3T3 cells

Zfp143 peaks <= 2kb from TSS			Repeats from repeatMasker (USCS) table					
Chromosome	Start	End	Chromosome	Start	End	repName	repClass	repFamily
chr1	6204523	6204924	.	.	.	.	.	.
chr1	9535119	9535520	.	.	.	.	.	.
chr1	9620524	9620925	.	.	.	.	.	.
chr1	9690531	9690932	chr1	9690510	9690675	G-rich	Low_comple	Low_complexity
chr1	9738422	9738823	.	.	.	.	.	.
chr1	16094646	16095047	chr1	16094682	16094708	(T)n	Simple_repe	Simple_repeat
chr1	16647066	16647467	.	.	.	.	.	.
chr1	16655064	16655465	.	.	.	.	.	.
chr1	17135240	17135641	.	.	.	.	.	.
chr1	20810367	20810768	chr1	20810614	20810641	(T)n	Simple_repe	Simple_repeat
chr1	20810367	20810768	chr1	20810726	20810812	B4A	SINE	B4
chr1	24685267	24685668	chr1	24685526	24685557	(TCCCG)n	Simple_repe	Simple_repeat
chr1	26744088	26744489	.	.	.	.	.	.
chr1	33871236	33871637	chr1	33871227	33871269	(CCG)n	Simple_repe	Simple_repeat
chr1	34496129	34496530	.	.	.	.	.	.
chr1	36301630	36302031	chr1	36301667	36301795	Lx8	LINE	L1
chr1	36301630	36302031	chr1	36301866	36302144	B4A	SINE	B4
chr1	36364260	36364661	.	.	.	.	.	.
chr1	36526777	36527178	.	.	.	.	.	.
chr1	36748096	36748497	.	.	.	.	.	.
chr1	37486156	37486557	chr1	37486528	37486618	MIRb	SINE	MIR
chr1	37929045	37929446	.	.	.	.	.	.
chr1	37947149	37947550	.	.	.	.	.	.
chr1	38054033	38054434	.	.	.	.	.	.
chr1	39424496	39424897	.	.	.	.	.	.
chr1	40282444	40282845	chr1	40282782	40282824	(CA)n	Simple_repe	Simple_repeat
chr1	43155378	43155779	.	.	.	.	.	.
chr1	43990517	43990918	.	.	.	.	.	.
chr1	44159132	44159533	.	.	.	.	.	.
chr1	44175556	44175957	chr1	44175851	44175912	CT-rich	Low_comple	Low_complexity
chr1	45852056	45852457	.	.	.	.	.	.
chr1	54307341	54307742	.	.	.	.	.	.
chr1	54495663	54496064	chr1	54495995	54496203	B2_Mm2	SINE	B2
chr1	55084168	55084569	chr1	55084487	55084622	B1_Mm	SINE	Alu
chr1	55144688	55145089	chr1	55144725	55144772	GC_rich	Low_comple	Low_complexity
chr1	55144688	55145089	chr1	55144804	55144825	GC_rich	Low_comple	Low_complexity
chr1	55187782	55188183	chr1	55188034	55188082	(CCCCG)n	Simple_repe	Simple_repeat
chr1	55285060	55285461	.	.	.	.	.	.
chr1	57463377	57463778	.	.	.	.	.	.
chr1	58052595	58052996	.	.	.	.	.	.
chr1	58502142	58502543	.	.	.	.	.	.
chr1	58561743	58562144	chr1	58562124	58562146	(A)n	Simple_repe	Simple_repeat
chr1	58643032	58643433	.	.	.	.	.	.
chr1	59030139	59030540	.	.	.	.	.	.
chr1	59741630	59742031	chr1	59741675	59741696	(A)n	Simple_repe	Simple_repeat
chr1	60154587	60154988	.	.	.	.	.	.
chr1	63223391	63223792	.	.	.	.	.	.
chr1	64577640	64578041	.	.	.	.	.	.
chr1	65232911	65233312	.	.	.	.	.	.
chr1	72629575	72629976	.	.	.	.	.	.
chr1	74331340	74331741	.	.	.	.	.	.
chr1	74552632	74553033	.	.	.	.	.	.
chr1	74707884	74708285	chr1	74708169	74708217	C-rich	Low_comple	Low_complexity
chr1	75121417	75121818	.	.	.	.	.	.
chr1	75232687	75233088	chr1	75232487	75232703	L2a	LINE	L2
chr1	75232687	75233088	chr1	75232965	75232993	(CCCCCG)n	Simple_repe	Simple_repeat
chr1	75432288	75432689	.	.	.	.	.	.
chr1	78485355	78485756	.	.	.	.	.	.
chr1	79772411	79772812	.	.	.	.	.	.
chr1	84835981	84836382	.	.	.	.	.	.
chr1	88051074	88051475	.	.	.	.	.	.
chr1	88479233	88479634	.	.	.	.	.	.
chr1	88600167	88600568	.	.	.	.	.	.
chr1	89904963	89905364	.	.	.	.	.	.
chr1	90173999	90174400	.	.	.	.	.	.
chr1	91351026	91351427	chr1	91351314	91351356	GC_rich	Low_comple	Low_complexity
chr1	93295219	93295620	chr1	93295321	93295343	(CGG)n	Simple_repe	Simple_repeat
chr1	93295219	93295620	chr1	93295406	93295427	GC_rich	Low_comple	Low_complexity
chr1	93390991	93391392	.	.	.	.	.	.
chr1	94830778	94831179	.	.	.	.	.	.
chr1	95239918	95240319	.	.	.	.	.	.
chr1	95532165	95532566	.	.	.	.	.	.
chr1	95581817	95582218	chr1	95581807	95581914	B3	SINE	B2
chr1	99666529	99666930	.	.	.	.	.	.
chr1	108067809	108068210	.	.	.	.	.	.
chr1	108693114	108693515	chr1	108693367	108693589	L1MD3	LINE	L1
chr1	120284656	120285057	chr1	120284532	120284720	L1MB2	LINE	L1
chr1	120355799	120356200	.	.	.	.	.	.
chr1	121809571	121809972	.	.	.	.	.	.
chr1	122017599	122018000	.	.	.	.	.	.
chr1	122498714	122499115	.	.	.	.	.	.
chr1	123464384	123464785	.	.	.	.	.	.
chr1	129670321	129670722	.	.	.	.	.	.
chr1	129765174	129765575	.	.	.	.	.	.
chr1	129999107	129999508	.	.	.	.	.	.
chr1	130140464	130140865	.	.	.	.	.	.
chr1	133035752	133036153	.	.	.	.	.	.
chr1	133587057	133587458	.	.	.	.	.	.
chr1	133763551	133763952	chr1	133763502	133763614	ID_B1	SINE	B4
chr1	134313757	134314158	.	.	.	.	.	.
chr1	134373497	134373898	.	.	.	.	.	.
chr1	134921812	134922213	chr1	134922106	134922226	B1_Mus2	SINE	Alu

repName count

GC_rich	191
(CGG)n	41
ID_B1	26
AT_rich	26
(A)n	25
(CCG)n	24
B3	24
(T)n	23
PB1D10	23
G-rich	22
B1_Mus1	20
GA-rich	20
(CCCCG)n	16
(CA)n	15
B1_Mus2	15
(CGGGG)n	15
C-rich	13
(TG)n	13
RSINE1	13
B2_Mm2	11
(TTTG)n	11
PB1D7	11
B1_Mur1	11
MIRb	9
CT-rich	9
(GA)n	9
PB1D9	9
(CCCG)n	9
RLTR15	9
B4A	8
(GGA)n	8
B1F	8
B1_Mm	7
B1_Mur4	7
B1_Mur2	7
L2a	6
PB1	6
B4	6
MIR	6
T-rich	5
(TC)n	5
B1F2	5
(CGCGG)n	4
B3A	4
L2b	4
ID4	4
MIRm	4
L2	4
(CAAAA)n	4
(CCGGG)n	4
Lx8	3
(CCCCCG)n	3
URR1B	3
B1_Mur3	3
(CGAG)n	3
(TCC)n	3
MIRc	3
(CAG)n	3
B1F1	3
ID	3
MT2B2	3
MIR3	3
(CGGG)n	3
tRNA-Ala-GC	3
(TCTG)n	3
(TAAA)n	3
(TTTC)n	3
(GGGA)n	3
RLTR42	3
RMER17B	3
MLT1J1	2
(CACG)n	2
(CAGAGA)n	2
B2_Mm1t	2
(TCTCTG)n	2
RMER30	2
(CCCCCA)n	2
(CAAA)n	2
U1	2
MER5B	2
(CTGGGG)n	2
(CGTG)n	2
(G)n	2
LSU-rRNA_H	2
MT2B	2
(C)n	2
A-rich	2
MTC	2
L2c	2
(TTTTG)n	2
URR1A	2
MER53	2

repClass count

Simple_repe	314
Low_comple	288
SINE	262
LTR	53
LINE	33
DNA	21
tRNA	9
snRNA	8
rRNA	2
Satellite	2
Unknown	1
srpRNA	1
scRNA	1
RNA	1

repFamily count

Simple_repe	314
Low_comple	288
Alu	135
B4	53
B2	41
MIR	25
ERVK	22
L1	16
L2	16
ERVL	14
MER1_type	12
MaLR	10
tRNA	9
snRNA	8
ID	8
ERV1	6
MER2_type	4
AcHobo	2
rRNA	2
hAT	2
Satellite	2
Y-chromoso	1
srpRNA	1
Tip100	1
scRNA	1
RTE	1
Gypsy?	1
RNA	1

chr1	135506651	135507052	.	.	.	.	.	.
chr1	135557827	135558228	.	.	.	.	.	.
chr1	136006569	136006970	chr1	136006546	136006592	G-rich	Low_comple	Low_complexity
chr1	136006569	136006970	chr1	136006701	136006745	(CA)n	Simple_repe	Simple_repeat
chr1	136006569	136006970	chr1	136006754	136006847	MLT1J1	LTR	MaLR
chr1	136006569	136006970	chr1	136006947	136006996	(TG)n	Simple_repe	Simple_repeat
chr1	136302323	136302724	.	.	.	.	.	.
chr1	136852430	136852831	.	.	.	.	.	.
chr1	137210179	137210580	chr1	137210553	137210679	B1_Mus1	SINE	Alu
chr1	137269891	137270292	.	.	.	.	.	.
chr1	137662520	137662921	.	.	.	.	.	.
chr1	138521296	138521697	chr1	138521597	138521623	(CGG)n	Simple_repe	Simple_repeat
chr1	138521296	138521697	chr1	138521640	138521762	(CGGGG)n	Simple_repe	Simple_repeat
chr1	138592413	138592814	.	.	.	.	.	.
chr1	140516147	140516548	.	.	.	.	.	.
chr1	145624161	145624562	chr1	145624159	145624208	(CCCCG)n	Simple_repe	Simple_repeat
chr1	151807919	151808320	.	.	.	.	.	.
chr1	152240147	152240548	.	.	.	.	.	.
chr1	153275378	153275779	.	.	.	.	.	.
chr1	153602005	153602406	.	.	.	.	.	.
chr1	155180156	155180557	.	.	.	.	.	.
chr1	157820237	157820638	chr1	157820327	157820360	(CGG)n	Simple_repe	Simple_repeat
chr1	157883016	157883417	.	.	.	.	.	.
chr1	157887793	157888194	.	.	.	.	.	.
chr1	162964762	162965163	.	.	.	.	.	.
chr1	163000818	163001219	.	.	.	.	.	.
chr1	163061471	163061872	.	.	.	.	.	.
chr1	163806958	163807359	.	.	.	.	.	.
chr1	163899140	163899541	.	.	.	.	.	.
chr1	164478512	164478913	.	.	.	.	.	.
chr1	165924728	165925129	.	.	.	.	.	.
chr1	166178649	166179050	.	.	.	.	.	.
chr1	166237347	166237748	.	.	.	.	.	.
chr1	167166909	167167310	.	.	.	.	.	.
chr1	169238671	169239072	.	.	.	.	.	.
chr1	172798590	172798991	chr1	172798919	172798958	(CACG)n	Simple_repe	Simple_repeat
chr1	172798590	172798991	chr1	172798958	172799016	(CATA)n	Simple_repe	Simple_repeat
chr1	173177154	173177555	.	.	.	.	.	.
chr1	173223476	173223877	chr1	173223430	173223857	RMER4A	LTR	ERVK
chr1	173258921	173259322	.	.	.	.	.	.
chr1	173433264	173433665	chr1	173433177	173433294	U5	snRNA	snRNA
chr1	174412013	174412414	.	.	.	.	.	.
chr1	177555719	177556120	.	.	.	.	.	.
chr1	177810459	177810860	.	.	.	.	.	.
chr1	178744725	178745126	.	.	.	.	.	.
chr1	179726767	179727168	.	.	.	.	.	.
chr1	180117336	180117737	.	.	.	.	.	.
chr1	181476233	181476634	.	.	.	.	.	.
chr1	181733828	181734229	.	.	.	.	.	.
chr1	182571273	182571674	chr1	182571306	182571405	GC_rich	Low_comple	Low_complexity
chr1	182655903	182656304	.	.	.	.	.	.
chr1	182945669	182946070	.	.	.	.	.	.
chr1	183074196	183074597	.	.	.	.	.	.
chr1	183080837	183081238	.	.	.	.	.	.
chr1	192735459	192735860	.	.	.	.	.	.
chr1	192752255	192752656	.	.	.	.	.	.
chr1	193149557	193149958	.	.	.	.	.	.
chr1	193645058	193645459	.	.	.	.	.	.
chr1	196957527	196957928	.	.	.	.	.	.
chr10	7382872	7383273	.	.	.	.	.	.
chr10	7400689	7401090	.	.	.	.	.	.
chr10	9621775	9622176	.	.	.	.	.	.
chr10	12727974	12728375	.	.	.	.	.	.
chr10	17954848	17955249	.	.	.	.	.	.
chr10	20031991	20032392	.	.	.	.	.	.
chr10	24589511	24589912	.	.	.	.	.	.
chr10	33670864	33671265	.	.	.	.	.	.
chr10	39966723	39967124	.	.	.	.	.	.
chr10	39978147	39978548	chr10	39978272	39978485	U3	snRNA	snRNA
chr10	40020388	40020789	.	.	.	.	.	.
chr10	40068830	40069231	.	.	.	.	.	.
chr10	40602974	40603375	.	.	.	.	.	.
chr10	41529274	41529675	.	.	.	.	.	.
chr10	42198187	42198588	.	.	.	.	.	.
chr10	42221611	42222012	.	.	.	.	.	.
chr10	45297417	45297818	.	.	.	.	.	.
chr10	57785592	57785993	.	.	.	.	.	.
chr10	59165122	59165523	.	.	.	.	.	.
chr10	59342513	59342914	.	.	.	.	.	.
chr10	59465721	59466122	.	.	.	.	.	.
chr10	60215167	60215568	.	.	.	.	.	.
chr10	62114006	62114407	chr10	62114372	62114400	(CCCCG)n	Simple_repe	Simple_repeat
chr10	62845370	62845771	chr10	62845746	62845808	B1_Mm	SINE	Alu
chr10	67011863	67012264	.	.	.	.	.	.
chr10	67375283	67375684	.	.	.	.	.	.
chr10	70700596	70700997	.	.	.	.	.	.
chr10	70747855	70748256	chr10	70748029	70748050	GC_rich	Low_comple	Low_complexity
chr10	72117427	72117828	.	.	.	.	.	.
chr10	74980553	74980954	.	.	.	.	.	.
chr10	75226913	75227314	chr10	75227280	75227336	T-rich	Low_comple	Low_complexity
chr10	76495793	76496194	.	.	.	.	.	.
chr10	76978377	76978778	.	.	.	.	.	.
chr10	77084855	77085256	chr10	77085207	77085252	(CGCGG)n	Simple_repe	Simple_repeat
chr10	78054647	78055048	chr10	78054638	78054719	GC_rich	Low_comple	Low_complexity
chr10	78054647	78055048	chr10	78054758	78054785	(T)n	Simple_repe	Simple_repeat

GSAT_MM	2
(CACCC)n	2
(CTCG)n	2
RMER2	2
Tigger7	2
(TGG)n	2
(TCCCG)n	1
L1MD3	1
L1MB2	1
(CATA)n	1
RMER4A	1
U5	1
U3	1
U6	1
tRNA-Asn-AA	1
(CTCGG)n	1
Lx5	1
CYRA11_Mm	1
(TCTA)n	1
RLTR24	1
L1ME3A	1
(GTTTG)n	1
MER74B	1
(TAAAAA)n	1
U2	1
MTE2b	1
RMER15	1
(CTAAT)n	1
ORR1E	1
7SLRNA	1
MER2B	1
MER81	1
(CGGGGG)n	1
ID4_	1
(GGAGAA)n	1
tRNA-Arg-CG	1
LTR33B	1
LTR33A	1
(CCCGG)n	1
RLTR6-int	1
MERVL-int	1
(CG)n	1
(TAGA)n	1
MER57D	1
MER54B	1
(GAAA)n	1
(TTA)n	1
(CAGCC)n	1
tRNA-Gly-GG	1
(CAAAAA)n	1
L1MC	1
RLTR42-int	1
(TCCA)n	1
MER5A	1
FordPrefect	1
(CTAA)n	1
(TGGGGG)n	1
RMER17C	1
ORR1C2	1
MLT1B	1
(TTGG)n	1
RCHARR1	1
(TGGG)n	1
L1MC3	1
(CATATA)n	1
BC1_Mm	1
(CCCCCT)n	1
Lx7	1
Lx	1
L4	1
tRNA-Arg-AG	1
(CAT)n	1
U7	1
(TCCC)n	1
LTR88b	1
(GGAA)n	1
(TTG)n	1
RLTR19	1
Lx2B	1
(TTTA)n	1
MT2A	1
(GGGGA)n	1
ORR1C1	1
tRNA-Arg-CG	1
(CAGA)n	1
tRNA-Leu-CT	1
MLT1J	1
RMER16-int	1
MMVL30-int	1
IAPEy-int	1
RLTR13D3	1
U13	1
MER63D	1
(GGGTG)n	1
(TTTTTG)n	1

chr10	79132388	79132789	.	.	.	.	.	.
chr10	79144503	79144904	.	.	.	.	.	.
chr10	79209182	79209583	.	.	.	.	.	.
chr10	79316943	79317344	.	.	.	.	.	.
chr10	79371405	79371806	chr10	79371566	79371601	GC_rich	Low_comple	Low_complexity
chr10	79422647	79423048	.	.	.	.	.	.
chr10	79447873	79448274	chr10	79448250	79448356	U6	snRNA	snRNA
chr10	79577769	79578170	chr10	79577720	79577880	RSINE1	SINE	B4
chr10	79604815	79605216	.	.	.	.	.	.
chr10	79635458	79635859	.	.	.	.	.	.
chr10	79711945	79712346	chr10	79711903	79711977	tRNA-Asn-AA	tRNA	tRNA
chr10	79727375	79727776	chr10	79727671	79727759	GC_rich	Low_comple	Low_complexity
chr10	79754954	79755355	chr10	79754967	79755028	(CAGAGA)n	Simple_repe	Simple_repeat
chr10	79861571	79861972	.	.	.	.	.	.
chr10	79896512	79896913	.	.	.	.	.	.
chr10	80024158	80024559	.	.	.	.	.	.
chr10	80041086	80041487	.	.	.	.	.	.
chr10	80065371	80065772	.	.	.	.	.	.
chr10	80261194	80261595	.	.	.	.	.	.
chr10	80363517	80363918	.	.	.	.	.	.
chr10	80380844	80381245	.	.	.	.	.	.
chr10	80599972	80600373	chr10	80599985	80600022	(A)n	Simple_repe	Simple_repeat
chr10	80641279	80641680	.	.	.	.	.	.
chr10	80730717	80731118	.	.	.	.	.	.
chr10	80814417	80814818	chr10	80814347	80814463	B2_Mm1t	SINE	B2
chr10	80814417	80814818	chr10	80814487	80814565	B3A	SINE	B2
chr10	80841340	80841741	.	.	.	.	.	.
chr10	80959016	80959417	.	.	.	.	.	.
chr10	81007872	81008273	chr10	81008121	81008211	(CTCGG)n	Simple_repe	Simple_repeat
chr10	81068844	81069245	.	.	.	.	.	.
chr10	81090064	81090465	.	.	.	.	.	.
chr10	82092299	82092700	chr10	82091960	82092318	Lx5	LINE	L1
chr10	82161680	82162081	.	.	.	.	.	.
chr10	83006427	83006828	.	.	.	.	.	.
chr10	83111334	83111735	.	.	.	.	.	.
chr10	83994985	83995386	.	.	.	.	.	.
chr10	84084853	84085254	.	.	.	.	.	.
chr10	84379758	84380159	chr10	84379732	84379788	(A)n	Simple_repe	Simple_repeat
chr10	86168586	86168987	.	.	.	.	.	.
chr10	87609555	87609956	.	.	.	.	.	.
chr10	87663635	87664036	chr10	87663582	87663655	(TCTCTG)n	Simple_repe	Simple_repeat
chr10	92915893	92916294	.	.	.	.	.	.
chr10	93052254	93052655	.	.	.	.	.	.
chr10	93352353	93352754	chr10	93352440	93352482	(GA)n	Simple_repe	Simple_repeat
chr10	93498367	93498768	.	.	.	.	.	.
chr10	94786575	94786976	chr10	94786858	94786912	CYRA11_Mm	Unknown	Y-chromosome
chr10	94786575	94786976	chr10	94786912	94787099	URR1B	DNA	MER1_type
chr10	94964398	94964799	.	.	.	.	.	.
chr10	94977513	94977914	chr10	94977909	94977933	GC_rich	Low_comple	Low_complexity
chr10	99949834	99950235	.	.	.	.	.	.
chr10	100051722	100052123	.	.	.	.	.	.
chr10	110446870	110447271	.	.	.	.	.	.
chr10	111409478	111409879	chr10	111409476	111409566	CT-rich	Low_comple	Low_complexity
chr10	114821686	114822087	.	.	.	.	.	.
chr10	116018378	116018779	.	.	.	.	.	.
chr10	116585367	116585768	.	.	.	.	.	.
chr10	117147115	117147516	chr10	117147313	117147336	GC_rich	Low_comple	Low_complexity
chr10	117147115	117147516	chr10	117147346	117147458	C-rich	Low_comple	Low_complexity
chr10	117229541	117229942	.	.	.	.	.	.
chr10	118677414	118677815	.	.	.	.	.	.
chr10	119645631	119646032	.	.	.	.	.	.
chr10	119663927	119664328	.	.	.	.	.	.
chr10	120335828	120336229	.	.	.	.	.	.
chr10	121063385	121063786	.	.	.	.	.	.
chr10	122513238	122513639	chr10	122513479	122513503	GC_rich	Low_comple	Low_complexity
chr10	122633815	122634216	chr10	122633847	122633868	GC_rich	Low_comple	Low_complexity
chr10	122633815	122634216	chr10	122633989	122634015	(CGG)n	Simple_repe	Simple_repeat
chr10	122633815	122634216	chr10	122634043	122634064	GC_rich	Low_comple	Low_complexity
chr10	126479946	126480347	.	.	.	.	.	.
chr10	126703113	126703514	.	.	.	.	.	.
chr10	126748584	126748985	.	.	.	.	.	.
chr10	126959357	126959758	chr10	126959716	126959740	(TTTG)n	Simple_repe	Simple_repeat
chr10	127452005	127452406	chr10	127451895	127452019	B1_Mus1	SINE	Alu
chr10	127472432	127472833	.	.	.	.	.	.
chr10	127495985	127496386	chr10	127496018	127496039	GC_rich	Low_comple	Low_complexity
chr10	127740498	127740899	.	.	.	.	.	.
chr10	127759120	127759521	chr10	127759208	127759236	(TTTG)n	Simple_repe	Simple_repeat
chr10	127805919	127806320	.	.	.	.	.	.
chr10	127935572	127935973	chr10	127935972	127936031	(CGGGG)n	Simple_repe	Simple_repeat
chr10	127984684	127985085	.	.	.	.	.	.
chr10	127986222	127986623	chr10	127986520	127986576	B1_Mur3	SINE	Alu
chr10	127986222	127986623	chr10	127986576	127986604	AT_rich	Low_comple	Low_complexity
chr10	128002923	128003324	chr10	128002988	128003049	(CGAG)n	Simple_repe	Simple_repeat
chr10	128063683	128064084	.	.	.	.	.	.
chr10	128133335	128133736	chr10	128133310	128133347	(TCC)n	Simple_repe	Simple_repeat
chr10	128242396	128242797	.	.	.	.	.	.
chr11	3023933	3024334	chr11	3024264	3024302	AT_rich	Low_comple	Low_complexity
chr11	3023933	3024334	chr11	3024318	3024351	(TCTA)n	Simple_repe	Simple_repeat
chr11	3188482	3188883	chr11	3188456	3188562	MIRc	SINE	MIR
chr11	3352143	3352544	.	.	.	.	.	.
chr11	3439222	3439623	.	.	.	.	.	.
chr11	3863540	3863941	chr11	3863564	3863679	B1_Mus2	SINE	Alu
chr11	3996566	3996967	.	.	.	.	.	.
chr11	4060472	4060873	.	.	.	.	.	.
chr11	4537674	4538075	.	.	.	.	.	.

