998-30,609,301	16357	16498	(11200) + KORV_I-int	LTR/ERV1	5813	5954	(1470)	394
291	28.4	0.0	0.0	scaffold7_30,636,998-30,609,301	16537	16610	(11088) + KORV_I-int	LTR/ERV1	6023	6096	(1328)	394
891	33.4	3.0	2.6	scaffold7_30,636,998-30,609,301	16658	17118	(10580) + KORV_I-int	LTR/ERV1	6962	7424	(0)	394
491	21.7	5.1	2.5	scaffold7_30,636,998-30,609,301	17532	17687	(10011) + LTRIS4	LTR/ERV1	309	468	(39)	395
470	28.4	5.7	4.4	scaffold7_30,636,998-30,609,301	17751	17997	(9701) + L2a	LINE/L2	3075	3324	(102)	392
239	28.1	0.0	0.0	scaffold7_30,636,998-30,609,301	18017	18080	(9618) + L2b_ME	LINE/L2	3383	3446	(1)	396
878	24.2	7.3	2.4	scaffold7_30,636,998-30,609,301	19798	20110	(7588) C LIME4a	LINE/L1	(4)	6120	5793	397
589	42.8	7.4	0.5	scaffold7_30,636,998-30,609,301	20154	20355	(7343) + SINEC1B_Ame	SINE/rRNA	1	216	(12)	398
677	11.7	1.9	1.9	scaffold7_30,636,998-30,609,301	20592	20696	(7002) + SINEC_old	SINE/rRNA	1	105	(7)	399
421	27.3	1.6	0.8	scaffold7_30,636,998-30,609,301	20699	20820	(6878) + SINEC2_Ame	SINE/rRNA	2	124	(9)	400
23	13.1	0.0	2.3	scaffold7_30,636,998-30,609,301	20851	20894	(6804) + A-rich	Low_complexity	1	43	(0)	401
338	22.9	2.9	0.0	scaffold7_30,636,998-30,609,301	20981	21050	(6644) + rRNA-Lys-AAG	rRNA	2	73	(3)	402
15	15.8	0.0	2.8	scaffold7_30,636,998-30,609,301	21062	21098	(6600) + A-rich	Low_complexity	1	36	(0)	403
691	18.8	13.1	4.0	scaffold7_30,636,998-30,609,301	21143	21325	(6373) C SINEC1_Ame	SINE/rRNA	(2)	199	1	404
315	21.8	10.8	0.9	scaffold7_30,636,998-30,609,301	21326	21439	(6259) + LIME4c	LINE/L1	5459	5582	(501)	405
421	13.6	0.0	0.0	scaffold7_30,636,998-30,609,301	21525	21590	(6108) C CorL1R1-int	LTR/ERV1	(517)	6098	6033	406
1638	21.8	9.4	0.0	scaffold7_30,636,998-30,609,301	21736	22350	(5348) C CorERV2-int	LTR/ERV1	(1380)	6232	5560	407
4729	20.8	2.5	1.2	scaffold7_30,636,998-30,609,301	22361	23325	(4373) C CorERV2-int	LTR/ERV1	(2702)	4910	3934	407
284	32.8	6.7	0.8	scaffold7_30,636,998-30,609,301	23327	23446	(4252) C CorERV2-int	LTR/ERV1	(3927)	3497	3371	407
2821	13.7	5.5	0.8	scaffold7_30,636,998-30,609,301	23448	23904	(3794) C CorERV2-int	LTR/ERV1	(3809)	3803	3326	408
226	37.9	4.9	0.4	scaffold7_30,636,998-30,609,301	23905	24169	(3529) C CorERV2-int	LTR/ERV1	(4534)	2890	2614	408
3844	18.4	3.6	0.4	scaffold7_30,636,998-30,609,301	24170	25154	(2544) C CorERV2-int	LTR/ERV1	(4560)	3052	2008	409
672	12.3	0.0	1.9	scaffold7_30,636,998-30,609,301	25158	25265	(2433) + SINEC_old	SINE/rRNA	7	112	(0)	410
2306	22.1	6.4	2.3	scaffold7_30,636,998-30,609,301	25271	25626	(2872) C CorERV2-int	LTR/ERV1	(5599)	2013	1556	409
42	0.0	0.0	0.0	scaffold7_30,636,998-30,609,301	25627	25662	(2036) + (AC)n	Simple_repeat	1	36	(0)	411
2306	23.0	5.3	1.7	scaffold7_30,636,998-30,609,301	25663	26010	(1688) C CorERV2-int	LTR/ERV1	(5959)	1653	1290	409 *
4009	16.6	5.0	3.2	scaffold7_30,636,998-30,609,301	25999	27328	(370) C CorERV2-int	LTR/ERV1	(6233)	1379	1	409
1324	22.9	2.9	2.5	scaffold7_30,636,998-30,609,301	27329	27677	(21) C CorL1R1B2	LTR/ERV1	(4)	542	144	409