L1ME2	1
MER82	1
Lx9	1
HAL1-3A_ME	1
LTR33C	1
L1MEe	1
(CTG)n	1
LTR16E1	1
7SK	1
(CCGCG)n	1
(CAGGC)n	1
Cheshire	1

chr11	4604383	4604784	.	.	.	.	.	.	
chr11	4795091	4795492	.	.	.	.	.	.	
chr11	5442055	5442456	chr11	5442392	5442524	ID_B1	SINE	B4	
chr11	5661918	5662319	.	.	.	.	.	.	
chr11	5759995	5760396	.	.	.	.	.	.	
chr11	5762690	5763091	.	.	.	.	.	.	
chr11	6100011	6100412	.	.	.	.	.	.	
chr11	6167646	6168047	.	.	.	.	.	.	
chr11	6288121	6288522	chr11	6287987	6288166	RMER30	DNA	MER1_type	
chr11	6288121	6288522	chr11	6288415	6288453	AT_rich	Low_comple	Low_complexity	
chr11	6288121	6288522	chr11	6288512	6288551	B2_Mm2	SINE	B2	
chr11	6446307	6446708	chr11	6446261	6446347	PB1D10	SINE	Alu	
chr11	11708446	11708847	.	.	.	.	.	.	
chr11	16851068	16851469	.	.	.	.	.	.	
chr11	17111676	17112077	.	.	.	.	.	.	
chr11	20012833	20013234	.	.	.	.	.	.	
chr11	20101091	20101492	.	.	.	.	.	.	
chr11	20641401	20641802	chr11	20641504	20641567	(CCG)n	Simple_repe	Simple_repeat	
chr11	20991031	20991432	chr11	20991391	20991443	(CAG)n	Simple_repe	Simple_repeat	
chr11	21138589	21138990	chr11	21138911	21139098	(CGG)n	Simple_repe	Simple_repeat	
chr11	21471714	21472115	.	.	.	.	.	.	
chr11	23566182	23566583	.	.	.	.	.	.	
chr11	23795056	23795457	.	.	.	.	.	.	
chr11	29071824	29072225	.	.	.	.	.	.	
chr11	29273394	29273795	chr11	29273466	29273495	GC_rich	Low_comple	Low_complexity	
chr11	29426215	29426616	.	.	.	.	.	.	
chr11	29447988	29448389	.	.	.	.	.	.	
chr11	29925985	29926386	.	.	.	.	.	.	
chr11	30854203	30854604	chr11	30854123	30854275	(GGA)n	Simple_repe	Simple_repeat	
chr11	30886213	30886614	.	.	.	.	.	.	
chr11	31571759	31572160	chr11	31571788	31571830	(CGG)n	Simple_repe	Simple_repeat	
chr11	32124838	32125239	.	.	.	.	.	.	
chr11	32432938	32433339	chr11	32433270	32433299	GC_rich	Low_comple	Low_complexity	
chr11	32542398	32542799	.	.	.	.	.	.	
chr11	35582767	35583168	chr11	35583108	35583131	(CGG)n	Simple_repe	Simple_repeat	
chr11	40547111	40547512	.	.	.	.	.	.	
chr11	40568766	40569167	chr11	40569035	40569086	T-rich	Low_comple	Low_complexity	
chr11	43247055	43247456	chr11	43246958	43247067	B2_Mm2	SINE	B2	
chr11	43247055	43247456	chr11	43247140	43247176	(A)n	Simple_repe	Simple_repeat	
chr11	43494874	43495275	chr11	43494860	43494956	L2a	LINE	L2	
chr11	43561370	43561771	.	.	.	.	.	.	
chr11	45665202	45665603	chr11	45665403	45665431	GC_rich	Low_comple	Low_complexity	
chr11	48613602	48614003	.	.	.	.	.	.	
chr11	48630545	48630946	.	.	.	.	.	.	
chr11	50139222	50139623	.	.	.	.	.	.	
chr11	50641068	50641469	chr11	50641433	50641527	B1F1	SINE	Alu	
chr11	50654928	50655329	.	.	.	.	.	.	
chr11	50700975	50701376	.	.	.	.	.	.	
chr11	50729485	50729886	.	.	.	.	.	.	
chr11	50744976	50745377	.	.	.	.	.	.	
chr11	50872530	50872931	chr11	50872509	50872539	(A)n	Simple_repe	Simple_repeat	
chr11	51502250	51502651	.	.	.	.	.	.	
chr11	51576964	51577365	chr11	51576888	51576999	B1_Mur4	SINE	Alu	
chr11	51780924	51781325	.	.	.	.	.	.	
chr11	51817537	51817938	chr11	51817597	51817630	(CCCCCA)n	Simple_repe	Simple_repeat	
chr11	53113954	53114355	.	.	.	.	.	.	
chr11	53137993	53138394	.	.	.	.	.	.	
chr11	53333014	53333415	chr11	53333320	53333374	GC_rich	Low_comple	Low_complexity	
chr11	53520698	53521099	chr11	53520979	53521073	PB1D7	SINE	Alu	
chr11	53914148	53914549	chr11	53914407	53914510	G-rich	Low_comple	Low_complexity	
chr11	54674062	54674463	.	.	.	.	.	.	
chr11	55282369	55282770	.	.	.	.	.	.	
chr11	57331959	57332360	.	.	.	.	.	.	
chr11	57917427	57917828	.	.	.	.	.	.	
chr11	57984910	57985311	chr11	57984562	57984932	RLTR24	LTR	ERV1	
chr11	58120327	58120728	.	.	.	.	.	.	
chr11	58752314	58752715	chr11	58752266	58752322	GC_rich	Low_comple	Low_complexity	
chr11	58752314	58752715	chr11	58752404	58752433	GC_rich	Low_comple	Low_complexity	
chr11	58791390	58791791	.	.	.	.	.	.	
chr11	58793197	58793598	chr11	58793485	58793678	B3A	SINE	B2	
chr11	59041577	59041978	.	.	.	.	.	.	
chr11	59285529	59285930	.	.	.	.	.	.	
chr11	60166622	60167023	.	.	.	.	.	.	
chr11	60230477	60230878	chr11	60230779	60230923	(TG)n	Simple_repe	Simple_repeat	
chr11	60267863	60268264	.	.	.	.	.	.	
chr11	60512923	60513324	chr11	60513151	60513192	GC_rich	Low_comple	Low_complexity	
chr11	60541698	60542099	.	.	.	.	.	.	
chr11	60590630	60591031	.	.	.	.	.	.	
chr11	60643883	60644284	chr11	60643856	60643973	PB1D10	SINE	Alu	
chr11	60692181	60692582	.	.	.	.	.	.	
chr11	61393559	61393960	chr11	61393606	61393693	L1ME3A	LINE	L1	
chr11	61743530	61743931	chr11	61743512	61743547	GC_rich	Low_comple	Low_complexity	
chr11	61743530	61743931	chr11	61743791	61743817	GC_rich	Low_comple	Low_complexity	
chr11	62363396	62363797	.	.	.	.	.	.	
chr11	62416064	62416465	chr11	62415948	62416069	PB1	SINE	Alu	
chr11	64792077	64792478	.	.	.	.	.	.	
chr11	64976286	64976687	.	.	.	.	.	.	
chr11	67346124	67346525	chr11	67346428	67346687	L2b	LINE	L2	
chr11	67399965	67400366	.	.	.	.	.	.	
chr11	68829373	68829774	chr11	68829392	68829492	B1F1	SINE	Alu	
chr11	69209371	69209772	.	.	.	.	.	.	
chr11	69392698	69393099	chr11	69393071	69393128	CT-rich	Low_comple	Low_complexity	
chr11	69572005	69572406	.	.	.	.	.	.	
chr11	69727254	69727655	.	.	.	.	.	.	
chr11	69733300	69733701	.	.	.	.	.	.	

chr11	69794006	69794407	.	.	.	.	.	.
chr11	69808971	69809372	chr11	69809281	69809308	(GGA)n	Simple_repe	Simple_repeat
chr11	69828746	69829147	.	.	.	.	.	.
chr11	70265158	70265559	chr11	70265205	70265262	PB1D9	SINE	Alu
chr11	70338592	70338993	.	.	.	.	.	.
chr11	70460309	70460710	.	.	.	.	.	.
chr11	70783746	70784147	.	.	.	.	.	.
chr11	70796350	70796751	.	.	.	.	.	.
chr11	70817860	70818261	.	.	.	.	.	.
chr11	70833141	70833542	.	.	.	.	.	.
chr11	72028363	72028764	.	.	.	.	.	.
chr11	72114846	72115247	.	.	.	.	.	.
chr11	72254634	72255035	.	.	.	.	.	.
chr11	72951663	72952064	.	.	.	.	.	.
chr11	72990300	72990701	.	.	.	.	.	.
chr11	73012391	73012792	.	.	.	.	.	.
chr11	74462742	74463143	.	.	.	.	.	.
chr11	75234695	75235096	.	.	.	.	.	.
chr11	75274596	75274997	.	.	.	.	.	.
chr11	75444099	75444500	.	.	.	.	.	.
chr11	75492534	75492935	.	.	.	.	.	.
chr11	75992954	75993355	.	.	.	.	.	.
chr11	76220265	76220666	.	.	.	.	.	.
chr11	76576944	76577345	.	.	.	.	.	.
chr11	76891736	76892137	.	.	.	.	.	.
chr11	77303414	77303815	chr11	77303394	77303424	GC_rich	Low_comple	Low_complexity
chr11	77303414	77303815	chr11	77303425	77303446	(CCG)n	Simple_repe	Simple_repeat
chr11	77499191	77499592	chr11	77499236	77499273	(CA)n	Simple_repe	Simple_repeat
chr11	77707198	77707599	.	.	.	.	.	.
chr11	77795127	77795528	.	.	.	.	.	.
chr11	77893663	77894064	.	.	.	.	.	.
chr11	77979694	77980095	.	.	.	.	.	.
chr11	77996955	77997356	chr11	77997256	77997279	(GTTTG)n	Simple_repe	Simple_repeat
chr11	77996955	77997356	chr11	77997326	77997382	B2_Mm2	SINE	B2
chr11	78325539	78325940	chr11	78325687	78325710	GC_rich	Low_comple	Low_complexity
chr11	78325539	78325940	chr11	78325739	78325779	GC_rich	Low_comple	Low_complexity
chr11	78349634	78350035	.	.	.	.	.	.
chr11	78959850	78960251	.	.	.	.	.	.
chr11	79806137	79806538	chr11	79806516	79806548	GC_rich	Low_comple	Low_complexity
chr11	80191230	80191631	chr11	80191298	80191341	GC_rich	Low_comple	Low_complexity
chr11	80196590	80196991	.	.	.	.	.	.
chr11	80241854	80242255	.	.	.	.	.	.
chr11	80623636	80624037	.	.	.	.	.	.
chr11	83105002	83105403	.	.	.	.	.	.
chr11	83390619	83391020	chr11	83390901	83391265	MER74B	LTR	ERVL
chr11	83566964	83567365	.	.	.	.	.	.
chr11	83755443	83755844	.	.	.	.	.	.
chr11	84693491	84693892	.	.	.	.	.	.
chr11	84729680	84730081	chr11	84730016	84730106	PB1D10	SINE	Alu
chr11	85165989	85166390	.	.	.	.	.	.
chr11	86497363	86497764	.	.	.	.	.	.
chr11	86570944	86571345	.	.	.	.	.	.
chr11	86620359	86620760	.	.	.	.	.	.
chr11	86900128	86900529	.	.	.	.	.	.
chr11	87239855	87240256	chr11	87239846	87239872	(CAAA)n	Simple_repe	Simple_repeat
chr11	87239855	87240256	chr11	87240217	87240381	U1	snRNA	snRNA
chr11	87550839	87551240	.	.	.	.	.	.
chr11	87801018	87801419	chr11	87801039	87801084	C-rich	Low_comple	Low_complexity
chr11	87801018	87801419	chr11	87801170	87801220	G-rich	Low_comple	Low_complexity
chr11	87860659	87861060	.	.	.	.	.	.
chr11	88017735	88018136	.	.	.	.	.	.
chr11	90499297	90499698	.	.	.	.	.	.
chr11	93829441	93829842	.	.	.	.	.	.
chr11	93856433	93856834	.	.	.	.	.	.
chr11	94183059	94183460	.	.	.	.	.	.
chr11	94410155	94410556	.	.	.	.	.	.
chr11	94490822	94491223	chr11	94491103	94491200	G-rich	Low_comple	Low_complexity
chr11	94514856	94515257	.	.	.	.	.	.
chr11	94850980	94851381	chr11	94851080	94851149	G-rich	Low_comple	Low_complexity
chr11	94902603	94903004	.	.	.	.	.	.
chr11	95171428	95171829	.	.	.	.	.	.
chr11	95245614	95246015	.	.	.	.	.	.
chr11	95527953	95528354	.	.	.	.	.	.
chr11	95718621	95719022	chr11	95718554	95718685	B1_Mus1	SINE	Alu
chr11	95718621	95719022	chr11	95718766	95718908	B4	SINE	B4
chr11	95895997	95896398	chr11	95896298	95896322	GC_rich	Low_comple	Low_complexity
chr11	95926511	95926912	chr11	95926475	95926594	(CCG)n	Simple_repe	Simple_repeat
chr11	95937164	95937565	.	.	.	.	.	.
chr11	96638667	96639068	.	.	.	.	.	.
chr11	96650184	96650585	chr11	96650131	96650230	PB1D10	SINE	Alu
chr11	96839126	96839527	.	.	.	.	.	.
chr11	96902671	96903072	chr11	96902814	96902848	(T)n	Simple_repe	Simple_repeat
chr11	97049527	97049928	.	.	.	.	.	.
chr11	97176985	97177386	.	.	.	.	.	.
chr11	97564387	97564788	.	.	.	.	.	.
chr11	97627813	97628214	.	.	.	.	.	.
chr11	97643504	97643905	.	.	.	.	.	.
chr11	97745314	97745715	chr11	97745326	97745363	(TAAAAA)n	Simple_repe	Simple_repeat
chr11	98261400	98261801	.	.	.	.	.	.
chr11	98299971	98300372	.	.	.	.	.	.
chr11	98448427	98448828	.	.	.	.	.	.
chr11	98543668	98544069	.	.	.	.	.	.
chr11	98590610	98591011	.	.	.	.	.	.
chr11	98636541	98636942	.	.	.	.	.	.
chr11	98670897	98671298	chr11	98671259	98671348	(CGG)n	Simple_repe	Simple_repeat

chr11	98724775	98725176	chr11	98724668	98724798	MER5B	DNA	MER1_type
chr11	98724775	98725176	chr11	98725014	98725099	(GA)n	Simple_repe	Simple_repeat
chr11	98768725	98769126	chr11	98768892	98768917	(A)n	Simple_repe	Simple_repeat
chr11	98821402	98821803	chr11	98821690	98821718	GC_rich	Low_comple	Low_complexity
chr11	98821402	98821803	chr11	98821794	98821829	GC_rich	Low_comple	Low_complexity
chr11	99092173	99092574	.	.	.	.	.	.
chr11	100259249	100259650	.	.	.	.	.	.
chr11	100302133	100302534	.	.	.	.	.	.
chr11	100333916	100334317	chr11	100333995	100334055	(CCG)n	Simple_repe	Simple_repeat
chr11	100389155	100389556	.	.	.	.	.	.
chr11	100483969	100484370	chr11	100483920	100483974	ID	SINE	ID
chr11	100483969	100484370	chr11	100483974	100483995	ID4	SINE	ID
chr11	100573608	100574009	chr11	100573554	100573657	(CTGGGG)n	Simple_repe	Simple_repeat
chr11	100599425	100599826	.	.	.	.	.	.
chr11	100800872	100801273	.	.	.	.	.	.
chr11	100870462	100870863	chr11	100870835	100870874	(CGG)n	Simple_repe	Simple_repeat
chr11	100943836	100944237	chr11	100943858	100943893	(CCCCG)n	Simple_repe	Simple_repeat
chr11	101114789	101115190	chr11	101114830	101114854	GC_rich	Low_comple	Low_complexity
chr11	101140103	101140504	.	.	.	.	.	.
chr11	101163425	101163826	chr11	101163805	101163844	(TTTG)n	Simple_repe	Simple_repeat
chr11	101177088	101177489	.	.	.	.	.	.
chr11	101303405	101303806	.	.	.	.	.	.
chr11	101326031	101326432	.	.	.	.	.	.
chr11	101413439	101413840	.	.	.	.	.	.
chr11	101488343	101488744	chr11	101488679	101488866	U2	snRNA	snRNA
chr11	101594057	101594458	.	.	.	.	.	.
chr11	102017469	102017870	.	.	.	.	.	.
chr11	102050709	102051110	chr11	102051063	102051086	GC_rich	Low_comple	Low_complexity
chr11	102146204	102146605	.	.	.	.	.	.
chr11	102156485	102156886	.	.	.	.	.	.
chr11	102292318	102292719	chr11	102292697	102292824	B1F	SINE	Alu
chr11	102292318	102292719	chr11	102292715	102292860	MT2B2	LTR	ERVL
chr11	102417506	102417907	.	.	.	.	.	.
chr11	102485520	102485921	.	.	.	.	.	.
chr11	102558819	102559220	.	.	.	.	.	.
chr11	102786652	102787053	chr11	102786745	102786871	B1_Mur1	SINE	Alu
chr11	102889595	102889996	.	.	.	.	.	.
chr11	102963960	102964361	.	.	.	.	.	.
chr11	102977252	102977653	chr11	102977579	102977666	GA-rich	Low_comple	Low_complexity
chr11	102994375	102994776	chr11	102994439	102994486	(T)n	Simple_repe	Simple_repeat
chr11	104304151	104304552	.	.	.	.	.	.
chr11	105897623	105898024	.	.	.	.	.	.
chr11	105927120	105927521	chr11	105927084	105927137	MIR3	SINE	MIR
chr11	105945611	105946012	.	.	.	.	.	.
chr11	106055242	106055643	.	.	.	.	.	.
chr11	106077550	106077951	chr11	106077675	106077703	GC_rich	Low_comple	Low_complexity
chr11	106117195	106117596	.	.	.	.	.	.
chr11	106134339	106134740	.	.	.	.	.	.
chr11	106362695	106363096	chr11	106363078	106363131	B1_Mus2	SINE	Alu
chr11	106577810	106578211	.	.	.	.	.	.
chr11	106640679	106641080	.	.	.	.	.	.
chr11	106649667	106650068	.	.	.	.	.	.
chr11	106860799	106861200	chr11	106861175	106861266	PB1D9	SINE	Alu
chr11	106993759	106994160	.	.	.	.	.	.
chr11	107050420	107050821	.	.	.	.	.	.
chr11	107330095	107330496	.	.	.	.	.	.
chr11	107340568	107340969	.	.	.	.	.	.
chr11	107409085	107409486	chr11	107409154	107409211	G-rich	Low_comple	Low_complexity
chr11	109287255	109287656	.	.	.	.	.	.
chr11	109582271	109582672	.	.	.	.	.	.
chr11	110260187	110260588	.	.	.	.	.	.
chr11	113063052	113063453	chr11	113063404	113063477	MTE2b	LTR	MaLR
chr11	113426952	113427353	.	.	.	.	.	.
chr11	113545272	113545673	.	.	.	.	.	.
chr11	113612730	113613131	.	.	.	.	.	.
chr11	114529615	114530016	chr11	114529486	114529632	B1_Mm	SINE	Alu
chr11	114529615	114530016	chr11	114529632	114529663	AT_rich	Low_comple	Low_complexity
chr11	115264852	115265253	chr11	115264774	115264860	PB1D10	SINE	Alu
chr11	115281164	115281565	chr11	115281443	115281478	GC_rich	Low_comple	Low_complexity
chr11	115353065	115353466	.	.	.	.	.	.
chr11	115397710	115398111	.	.	.	.	.	.
chr11	115425493	115425894	.	.	.	.	.	.
chr11	115474649	115475050	chr11	115474671	115475069	RMER15	LTR	ERVL
chr11	115489432	115489833	.	.	.	.	.	.
chr11	115626508	115626909	.	.	.	.	.	.
chr11	115675201	115675602	.	.	.	.	.	.
chr11	115794669	115795070	.	.	.	.	.	.
chr11	115872742	115873143	chr11	115872643	115872754	B1_Mur2	SINE	Alu
chr11	115891311	115891712	.	.	.	.	.	.
chr11	115948273	115948674	.	.	.	.	.	.
chr11	115970183	115970584	chr11	115970461	115970512	(TC)n	Simple_repe	Simple_repeat
chr11	115991809	115992210	.	.	.	.	.	.
chr11	116029379	116029780	.	.	.	.	.	.
chr11	116060477	116060878	.	.	.	.	.	.
chr11	116135282	116135683	chr11	116135334	116135396	(CCG)n	Simple_repe	Simple_repeat
chr11	116135282	116135683	chr11	116135650	116135769	B4A	SINE	B4
chr11	116167866	116168267	.	.	.	.	.	.
chr11	116351740	116352141	.	.	.	.	.	.
chr11	116453694	116454095	.	.	.	.	.	.
chr11	116519223	116519624	.	.	.	.	.	.
chr11	116532704	116533105	.	.	.	.	.	.
chr11	116704674	116705075	.	.	.	.	.	.
chr11	116714825	116715226	.	.	.	.	.	.
chr11	116937896	116938297	.	.	.	.	.	.
chr11	117192574	117192975	.	.	.	.	.	.

chr11	117515263	117515664	.	.	.	.	.	.	
chr11	117642010	117642411	chr11	117642395	117642469	MIR	SINE	MIR	
chr11	117710368	117710769	.	.	.	.	.	.	
chr11	117734633	117735034	.	.	.	.	.	.	
chr11	118280301	118280702	.	.	.	.	.	.	
chr11	119464105	119464506	.	.	.	.	.	.	
chr11	119960087	119960488	.	.	.	.	.	.	
chr11	120012344	120012745	.	.	.	.	.	.	
chr11	120575024	120575425	.	.	.	.	.	.	
chr11	120645379	120645780	chr11	120645376	120645415	(CAG)n	Simple_repe	Simple_repeat	
chr11	120645379	120645780	chr11	120645481	120645528	GC_rich	Low_comple	Low_complexity	
chr11	120645379	120645780	chr11	120645712	120645752	(CGGGG)n	Simple_repe	Simple_repeat	
chr11	120794039	120794440	.	.	.	.	.	.	
chr11	121313051	121313452	.	.	.	.	.	.	
chr12	3235127	3235528	.	.	.	.	.	.	
chr12	3364905	3365306	chr12	3365271	3365293	GC_rich	Low_comple	Low_complexity	
chr12	3427650	3428051	chr12	3427874	3428028	T-rich	Low_comple	Low_complexity	
chr12	4233806	4234207	.	.	.	.	.	.	
chr12	4849876	4850277	chr12	4849811	4849937	B1_Mus2	SINE	Alu	
chr12	8214707	8215108	.	.	.	.	.	.	
chr12	8680778	8681179	chr12	8680899	8680940	GC_rich	Low_comple	Low_complexity	
chr12	8680778	8681179	chr12	8681109	8681178	GA-rich	Low_comple	Low_complexity	
chr12	8980587	8980988	.	.	.	.	.	.	
chr12	9036647	9037048	chr12	9036582	9036684	(CTAAT)n	Simple_repe	Simple_repeat	
chr12	10397336	10397737	.	.	.	.	.	.	
chr12	11272176	11272577	.	.	.	.	.	.	
chr12	17551225	17551626	chr12	17551602	17551638	GC_rich	Low_comple	Low_complexity	
chr12	21379340	21379741	chr12	21379558	21379583	GC_rich	Low_comple	Low_complexity	
chr12	29320665	29321066	.	.	.	.	.	.	
chr12	31595680	31596081	chr12	31595901	31595998	ORR1E	LTR	MaLR	
chr12	32184542	32184943	.	.	.	.	.	.	
chr12	32635213	32635614	.	.	.	.	.	.	
chr12	40949738	40950139	.	.	.	.	.	.	
chr12	41172375	41172776	.	.	.	.	.	.	
chr12	52478358	52478759	.	.	.	.	.	.	
chr12	52792774	52793175	chr12	52792756	52792793	GC_rich	Low_comple	Low_complexity	
chr12	52792774	52793175	chr12	52792928	52792962	(GGA)n	Simple_repe	Simple_repeat	
chr12	55797406	55797807	chr12	55797768	55797933	U1	snRNA	snRNA	
chr12	55963509	55963910	chr12	55963858	55963901	(CGGG)n	Simple_repe	Simple_repeat	
chr12	56181240	56181641	.	.	.	.	.	.	
chr12	56404008	56404409	.	.	.	.	.	.	
chr12	56499596	56499997	.	.	.	.	.	.	
chr12	56594448	56594849	.	.	.	.	.	.	
chr12	56937001	56937402	.	.	.	.	.	.	
chr12	66066452	66066853	.	.	.	.	.	.	
chr12	66273604	66274005	.	.	.	.	.	.	
chr12	70259947	70260348	chr12	70260281	70260581	7SLRNA	srpRNA	srpRNA	
chr12	70269623	70270024	.	.	.	.	.	.	
chr12	70397406	70397807	chr12	70397710	70397738	GC_rich	Low_comple	Low_complexity	
chr12	71087869	71088270	chr12	71087769	71087892	(CCG)n	Simple_repe	Simple_repeat	
chr12	71087869	71088270	chr12	71088114	71088142	GC_rich	Low_comple	Low_complexity	
chr12	72931800	72932201	.	.	.	.	.	.	
chr12	73636806	73637207	.	.	.	.	.	.	
chr12	73765770	73766171	.	.	.	.	.	.	
chr12	75065343	75065744	chr12	75065217	75065355	B1_Mur1	SINE	Alu	
chr12	76770863	76771264	.	.	.	.	.	.	
chr12	77470215	77470616	chr12	77470608	77470656	(CGTG)n	Simple_repe	Simple_repeat	
chr12	77938516	77938917	.	.	.	.	.	.	
chr12	78063170	78063571	.	.	.	.	.	.	
chr12	80273482	80273883	.	.	.	.	.	.	
chr12	80292687	80293088	.	.	.	.	.	.	
chr12	80309643	80310044	chr12	80309572	80309692	PB1	SINE	Alu	
chr12	80398042	80398443	.	.	.	.	.	.	
chr12	81362256	81362657	chr12	81362627	81362777	MER2B	DNA	MER2_type	
chr12	81744719	81745120	.	.	.	.	.	.	
chr12	81891231	81891632	.	.	.	.	.	.	
chr12	82633732	82634133	chr12	82634132	82634180	(TG)n	Simple_repe	Simple_repeat	
chr12	82695790	82696191	.	.	.	.	.	.	
chr12	84938075	84938476	.	.	.	.	.	.	
chr12	84972943	84973344	.	.	.	.	.	.	
chr12	85291381	85291782	chr12	85291242	85291395	B1_Mur2	SINE	Alu	
chr12	85702698	85703099	.	.	.	.	.	.	
chr12	86311648	86312049	chr12	86312001	86312031	(TTTG)n	Simple_repe	Simple_repeat	
chr12	86560266	86560667	.	.	.	.	.	.	
chr12	86621337	86621738	.	.	.	.	.	.	
chr12	86680159	86680560	.	.	.	.	.	.	
chr12	86715713	86716114	.	.	.	.	.	.	
chr12	87165649	87166050	.	.	.	.	.	.	
chr12	88488442	88488843	.	.	.	.	.	.	
chr12	88607153	88607554	.	.	.	.	.	.	
chr12	88784620	88785021	.	.	.	.	.	.	
chr12	88813108	88813509	.	.	.	.	.	.	
chr12	89598740	89599141	.	.	.	.	.	.	
chr12	92622728	92623129	.	.	.	.	.	.	
chr12	93087650	93088051	.	.	.	.	.	.	
chr12	101397692	101398093	.	.	.	.	.	.	
chr12	102017113	102017514	chr12	102016991	102017116	MER5B	DNA	MER1_type	
chr12	103151183	103151584	.	.	.	.	.	.	
chr12	103995836	103996237	.	.	.	.	.	.	
chr12	104663904	104664305	.	.	.	.	.	.	
chr12	105990185	105990586	.	.	.	.	.	.	
chr12	106270322	106270723	.	.	.	.	.	.	
chr12	107022645	107023046	chr12	107022777	107022805	(G)n	Simple_repe	Simple_repeat	
chr12	107248157	107248558	.	.	.	.	.	.	
chr12	110132268	110132669	.	.	.	.	.	.	

chr12	111839316	111839717	chr12	111839618	111839651	GC_rich	Low_comple	Low_complexity
chr12	112127247	112127648	.	.	.	.	.	.
chr12	112775974	112776375	.	.	.	.	.	.
chr12	112916088	112916489	.	.	.	.	.	.
chr12	112951242	112951643	chr12	112951367	112951392	GC_rich	Low_comple	Low_complexity
chr12	112996866	112997267	chr12	112997069	112997090	GC_rich	Low_comple	Low_complexity
chr12	113205047	113205448	chr12	113205386	113205476	MER81	DNA	AcHobo
chr12	114067643	114068044	chr12	114067738	114067761	GC_rich	Low_comple	Low_complexity
chr12	117285633	117286034	.	.	.	.	.	.
chr12	117501310	117501711	.	.	.	.	.	.
chr12	119540348	119540749	.	.	.	.	.	.
chr13	3610370	3610771	.	.	.	.	.	.
chr13	3633040	3633441	.	.	.	.	.	.
chr13	8870149	8870550	.	.	.	.	.	.
chr13	12350343	12350744	.	.	.	.	.	.
chr13	12657873	12658274	.	.	.	.	.	.
chr13	14046512	14046913	.	.	.	.	.	.
chr13	14131776	14132177	chr13	14132065	14132123	B1F	SINE	Alu
chr13	14155606	14156007	chr13	14155979	14156049	G-rich	Low_comple	Low_complexity
chr13	14705233	14705634	.	.	.	.	.	.
chr13	18035867	18036268	chr13	18035951	18035986	(CGG)n	Simple_repe	Simple_repeat
chr13	18035867	18036268	chr13	18036066	18036096	GC_rich	Low_comple	Low_complexity
chr13	18085006	18085407	.	.	.	.	.	.
chr13	18808927	18809328	.	.	.	.	.	.
chr13	22036622	22037023	chr13	22036550	22036632	ID_B1	SINE	B4
chr13	23523157	23523558	chr13	23523153	23523188	(CCCCCA)n	Simple_repe	Simple_repeat
chr13	23523157	23523558	chr13	23523280	23523353	tRNA-Ala-GC	tRNA	tRNA
chr13	23831507	23831908	.	.	.	.	.	.
chr13	31065788	31066189	chr13	31066090	31066263	GA-rich	Low_comple	Low_complexity
chr13	32893629	32894030	.	.	.	.	.	.
chr13	34056524	34056925	.	.	.	.	.	.
chr13	35997698	35998099	.	.	.	.	.	.
chr13	38296557	38296958	.	.	.	.	.	.
chr13	41344891	41345292	.	.	.	.	.	.
chr13	43493546	43493947	chr13	43493555	43493580	(A)n	Simple_repe	Simple_repeat
chr13	44825888	44826289	chr13	44825883	44825925	GC_rich	Low_comple	Low_complexity
chr13	46823263	46823664	chr13	46823247	46823304	(CCG)n	Simple_repe	Simple_repeat
chr13	47025667	47026068	.	.	.	.	.	.
chr13	48608683	48609084	.	.	.	.	.	.
chr13	49436612	49437013	chr13	49436936	49436982	(CGG)n	Simple_repe	Simple_repeat
chr13	49748318	49748719	.	.	.	.	.	.
chr13	49777209	49777610	.	.	.	.	.	.
chr13	51741226	51741627	.	.	.	.	.	.
chr13	54570094	54570495	chr13	54570382	54570532	B1_Mus1	SINE	Alu
chr13	54666561	54666962	.	.	.	.	.	.
chr13	54676158	54676559	chr13	54676124	54676203	MIRm	SINE	MIR
chr13	54691271	54691672	.	.	.	.	.	.
chr13	54795733	54796134	.	.	.	.	.	.
chr13	55464100	55464501	.	.	.	.	.	.
chr13	55637776	55638177	.	.	.	.	.	.
chr13	55672349	55672750	chr13	55672389	55672437	(CCG)n	Simple_repe	Simple_repeat
chr13	55694248	55694649	.	.	.	.	.	.
chr13	55701149	55701550	chr13	55701405	55701427	GC_rich	Low_comple	Low_complexity
chr13	56236681	56237082	chr13	56236750	56236834	(CCCG)n	Simple_repe	Simple_repeat
chr13	56236681	56237082	chr13	56237043	56237067	GC_rich	Low_comple	Low_complexity
chr13	58316864	58317265	.	.	.	.	.	.
chr13	59686277	59686678	.	.	.	.	.	.
chr13	59871090	59871491	.	.	.	.	.	.
chr13	62568028	62568429	.	.	.	.	.	.
chr13	63532860	63533261	.	.	.	.	.	.
chr13	65379891	65380292	.	.	.	.	.	.
chr13	67006043	67006444	.	.	.	.	.	.
chr13	67161949	67162350	.	.	.	.	.	.
chr13	67182304	67182705	.	.	.	.	.	.
chr13	67228929	67229330	.	.	.	.	.	.
chr13	67273812	67274213	.	.	.	.	.	.
chr13	67295187	67295588	.	.	.	.	.	.
chr13	67369904	67370305	.	.	.	.	.	.
chr13	67379298	67379699	.	.	.	.	.	.
chr13	67407231	67407632	.	.	.	.	.	.
chr13	67433359	67433760	.	.	.	.	.	.
chr13	67461376	67461777	.	.	.	.	.	.
chr13	67476573	67476974	.	.	.	.	.	.
chr13	67500562	67500963	.	.	.	.	.	.
chr13	67552377	67552778	.	.	.	.	.	.
chr13	67585008	67585409	.	.	.	.	.	.
chr13	67601283	67601684	.	.	.	.	.	.
chr13	67626967	67627368	.	.	.	.	.	.
chr13	67653908	67654309	.	.	.	.	.	.
chr13	67710444	67710845	chr13	67710807	67710954	B1_Mus1	SINE	Alu
chr13	67738537	67738938	.	.	.	.	.	.
chr13	67784287	67784688	.	.	.	.	.	.
chr13	67829909	67830310	.	.	.	.	.	.
chr13	67855962	67856363	.	.	.	.	.	.
chr13	67880407	67880808	chr13	67880375	67880498	B1_Mus1	SINE	Alu
chr13	67880407	67880808	chr13	67880498	67880575	B4	SINE	B4
chr13	67914490	67914891	.	.	.	.	.	.
chr13	70776872	70777273	.	.	.	.	.	.
chr13	73465693	73466094	.	.	.	.	.	.
chr13	73741222	73741623	chr13	73741564	73741588	GC_rich	Low_comple	Low_complexity
chr13	74075059	74075460	.	.	.	.	.	.
chr13	76235910	76236311	.	.	.	.	.	.
chr13	77274578	77274979	.	.	.	.	.	.
chr13	86186260	86186661	.	.	.	.	.	.
chr13	91062384	91062785	.	.	.	.	.	.

chr13	93614507	93614908	.	.	.	.	.	.	
chr13	93962179	93962580	.	.	.	.	.	.	
chr13	96145205	96145606	.	.	.	.	.	.	
chr13	97312255	97312656	chr13	97312586	97312692	GA-rich	Low_comple	Low_complexity	
chr13	97907707	97908108	.	.	.	.	.	.	
chr13	100894580	100894981	chr13	100894535	100894609	PB1D10	SINE	Alu	
chr13	101603133	101603534	.	.	.	.	.	.	
chr13	104968364	104968765	.	.	.	.	.	.	
chr13	107726810	107727211	.	.	.	.	.	.	
chr13	107736925	107737326	.	.	.	.	.	.	
chr13	111070238	111070639	.	.	.	.	.	.	
chr13	113450683	113451084	.	.	.	.	.	.	
chr13	113717420	113717821	.	.	.	.	.	.	
chr13	119175837	119176238	.	.	.	.	.	.	
chr13	120276390	120276791	chr13	120276694	120276750	B2_Mm2	SINE	B2	
chr14	8930404	8930805	chr14	8930698	8930823	(CGG)n	Simple_repe	Simple_repeat	
chr14	14793587	14793988	chr14	14793722	14793743	GC_rich	Low_comple	Low_complexity	
chr14	14793587	14793988	chr14	14793850	14793975	GC_rich	Low_comple	Low_complexity	
chr14	19103381	19103782	.	.	.	.	.	.	
chr14	21113633	21114034	chr14	21113522	21113658	B4A	SINE	B4	
chr14	21365605	21366006	chr14	21365609	21365632	(CGGGGG)n	Simple_repe	Simple_repeat	
chr14	21365605	21366006	chr14	21365632	21365660	GC_rich	Low_comple	Low_complexity	
chr14	21522082	21522483	.	.	.	.	.	.	
chr14	21526273	21526674	.	.	.	.	.	.	
chr14	22569557	22569958	.	.	.	.	.	.	
chr14	25063566	25063967	.	.	.	.	.	.	
chr14	26513437	26513838	.	.	.	.	.	.	
chr14	26587034	26587435	.	.	.	.	.	.	
chr14	27354334	27354735	.	.	.	.	.	.	
chr14	27457265	27457666	.	.	.	.	.	.	
chr14	28435271	28435672	chr14	28435594	28435695	(CCCCG)n	Simple_repe	Simple_repeat	
chr14	30781281	30781682	.	.	.	.	.	.	
chr14	30791320	30791721	chr14	30791342	30791422	ID4_	SINE	ID	
chr14	30791320	30791721	chr14	30791423	30791470	(A)n	Simple_repe	Simple_repeat	
chr14	30791320	30791721	chr14	30791677	30791717	(GGAGAA)n	Simple_repe	Simple_repeat	
chr14	31292508	31292909	.	.	.	.	.	.	
chr14	31764344	31764745	.	.	.	.	.	.	
chr14	31814327	31814728	.	.	.	.	.	.	
chr14	32454327	32454728	.	.	.	.	.	.	
chr14	35486767	35487168	chr14	35486994	35487029	GC_rich	Low_comple	Low_complexity	
chr14	45949353	45949754	chr14	45949424	45949472	C-rich	Low_comple	Low_complexity	
chr14	47407810	47408211	.	.	.	.	.	.	
chr14	48187896	48188297	.	.	.	.	.	.	
chr14	51427311	51427712	.	.	.	.	.	.	
chr14	52504343	52504744	.	.	.	.	.	.	
chr14	52639197	52639598	.	.	.	.	.	.	
chr14	52816730	52817131	.	.	.	.	.	.	
chr14	55136252	55136653	chr14	55136532	55136605	tRNA-Arg-CG	tRNA	tRNA	
chr14	55272298	55272699	.	.	.	.	.	.	
chr14	55305595	55305996	.	.	.	.	.	.	
chr14	55711084	55711485	chr14	55711148	55711177	(TCC)n	Simple_repe	Simple_repeat	
chr14	55713421	55713822	.	.	.	.	.	.	
chr14	56290799	56291200	.	.	.	.	.	.	
chr14	57190574	57190975	.	.	.	.	.	.	
chr14	57286590	57286991	chr14	57286543	57286633	RSINE1	SINE	B4	
chr14	57397255	57397656	.	.	.	.	.	.	
chr14	58042646	58043047	.	.	.	.	.	.	
chr14	58283571	58283972	.	.	.	.	.	.	
chr14	60870170	60870571	.	.	.	.	.	.	
chr14	60883694	60884095	.	.	.	.	.	.	
chr14	62058754	62059155	chr14	62058737	62058759	GC_rich	Low_comple	Low_complexity	
chr14	63378523	63378924	chr14	63378866	63378995	G-rich	Low_comple	Low_complexity	
chr14	63455888	63456289	.	.	.	.	.	.	
chr14	65271059	65271460	chr14	65271120	65271186	GA-rich	Low_comple	Low_complexity	
chr14	65568577	65568978	.	.	.	.	.	.	
chr14	66452824	66453225	.	.	.	.	.	.	
chr14	70689158	70689559	chr14	70689155	70689211	GC_rich	Low_comple	Low_complexity	
chr14	71167272	71167673	chr14	71167396	71167593	LTR33B	LTR	ERVL	
chr14	76154203	76154604	chr14	76154329	76154357	GC_rich	Low_comple	Low_complexity	
chr14	76244723	76245124	.	.	.	.	.	.	
chr14	79797408	79797809	.	.	.	.	.	.	
chr14	79825995	79826396	chr14	79825892	79826033	B1_Mur2	SINE	Alu	
chr14	79851342	79851743	.	.	.	.	.	.	
chr14	79987278	79987679	.	.	.	.	.	.	
chr14	99498903	99499304	.	.	.	.	.	.	
chr14	105576370	105576771	.	.	.	.	.	.	
chr14	120876494	120876895	.	.	.	.	.	.	
chr15	3945720	3946121	.	.	.	.	.	.	
chr15	5066416	5066817	.	.	.	.	.	.	
chr15	5135346	5135747	.	.	.	.	.	.	
chr15	8049009	8049410	.	.	.	.	.	.	
chr15	8059081	8059482	chr15	8059106	8059186	C-rich	Low_comple	Low_complexity	
chr15	9069984	9070385	chr15	9070264	9070289	(GGA)n	Simple_repe	Simple_repeat	
chr15	10415547	10415948	.	.	.	.	.	.	
chr15	10929563	10929964	chr15	10929657	10929688	(TTTG)n	Simple_repe	Simple_repeat	
chr15	10929563	10929964	chr15	10929689	10929809	LTR33A	LTR	ERVL	
chr15	10929563	10929964	chr15	10929853	10929940	L2b	LINE	L2	
chr15	12047339	12047740	.	.	.	.	.	.	
chr15	12754277	12754678	.	.	.	.	.	.	
chr15	25913852	25914253	.	.	.	.	.	.	
chr15	27560271	27560672	chr15	27560265	27560306	GC_rich	Low_comple	Low_complexity	
chr15	34372798	34373199	.	.	.	.	.	.	
chr15	34424815	34425216	.	.	.	.	.	.	
chr15	36539140	36539541	.	.	.	.	.	.	
chr15	38763986	38764387	chr15	38764060	38764156	MIRb	SINE	MIR	