458	16.9	16.8	0.7	scaffold80_7,084,287-7,112,941	4	122	(28533) C MLTIC	LTR/ERV1-MaLR	(59)	408	271	412
15	9.8	0.0	0.0	scaffold80_7,084,287-7,112,941	210	231	(28424) + (ATT)n	Simple_repeat	1	22	(0)	413
20	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	233	254	(28401) + (GA)n	Simple_repeat	1	22	(0)	414
16	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	333	350	(28305) + (A)n	Simple_repeat	1	18	(0)	415
389	16.9	0.0	3.4	scaffold80_7,084,287-7,112,941	419	510	(28145) + L1-1_Ame	LINE/L1	6751	6839	(8)	416
532	26.8	3.9	0.5	scaffold80_7,084,287-7,112,941	511	690	(27965) C MER20B	DNA/HAT-Charlie	(401)	382	197	417
234	11.6	0.0	2.3	scaffold80_7,084,287-7,112,941	705	748	(27907) C MER20B	DNA/HAT-Charlie	(702)	81	39	417
201	36.4	10.1	0.0	scaffold80_7,084,287-7,112,941	1345	1452	(27122) + L3	LINE/IR1	3562	3670	(429)	418
3152	16.3	6.0	3.2	scaffold80_7,084,287-7,112,941	1628	1694	(26961) C LIMB1	LINE/L1	(5)	6163	6111	419
1597	7.5	0.0	0.0	scaffold80_7,084,287-7,112,941	1695	1894	(26761) + SINEC1_Ame	SINE/rRNA	1	200	(1)	420
3152	16.3	6.0	3.2	scaffold80_7,084,287-7,112,941	1895	2471	(26184) C LIMB1	LINE/L1	(58)	6110	5501	419
21	23.9	1.7	0.0	scaffold80_7,084,287-7,112,941	2480	2538	(26117) + (TATA)n	Simple_repeat	1	60	(0)	421
499	23.9	2.4	0.4	scaffold80_7,084,287-7,112,941	2540	2684	(25971) C LIMB1	LINE/L1	(1368)	4977	4814	419
333	33.7	1.7	1.1	scaffold80_7,084,287-7,112,941	2685	2858	(25797) C Sor-1_T5y	Satellite	(1280)	1956	1782	422
1063	16.0	2.8	2.3	scaffold80_7,084,287-7,112,941	2859	2885	(25770) C LIMB1	LINE/L1	(1508)	4637	4611	419
60	0.0	3.3	0.0	scaffold80_7,084,287-7,112,941	2886	2946	(25709) + (AAA)n	Simple_repeat	1	63	(0)	423
1063	16.0	2.8	2.3	scaffold80_7,084,287-7,112,941	2947	3136	(25519) C LIMB1	LINE/L1	(1530)	4610	4419	419
378	29.4	4.2	3.6	scaffold80_7,084,287-7,112,941	3581	3746	(24909) C Tigger15a	DNA/TcMar-Tigger	(416)	299	133	424
47	27.0	1.6	4.4	scaffold80_7,084,287-7,112,941	4771	4955	(23700) + (TTTC)n	Simple_repeat	1	180	(0)	425
15	26.9	3.3	1.6	scaffold80_7,084,287-7,112,941	5352	5592	(23863) + (ATGATA)n	Simple_repeat	1	62	(0)	426
70	13.6	0.0	2.4	scaffold80_7,084,287-7,112,941	5671	5798	(23857) + (TATATA)n	Simple_repeat	1	125	(0)	427
34	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	5802	5830	(22825) + (TG)n	Simple_repeat	1	29	(0)	428
257	34.2	0.8	1.7	scaffold80_7,084,287-7,112,941	5841	5959	(22696) + MER5A	DNA/HAT-Charlie	72	189	(0)	429
555	33.0	2.3	0.5	scaffold80_7,084,287-7,112,941	7017	7235	(21420) + MIRb	SINE/MIR	30	252	(16)	430
346	29.9	12.1	1.7	scaffold80_7,084,287-7,112,941	7707	8047	(20608) C L2b	LINE/L2	(0)	3426	3055	431
626	22.3	2.9	8.0	scaffold80_7,084,287-7,112,941	8126	8335	(20320) + SINEC1_Ame	SINE/rRNA	1	200	(1)	432
17	19.5	0.0	0.0	scaffold80_7,084,287-7,112,941	8337	8367	(20288) + A-rich	Low_complexity	1	31	(0)	433
379	22.7	6.1	4.3	scaffold80_7,084,287-7,112,941	10071	10185	(18470) + MIRb	SINE/MIR	20	136	(132)	434
16	21.8	2.6	0.0	scaffold80_7,084,287-7,112,941	11842	11879	(16776) + (TA)n	Simple_repeat	1	39	(0)	435
522	21.4	4.1	4.0	scaffold80_7,084,287-7,112,941	12014	12219	(16436) C LTRIS4	LTR/ERV1	(42)	465	205	436
353	26.1	7.7	2.1	scaffold80_7,084,287-7,112,941	12960	13129	(15526) + Monig0	SINE/MIR	1	179	(115)	437
239	24.7	5.7	3.3	scaffold80_7,084,287-7,112,941	14690	14777	(13878) + MIR3	SINE/MIR	15	104	(104)	438
541	23.4	7.6	5.3	scaffold80_7,084,287-7,112,941	14912	15096	(13559) + MER5A	DNA/HAT-Charlie	1	189	(0)	439
190	33.3	6.4	1.0	scaffold80_7,084,287-7,112,941	15225	15318	(13337) + L2b	LINE/L2	3264	3362	(13)	440
285	31.1	2.4	2.4	scaffold80_7,084,287-7,112,941	15330	15454	(13201) + MIRb	SINE/MIR	86	210	(58)	441
45	6.0	0.0	0.0	scaffold80_7,084,287-7,112,941	15483	15534	(13121) + (GT)n	Simple_repeat	1	52	(0)	442
400	37.2	7.7	3.0	scaffold80_7,084,287-7,112,941	15622	16037	(12618) C MonGypLTRic	LTR/gypsy	(119)	684	250	443
293	29.5	14.3	0.0	scaffold80_7,084,287-7,112,941	16158	16262	(12393) C MonGypLTRic	LTR/gypsy	(620)	193	74	443
678	27.3	1.4	2.3	scaffold80_7,084,287-7,112,941	16297	16517	(12138) + MER20	DNA/HAT-Charlie	1	219	(0)	444
456	22.4	1.0	0.0	scaffold80_7,084,287-7,112,941	17181	17278	(11377) C MER45C	DNA/HAT-Tip100	(11)	942	844	445
816	9.4	24.5	4.3	scaffold80_7,084,287-7,112,941	17279	17433	(11222) + SINEC_b1	SINE/rRNA	1	185	(9)	446
39	4.1	3.4	8.2	scaffold80_7,084,287-7,112,941	17438	17526	(11129) + (TA)n	Simple_repeat	1	85	(0)	447
39	6.8	0.0	0.0	scaffold80_7,084,287-7,112,941	17527	17573	(11082) + (TG)n	Simple_repeat	1	47	(0)	448
292	19.5	0.0	3.9	scaffold80_7,084,287-7,112,941	17538	17667	(10985) C MER45C	DNA/HAT-Tip100	(97)	856	780	445
1333	23.8	2.0	3.3	scaffold80_7,084,287-7,112,941	18914	19460	(9195) + Arthur2	DNA/HAT-Tip100	442	981	(2719)	449
13	22.2	3.5	5.3	scaffold80_7,084,287-7,112,941	19894	19951	(8704) + (ATT)n	Simple_repeat	1	57	(0)	450
1367	21.2	10.3	0.6	scaffold80_7,084,287-7,112,941	20099	20492	(8163) C LIMA7	LINE/L1	(0)	6894	6510	451
75	13.4	5.4	0.0	scaffold80_7,084,287-7,112,941	20862	21008	(7647) + (AT)n	Simple_repeat	1	155	(0)	452
17	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	21198	21216	(7439) + (TG)n	Simple_repeat	1	19	(0)	453
16	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	21216	21235	(7420) + (TA)n	Simple_repeat	1	21	(0)	454 *
463	29.6	6.6	0.6	scaffold80_7,084,287-7,112,941	21332	21494	(7161) C MLT1H	LTR/ERV1-MaLR	(0)	549	374	455
266	37.1	1.0	7.2	scaffold80_7,084,287-7,112,941	21541	21746	(6909) C L2c	LINE/L2	(200)	3187	2994	456
51	2.1	0.0	0.0	scaffold80_7,084,287-7,112,941	22417	22464	(6191) + (AC)n	Simple_repeat	1	48	(0)	457
465	27.2	2.3	1.6	scaffold80_7,084,287-7,112,941	22742	22937	(5718) + LIMB7	LINE/L1	5983	6183	(1)	458
231	35.6	3.3	0.0	scaffold80_7,084,287-7,112,941	23168	23257	(5398) C L2a	LINE/L2	(30)	3396	3304	459
37	0.0	0.0	0.0	scaffold80_7,084,287-7,112,941	23468	23499	(5156) + (TG)n	Simple_repeat	1	32	(0)	460
782	28.3	1.5	1.5	scaffold80_7,084,287-7,112,941	23891	24091	(4564) C MER20	DNA/HAT-Charlie	(3)	216	16	461
459	28.2	2.3	0.0	scaffold80_7,084,287-7,112,941								