chr15	43308678	43309079	.	.	.	.	.	.
chr15	43701453	43701854	chr15	43701601	43701629	(CGGGG)n	Simple_repe	Simple_repeat
chr15	44259324	44259725	.	.	.	.	.	.
chr15	44450889	44451290	.	.	.	.	.	.
chr15	51708771	51709172	.	.	.	.	.	.
chr15	52543683	52544084	.	.	.	.	.	.
chr15	54903527	54903928	.	.	.	.	.	.
chr15	55388687	55389088	.	.	.	.	.	.
chr15	57723437	57723838	.	.	.	.	.	.
chr15	57743365	57743766	.	.	.	.	.	.
chr15	57865726	57866127	.	.	.	.	.	.
chr15	57907621	57908022	.	.	.	.	.	.
chr15	57966506	57966907	.	.	.	.	.	.
chr15	58765156	58765557	.	.	.	.	.	.
chr15	59479991	59480392	chr15	59480158	59480192	(GGA)n	Simple_repe	Simple_repeat
chr15	61870554	61870955	chr15	61870587	61870684	(TG)n	Simple_repe	Simple_repeat
chr15	66722667	66723068	.	.	.	.	.	.
chr15	68090336	68090737	.	.	.	.	.	.
chr15	72920652	72921053	.	.	.	.	.	.
chr15	75760083	75760484	.	.	.	.	.	.
chr15	75771168	75771569	.	.	.	.	.	.
chr15	75799459	75799860	.	.	.	.	.	.
chr15	75900053	75900454	.	.	.	.	.	.
chr15	75911204	75911605	.	.	.	.	.	.
chr15	76027068	76027469	.	.	.	.	.	.
chr15	76157606	76158007	.	.	.	.	.	.
chr15	76161509	76161910	.	.	.	.	.	.
chr15	76173759	76174160	.	.	.	.	.	.
chr15	76181984	76182385	.	.	.	.	.	.
chr15	76199062	76199463	.	.	.	.	.	.
chr15	76211292	76211693	.	.	.	.	.	.
chr15	76342297	76342698	.	.	.	.	.	.
chr15	76353553	76353954	.	.	.	.	.	.
chr15	76369008	76369409	.	.	.	.	.	.
chr15	76437766	76438167	chr15	76438159	76438299	B1_Mus2	SINE	Alu
chr15	76456314	76456715	.	.	.	.	.	.
chr15	76470279	76470680	chr15	76470639	76470659	(T)n	Simple_repe	Simple_repeat
chr15	76470279	76470680	chr15	76470665	76470811	B1_Mus2	SINE	Alu
chr15	76501815	76502216	chr15	76501873	76501894	AT_rich	Low_comple	Low_complexity
chr15	76531703	76532104	.	.	.	.	.	.
chr15	76540863	76541264	.	.	.	.	.	.
chr15	76734236	76734637	.	.	.	.	.	.
chr15	77801312	77801713	chr15	77801345	77801365	(A)n	Simple_repe	Simple_repeat
chr15	78236190	78236591	.	.	.	.	.	.
chr15	78258843	78259244	chr15	78259143	78259171	GC_rich	Low_comple	Low_complexity
chr15	78765161	78765562	.	.	.	.	.	.
chr15	78777893	78778294	chr15	78777800	78777974	ID_B1	SINE	B4
chr15	78905396	78905797	chr15	78905291	78905414	B1F	SINE	Alu
chr15	78971552	78971953	.	.	.	.	.	.
chr15	79059391	79059792	.	.	.	.	.	.
chr15	79377133	79377534	.	.	.	.	.	.
chr15	79501073	79501474	.	.	.	.	.	.
chr15	79722655	79723056	.	.	.	.	.	.
chr15	79913685	79914086	.	.	.	.	.	.
chr15	79963380	79963781	.	.	.	.	.	.
chr15	80064319	80064720	.	.	.	.	.	.
chr15	80085490	80085891	.	.	.	.	.	.
chr15	80807981	80808382	.	.	.	.	.	.
chr15	81022633	81023034	.	.	.	.	.	.
chr15	81191059	81191460	.	.	.	.	.	.
chr15	81494041	81494442	chr15	81494002	81494147	B1_Mus2	SINE	Alu
chr15	81560355	81560756	.	.	.	.	.	.
chr15	81642066	81642467	chr15	81642210	81642234	GC_rich	Low_comple	Low_complexity
chr15	81702156	81702557	.	.	.	.	.	.
chr15	81812610	81813011	.	.	.	.	.	.
chr15	82952965	82953366	chr15	82953334	82953432	B3	SINE	B2
chr15	82979689	82980090	.	.	.	.	.	.
chr15	83386111	83386512	.	.	.	.	.	.
chr15	83425487	83425888	chr15	83425830	83425859	AT_rich	Low_comple	Low_complexity
chr15	83425487	83425888	chr15	83425859	83426047	B3	SINE	B2
chr15	84022431	84022832	.	.	.	.	.	.
chr15	85689862	85690263	.	.	.	.	.	.
chr15	86044906	86045307	.	.	.	.	.	.
chr15	88692608	88693009	chr15	88692590	88692611	GC_rich	Low_comple	Low_complexity
chr15	88906159	88906560	chr15	88906394	88906428	GC_rich	Low_comple	Low_complexity
chr15	88906159	88906560	chr15	88906451	88906526	(CCCGG)n	Simple_repe	Simple_repeat
chr15	88919262	88919663	.	.	.	.	.	.
chr15	90054518	90054919	chr15	90054845	90054868	(CCCG)n	Simple_repe	Simple_repeat
chr15	96012731	96013132	chr15	96012887	96013026	RLTR15	LTR	ERVK
chr15	96012731	96013132	chr15	96013063	96013275	RLTR15	LTR	ERVK
chr15	96291305	96291706	chr15	96291344	96291368	(CGGG)n	Simple_repe	Simple_repeat
chr15	96473185	96473586	.	.	.	.	.	.
chr15	97536053	97536454	chr15	97536086	97536130	GC_rich	Low_comple	Low_complexity
chr15	97923684	97924085	.	.	.	.	.	.
chr15	97975888	97976289	.	.	.	.	.	.
chr15	98398060	98398461	.	.	.	.	.	.
chr15	98493206	98493607	.	.	.	.	.	.
chr15	98702495	98702896	.	.	.	.	.	.
chr15	98711437	98711838	.	.	.	.	.	.
chr15	98861068	98861469	.	.	.	.	.	.
chr15	98904889	98905290	.	.	.	.	.	.
chr15	99082178	99082579	.	.	.	.	.	.
chr15	99223025	99223426	.	.	.	.	.	.
chr15	99532281	99532682	chr15	99532640	99532661	GC_rich	Low_comple	Low_complexity
chr15	99532281	99532682	chr15	99532679	99532704	GC_rich	Low_comple	Low_complexity

chr15	99555810	99556211	.	.	.	.	.	.
chr15	99802988	99803389	.	.	.	.	.	.
chr15	100253229	100253630	.	.	.	.	.	.
chr15	100299330	100299731	chr15	100299418	100299453	GC_rich	Low_comple	Low_complexity
chr15	100325586	100325987	.	.	.	.	.	.
chr15	101114190	101114591	.	.	.	.	.	.
chr15	101198863	101199264	chr15	101198906	101198960	(TCTG)n	Simple_repe	Simple_repeat
chr15	101198863	101199264	chr15	101198991	101199103	MIRb	SINE	MIR
chr15	101903882	101904283	chr15	101904239	101904260	GC_rich	Low_comple	Low_complexity
chr15	101975743	101976144	.	.	.	.	.	.
chr15	102061009	102061410	chr15	102060970	102061120	B3	SINE	B2
chr15	102126437	102126838	.	.	.	.	.	.
chr15	102161923	102162324	.	.	.	.	.	.
chr15	102180996	102181397	.	.	.	.	.	.
chr15	102236157	102236558	.	.	.	.	.	.
chr15	102300663	102301064	chr15	102301018	102301073	(CCCG)n	Simple_repe	Simple_repeat
chr15	102348923	102349324	.	.	.	.	.	.
chr15	102552450	102552851	.	.	.	.	.	.
chr15	102993599	102994000	.	.	.	.	.	.
chr15	103070354	103070755	.	.	.	.	.	.
chr16	3743485	3743886	.	.	.	.	.	.
chr16	3846910	3847311	.	.	.	.	.	.
chr16	3884397	3884798	.	.	.	.	.	.
chr16	3908445	3908846	.	.	.	.	.	.
chr16	4558466	4558867	.	.	.	.	.	.
chr16	4683631	4684032	.	.	.	.	.	.
chr16	4789772	4790173	.	.	.	.	.	.
chr16	4879686	4880087	.	.	.	.	.	.
chr16	4964121	4964522	.	.	.	.	.	.
chr16	5049772	5050173	.	.	.	.	.	.
chr16	8637538	8637939	.	.	.	.	.	.
chr16	10447323	10447724	chr16	10447717	10447742	(CAAA)n	Simple_repe	Simple_repeat
chr16	10545212	10545613	.	.	.	.	.	.
chr16	11008268	11008669	chr16	11008189	11008332	B1F	SINE	Alu
chr16	11203248	11203649	.	.	.	.	.	.
chr16	11254286	11254687	.	.	.	.	.	.
chr16	11322719	11323120	chr16	11322627	11322755	ID_B1	SINE	B4
chr16	11322719	11323120	chr16	11322681	11322768	PB1D10	SINE	Alu
chr16	11322719	11323120	chr16	11322954	11322984	GC_rich	Low_comple	Low_complexity
chr16	11322719	11323120	chr16	11323006	11323083	(CGG)n	Simple_repe	Simple_repeat
chr16	13819037	13819438	chr16	13819375	13819413	(CGGGG)n	Simple_repe	Simple_repeat
chr16	14159497	14159898	chr16	14159425	14159614	CT-rich	Low_comple	Low_complexity
chr16	14360973	14361374	chr16	14360843	14360986	B1_Mus1	SINE	Alu
chr16	14360973	14361374	chr16	14360991	14361092	ID_B1	SINE	B4
chr16	14360973	14361374	chr16	14361261	14361329	MIR	SINE	MIR
chr16	16302849	16303250	.	.	.	.	.	.
chr16	16358945	16359346	.	.	.	.	.	.
chr16	16870630	16871031	.	.	.	.	.	.
chr16	17111182	17111583	.	.	.	.	.	.
chr16	17201411	17201812	chr16	17201671	17201835	L2a	LINE	L2
chr16	17508830	17509231	.	.	.	.	.	.
chr16	17722818	17723219	chr16	17723095	17723197	GA-rich	Low_comple	Low_complexity
chr16	17722818	17723219	chr16	17723181	17723307	(CAGAGA)n	Simple_repe	Simple_repeat
chr16	17911271	17911672	.	.	.	.	.	.
chr16	17928823	17929224	.	.	.	.	.	.
chr16	18248718	18249119	.	.	.	.	.	.
chr16	18289397	18289798	chr16	18289538	18289559	GC_rich	Low_comple	Low_complexity
chr16	18498623	18499024	.	.	.	.	.	.
chr16	18811940	18812341	.	.	.	.	.	.
chr16	20097358	20097759	.	.	.	.	.	.
chr16	20302292	20302693	chr16	20302467	20302490	(A)n	Simple_repe	Simple_repeat
chr16	20426328	20426729	.	.	.	.	.	.
chr16	20498678	20499079	chr16	20499037	20499066	GC_rich	Low_comple	Low_complexity
chr16	20535212	20535613	.	.	.	.	.	.
chr16	20651523	20651924	.	.	.	.	.	.
chr16	23107263	23107664	.	.	.	.	.	.
chr16	23127600	23128001	.	.	.	.	.	.
chr16	29579208	29579609	.	.	.	.	.	.
chr16	30587720	30588121	.	.	.	.	.	.
chr16	31948368	31948769	.	.	.	.	.	.
chr16	32003091	32003492	.	.	.	.	.	.
chr16	32079333	32079734	chr16	32079431	32079461	GC_rich	Low_comple	Low_complexity
chr16	32079333	32079734	chr16	32079723	32079827	B1_Mur4	SINE	Alu
chr16	32419694	32420095	.	.	.	.	.	.
chr16	32430623	32431024	.	.	.	.	.	.
chr16	32868271	32868672	.	.	.	.	.	.
chr16	32877599	32878000	.	.	.	.	.	.
chr16	33056309	33056710	.	.	.	.	.	.
chr16	33380630	33381031	chr16	33380912	33380967	(GGA)n	Simple_repe	Simple_repeat
chr16	35363769	35364170	.	.	.	.	.	.
chr16	35490812	35491213	.	.	.	.	.	.
chr16	35938345	35938746	chr16	35938442	35938509	ID4	SINE	ID
chr16	35981622	35982023	chr16	35981667	35981748	LSU-rRNA_H	rRNA	rRNA
chr16	35981622	35982023	chr16	35981743	35981907	LSU-rRNA_H	rRNA	rRNA
chr16	35981622	35982023	chr16	35981909	35982195	RLTR6-int	LTR	ERV1
chr16	35983129	35983530	chr16	35983379	35983400	GC_rich	Low_comple	Low_complexity
chr16	36040987	36041388	chr16	36040848	36041009	B3	SINE	B2
chr16	37011602	37012003	.	.	.	.	.	.
chr16	37539956	37540357	chr16	37540243	37540425	MERVL-int	LTR	ERVL
chr16	43889749	43890150	.	.	.	.	.	.
chr16	44724492	44724893	.	.	.	.	.	.
chr16	44746326	44746727	.	.	.	.	.	.
chr16	45742787	45743188	chr16	45743144	45743167	GC_rich	Low_comple	Low_complexity
chr16	55934509	55934910	.	.	.	.	.	.
chr16	55966259	55966660	.	.	.	.	.	.

chr16	56037723	56038124	.	.	.	.	.	.
chr16	57121604	57122005	chr16	57121933	57121962	GC_rich	Low_comple	Low_complexity
chr16	57231502	57231903	.	.	.	.	.	.
chr16	58670196	58670597	.	.	.	.	.	.
chr16	58727776	58728177	.	.	.	.	.	.
chr16	59639014	59639415	.	.	.	.	.	.
chr16	75766924	75767325	chr16	75767320	75767349	(A)n	Simple_repe	Simple_repeat
chr16	84834980	84835381	.	.	.	.	.	.
chr16	87454991	87455392	.	.	.	.	.	.
chr16	87495900	87496301	chr16	87495884	87495906	GC_rich	Low_comple	Low_complexity
chr16	90284549	90284950	chr16	90284762	90284822	(CCCCG)n	Simple_repe	Simple_repeat
chr16	90727385	90727786	.	.	.	.	.	.
chr16	90935195	90935596	.	.	.	.	.	.
chr16	91619095	91619496	chr16	91619484	91619561	B1_Mus1	SINE	Alu
chr16	91647906	91648307	.	.	.	.	.	.
chr16	91728793	91729194	.	.	.	.	.	.
chr16	91931731	91932132	.	.	.	.	.	.
chr16	92301299	92301700	.	.	.	.	.	.
chr16	94748085	94748486	chr16	94748188	94748210	(CG)n	Simple_repe	Simple_repeat
chr16	96349461	96349862	chr16	96349491	96349550	GC_rich	Low_comple	Low_complexity
chr16	96413669	96414070	.	.	.	.	.	.
chr16	98073266	98073667	chr16	98073243	98073325	GC_rich	Low_comple	Low_complexity
chr17	3082536	3082937	.	.	.	.	.	.
chr17	3083753	3084154	chr17	3083745	3083784	(TAGA)n	Simple_repe	Simple_repeat
chr17	3083753	3084154	chr17	3083794	3083831	AT_rich	Low_comple	Low_complexity
chr17	3557708	3558109	chr17	3558105	3558394	MER57D	LTR	ERV1
chr17	5440070	5440471	.	.	.	.	.	.
chr17	5491311	5491712	chr17	5491240	5491400	MIRb	SINE	MIR
chr17	11032977	11033378	.	.	.	.	.	.
chr17	13109097	13109498	.	.	.	.	.	.
chr17	13185256	13185657	.	.	.	.	.	.
chr17	13200536	13200937	.	.	.	.	.	.
chr17	15079977	15080378	.	.	.	.	.	.
chr17	17511325	17511726	.	.	.	.	.	.
chr17	17965422	17965823	chr17	17965785	17965841	CT-rich	Low_comple	Low_complexity
chr17	21145711	21146112	.	.	.	.	.	.
chr17	21560257	21560658	chr17	21560354	21560409	L2	LINE	L2
chr17	21587305	21587706	.	.	.	.	.	.
chr17	21870535	21870936	.	.	.	.	.	.
chr17	23700994	23701395	.	.	.	.	.	.
chr17	23810335	23810736	.	.	.	.	.	.
chr17	23939824	23940225	.	.	.	.	.	.
chr17	23966007	23966408	chr17	23966003	23966160	(CCCCG)n	Simple_repe	Simple_repeat
chr17	23966007	23966408	chr17	23966361	23966537	B3	SINE	B2
chr17	24210339	24210740	.	.	.	.	.	.
chr17	24615869	24616270	.	.	.	.	.	.
chr17	24664654	24665055	.	.	.	.	.	.
chr17	24769402	24769803	.	.	.	.	.	.
chr17	24861227	24861628	.	.	.	.	.	.
chr17	25031822	25032223	.	.	.	.	.	.
chr17	25252691	25253092	.	.	.	.	.	.
chr17	25270096	25270497	.	.	.	.	.	.
chr17	25321279	25321680	.	.	.	.	.	.
chr17	25716181	25716582	.	.	.	.	.	.
chr17	25892989	25893390	chr17	25893356	25893871	MER54B	LTR	ERVL
chr17	25910479	25910880	.	.	.	.	.	.
chr17	25929214	25929615	.	.	.	.	.	.
chr17	25960327	25960728	chr17	25960376	25960410	(CAAAA)n	Simple_repe	Simple_repeat
chr17	25965776	25966177	chr17	25965827	25965862	(TG)n	Simple_repe	Simple_repeat
chr17	25998289	25998690	.	.	.	.	.	.
chr17	26012217	26012618	.	.	.	.	.	.
chr17	26078743	26079144	.	.	.	.	.	.
chr17	26227261	26227662	.	.	.	.	.	.
chr17	26275125	26275526	.	.	.	.	.	.
chr17	26389608	26390009	chr17	26389590	26389619	AT_rich	Low_comple	Low_complexity
chr17	26852155	26852556	.	.	.	.	.	.
chr17	27053615	27054016	.	.	.	.	.	.
chr17	27957691	27958092	.	.	.	.	.	.
chr17	27976796	27977197	chr17	27976667	27976860	URR1B	DNA	MER1_type
chr17	29089189	29089590	chr17	29089332	29089363	GC_rich	Low_comple	Low_complexity
chr17	29215793	29216194	chr17	29215781	29215817	(GAAA)n	Simple_repe	Simple_repeat
chr17	29227692	29228093	.	.	.	.	.	.
chr17	29405643	29406044	chr17	29405617	29405649	(TTA)n	Simple_repe	Simple_repeat
chr17	29405643	29406044	chr17	29405738	29405760	GC_rich	Low_comple	Low_complexity
chr17	29405643	29406044	chr17	29405957	29406022	GC_rich	Low_comple	Low_complexity
chr17	30749469	30749870	chr17	30749744	30749764	(A)n	Simple_repe	Simple_repeat
chr17	32457964	32458365	.	.	.	.	.	.
chr17	32487543	32487944	.	.	.	.	.	.
chr17	33084175	33084576	.	.	.	.	.	.
chr17	33226169	33226570	chr17	33226157	33226191	(G)n	Simple_repe	Simple_repeat
chr17	33918071	33918472	.	.	.	.	.	.
chr17	33961311	33961712	.	.	.	.	.	.
chr17	34027642	34028043	.	.	.	.	.	.
chr17	34046110	34046511	.	.	.	.	.	.
chr17	34066167	34066568	.	.	.	.	.	.
chr17	34077104	34077505	.	.	.	.	.	.
chr17	34088268	34088669	.	.	.	.	.	.
chr17	34092579	34092980	.	.	.	.	.	.
chr17	34168769	34169170	chr17	34169044	34169097	(CGG)n	Simple_repe	Simple_repeat
chr17	34740463	34740864	chr17	34740462	34740516	(CA)n	Simple_repe	Simple_repeat
chr17	34783752	34784153	.	.	.	.	.	.
chr17	35034511	35034912	.	.	.	.	.	.
chr17	35258119	35258520	.	.	.	.	.	.
chr17	35271673	35272074	.	.	.	.	.	.
chr17	35301693	35302094	.	.	.	.	.	.

chr17	35372616	35373017	chr17	35372937	35373020	B1_Mur3	SINE	Alu
chr17	35810519	35810920	.	.	.	.	.	.
chr17	35975161	35975562	.	.	.	.	.	.
chr17	35997961	35998362	.	.	.	.	.	.
chr17	36016474	36016875	chr17	36016295	36016475	B3	SINE	B2
chr17	36046663	36047064	.	.	.	.	.	.
chr17	36053594	36053995	.	.	.	.	.	.
chr17	36116114	36116515	.	.	.	.	.	.
chr17	36394635	36395036	.	.	.	.	.	.
chr17	37088456	37088857	.	.	.	.	.	.
chr17	37095351	37095752	.	.	.	.	.	.
chr17	41071183	41071584	chr17	41071296	41071321	(CAAAA)n	Simple_repe	Simple_repeat
chr17	43803951	43804352	chr17	43804274	43804294	(CAGCC)n	Simple_repe	Simple_repeat
chr17	43803951	43804352	chr17	43804307	43804338	(T)n	Simple_repe	Simple_repeat
chr17	45643597	45643998	.	.	.	.	.	.
chr17	45710646	45711047	.	.	.	.	.	.
chr17	45733495	45733896	.	.	.	.	.	.
chr17	46247741	46248142	.	.	.	.	.	.
chr17	46290273	46290674	.	.	.	.	.	.
chr17	46297649	46298050	chr17	46298018	46298089	(CGG)n	Simple_repe	Simple_repeat
chr17	46419757	46420158	.	.	.	.	.	.
chr17	46817721	46818122	.	.	.	.	.	.
chr17	46848175	46848576	.	.	.	.	.	.
chr17	46909537	46909938	.	.	.	.	.	.
chr17	47147356	47147757	.	.	.	.	.	.
chr17	47505628	47506029	chr17	47505653	47505698	(TAAA)n	Simple_repe	Simple_repeat
chr17	47505628	47506029	chr17	47505699	47505728	AT_rich	Low_comple	Low_complexity
chr17	47639045	47639446	.	.	.	.	.	.
chr17	47831846	47832247	chr17	47832110	47832247	(CGGGG)n	Simple_repe	Simple_repeat
chr17	47873727	47874128	.	.	.	.	.	.
chr17	48549329	48549730	.	.	.	.	.	.
chr17	49567423	49567824	chr17	49567400	49567444	MT2B	LTR	ERVL
chr17	49754221	49754622	.	.	.	.	.	.
chr17	56098259	56098660	chr17	56098198	56098337	B1_Mur2	SINE	Alu
chr17	56218241	56218642	.	.	.	.	.	.
chr17	56220521	56220922	.	.	.	.	.	.
chr17	56358173	56358574	chr17	56358009	56358178	(CGCGG)n	Simple_repe	Simple_repeat
chr17	56358173	56358574	chr17	56358556	56358617	tRNA-Gly-GG	tRNA	tRNA
chr17	56395913	56396314	.	.	.	.	.	.
chr17	56416261	56416662	chr17	56416482	56416590	PB1D7	SINE	Alu
chr17	56464942	56465343	.	.	.	.	.	.
chr17	56723768	56724169	chr17	56724100	56724123	(C)n	Simple_repe	Simple_repeat
chr17	56749063	56749464	.	.	.	.	.	.
chr17	56752595	56752996	chr17	56752416	56752609	B2_Mm2	SINE	B2
chr17	56766147	56766548	.	.	.	.	.	.
chr17	56812527	56812928	chr17	56812764	56812787	GC_rich	Low_comple	Low_complexity
chr17	56812527	56812928	chr17	56812842	56812886	GC_rich	Low_comple	Low_complexity
chr17	56856991	56857392	.	.	.	.	.	.
chr17	56904328	56904729	.	.	.	.	.	.
chr17	57129498	57129899	.	.	.	.	.	.
chr17	57150691	57151092	.	.	.	.	.	.
chr17	57170735	57171136	chr17	57170670	57170798	GC_rich	Low_comple	Low_complexity
chr17	57387194	57387595	.	.	.	.	.	.
chr17	59152562	59152963	chr17	59152947	59152975	(T)n	Simple_repe	Simple_repeat
chr17	63232183	63232584	chr17	63232546	63232590	C-rich	Low_comple	Low_complexity
chr17	65963067	65963468	.	.	.	.	.	.
chr17	66234155	66234556	.	.	.	.	.	.
chr17	66450792	66451193	chr17	66450868	66450916	GC_rich	Low_comple	Low_complexity
chr17	66868990	66869391	chr17	66868981	66869007	(CCG)n	Simple_repe	Simple_repeat
chr17	71876012	71876413	.	.	.	.	.	.
chr17	71947963	71948364	.	.	.	.	.	.
chr17	74888617	74889018	.	.	.	.	.	.
chr17	74927546	74927947	chr17	74927934	74927970	GC_rich	Low_comple	Low_complexity
chr17	75116907	75117308	.	.	.	.	.	.
chr17	79135824	79136225	chr17	79135950	79135975	GC_rich	Low_comple	Low_complexity
chr17	79281706	79282107	.	.	.	.	.	.
chr17	79315810	79316211	.	.	.	.	.	.
chr17	79336193	79336594	.	.	.	.	.	.
chr17	79420089	79420490	chr17	79420175	79420225	GC_rich	Low_comple	Low_complexity
chr17	80014626	80015027	.	.	.	.	.	.
chr17	80526584	80526985	chr17	80526505	80526665	(GA)n	Simple_repe	Simple_repeat
chr17	80606635	80607036	.	.	.	.	.	.
chr17	80623567	80623968	.	.	.	.	.	.
chr17	80689341	80689742	.	.	.	.	.	.
chr17	83751704	83752105	.	.	.	.	.	.
chr17	85025556	85025957	chr17	85025606	85025627	(CAAAAA)n	Simple_repe	Simple_repeat
chr17	85190009	85190410	.	.	.	.	.	.
chr17	85489735	85490136	.	.	.	.	.	.
chr17	87361573	87361974	.	.	.	.	.	.
chr17	95148806	95149207	.	.	.	.	.	.
chr17	95233977	95234378	.	.	.	.	.	.
chr18	4375365	4375766	.	.	.	.	.	.
chr18	5334550	5334951	chr18	5334830	5334851	GC_rich	Low_comple	Low_complexity
chr18	6490642	6491043	chr18	6490904	6490958	GC_rich	Low_comple	Low_complexity
chr18	6490642	6491043	chr18	6490971	6491042	(CCCG)n	Simple_repe	Simple_repeat
chr18	13130501	13130902	.	.	.	.	.	.
chr18	21054678	21055079	.	.	.	.	.	.
chr18	24147932	24148333	.	.	.	.	.	.
chr18	24178712	24179113	.	.	.	.	.	.
chr18	24280268	24280669	chr18	24280541	24280588	B4A	SINE	B4
chr18	24280268	24280669	chr18	24280588	24280738	B1F2	SINE	Alu
chr18	25327053	25327454	chr18	25327131	25327154	(CGG)n	Simple_repe	Simple_repeat
chr18	31793703	31794104	.	.	.	.	.	.
chr18	31919045	31919446	.	.	.	.	.	.
chr18	32227113	32227514	.	.	.	.	.	.

chr18	32996672	32997073	.	.	.	.	.	.	
chr18	33954297	33954698	.	.	.	.	.	.	
chr18	34784066	34784467	.	.	.	.	.	.	
chr18	34918539	34918940	.	.	.	.	.	.	
chr18	35658330	35658731	.	.	.	.	.	.	
chr18	35721665	35722066	.	.	.	.	.	.	
chr18	35862596	35862997	.	.	.	.	.	.	
chr18	35930850	35931251	chr18	35931196	35931234	GC_rich	Low_comple	Low_complexity	
chr18	36839027	36839428	.	.	.	.	.	.	
chr18	36894876	36895277	.	.	.	.	.	.	
chr18	36904142	36904543	.	.	.	.	.	.	
chr18	36942668	36943069	.	.	.	.	.	.	
chr18	36953276	36953677	.	.	.	.	.	.	
chr18	40378859	40379260	chr18	40378890	40378915	(CGG)n	Simple_repe	Simple_repeat	
chr18	42421671	42422072	.	.	.	.	.	.	
chr18	42670733	42671134	.	.	.	.	.	.	
chr18	43554446	43554847	chr18	43554759	43554790	(TCTCTG)n	Simple_repe	Simple_repeat	
chr18	46440317	46440718	.	.	.	.	.	.	
chr18	46757061	46757462	.	.	.	.	.	.	
chr18	49991765	49992166	chr18	49991931	49991955	GC_rich	Low_comple	Low_complexity	
chr18	50287638	50288039	.	.	.	.	.	.	
chr18	60720191	60720592	.	.	.	.	.	.	
chr18	60934055	60934456	.	.	.	.	.	.	
chr18	61008426	61008827	chr18	61008765	61008788	(A)n	Simple_repe	Simple_repeat	
chr18	61336508	61336909	.	.	.	.	.	.	
chr18	61714734	61715135	.	.	.	.	.	.	
chr18	63137300	63137701	.	.	.	.	.	.	
chr18	63851857	63852258	.	.	.	.	.	.	
chr18	64676046	64676447	.	.	.	.	.	.	
chr18	65959891	65960292	.	.	.	.	.	.	
chr18	66162086	66162487	.	.	.	.	.	.	
chr18	68459724	68460125	.	.	.	.	.	.	
chr18	70631996	70632397	.	.	.	.	.	.	
chr18	70690156	70690557	chr18	70690140	70690165	(TTTC)n	Simple_repe	Simple_repeat	
chr18	70690156	70690557	chr18	70690170	70690375	B3A	SINE	B2	
chr18	75159930	75160331	chr18	75159992	75160015	AT_rich	Low_comple	Low_complexity	
chr18	75178158	75178559	.	.	.	.	.	.	
chr18	75857192	75857593	chr18	75857212	75857266	(GGGA)n	Simple_repe	Simple_repeat	
chr18	77182647	77183048	.	.	.	.	.	.	
chr18	78006392	78006793	.	.	.	.	.	.	
chr18	78012485	78012886	chr18	78012607	78012648	A-rich	Low_comple	Low_complexity	
chr18	80666566	80666967	.	.	.	.	.	.	
chr18	85120776	85121177	.	.	.	.	.	.	
chr18	89141083	89141484	.	.	.	.	.	.	
chr19	3282796	3283197	.	.	.	.	.	.	
chr19	3576117	3576518	chr19	3576262	3576335	tRNA-Ala-GC	tRNA	tRNA	
chr19	3912270	3912671	chr19	3912241	3912397	MIR	SINE	MIR	
chr19	4012635	4013036	.	.	.	.	.	.	
chr19	4125706	4126107	chr19	4125686	4125725	C-rich	Low_comple	Low_complexity	
chr19	4148363	4148764	chr19	4148265	4148378	PB1D9	SINE	Alu	
chr19	4163199	4163600	.	.	.	.	.	.	
chr19	4201401	4201802	.	.	.	.	.	.	
chr19	4213469	4213870	.	.	.	.	.	.	
chr19	4615716	4616117	chr19	4615797	4615857	(CCCCG)n	Simple_repe	Simple_repeat	
chr19	4793706	4794107	.	.	.	.	.	.	
chr19	4877852	4878253	chr19	4878088	4878170	MIR	SINE	MIR	
chr19	4961918	4962319	.	.	.	.	.	.	
chr19	5024201	5024602	.	.	.	.	.	.	
chr19	5041126	5041527	.	.	.	.	.	.	
chr19	5050497	5050898	.	.	.	.	.	.	
chr19	5088432	5088833	.	.	.	.	.	.	
chr19	5106901	5107302	.	.	.	.	.	.	
chr19	5118092	5118493	.	.	.	.	.	.	
chr19	5295368	5295769	.	.	.	.	.	.	
chr19	5366720	5367121	.	.	.	.	.	.	
chr19	5388538	5388939	.	.	.	.	.	.	
chr19	5408312	5408713	chr19	5408353	5408498	B1_Mur4	SINE	Alu	
chr19	5408312	5408713	chr19	5408530	5408632	L2	LINE	L2	
chr19	5460410	5460811	.	.	.	.	.	.	
chr19	5490248	5490649	.	.	.	.	.	.	
chr19	5601625	5602026	chr19	5601689	5601746	ID_B1	SINE	B4	
chr19	5688816	5689217	.	.	.	.	.	.	
chr19	5724598	5724999	chr19	5724904	5724992	MIRc	SINE	MIR	
chr19	5731636	5732037	.	.	.	.	.	.	
chr19	6077074	6077475	.	.	.	.	.	.	
chr19	6084778	6085179	.	.	.	.	.	.	
chr19	6118334	6118735	.	.	.	.	.	.	
chr19	6127818	6128219	.	.	.	.	.	.	
chr19	6141046	6141447	.	.	.	.	.	.	
chr19	6236113	6236514	.	.	.	.	.	.	
chr19	6334761	6335162	.	.	.	.	.	.	
chr19	6341558	6341959	.	.	.	.	.	.	
chr19	6984384	6984785	.	.	.	.	.	.	
chr19	7016099	7016500	.	.	.	.	.	.	
chr19	7048715	7049116	.	.	.	.	.	.	
chr19	7114793	7115194	.	.	.	.	.	.	
chr19	7131026	7131427	.	.	.	.	.	.	
chr19	7280576	7280977	.	.	.	.	.	.	
chr19	7291920	7292321	.	.	.	.	.	.	
chr19	7491847	7492248	chr19	7492160	7492253	GC_rich	Low_comple	Low_complexity	
chr19	7568544	7568945	.	.	.	.	.	.	
chr19	8797705	8798106	chr19	8798026	8798069	T-rich	Low_comple	Low_complexity	
chr19	8797705	8798106	chr19	8798069	8798217	B1_Mm	SINE	Alu	
chr19	8810137	8810538	chr19	8810021	8810156	B1_Mur4	SINE	Alu	
chr19	8810137	8810538	chr19	8810168	8810213	GA-rich	Low_comple	Low_complexity	

chr19	8872822	8873223	chr19	8873146	8873210	B1_Mus2	SINE	Alu
chr19	8872822	8873223	chr19	8873213	8873270	A-rich	Low_comple	Low_complexity
chr19	8893356	8893757	.	.	.	.	.	.
chr19	8924837	8925238	chr19	8924772	8924872	PB1D10	SINE	Alu
chr19	8967240	8967641	chr19	8967124	8967271	B1_Mus1	SINE	Alu
chr19	8994619	8995020	chr19	8994946	8995005	GC_rich	Low_comple	Low_complexity
chr19	9003803	9004204	chr19	9004103	9004132	GC_rich	Low_comple	Low_complexity
chr19	9028073	9028474	.	.	.	.	.	.
chr19	9974138	9974539	.	.	.	.	.	.
chr19	10278347	10278748	.	.	.	.	.	.
chr19	10630058	10630459	.	.	.	.	.	.
chr19	10651667	10652068	.	.	.	.	.	.
chr19	10679826	10680227	.	.	.	.	.	.
chr19	10969433	10969834	chr19	10969553	10969573	(A)n	Simple_repe	Simple_repeat
chr19	11023565	11023966	.	.	.	.	.	.
chr19	11844564	11844965	.	.	.	.	.	.
chr19	12576506	12576907	chr19	12576488	12576554	(CA)n	Simple_repe	Simple_repeat
chr19	12870512	12870913	.	.	.	.	.	.
chr19	14672448	14672849	.	.	.	.	.	.
chr19	18787413	18787814	.	.	.	.	.	.
chr19	21727108	21727509	.	.	.	.	.	.
chr19	23348124	23348525	chr19	23348501	23348649	(TG)n	Simple_repe	Simple_repeat
chr19	23761637	23762038	chr19	23761869	23761891	GC_rich	Low_comple	Low_complexity
chr19	27504319	27504720	.	.	.	.	.	.
chr19	29064691	29065092	.	.	.	.	.	.
chr19	29175705	29176106	.	.	.	.	.	.
chr19	31157257	31157658	.	.	.	.	.	.
chr19	32284995	32285396	.	.	.	.	.	.
chr19	32786628	32787029	.	.	.	.	.	.
chr19	34624926	34625327	.	.	.	.	.	.
chr19	34996633	34997034	.	.	.	.	.	.
chr19	36157970	36158371	.	.	.	.	.	.
chr19	36908377	36908778	.	.	.	.	.	.
chr19	36993184	36993585	.	.	.	.	.	.
chr19	37281772	37282173	chr19	37281879	37281928	GC_rich	Low_comple	Low_complexity
chr19	37336843	37337244	chr19	37337192	37337204	B4A	SINE	B4
chr19	37336843	37337244	chr19	37337204	37337347	B1F	SINE	Alu
chr19	37338957	37339358	chr19	37338868	37339291	L1MC	LINE	L1
chr19	37450595	37450996	.	.	.	.	.	.
chr19	40686555	40686956	.	.	.	.	.	.
chr19	41876528	41876929	.	.	.	.	.	.
chr19	42007684	42008085	.	.	.	.	.	.
chr19	42593044	42593445	.	.	.	.	.	.
chr19	43749281	43749682	chr19	43749285	43749316	(CCG)n	Simple_repe	Simple_repeat
chr19	43827288	43827689	.	.	.	.	.	.
chr19	44183447	44183848	chr19	44183545	44183901	RLTR15	LTR	ERVK
chr19	44209919	44210320	.	.	.	.	.	.
chr19	44367994	44368395	.	.	.	.	.	.
chr19	44406282	44406683	chr19	44406533	44406653	MIRb	SINE	MIR
chr19	44629829	44630230	.	.	.	.	.	.
chr19	44637073	44637474	.	.	.	.	.	.
chr19	45005876	45006277	.	.	.	.	.	.
chr19	45080766	45081167	.	.	.	.	.	.
chr19	45122630	45123031	.	.	.	.	.	.
chr19	45437877	45438278	.	.	.	.	.	.
chr19	45634850	45635251	.	.	.	.	.	.
chr19	45858010	45858411	.	.	.	.	.	.
chr19	46072938	46073339	chr19	46073251	46073349	MTC	LTR	MaLR
chr19	46118818	46119219	.	.	.	.	.	.
chr19	46130749	46131150	.	.	.	.	.	.
chr19	46150182	46150583	.	.	.	.	.	.
chr19	46226799	46227200	.	.	.	.	.	.
chr19	46402811	46403212	.	.	.	.	.	.
chr19	46413007	46413408	.	.	.	.	.	.
chr19	46470121	46470522	.	.	.	.	.	.
chr19	46673163	46673564	chr19	46673557	46673708	GA-rich	Low_comple	Low_complexity
chr19	46764453	46764854	.	.	.	.	.	.
chr19	47125229	47125630	chr19	47125181	47125240	G-rich	Low_comple	Low_complexity
chr19	47251614	47252015	chr19	47251712	47251759	(TC)n	Simple_repe	Simple_repeat
chr19	47251614	47252015	chr19	47251759	47251784	(TG)n	Simple_repe	Simple_repeat
chr19	47251614	47252015	chr19	47251938	47251961	(CTGGGG)n	Simple_repe	Simple_repeat
chr19	53403590	53403991	chr19	53403962	53404062	GC_rich	Low_comple	Low_complexity
chr19	53465066	53465467	chr19	53465404	53465521	B1_Mur1	SINE	Alu
chr19	54018782	54019183	.	.	.	.	.	.
chr19	57434941	57435342	chr19	57435336	57435450	(CCCCG)n	Simple_repe	Simple_repeat
chr19	57527181	57527582	.	.	.	.	.	.
chr19	60019405	60019806	chr19	60019506	60019531	GC_rich	Low_comple	Low_complexity
chr19	60965840	60966241	chr19	60966180	60966298	G-rich	Low_comple	Low_complexity
chr2	3429893	3430294	.	.	.	.	.	.
chr2	4802718	4803119	chr2	4802788	4802808	(T)n	Simple_repe	Simple_repeat
chr2	4802718	4803119	chr2	4803105	4803147	(CCG)n	Simple_repe	Simple_repeat
chr2	5766030	5766431	.	.	.	.	.	.
chr2	6134201	6134602	.	.	.	.	.	.
chr2	11524724	11525125	.	.	.	.	.	.
chr2	11699189	11699590	.	.	.	.	.	.
chr2	13995487	13995888	.	.	.	.	.	.
chr2	17977929	17978330	.	.	.	.	.	.
chr2	22750791	22751192	.	.	.	.	.	.
chr2	22895659	22896060	chr2	22895716	22895770	CT-rich	Low_comple	Low_complexity
chr2	22923526	22923927	.	.	.	.	.	.
chr2	23011800	23012201	.	.	.	.	.	.
chr2	25283820	25284221	chr2	25284192	25284288	(CGCGG)n	Simple_repe	Simple_repeat
chr2	25877290	25877691	chr2	25877624	25877803	ID_B1	SINE	B4
chr2	26236014	26236415	.	.	.	.	.	.
chr2	26495638	26496039	.	.	.	.	.	.

chr2	26758241	26758642	.	.	.	.	.	.
chr2	26766156	26766557	.	.	.	.	.	.
chr2	26819691	26820092	.	.	.	.	.	.
chr2	26865298	26865699	chr2	26865517	26865557	GC_rich	Low_comple	Low_complexity
chr2	27102655	27103056	.	.	.	.	.	.
chr2	27331022	27331423	chr2	27331031	27331063	(CCG)n	Simple_repe	Simple_repeat
chr2	27331022	27331423	chr2	27331326	27331385	(CCCG)n	Simple_repe	Simple_repeat
chr2	27370372	27370773	chr2	27370769	27370798	GC_rich	Low_comple	Low_complexity
chr2	28695652	28696053	.	.	.	.	.	.
chr2	29202090	29202491	.	.	.	.	.	.
chr2	29643061	29643462	chr2	29643363	29643495	ID_B1	SINE	B4
chr2	29657909	29658310	.	.	.	.	.	.
chr2	29682668	29683069	.	.	.	.	.	.
chr2	29790729	29791130	.	.	.	.	.	.
chr2	29904266	29904667	.	.	.	.	.	.
chr2	29949357	29949758	chr2	29949622	29949706	MIR	SINE	MIR
chr2	30092905	30093306	.	.	.	.	.	.
chr2	30219331	30219732	chr2	30219347	30219402	(TG)n	Simple_repe	Simple_repeat
chr2	30683665	30684066	.	.	.	.	.	.
chr2	30837463	30837864	.	.	.	.	.	.
chr2	31007660	31008061	.	.	.	.	.	.
chr2	31543535	31543936	.	.	.	.	.	.
chr2	31829755	31830156	.	.	.	.	.	.
chr2	31950834	31951235	.	.	.	.	.	.
chr2	32091930	32092331	.	.	.	.	.	.
chr2	32143609	32144010	.	.	.	.	.	.
chr2	32173049	32173450	.	.	.	.	.	.
chr2	32208738	32209139	.	.	.	.	.	.
chr2	32218397	32218798	.	.	.	.	.	.
chr2	32426105	32426506	.	.	.	.	.	.
chr2	32480735	32481136	chr2	32480862	32480921	CT-rich	Low_comple	Low_complexity
chr2	32549677	32550078	chr2	32549683	32549709	(CCCCG)n	Simple_repe	Simple_repeat
chr2	32568162	32568563	chr2	32568190	32568239	(CCG)n	Simple_repe	Simple_repeat
chr2	32568162	32568563	chr2	32568407	32568449	(CCG)n	Simple_repe	Simple_repeat
chr2	32612544	32612945	.	.	.	.	.	.
chr2	33323875	33324276	.	.	.	.	.	.
chr2	34609798	34610199	chr2	34609951	34609972	GC_rich	Low_comple	Low_complexity
chr2	34609798	34610199	chr2	34610145	34610238	(TC)n	Simple_repe	Simple_repeat
chr2	34627165	34627566	.	.	.	.	.	.
chr2	34726325	34726726	.	.	.	.	.	.
chr2	37278559	37278960	.	.	.	.	.	.
chr2	37286231	37286632	.	.	.	.	.	.
chr2	37298530	37298931	.	.	.	.	.	.
chr2	38142763	38143164	.	.	.	.	.	.
chr2	38499236	38499637	.	.	.	.	.	.
chr2	38860544	38860945	.	.	.	.	.	.
chr2	39081800	39082201	chr2	39081775	39081828	(CGG)n	Simple_repe	Simple_repeat
chr2	48804747	48805148	.	.	.	.	.	.
chr2	49306841	49307242	chr2	49306944	49306982	(GGGA)n	Simple_repe	Simple_repeat
chr2	49306841	49307242	chr2	49307125	49307147	GC_rich	Low_comple	Low_complexity
chr2	50151996	50152397	chr2	50151979	50152000	(CCGGG)n	Simple_repe	Simple_repeat
chr2	52716519	52716920	chr2	52716736	52716778	GC_rich	Low_comple	Low_complexity
chr2	52716519	52716920	chr2	52716893	52716923	GC_rich	Low_comple	Low_complexity
chr2	53050104	53050505	.	.	.	.	.	.
chr2	61430996	61431397	.	.	.	.	.	.
chr2	61549656	61550057	chr2	61549710	61549730	(C)n	Simple_repe	Simple_repeat
chr2	65506541	65506942	chr2	65506767	65506796	AT_rich	Low_comple	Low_complexity
chr2	69044145	69044546	.	.	.	.	.	.
chr2	69551404	69551805	chr2	69551795	69551882	RSINE1	SINE	B4
chr2	69560640	69561041	.	.	.	.	.	.
chr2	69699461	69699862	chr2	69699836	69699865	GC_rich	Low_comple	Low_complexity
chr2	69723555	69723956	.	.	.	.	.	.
chr2	70499413	70499814	.	.	.	.	.	.
chr2	70893538	70893939	.	.	.	.	.	.
chr2	71049529	71049930	.	.	.	.	.	.
chr2	73150456	73150857	.	.	.	.	.	.
chr2	73730496	73730897	.	.	.	.	.	.
chr2	74416804	74417205	.	.	.	.	.	.
chr2	75670050	75670451	chr2	75670116	75670174	(CGGGG)n	Simple_repe	Simple_repeat
chr2	75670050	75670451	chr2	75670397	75670420	GC_rich	Low_comple	Low_complexity
chr2	75776503	75776904	.	.	.	.	.	.
chr2	75819887	75820288	.	.	.	.	.	.
chr2	76485600	76486001	.	.	.	.	.	.
chr2	76513141	76513542	chr2	76513527	76513621	GC_rich	Low_comple	Low_complexity
chr2	77784271	77784672	.	.	.	.	.	.
chr2	80155611	80156012	chr2	80155825	80155856	GC_rich	Low_comple	Low_complexity
chr2	80478750	80479151	chr2	80478661	80478801	B1_Mus1	SINE	Alu
chr2	83484444	83484845	.	.	.	.	.	.
chr2	84316769	84317170	chr2	84316782	84317019	RLTR42	LTR	ERVK
chr2	84316769	84317170	chr2	84317024	84318538	RLTR42-int	LTR	ERVK
chr2	84518156	84518557	.	.	.	.	.	.
chr2	84567323	84567724	.	.	.	.	.	.
chr2	84666934	84667335	.	.	.	.	.	.
chr2	90893893	90894294	chr2	90893836	90893974	B1_Mus2	SINE	Alu
chr2	90893893	90894294	chr2	90893838	90894027	B4	SINE	B4
chr2	90910380	90910781	chr2	90910385	90910419	(CCCCG)n	Simple_repe	Simple_repeat
chr2	91023350	91023751	.	.	.	.	.	.
chr2	91042770	91043171	.	.	.	.	.	.
chr2	91105279	91105680	.	.	.	.	.	.
chr2	91284686	91285087	.	.	.	.	.	.
chr2	92031972	92032373	.	.	.	.	.	.
chr2	93850802	93851203	.	.	.	.	.	.
chr2	94246668	94247069	.	.	.	.	.	.
chr2	101469033	101469434	.	.	.	.	.	.
chr2	101726160	101726561	.	.	.	.	.	.

chr2	103601346	103601747	.	.	.	.	.	.
chr2	104430332	104430733	chr2	104430672	104430701	(CGG)n	Simple_repe	Simple_repeat
chr2	104656992	104657393	chr2	104656992	104657050	GC_rich	Low_comple	Low_complexity
chr2	104656992	104657393	chr2	104657157	104657206	GC_rich	Low_comple	Low_complexity
chr2	104857021	104857422	.	.	.	.	.	.
chr2	109857779	109858180	.	.	.	.	.	.
chr2	112101832	112102233	.	.	.	.	.	.
chr2	112105464	112105865	chr2	112105856	112105902	GC_rich	Low_comple	Low_complexity
chr2	112219207	112219608	chr2	112219376	112219398	GC_rich	Low_comple	Low_complexity
chr2	112294979	112295380	.	.	.	.	.	.
chr2	114000872	114001273	.	.	.	.	.	.
chr2	114027029	114027430	.	.	.	.	.	.
chr2	115406937	115407338	.	.	.	.	.	.
chr2	118423698	118424099	.	.	.	.	.	.
chr2	118938128	118938529	.	.	.	.	.	.
chr2	118999899	119000300	.	.	.	.	.	.
chr2	119034467	119034868	.	.	.	.	.	.
chr2	119114204	119114605	.	.	.	.	.	.
chr2	120676209	120676610	.	.	.	.	.	.
chr2	121282666	121283067	.	.	.	.	.	.
chr2	121299610	121300011	.	.	.	.	.	.
chr2	121332254	121332655	.	.	.	.	.	.
chr2	121943985	121944386	.	.	.	.	.	.
chr2	122456118	122456519	.	.	.	.	.	.
chr2	125684602	125685003	.	.	.	.	.	.
chr2	125973446	125973847	chr2	125973499	125973557	(TTTG)n	Simple_repe	Simple_repeat
chr2	125973446	125973847	chr2	125973571	125973681	PB1D10	SINE	Alu
chr2	126501067	126501468	.	.	.	.	.	.
chr2	126532853	126533254	.	.	.	.	.	.
chr2	127033811	127034212	.	.	.	.	.	.
chr2	127073334	127073735	.	.	.	.	.	.
chr2	127410306	127410707	.	.	.	.	.	.
chr2	128254958	128255359	chr2	128254991	128255028	(A)n	Simple_repe	Simple_repeat
chr2	128512898	128513299	.	.	.	.	.	.
chr2	128891327	128891728	chr2	128891301	128891379	ID	SINE	ID
chr2	128891327	128891728	chr2	128891653	128891699	GC_rich	Low_comple	Low_complexity
chr2	128926509	128926910	chr2	128926488	128926613	B1_Mur3	SINE	Alu
chr2	128926509	128926910	chr2	128926613	128926631	ID_B1	SINE	B4
chr2	128955185	128955586	.	.	.	.	.	.
chr2	130100320	130100721	chr2	130100553	130100576	GC_rich	Low_comple	Low_complexity
chr2	130389268	130389669	.	.	.	.	.	.
chr2	131000408	131000809	.	.	.	.	.	.
chr2	131035855	131036256	.	.	.	.	.	.
chr2	131737027	131737428	chr2	131737125	131737245	B1F	SINE	Alu
chr2	132424871	132425272	chr2	132424848	132424945	PB1D10	SINE	Alu
chr2	136717715	136718116	.	.	.	.	.	.
chr2	139996118	139996519	.	.	.	.	.	.
chr2	142888573	142888974	.	.	.	.	.	.
chr2	144096503	144096904	.	.	.	.	.	.
chr2	144284839	144285240	.	.	.	.	.	.
chr2	144353188	144353589	.	.	.	.	.	.
chr2	144376396	144376797	.	.	.	.	.	.
chr2	144419568	144419969	.	.	.	.	.	.
chr2	145728754	145729155	.	.	.	.	.	.
chr2	145760555	145760956	.	.	.	.	.	.
chr2	146337852	146338253	.	.	.	.	.	.
chr2	146681418	146681819	.	.	.	.	.	.
chr2	146838527	146838928	.	.	.	.	.	.
chr2	148498073	148498474	.	.	.	.	.	.
chr2	148558027	148558428	chr2	148558386	148558458	(GA)n	Simple_repe	Simple_repeat
chr2	149962271	149962672	.	.	.	.	.	.
chr2	150730360	150730761	.	.	.	.	.	.
chr2	151319736	151320137	.	.	.	.	.	.
chr2	151566883	151567284	.	.	.	.	.	.
chr2	152052053	152052454	.	.	.	.	.	.
chr2	152157954	152158355	.	.	.	.	.	.
chr2	152221756	152222157	.	.	.	.	.	.
chr2	152240332	152240733	.	.	.	.	.	.
chr2	152673357	152673758	chr2	152673342	152673497	ID_B1	SINE	B4
chr2	152788258	152788659	chr2	152788600	152788676	(TCCA)n	Simple_repe	Simple_repeat
chr2	152986861	152987262	.	.	.	.	.	.
chr2	153066903	153067304	chr2	153067204	153067229	GC_rich	Low_comple	Low_complexity
chr2	153116976	153117377	.	.	.	.	.	.
chr2	153171250	153171651	chr2	153171577	153171616	(CA)n	Simple_repe	Simple_repeat
chr2	154438791	154439192	chr2	154439175	154439261	GC_rich	Low_comple	Low_complexity
chr2	154482410	154482811	chr2	154482734	154482849	G-rich	Low_comple	Low_complexity
chr2	154718497	154718898	.	.	.	.	.	.
chr2	154899688	154900089	.	.	.	.	.	.
chr2	154958977	154959378	chr2	154958802	154958986	MER5A	DNA	MER1_type
chr2	154958977	154959378	chr2	154959022	154959093	GA-rich	Low_comple	Low_complexity
chr2	155183063	155183464	.	.	.	.	.	.
chr2	155517980	155518381	.	.	.	.	.	.
chr2	155555017	155555418	.	.	.	.	.	.
chr2	155644938	155645339	chr2	155645330	155645443	B1F2	SINE	Alu
chr2	155755605	155756006	.	.	.	.	.	.
chr2	155969736	155970137	.	.	.	.	.	.
chr2	156005813	156006214	.	.	.	.	.	.
chr2	156373098	156373499	.	.	.	.	.	.
chr2	156547979	156548380	.	.	.	.	.	.
chr2	156817687	156818088	chr2	156817764	156817808	(CAG)n	Simple_repe	Simple_repeat
chr2	157030099	157030500	.	.	.	.	.	.
chr2	157193160	157193561	chr2	157193124	157193204	PB1D7	SINE	Alu
chr2	157392235	157392636	chr2	157392609	157392650	MIRm	SINE	MIR
chr2	157854189	157854590	.	.	.	.	.	.
chr2	158187065	158187466	chr2	158187373	158187403	AT_rich	Low_comple	Low_complexity

chr2	158235233	158235634	.	.	.	.	.	.
chr2	158620455	158620856	.	.	.	.	.	.
chr2	162842915	162843316	.	.	.	.	.	.
chr2	163245311	163245712	.	.	.	.	.	.
chr2	164286258	164286659	.	.	.	.	.	.
chr2	164322805	164323206	.	.	.	.	.	.
chr2	164630261	164630662	.	.	.	.	.	.
chr2	164736982	164737383	.	.	.	.	.	.
chr2	165152051	165152452	.	.	.	.	.	.
chr2	165213671	165214072	.	.	.	.	.	.
chr2	165817902	165818303	chr2	165818110	165818133	GC_rich	Low_comple	Low_complexity
chr2	166619041	166619442	chr2	166619052	166619080	(GA)n	Simple_repe	Simple_repeat
chr2	166821739	166822140	chr2	166821784	166821816	GC_rich	Low_comple	Low_complexity
chr2	166821739	166822140	chr2	166822061	166822196	L2c	LINE	L2
chr2	166888423	166888824	.	.	.	.	.	.
chr2	167318181	167318582	.	.	.	.	.	.
chr2	167516666	167517067	.	.	.	.	.	.
chr2	172196264	172196665	.	.	.	.	.	.
chr2	172847141	172847542	.	.	.	.	.	.
chr2	173901554	173901955	.	.	.	.	.	.
chr2	174241342	174241743	.	.	.	.	.	.
chr2	174289517	174289918	.	.	.	.	.	.
chr2	177574915	177575316	chr2	177574531	177574921	RMER17B	LTR	ERVK
chr2	177691871	177692272	chr2	177691495	177691892	RMER17B	LTR	ERVK
chr2	177757758	177758159	chr2	177758106	177758494	RMER17B	LTR	ERVK
chr2	179805130	179805531	chr2	179805114	179805218	PB1D7	SINE	Alu
chr2	179805130	179805531	chr2	179805505	179805613	PB1	SINE	Alu
chr2	179905935	179906336	chr2	179905898	179906039	FordPrefect	DNA	Tip100
chr2	179991826	179992227	chr2	179992165	179992206	(CCGGG)n	Simple_repe	Simple_repeat
chr2	180655482	180655883	chr2	180655427	180655544	GC_rich	Low_comple	Low_complexity
chr2	180701713	180702114	.	.	.	.	.	.
chr2	181054434	181054835	chr2	181054821	181054966	B1_Mus2	SINE	Alu
chr2	181099870	181100271	chr2	181099945	181099974	(CCG)n	Simple_repe	Simple_repeat
chr2	181316548	181316949	.	.	.	.	.	.
chr2	181335830	181336231	.	.	.	.	.	.
chr2	181414707	181415108	chr2	181414974	181414995	(T)n	Simple_repe	Simple_repeat
chr2	181598859	181599260	.	.	.	.	.	.
chr3	5218284	5218685	chr3	5218484	5218531	CT-rich	Low_comple	Low_complexity
chr3	5576126	5576527	.	.	.	.	.	.
chr3	8923591	8923992	.	.	.	.	.	.
chr3	10440157	10440558	.	.	.	.	.	.
chr3	19063070	19063471	.	.	.	.	.	.
chr3	19794469	19794870	.	.	.	.	.	.
chr3	27483303	27483704	.	.	.	.	.	.
chr3	30501066	30501467	.	.	.	.	.	.
chr3	30894157	30894558	.	.	.	.	.	.
chr3	32263057	32263458	.	.	.	.	.	.
chr3	32635647	32636048	.	.	.	.	.	.
chr3	33698874	33699275	.	.	.	.	.	.
chr3	33743052	33743453	.	.	.	.	.	.
chr3	33918867	33919268	chr3	33918923	33918984	C-rich	Low_comple	Low_complexity
chr3	33918867	33919268	chr3	33919088	33919109	GC_rich	Low_comple	Low_complexity
chr3	33980132	33980533	.	.	.	.	.	.
chr3	36470811	36471212	.	.	.	.	.	.
chr3	37318951	37319352	.	.	.	.	.	.
chr3	40547949	40548350	.	.	.	.	.	.
chr3	51219659	51220060	chr3	51220021	51220074	GA-rich	Low_comple	Low_complexity
chr3	53267469	53267870	chr3	53267691	53267712	GC_rich	Low_comple	Low_complexity
chr3	57455411	57455812	.	.	.	.	.	.
chr3	58218508	58218909	chr3	58218479	58218510	AT_rich	Low_comple	Low_complexity
chr3	58218508	58218909	chr3	58218634	58218677	(CGG)n	Simple_repe	Simple_repeat
chr3	58218508	58218909	chr3	58218800	58218824	(TTTTG)n	Simple_repe	Simple_repeat
chr3	58329760	58330161	.	.	.	.	.	.
chr3	61167114	61167515	.	.	.	.	.	.
chr3	62310777	62311178	chr3	62310735	62310794	(CCG)n	Simple_repe	Simple_repeat
chr3	63768405	63768806	.	.	.	.	.	.
chr3	65196447	65196848	chr3	65196800	65196836	(CTAA)n	Simple_repe	Simple_repeat
chr3	65762037	65762438	.	.	.	.	.	.
chr3	67233819	67234220	chr3	67233838	67233859	AT_rich	Low_comple	Low_complexity
chr3	67386398	67386799	.	.	.	.	.	.
chr3	68808651	68809052	.	.	.	.	.	.
chr3	75360605	75361006	.	.	.	.	.	.
chr3	79432605	79433006	.	.	.	.	.	.
chr3	79689926	79690327	.	.	.	.	.	.
chr3	82161573	82161974	.	.	.	.	.	.
chr3	84024626	84025027	.	.	.	.	.	.
chr3	85377779	85378180	.	.	.	.	.	.
chr3	85946417	85946818	.	.	.	.	.	.
chr3	87689530	87689931	.	.	.	.	.	.
chr3	87723173	87723574	.	.	.	.	.	.
chr3	87733918	87734319	chr3	87734304	87734346	(CCCCCG)n	Simple_repe	Simple_repeat
chr3	87846849	87847250	chr3	87846850	87846873	(TGGGGG)n	Simple_repe	Simple_repeat
chr3	87885704	87886105	.	.	.	.	.	.
chr3	87944165	87944566	.	.	.	.	.	.
chr3	88100326	88100727	chr3	88100248	88100435	B3	SINE	B2
chr3	88307030	88307431	.	.	.	.	.	.
chr3	88335596	88335997	chr3	88335799	88335826	GC_rich	Low_comple	Low_complexity
chr3	88356736	88357137	.	.	.	.	.	.
chr3	88383312	88383713	.	.	.	.	.	.
chr3	88753892	88754293	chr3	88754248	88754289	(GGA)n	Simple_repe	Simple_repeat
chr3	88905699	88906100	.	.	.	.	.	.
chr3	88981008	88981409	.	.	.	.	.	.
chr3	89006628	89007029	.	.	.	.	.	.
chr3	89017618	89018019	.	.	.	.	.	.
chr3	89050291	89050692	.	.	.	.	.	.

chr3	89070247	89070648	.	.	.	.	.	.
chr3	89215700	89216101	.	.	.	.	.	.
chr3	89222352	89222753	.	.	.	.	.	.
chr3	89577051	89577452	chr3	89577422	89577488	GC_rich	Low_comple	Low_complexity
chr3	89856549	89856950	chr3	89856600	89856626	(CCCCG)n	Simple_repe	Simple_repeat
chr3	89856549	89856950	chr3	89856826	89856848	(T)n	Simple_repe	Simple_repeat
chr3	90017508	90017909	.	.	.	.	.	.
chr3	90035298	90035699	.	.	.	.	.	.
chr3	90057901	90058302	chr3	90058260	90058345	G-rich	Low_comple	Low_complexity
chr3	90294787	90295188	chr3	90295142	90295297	(TTTC)n	Simple_repe	Simple_repeat
chr3	93360537	93360938	chr3	93360512	93360546	(TTTG)n	Simple_repe	Simple_repeat
chr3	93360537	93360938	chr3	93360752	93360795	(GA)n	Simple_repe	Simple_repeat
chr3	94386496	94386897	chr3	94386518	94386570	GC_rich	Low_comple	Low_complexity
chr3	94386496	94386897	chr3	94386794	94386915	B1_Mus2	SINE	Alu
chr3	94846382	94846783	.	.	.	.	.	.
chr3	94914759	94915160	chr3	94914628	94914762	B1_Mur1	SINE	Alu
chr3	94937776	94938177	chr3	94938062	94938089	AT_rich	Low_comple	Low_complexity
chr3	95021651	95022052	.	.	.	.	.	.
chr3	95031924	95032325	.	.	.	.	.	.
chr3	95085611	95086012	chr3	95086010	95086105	PB1D10	SINE	Alu
chr3	95161031	95161432	chr3	95161400	95161430	AT_rich	Low_comple	Low_complexity
chr3	95543383	95543784	.	.	.	.	.	.
chr3	95697576	95697977	.	.	.	.	.	.
chr3	95861621	95862022	.	.	.	.	.	.
chr3	95964161	95964562	.	.	.	.	.	.
chr3	95976247	95976648	chr3	95976382	95976410	GC_rich	Low_comple	Low_complexity
chr3	96001412	96001813	chr3	96001796	96001887	ID_B1	SINE	B4
chr3	96073332	96073733	.	.	.	.	.	.
chr3	96433635	96434036	chr3	96433635	96433710	B1_Mur1	SINE	Alu
chr3	96962468	96962869	.	.	.	.	.	.
chr3	97413925	97414326	chr3	97413951	97413981	GC_rich	Low_comple	Low_complexity
chr3	97571755	97572156	.	.	.	.	.	.
chr3	98186116	98186517	.	.	.	.	.	.
chr3	100725786	100726187	.	.	.	.	.	.
chr3	102824766	102825167	.	.	.	.	.	.
chr3	103613191	103613592	chr3	103613419	103613441	GC_rich	Low_comple	Low_complexity
chr3	103718121	103718522	.	.	.	.	.	.
chr3	104667162	104667563	.	.	.	.	.	.
chr3	104857670	104858071	chr3	104857647	104857739	PB1D10	SINE	Alu
chr3	104857670	104858071	chr3	104857659	104857779	ID_B1	SINE	B4
chr3	105490207	105490608	.	.	.	.	.	.
chr3	106524269	106524670	.	.	.	.	.	.
chr3	107136711	107137112	.	.	.	.	.	.
chr3	107563071	107563472	chr3	107563245	107563282	(CA)n	Simple_repe	Simple_repeat
chr3	108013344	108013745	chr3	108013391	108013438	GC_rich	Low_comple	Low_complexity
chr3	108059797	108060198	.	.	.	.	.	.
chr3	108187391	108187792	chr3	108187546	108187693	RMER17C	LTR	ERVK
chr3	108187391	108187792	chr3	108187681	108187746	PB1D7	SINE	Alu
chr3	108340194	108340595	.	.	.	.	.	.
chr3	108357539	108357940	chr3	108357865	108357940	PB1D10	SINE	Alu
chr3	108365157	108365558	.	.	.	.	.	.
chr3	110053772	110054173	chr3	110054129	110054505	MT2B2	LTR	ERVL
chr3	113332874	113333275	.	.	.	.	.	.
chr3	115590775	115591176	.	.	.	.	.	.
chr3	115710967	115711368	.	.	.	.	.	.
chr3	116210874	116211275	.	.	.	.	.	.
chr3	116297709	116298110	.	.	.	.	.	.
chr3	120994756	120995157	.	.	.	.	.	.
chr3	121977083	121977484	.	.	.	.	.	.
chr3	122322587	122322988	chr3	122322646	122322677	(GGGA)n	Simple_repe	Simple_repeat
chr3	122322587	122322988	chr3	122322738	122322779	GC_rich	Low_comple	Low_complexity
chr3	123211091	123211492	.	.	.	.	.	.
chr3	127483094	127483495	.	.	.	.	.	.
chr3	129534110	129534511	.	.	.	.	.	.
chr3	130433112	130433513	.	.	.	.	.	.
chr3	132754626	132755027	.	.	.	.	.	.
chr3	133903081	133903482	chr3	133903054	133903118	(CGG)n	Simple_repe	Simple_repeat
chr3	134943918	134944319	.	.	.	.	.	.
chr3	137581256	137581657	chr3	137581416	137581439	GC_rich	Low_comple	Low_complexity
chr3	137806267	137806668	.	.	.	.	.	.
chr3	138189928	138190329	chr3	138190054	138190084	(A)n	Simple_repe	Simple_repeat
chr3	142222484	142222885	.	.	.	.	.	.
chr3	144781700	144782101	.	.	.	.	.	.
chr3	146184216	146184617	chr3	146184492	146184633	B1_Mus2	SINE	Alu
chr3	151856648	151857049	.	.	.	.	.	.
chr3	154756026	154756427	chr3	154756364	154756391	(CCCCG)n	Simple_repe	Simple_repeat
chr3	157694564	157694965	.	.	.	.	.	.
chr4	3762589	3762990	.	.	.	.	.	.
chr4	4720320	4720721	.	.	.	.	.	.
chr4	11003192	11003593	.	.	.	.	.	.
chr4	11412914	11413315	.	.	.	.	.	.
chr4	12014919	12015320	chr4	12015170	12015197	(A)n	Simple_repe	Simple_repeat
chr4	19969062	19969463	chr4	19969043	19969151	(CCCCG)n	Simple_repe	Simple_repeat
chr4	21774950	21775351	.	.	.	.	.	.
chr4	33397137	33397538	.	.	.	.	.	.
chr4	34497523	34497924	chr4	34497622	34497644	(T)n	Simple_repe	Simple_repeat
chr4	41222308	41222709	.	.	.	.	.	.
chr4	41450169	41450570	chr4	41450512	41450853	ORR1C2	LTR	MaLR
chr4	43023200	43023601	.	.	.	.	.	.
chr4	43044162	43044563	.	.	.	.	.	.
chr4	43575279	43575680	.	.	.	.	.	.
chr4	44085391	44085792	.	.	.	.	.	.
chr4	44768956	44769357	.	.	.	.	.	.
chr4	45309788	45310189	.	.	.	.	.	.
chr4	46151243	46151644	.	.	.	.	.	.

chr4	46401849	46402250	.	.	.	.	.	.	
chr4	48292360	48292761	.	.	.	.	.	.	
chr4	49533838	49534239	.	.	.	.	.	.	
chr4	55543581	55543982	.	.	.	.	.	.	
chr4	56815003	56815404	.	.	.	.	.	.	
chr4	56960193	56960594	.	.	.	.	.	.	
chr4	57314695	57315096	.	.	.	.	.	.	
chr4	58923808	58924209	.	.	.	.	.	.	
chr4	58956201	58956602	.	.	.	.	.	.	
chr4	59796616	59797017	chr4	59796993	59797038	(TCTG)n	Simple_repe	Simple_repeat	
chr4	61869377	61869778	.	.	.	.	.	.	
chr4	61947238	61947639	.	.	.	.	.	.	
chr4	62021560	62021961	.	.	.	.	.	.	
chr4	62069510	62069911	.	.	.	.	.	.	
chr4	62186043	62186444	.	.	.	.	.	.	
chr4	63064386	63064787	.	.	.	.	.	.	
chr4	63219914	63220315	chr4	63220053	63220132	MIR3	SINE	MIR	
chr4	65265754	65266155	.	.	.	.	.	.	
chr4	66489646	66490047	.	.	.	.	.	.	
chr4	70071345	70071746	.	.	.	.	.	.	
chr4	74924025	74924426	.	.	.	.	.	.	
chr4	83063361	83063762	.	.	.	.	.	.	
chr4	86221287	86221688	.	.	.	.	.	.	
chr4	86257869	86258270	.	.	.	.	.	.	
chr4	86503106	86503507	.	.	.	.	.	.	
chr4	88368132	88368533	chr4	88368439	88368485	G-rich	Low_comple	Low_complexity	
chr4	94269945	94270346	.	.	.	.	.	.	
chr4	94718902	94719303	.	.	.	.	.	.	
chr4	98460246	98460647	chr4	98460166	98460279	ID_B1	SINE	B4	
chr4	98460246	98460647	chr4	98460353	98460487	RLTR15	LTR	ERVK	
chr4	98460246	98460647	chr4	98460472	98460728	RLTR15	LTR	ERVK	
chr4	98860419	98860820	chr4	98860812	98860835	GC_rich	Low_comple	Low_complexity	
chr4	99495658	99496059	.	.	.	.	.	.	
chr4	100448532	100448933	chr4	100448511	100448609	(GA)n	Simple_repe	Simple_repeat	
chr4	100448532	100448933	chr4	100448615	100448795	MIRb	SINE	MIR	
chr4	106323358	106323759	.	.	.	.	.	.	
chr4	106351368	106351769	.	.	.	.	.	.	
chr4	106582676	106583077	.	.	.	.	.	.	
chr4	106739281	106739682	.	.	.	.	.	.	
chr4	106850784	106851185	.	.	.	.	.	.	
chr4	106986754	106987155	.	.	.	.	.	.	
chr4	107040192	107040593	chr4	107040165	107040300	B3	SINE	B2	
chr4	107476385	107476786	chr4	107476444	107476472	GC_rich	Low_comple	Low_complexity	
chr4	107562651	107563052	chr4	107562987	107563130	ID_B1	SINE	B4	
chr4	108000448	108000849	.	.	.	.	.	.	
chr4	108132388	108132789	chr4	108132578	108132611	C-rich	Low_comple	Low_complexity	
chr4	108132388	108132789	chr4	108132679	108132733	(CGG)n	Simple_repe	Simple_repeat	
chr4	108251517	108251918	.	.	.	.	.	.	
chr4	108292586	108292987	chr4	108292595	108292621	GC_rich	Low_comple	Low_complexity	
chr4	108506119	108506520	chr4	108506189	108506214	(CGG)n	Simple_repe	Simple_repeat	
chr4	108520241	108520642	.	.	.	.	.	.	
chr4	108643647	108644048	chr4	108643657	108643817	MLT1B	LTR	MaLR	
chr4	108672853	108673254	.	.	.	.	.	.	
chr4	108789135	108789536	.	.	.	.	.	.	
chr4	108952531	108952932	chr4	108952853	108952878	(CGGGG)n	Simple_repe	Simple_repeat	
chr4	109348829	109349230	chr4	109349196	109349253	(CGG)n	Simple_repe	Simple_repeat	
chr4	114078294	114078695	chr4	114078469	114078525	GA-rich	Low_comple	Low_complexity	
chr4	114078294	114078695	chr4	114078587	114078637	(CGAG)n	Simple_repe	Simple_repeat	
chr4	114078294	114078695	chr4	114078655	114078700	(CCCCG)n	Simple_repe	Simple_repeat	
chr4	114659247	114659648	.	.	.	.	.	.	
chr4	114672452	114672853	.	.	.	.	.	.	
chr4	115410096	115410497	.	.	.	.	.	.	
chr4	115457204	115457605	.	.	.	.	.	.	
chr4	115725913	115726314	chr4	115725944	115726053	GA-rich	Low_comple	Low_complexity	
chr4	115747544	115747945	.	.	.	.	.	.	
chr4	115796143	115796544	.	.	.	.	.	.	
chr4	116137557	116137958	chr4	116137859	116138124	L2	LINE	L2	
chr4	116180245	116180646	.	.	.	.	.	.	
chr4	116229491	116229892	.	.	.	.	.	.	
chr4	116270120	116270521	.	.	.	.	.	.	
chr4	116300368	116300769	.	.	.	.	.	.	
chr4	116324106	116324507	.	.	.	.	.	.	
chr4	116358243	116358644	.	.	.	.	.	.	
chr4	116380820	116381221	.	.	.	.	.	.	
chr4	116479757	116480158	.	.	.	.	.	.	
chr4	116691794	116692195	.	.	.	.	.	.	
chr4	116798587	116798988	.	.	.	.	.	.	
chr4	116828458	116828859	.	.	.	.	.	.	
chr4	116855037	116855438	chr4	116855331	116855357	(TTGG)n	Simple_repe	Simple_repeat	
chr4	116855037	116855438	chr4	116855371	116855503	B1_Mus2	SINE	Alu	
chr4	117222606	117223007	chr4	117222669	117222702	AT_rich	Low_comple	Low_complexity	
chr4	117354723	117355124	chr4	117355080	117355224	MIRb	SINE	MIR	
chr4	117559831	117560232	.	.	.	.	.	.	
chr4	117564494	117564895	chr4	117564884	117564945	RSINE1	SINE	B4	
chr4	117587665	117588066	.	.	.	.	.	.	
chr4	118081692	118082093	.	.	.	.	.	.	
chr4	118101307	118101708	.	.	.	.	.	.	
chr4	118293263	118293664	.	.	.	.	.	.	
chr4	118846753	118847154	.	.	.	.	.	.	
chr4	118967240	118967641	.	.	.	.	.	.	
chr4	118992985	118993386	.	.	.	.	.	.	
chr4	119211971	119212372	chr4	119212300	119212326	(CCG)n	Simple_repe	Simple_repeat	
chr4	120243712	120244113	chr4	120244038	120244468	L2c	LINE	L2	
chr4	120597449	120597850	.	.	.	.	.	.	
chr4	120770631	120771032	.	.	.	.	.	.	

chr4	122513263	122513664	.	.	.	.	.	.	
chr4	122562902	122563303	.	.	.	.	.	.	
chr4	122959672	122960073	.	.	.	.	.	.	
chr4	123395397	123395798	chr4	123395796	123395963	B3	SINE	B2	
chr4	124370717	124371118	.	.	.	.	.	.	
chr4	124391815	124392216	.	.	.	.	.	.	
chr4	124418892	124419293	.	.	.	.	.	.	
chr4	124614072	124614473	.	.	.	.	.	.	
chr4	124743695	124744096	chr4	124743675	124743749	PB1D7	SINE	Alu	
chr4	125723925	125724326	chr4	125723768	125723996	URR1A	DNA	MER1_type	
chr4	125735583	125735984	.	.	.	.	.	.	
chr4	125773593	125773994	chr4	125773571	125773670	(TTTC)n	Simple_repe	Simple_repeat	
chr4	125780893	125781294	chr4	125781293	125781321	GC_rich	Low_comple	Low_complexity	
chr4	125879770	125880171	.	.	.	.	.	.	
chr4	125939377	125939778	.	.	.	.	.	.	
chr4	125998825	125999226	chr4	125998858	125998958	(CCG)n	Simple_repe	Simple_repeat	
chr4	126145783	126146184	chr4	126145788	126145832	(CCG)n	Simple_repe	Simple_repeat	
chr4	126234292	126234693	chr4	126234691	126234721	(A)n	Simple_repe	Simple_repeat	
chr4	126286807	126287208	.	.	.	.	.	.	
chr4	126354631	126355032	.	.	.	.	.	.	
chr4	126430572	126430973	.	.	.	.	.	.	
chr4	126645306	126645707	.	.	.	.	.	.	
chr4	126738190	126738591	chr4	126738574	126738716	B1_Mur2	SINE	Alu	
chr4	126754060	126754461	chr4	126753985	126754177	B2_Mm2	SINE	B2	
chr4	126920829	126921230	chr4	126921030	126921060	GC_rich	Low_comple	Low_complexity	
chr4	127031897	127032298	.	.	.	.	.	.	
chr4	128287144	128287545	.	.	.	.	.	.	
chr4	128866953	128867354	.	.	.	.	.	.	
chr4	129012793	129013194	.	.	.	.	.	.	
chr4	129138720	129139121	.	.	.	.	.	.	
chr4	129277744	129278145	.	.	.	.	.	.	
chr4	129318197	129318598	.	.	.	.	.	.	
chr4	129495954	129496355	.	.	.	.	.	.	
chr4	130037027	130037428	.	.	.	.	.	.	
chr4	130219096	130219497	chr4	130219179	130219199	(CCCG)n	Simple_repe	Simple_repeat	
chr4	131767982	131768383	chr4	131768121	131768143	GC_rich	Low_comple	Low_complexity	
chr4	131826072	131826473	.	.	.	.	.	.	
chr4	131864320	131864721	.	.	.	.	.	.	
chr4	131909417	131909818	.	.	.	.	.	.	
chr4	131978223	131978624	.	.	.	.	.	.	
chr4	132066337	132066738	.	.	.	.	.	.	
chr4	132194758	132195159	.	.	.	.	.	.	
chr4	132398900	132399301	.	.	.	.	.	.	
chr4	132567188	132567589	chr4	132567475	132567575	GA-rich	Low_comple	Low_complexity	
chr4	132833591	132833992	.	.	.	.	.	.	
chr4	132895314	132895715	.	.	.	.	.	.	
chr4	132925380	132925781	chr4	132925326	132925464	MIR	SINE	MIR	
chr4	132925380	132925781	chr4	132925511	132925533	(T)n	Simple_repe	Simple_repeat	
chr4	133658199	133658600	.	.	.	.	.	.	
chr4	133951989	133952390	.	.	.	.	.	.	
chr4	134023987	134024388	.	.	.	.	.	.	
chr4	134067004	134067405	.	.	.	.	.	.	
chr4	134908854	134909255	.	.	.	.	.	.	
chr4	135429677	135430078	.	.	.	.	.	.	
chr4	135609114	135609515	.	.	.	.	.	.	
chr4	135841208	135841609	.	.	.	.	.	.	
chr4	136604574	136604975	.	.	.	.	.	.	
chr4	137149402	137149803	.	.	.	.	.	.	
chr4	137860534	137860935	.	.	.	.	.	.	
chr4	137990338	137990739	chr4	137990261	137990409	RSINE1	SINE	B4	
chr4	138908112	138908513	.	.	.	.	.	.	
chr4	140517087	140517488	.	.	.	.	.	.	
chr4	140542562	140542963	chr4	140542436	140542614	(TCTG)n	Simple_repe	Simple_repeat	
chr4	141346639	141347040	chr4	141346977	141347082	MIR3	SINE	MIR	
chr4	147222368	147222769	.	.	.	.	.	.	
chr4	147278815	147279216	chr4	147279115	147279186	G-rich	Low_comple	Low_complexity	
chr4	147412225	147412626	.	.	.	.	.	.	
chr4	148000214	148000615	.	.	.	.	.	.	
chr4	148473748	148474149	.	.	.	.	.	.	
chr4	148478018	148478419	.	.	.	.	.	.	
chr4	150283601	150284002	.	.	.	.	.	.	
chr4	151307595	151307996	chr4	151307482	151307654	(CA)n	Simple_repe	Simple_repeat	
chr4	151370236	151370637	.	.	.	.	.	.	
chr4	151699644	151700045	.	.	.	.	.	.	
chr4	153324502	153324903	chr4	153324621	153324797	RLTR15	LTR	ERVK	
chr4	153324502	153324903	chr4	153324880	153325070	RLTR15	LTR	ERVK	
chr4	153348994	153349395	.	.	.	.	.	.	
chr4	153385595	153385996	chr4	153385526	153385679	ID_B1	SINE	B4	
chr4	153516224	153516625	chr4	153516220	153516340	MER53	DNA	hAT	
chr4	154338380	154338781	.	.	.	.	.	.	
chr4	154998696	154999097	.	.	.	.	.	.	
chr4	155043154	155043555	.	.	.	.	.	.	
chr4	155177461	155177862	.	.	.	.	.	.	
chr4	155186254	155186655	chr4	155186638	155186689	(CGG)n	Simple_repe	Simple_repeat	
chr4	155205445	155205846	chr4	155205500	155205521	AT_rich	Low_comple	Low_complexity	
chr4	155483781	155484182	.	.	.	.	.	.	
chr4	155609906	155610307	chr4	155610003	155610040	GC_rich	Low_comple	Low_complexity	
chr4	155609906	155610307	chr4	155610190	155610219	GC_rich	Low_comple	Low_complexity	
chr5	3802958	3803359	.	.	.	.	.	.	
chr5	5514738	5515139	.	.	.	.	.	.	
chr5	15186375	15186776	.	.	.	.	.	.	
chr5	20562082	20562483	.	.	.	.	.	.	
chr5	20930492	20930893	.	.	.	.	.	.	
chr5	21207532	21207933	.	.	.	.	.	.	
chr5	21242771	21243172	.	.	.	.	.	.	

chr5	22938523	22938924	.	.	.	.	.	.
chr5	23900269	23900670	.	.	.	.	.	.
chr5	23929294	23929695	.	.	.	.	.	.
chr5	23950812	23951213	.	.	.	.	.	.
chr5	23953488	23953889	.	.	.	.	.	.
chr5	24083153	24083554	.	.	.	.	.	.
chr5	24092952	24093353	.	.	.	.	.	.
chr5	24191557	24191958	chr5	24191732	24191760	GC_rich	Low_comple	Low_complexity
chr5	24191557	24191958	chr5	24191890	24191994	G-rich	Low_comple	Low_complexity
chr5	28118018	28118419	.	.	.	.	.	.
chr5	28643487	28643888	chr5	28643802	28643845	GC_rich	Low_comple	Low_complexity
chr5	29761016	29761417	.	.	.	.	.	.
chr5	29895492	29895893	.	.	.	.	.	.
chr5	30062126	30062527	.	.	.	.	.	.
chr5	30339686	30340087	.	.	.	.	.	.
chr5	30558753	30559154	.	.	.	.	.	.
chr5	31171740	31172141	.	.	.	.	.	.
chr5	31190806	31191207	chr5	31190887	31190961	tRNA-Ala-GC	tRNA	tRNA
chr5	31251932	31252333	.	.	.	.	.	.
chr5	31351550	31351951	.	.	.	.	.	.
chr5	31482271	31482672	.	.	.	.	.	.
chr5	31495339	31495740	.	.	.	.	.	.
chr5	31504526	31504927	.	.	.	.	.	.
chr5	31593295	31593696	chr5	31593279	31593301	(T)n	Simple_repe	Simple_repeat
chr5	31829025	31829426	.	.	.	.	.	.
chr5	31916149	31916550	chr5	31916117	31916155	MIRb	SINE	MIR
chr5	33677801	33678202	.	.	.	.	.	.
chr5	33994956	33995357	.	.	.	.	.	.
chr5	34000462	34000863	.	.	.	.	.	.
chr5	34125299	34125700	.	.	.	.	.	.
chr5	34278902	34279303	.	.	.	.	.	.
chr5	34511898	34512299	.	.	.	.	.	.
chr5	34678728	34679129	.	.	.	.	.	.
chr5	34712170	34712571	chr5	34712483	34712534	GC_rich	Low_comple	Low_complexity
chr5	35002704	35003105	.	.	.	.	.	.
chr5	35104204	35104605	.	.	.	.	.	.
chr5	35917536	35917937	.	.	.	.	.	.
chr5	35925322	35925723	chr5	35925650	35925678	(CGGGG)n	Simple_repe	Simple_repeat
chr5	36807464	36807865	.	.	.	.	.	.
chr5	37141614	37142015	chr5	37141644	37141673	AT_rich	Low_comple	Low_complexity
chr5	37141614	37142015	chr5	37141728	37141832	B2_Mm2	SINE	B2
chr5	37141614	37142015	chr5	37141832	37141856	(T)n	Simple_repe	Simple_repeat
chr5	37222487	37222888	chr5	37222625	37222729	MLT1J1	LTR	MaLR
chr5	37222487	37222888	chr5	37222719	37222812	B3	SINE	B2
chr5	37222487	37222888	chr5	37222815	37223230	RCHARR1	DNA	MER1_type
chr5	38430268	38430669	.	.	.	.	.	.
chr5	42235361	42235762	chr5	42235324	42235395	(CGG)n	Simple_repe	Simple_repeat
chr5	45911271	45911672	chr5	45911609	45911631	GC_rich	Low_comple	Low_complexity
chr5	46248988	46249389	.	.	.	.	.	.
chr5	53060784	53061185	.	.	.	.	.	.
chr5	53174076	53174477	chr5	53174145	53174186	(TGGG)n	Simple_repe	Simple_repeat
chr5	54200723	54201124	.	.	.	.	.	.
chr5	65782500	65782901	.	.	.	.	.	.
chr5	65884014	65884415	.	.	.	.	.	.
chr5	67651661	67652062	.	.	.	.	.	.
chr5	69947936	69948337	chr5	69947924	69947970	(CA)n	Simple_repe	Simple_repeat
chr5	72950805	72951206	chr5	72950830	72950851	GC_rich	Low_comple	Low_complexity
chr5	72950805	72951206	chr5	72950976	72950998	(T)n	Simple_repe	Simple_repeat
chr5	73683847	73684248	.	.	.	.	.	.
chr5	73883581	73883982	.	.	.	.	.	.
chr5	76958129	76958530	chr5	76957971	76958177	URR1A	DNA	MER1_type
chr5	77380597	77380998	.	.	.	.	.	.
chr5	77403428	77403829	.	.	.	.	.	.
chr5	77739327	77739728	.	.	.	.	.	.
chr5	87233056	87233457	chr5	87233153	87233189	(CCCCCG)n	Simple_repe	Simple_repeat
chr5	88983260	88983661	.	.	.	.	.	.
chr5	91711833	91712234	.	.	.	.	.	.
chr5	92863994	92864395	.	.	.	.	.	.
chr5	96591726	96592127	.	.	.	.	.	.
chr5	96638901	96639302	.	.	.	.	.	.
chr5	100947103	100947504	.	.	.	.	.	.
chr5	101227459	101227860	.	.	.	.	.	.
chr5	101249785	101250186	.	.	.	.	.	.
chr5	104340133	104340534	chr5	104340140	104340203	GC_rich	Low_comple	Low_complexity
chr5	104340133	104340534	chr5	104340281	104340308	(CGGGG)n	Simple_repe	Simple_repeat
chr5	108494488	108494889	.	.	.	.	.	.
chr5	108561513	108561914	.	.	.	.	.	.
chr5	108697745	108698146	.	.	.	.	.	.
chr5	108741608	108742009	.	.	.	.	.	.
chr5	108863222	108863623	.	.	.	.	.	.
chr5	110538896	110539297	.	.	.	.	.	.
chr5	111268706	111269107	.	.	.	.	.	.
chr5	112755141	112755542	.	.	.	.	.	.
chr5	112770612	112771013	.	.	.	.	.	.
chr5	115016924	115017325	.	.	.	.	.	.
chr5	115372300	115372701	chr5	115372386	115372463	B1_Mur4	SINE	Alu
chr5	115372300	115372701	chr5	115372463	115372611	GSAT_MM	Satellite	Satellite
chr5	115372300	115372701	chr5	115372624	115372737	RSINE1	SINE	B4
chr5	115391949	115392350	chr5	115391980	115392028	GA-rich	Low_comple	Low_complexity
chr5	115722753	115723154	chr5	115723083	115723189	B1_Mur1	SINE	Alu
chr5	115729456	115729857	.	.	.	.	.	.
chr5	115750913	115751314	chr5	115750980	115751019	GC_rich	Low_comple	Low_complexity
chr5	115776930	115777331	chr5	115777208	115777361	(CGG)n	Simple_repe	Simple_repeat
chr5	115791072	115791473	.	.	.	.	.	.
chr5	115934240	115934641	chr5	115934600	115934707	PB1D9	SINE	Alu

chr5	116015029	116015430	chr5	116015323	116015476	(CGG)n	Simple_repe	Simple_repeat
chr5	116870959	116871360	chr5	116871234	116871374	L1MC3	LINE	L1
chr5	117565854	117566255	.	.	.	.	.	.
chr5	117806567	117806968	.	.	.	.	.	.
chr5	121654265	121654666	chr5	121654267	121654383	RSINE1	SINE	B4
chr5	121902604	121903005	.	.	.	.	.	.
chr5	121995682	121996083	chr5	121995596	121995715	(CCG)n	Simple_repe	Simple_repeat
chr5	121995682	121996083	chr5	121995743	121995777	GC_rich	Low_comple	Low_complexity
chr5	122044120	122044521	.	.	.	.	.	.
chr5	122298149	122298550	.	.	.	.	.	.
chr5	122714224	122714625	chr5	122714526	122714603	(CGGGG)n	Simple_repe	Simple_repeat
chr5	122734037	122734438	chr5	122733898	122734039	ID_B1	SINE	B4
chr5	122734037	122734438	chr5	122734305	122734444	G-rich	Low_comple	Low_complexity
chr5	122822278	122822679	.	.	.	.	.	.
chr5	123271253	123271654	.	.	.	.	.	.
chr5	123677976	123678377	chr5	123677852	123677985	B1_Mus2	SINE	Alu
chr5	124170910	124171311	.	.	.	.	.	.
chr5	124199256	124199657	.	.	.	.	.	.
chr5	124356964	124357365	.	.	.	.	.	.
chr5	124777302	124777703	.	.	.	.	.	.
chr5	124875905	124876306	chr5	124876044	124876072	(CACCC)n	Simple_repe	Simple_repeat
chr5	124875905	124876306	chr5	124876294	124876441	B1_Mus1	SINE	Alu
chr5	124889365	124889766	.	.	.	.	.	.
chr5	124990351	124990752	chr5	124990369	124990547	B3	SINE	B2
chr5	125342378	125342779	.	.	.	.	.	.
chr5	128097718	128098119	.	.	.	.	.	.
chr5	129525346	129525747	.	.	.	.	.	.
chr5	130175781	130176182	.	.	.	.	.	.
chr5	130230679	130231080	chr5	130230612	130230693	URR1B	DNA	MER1_type
chr5	130363210	130363611	chr5	130363459	130363526	PB1D10	SINE	Alu
chr5	130504960	130505361	chr5	130504886	130505016	B1F	SINE	Alu
chr5	130697982	130698383	chr5	130698350	130698385	GC_rich	Low_comple	Low_complexity
chr5	134575334	134575735	.	.	.	.	.	.
chr5	134652462	134652863	.	.	.	.	.	.
chr5	134790535	134790936	chr5	134790590	134790644	(T)n	Simple_repe	Simple_repeat
chr5	135662675	135663076	.	.	.	.	.	.
chr5	135870252	135870653	chr5	135870419	135870440	GC_rich	Low_comple	Low_complexity
chr5	135870252	135870653	chr5	135870490	135870551	ID_B1	SINE	B4
chr5	135870252	135870653	chr5	135870551	135870682	B1_Mur4	SINE	Alu
chr5	136108256	136108657	chr5	136108283	136108318	(TTTG)n	Simple_repe	Simple_repeat
chr5	136410680	136411081	chr5	136410756	136410782	(T)n	Simple_repe	Simple_repeat
chr5	136470459	136470860	chr5	136470339	136470501	RSINE1	SINE	B4
chr5	136470459	136470860	chr5	136470341	136470535	B2_Mm2	SINE	B2
chr5	136592345	136592746	.	.	.	.	.	.
chr5	136611800	136612201	.	.	.	.	.	.
chr5	137394779	137395180	.	.	.	.	.	.
chr5	137428945	137429346	.	.	.	.	.	.
chr5	137438023	137438424	.	.	.	.	.	.
chr5	137462580	137462981	.	.	.	.	.	.
chr5	137521292	137521693	.	.	.	.	.	.
chr5	137547127	137547528	chr5	137547411	137547490	PB1D10	SINE	Alu
chr5	137727853	137728254	chr5	137728190	137728214	GC_rich	Low_comple	Low_complexity
chr5	137748824	137749225	.	.	.	.	.	.
chr5	137790910	137791311	.	.	.	.	.	.
chr5	137928835	137929236	chr5	137928843	137928900	L2a	LINE	L2
chr5	137928835	137929236	chr5	137928928	137929123	B3	SINE	B2
chr5	137928835	137929236	chr5	137929155	137929206	(CATATA)n	Simple_repe	Simple_repeat
chr5	137928835	137929236	chr5	137929220	137929314	B4A	SINE	B4
chr5	137974241	137974642	.	.	.	.	.	.
chr5	138042184	138042585	chr5	138042568	138042590	AT_rich	Low_comple	Low_complexity
chr5	138179684	138180085	chr5	138179893	138179953	(TC)n	Simple_repe	Simple_repeat
chr5	138228719	138229120	.	.	.	.	.	.
chr5	138526059	138526460	.	.	.	.	.	.
chr5	138558154	138558555	.	.	.	.	.	.
chr5	138596808	138597209	.	.	.	.	.	.
chr5	138602112	138602513	chr5	138602094	138602185	ID_B1	SINE	B4
chr5	138602112	138602513	chr5	138602314	138602391	(CGG)n	Simple_repe	Simple_repeat
chr5	138612174	138612575	.	.	.	.	.	.
chr5	138628943	138629344	.	.	.	.	.	.
chr5	139820941	139821342	.	.	.	.	.	.
chr5	140251495	140251896	chr5	140251860	140251976	B1_Mus1	SINE	Alu
chr5	140302681	140303082	chr5	140303024	140303065	AT_rich	Low_comple	Low_complexity
chr5	140797486	140797887	chr5	140797746	140797855	PB1D9	SINE	Alu
chr5	140895070	140895471	.	.	.	.	.	.
chr5	143656744	143657145	chr5	143657047	143657111	L2	LINE	L2
chr5	143874649	143875050	chr5	143875047	143875246	B3	SINE	B2
chr5	143942363	143942764	.	.	.	.	.	.
chr5	144165265	144165666	.	.	.	.	.	.
chr5	144225191	144225592	.	.	.	.	.	.
chr5	144670604	144671005	.	.	.	.	.	.
chr5	144775603	144776004	chr5	144775655	144775697	GC_rich	Low_comple	Low_complexity
chr5	144775603	144776004	chr5	144775976	144775989	PB1D9	SINE	Alu
chr5	144775603	144776004	chr5	144775989	144776017	(TTTG)n	Simple_repe	Simple_repeat
chr5	145900745	145901146	chr5	145900856	145900882	(CGG)n	Simple_repe	Simple_repeat
chr5	145927846	145928247	chr5	145928103	145928133	(CGG)n	Simple_repe	Simple_repeat
chr5	145952238	145952639	chr5	145952604	145952685	BC1_Mm	scRNA	scRNA
chr5	145964773	145965174	chr5	145964822	145964892	RSINE1	SINE	B4
chr5	147032446	147032847	.	.	.	.	.	.
chr5	147042324	147042725	.	.	.	.	.	.
chr5	148213853	148214254	chr5	148213833	148213906	B4	SINE	B4
chr5	148213853	148214254	chr5	148213950	148214224	RLTR15	LTR	ERVK
chr5	148241531	148241932	chr5	148241928	148241968	GC_rich	Low_comple	Low_complexity
chr5	149210206	149210607	.	.	.	.	.	.
chr5	149364277	149364678	.	.	.	.	.	.
chr5	149740087	149740488	.	.	.	.	.	.

chr5	149761605	149762006	.	.	.	.	.	.
chr5	149995995	149996396	chr5	149995966	149996008	(CCCCCT)n	Simple_repe	Simple_repeat
chr5	150439114	150439515	.	.	.	.	.	.
chr5	151324938	151325339	.	.	.	.	.	.
chr5	151468037	151468438	.	.	.	.	.	.
chr5	152453677	152454078	.	.	.	.	.	.
chr6	3448178	3448579	.	.	.	.	.	.
chr6	4036795	4037196	.	.	.	.	.	.
chr6	5446458	5446859	.	.	.	.	.	.
chr6	6528481	6528882	.	.	.	.	.	.
chr6	6905736	6906137	.	.	.	.	.	.
chr6	8159498	8159899	.	.	.	.	.	.
chr6	11875680	11876081	chr6	11875640	11875744	Lx7	LINE	L1
chr6	11875680	11876081	chr6	11875739	11875779	Lx	LINE	L1
chr6	13821304	13821705	.	.	.	.	.	.
chr6	21899252	21899653	chr6	21899603	21899644	(T)n	Simple_repe	Simple_repeat
chr6	24477392	24477793	.	.	.	.	.	.
chr6	28211738	28212139	.	.	.	.	.	.
chr6	28371493	28371894	.	.	.	.	.	.
chr6	28429949	28430350	.	.	.	.	.	.
chr6	29114517	29114918	.	.	.	.	.	.
chr6	29297747	29298148	.	.	.	.	.	.
chr6	29417441	29417842	chr6	29417358	29417482	ID_B1	SINE	B4
chr6	29559653	29560054	.	.	.	.	.	.
chr6	29717995	29718396	chr6	29718367	29718535	G-rich	Low_comple	Low_complexity
chr6	30254432	30254833	chr6	30254403	30254468	(CTCG)n	Simple_repe	Simple_repeat
chr6	30340781	30341182	.	.	.	.	.	.
chr6	30350765	30351166	chr6	30350876	30351001	L4	LINE	RTE
chr6	33010208	33010609	.	.	.	.	.	.
chr6	33198763	33199164	.	.	.	.	.	.
chr6	33979204	33979605	.	.	.	.	.	.
chr6	34126926	34127327	.	.	.	.	.	.
chr6	34267418	34267819	.	.	.	.	.	.
chr6	34303711	34304112	chr6	34303677	34303719	C-rich	Low_comple	Low_complexity
chr6	34333976	34334377	.	.	.	.	.	.
chr6	34730125	34730526	.	.	.	.	.	.
chr6	35083621	35084022	.	.	.	.	.	.
chr6	35127243	35127644	chr6	35127154	35127303	B1_Mm	SINE	Alu
chr6	35489625	35490026	.	.	.	.	.	.
chr6	38483601	38484002	chr6	38483930	38484002	tRNA-Arg-AG	tRNA	tRNA
chr6	39327550	39327951	.	.	.	.	.	.
chr6	39542630	39543031	.	.	.	.	.	.
chr6	39760788	39761189	.	.	.	.	.	.
chr6	47780409	47780810	.	.	.	.	.	.
chr6	47827504	47827905	chr6	47827844	47827934	GC_rich	Low_comple	Low_complexity
chr6	47870383	47870784	chr6	47870615	47870640	(CGG)n	Simple_repe	Simple_repeat
chr6	47998362	47998763	chr6	47998365	47998404	GC_rich	Low_comple	Low_complexity
chr6	47998362	47998763	chr6	47998724	47998770	(CGG)n	Simple_repe	Simple_repeat
chr6	48345393	48345794	.	.	.	.	.	.
chr6	48454083	48454484	chr6	48454032	48454111	PB1D10	SINE	Alu
chr6	48505062	48505463	chr6	48505079	48505301	RLTR42	LTR	ERVK
chr6	48505062	48505463	chr6	48505369	48505415	RMER2	LTR	ERV1
chr6	48505062	48505463	chr6	48505415	48505442	(CA)n	Simple_repe	Simple_repeat
chr6	48505062	48505463	chr6	48505442	48505961	RMER2	LTR	ERV1
chr6	49269038	49269439	chr6	49269432	49269453	GC_rich	Low_comple	Low_complexity
chr6	50406198	50406599	chr6	50406378	50406437	L2a	LINE	L2
chr6	51420399	51420800	chr6	51420586	51420658	GC_rich	Low_comple	Low_complexity
chr6	52154374	52154775	.	.	.	.	.	.
chr6	55153544	55153945	.	.	.	.	.	.
chr6	56874036	56874437	.	.	.	.	.	.
chr6	65728892	65729293	.	.	.	.	.	.
chr6	66485027	66485428	.	.	.	.	.	.
chr6	67216671	67217072	.	.	.	.	.	.
chr6	70742071	70742472	chr6	70742050	70742090	GC_rich	Low_comple	Low_complexity
chr6	71391110	71391511	.	.	.	.	.	.
chr6	71583317	71583718	.	.	.	.	.	.
chr6	71781666	71782067	.	.	.	.	.	.
chr6	71858564	71858965	.	.	.	.	.	.
chr6	72305117	72305518	chr6	72305383	72305429	GC_rich	Low_comple	Low_complexity
chr6	72548224	72548625	.	.	.	.	.	.
chr6	72566592	72566993	.	.	.	.	.	.
chr6	73198226	73198627	.	.	.	.	.	.
chr6	81915757	81916158	.	.	.	.	.	.
chr6	83004365	83004766	chr6	83004565	83004609	(CA)n	Simple_repe	Simple_repeat
chr6	83058869	83059270	.	.	.	.	.	.
chr6	83075027	83075428	.	.	.	.	.	.
chr6	83456395	83456796	.	.	.	.	.	.
chr6	85019356	85019757	chr6	85019725	85019907	B3	SINE	B2
chr6	85283319	85283720	.	.	.	.	.	.
chr6	85381758	85382159	.	.	.	.	.	.
chr6	85401819	85402220	.	.	.	.	.	.
chr6	86388132	86388533	.	.	.	.	.	.
chr6	86476023	86476424	chr6	86476002	86476183	(CGG)n	Simple_repe	Simple_repeat
chr6	86634354	86634755	.	.	.	.	.	.
chr6	86799055	86799456	chr6	86799447	86799537	(CGGG)n	Simple_repe	Simple_repeat
chr6	87622039	87622440	.	.	.	.	.	.
chr6	87788540	87788941	.	.	.	.	.	.
chr6	88468740	88469141	chr6	88468797	88468834	GC_rich	Low_comple	Low_complexity
chr6	89545470	89545871	.	.	.	.	.	.
chr6	90319277	90319678	.	.	.	.	.	.
chr6	91423417	91423818	.	.	.	.	.	.
chr6	91465752	91466153	chr6	91465848	91465890	GC_rich	Low_comple	Low_complexity
chr6	91827803	91828204	.	.	.	.	.	.
chr6	92133855	92134256	.	.	.	.	.	.
chr6	92164711	92165112	.	.	.	.	.	.

chr6	94450122	94450523	.	.	.	.	.	.
chr6	95067509	95067910	.	.	.	.	.	.
chr6	97155353	97155754	chr6	97155676	97155697	GC_rich	Low_comple	Low_complexity
chr6	97756750	97757151	chr6	97757031	97757054	GC_rich	Low_comple	Low_complexity
chr6	106749885	106750286	.	.	.	.	.	.
chr6	108014816	108015217	.	.	.	.	.	.
chr6	108162811	108163212	chr6	108163142	108163204	GA-rich	Low_comple	Low_complexity
chr6	112646506	112646907	.	.	.	.	.	.
chr6	112995989	112996390	.	.	.	.	.	.
chr6	113276636	113277037	.	.	.	.	.	.
chr6	113588123	113588524	.	.	.	.	.	.
chr6	113646658	113647059	chr6	113646750	113646774	AT_rich	Low_comple	Low_complexity
chr6	113690492	113690893	.	.	.	.	.	.
chr6	115551524	115551925	chr6	115551388	115551597	B3	SINE	B2
chr6	115551524	115551925	chr6	115551613	115551650	(CAT)n	Simple_repe	Simple_repeat
chr6	115551524	115551925	chr6	115551904	115551949	(CGGGG)n	Simple_repe	Simple_repeat
chr6	115758628	115759029	.	.	.	.	.	.
chr6	116157781	116158182	.	.	.	.	.	.
chr6	117790991	117791392	.	.	.	.	.	.
chr6	117812882	117813283	.	.	.	.	.	.
chr6	117850684	117851085	chr6	117851074	117851106	(TG)n	Simple_repe	Simple_repeat
chr6	118369268	118369669	.	.	.	.	.	.
chr6	118429438	118429839	chr6	118429406	118429474	(CCCG)n	Simple_repe	Simple_repeat
chr6	119988653	119989054	chr6	119988715	119988748	GC_rich	Low_comple	Low_complexity
chr6	119988653	119989054	chr6	119989027	119989063	GA-rich	Low_comple	Low_complexity
chr6	120307306	120307707	.	.	.	.	.	.
chr6	120313886	120314287	.	.	.	.	.	.
chr6	120481228	120481629	.	.	.	.	.	.
chr6	121133651	121134052	.	.	.	.	.	.
chr6	122258431	122258832	.	.	.	.	.	.
chr6	124691137	124691538	chr6	124691242	124691304	U7	snRNA	snRNA
chr6	124778875	124779276	.	.	.	.	.	.
chr6	124958778	124959179	.	.	.	.	.	.
chr6	124989614	124990015	.	.	.	.	.	.
chr6	125094960	125095361	.	.	.	.	.	.
chr6	125141963	125142364	.	.	.	.	.	.
chr6	125181063	125181464	chr6	125181096	125181127	(A)n	Simple_repe	Simple_repeat
chr6	126798946	126799347	.	.	.	.	.	.
chr6	128374703	128375104	.	.	.	.	.	.
chr6	128387693	128388094	.	.	.	.	.	.
chr6	133055475	133055876	.	.	.	.	.	.
chr6	134590759	134591160	chr6	134590576	134590779	B2_Mm2	SINE	B2
chr6	134779875	134780276	.	.	.	.	.	.
chr6	134961415	134961816	chr6	134961420	134961441	AT_rich	Low_comple	Low_complexity
chr6	135147847	135148248	.	.	.	.	.	.
chr6	135312489	135312890	.	.	.	.	.	.
chr6	136753285	136753686	chr6	136753565	136753576	ID_B1	SINE	B4
chr6	136753285	136753686	chr6	136753576	136753661	B1F	SINE	Alu
chr6	137683406	137683807	chr6	137683696	137683730	(TCCC)n	Simple_repe	Simple_repeat
chr6	140569160	140569561	chr6	140569356	140569699	LTR88b	LTR	Gypsy?
chr6	142293976	142294377	.	.	.	.	.	.
chr6	142704973	142705374	chr6	142704923	142705030	GA-rich	Low_comple	Low_complexity
chr6	142704973	142705374	chr6	142705323	142705367	GC_rich	Low_comple	Low_complexity
chr6	143048514	143048915	.	.	.	.	.	.
chr6	143115536	143115937	.	.	.	.	.	.
chr6	148160602	148161003	.	.	.	.	.	.
chr6	149137180	149137581	.	.	.	.	.	.
chr7	3568731	3569132	chr7	3568589	3568751	B2_Mm2	SINE	B2
chr7	3581041	3581442	.	.	.	.	.	.
chr7	4397095	4397496	chr7	4397415	4397451	(GA)n	Simple_repe	Simple_repeat
chr7	4397095	4397496	chr7	4397451	4397556	(GGAA)n	Simple_repe	Simple_repeat
chr7	4453647	4454048	chr7	4453647	4453766	B1_Mus1	SINE	Alu
chr7	4453647	4454048	chr7	4453962	4453974	PB1D10	SINE	Alu
chr7	4453647	4454048	chr7	4453974	4454058	ID_B1	SINE	B4
chr7	4610383	4610784	.	.	.	.	.	.
chr7	4675091	4675492	.	.	.	.	.	.
chr7	4744295	4744696	.	.	.	.	.	.
chr7	4764232	4764633	.	.	.	.	.	.
chr7	4966745	4967146	chr7	4967100	4967129	GC_rich	Low_comple	Low_complexity
chr7	5031635	5032036	chr7	5031898	5031931	GC_rich	Low_comple	Low_complexity
chr7	6123753	6124154	.	.	.	.	.	.
chr7	6335679	6336080	.	.	.	.	.	.
chr7	7074067	7074468	chr7	7074446	7074569	B1_Mur1	SINE	Alu
chr7	7089314	7089715	.	.	.	.	.	.
chr7	7123792	7124193	.	.	.	.	.	.
chr7	7230801	7231202	.	.	.	.	.	.
chr7	7252018	7252419	chr7	7252024	7252064	(TTG)n	Simple_repe	Simple_repeat
chr7	11080622	11081023	.	.	.	.	.	.
chr7	13007908	13008309	.	.	.	.	.	.
chr7	13063440	13063841	.	.	.	.	.	.
chr7	13420109	13420510	.	.	.	.	.	.
chr7	13466287	13466688	.	.	.	.	.	.
chr7	13482870	13483271	chr7	13482795	13482913	B3	SINE	B2
chr7	13507373	13507774	.	.	.	.	.	.
chr7	13563183	13563584	.	.	.	.	.	.
chr7	13619902	13620303	.	.	.	.	.	.
chr7	13639588	13639989	.	.	.	.	.	.
chr7	13863869	13864270	chr7	13864249	13864276	(CGAG)n	Simple_repe	Simple_repeat
chr7	16893851	16894252	.	.	.	.	.	.
chr7	17037873	17038274	.	.	.	.	.	.
chr7	17323465	17323866	.	.	.	.	.	.
chr7	17612445	17612846	chr7	17612371	17612470	L2b	LINE	L2
chr7	19588115	19588516	.	.	.	.	.	.
chr7	19609407	19609808	.	.	.	.	.	.
chr7	19704917	19705318	.	.	.	.	.	.

chr7	19857018	19857419	.	.	.	.	.	.
chr7	19929918	19930319	chr7	19929852	19930014	L2b	LINE	L2
chr7	19929918	19930319	chr7	19930136	19930202	(TC)n	Simple_repe	Simple_repeat
chr7	19945715	19946116	chr7	19945994	19946123	B1_Mur1	SINE	Alu
chr7	19966988	19967389	chr7	19966912	19967020	B1_Mus1	SINE	Alu
chr7	19966988	19967389	chr7	19967020	19967045	B4	SINE	B4
chr7	20189657	20190058	chr7	20190039	20190142	B3	SINE	B2
chr7	20301167	20301568	.	.	.	.	.	.
chr7	20537876	20538277	chr7	20537845	20537956	ID_B1	SINE	B4
chr7	20537876	20538277	chr7	20538004	20538072	MIRm	SINE	MIR
chr7	20537876	20538277	chr7	20538234	20538522	RLTR19	LTR	ERVK
chr7	24866686	24867087	chr7	24866957	24867037	(TG)n	Simple_repe	Simple_repeat
chr7	24897133	24897534	.	.	.	.	.	.
chr7	24918948	24919349	.	.	.	.	.	.
chr7	24959848	24960249	chr7	24959904	24959929	(A)n	Simple_repe	Simple_repeat
chr7	24992994	24993395	.	.	.	.	.	.
chr7	25022553	25022954	chr7	25022818	25023371	Lx2B	LINE	L1
chr7	25039517	25039918	.	.	.	.	.	.
chr7	25055171	25055572	chr7	25055036	25055183	B1_Mus1	SINE	Alu
chr7	25084188	25084589	.	.	.	.	.	.
chr7	25101529	25101930	.	.	.	.	.	.
chr7	25292308	25292709	chr7	25292333	25292377	(CTCG)n	Simple_repe	Simple_repeat
chr7	25292308	25292709	chr7	25292693	25292720	(T)n	Simple_repe	Simple_repeat
chr7	25689176	25689577	.	.	.	.	.	.
chr7	25757594	25757995	.	.	.	.	.	.
chr7	26022983	26023384	.	.	.	.	.	.
chr7	26065406	26065807	.	.	.	.	.	.
chr7	26082847	26083248	chr7	26083109	26083260	B1_Mus1	SINE	Alu
chr7	26503867	26504268	.	.	.	.	.	.
chr7	27980592	27980993	.	.	.	.	.	.
chr7	28016877	28017278	chr7	28016805	28016922	MIRm	SINE	MIR
chr7	28139119	28139520	chr7	28139106	28139126	(TTTA)n	Simple_repe	Simple_repeat
chr7	28259541	28259942	.	.	.	.	.	.
chr7	28338046	28338447	.	.	.	.	.	.
chr7	28438744	28439145	.	.	.	.	.	.
chr7	28459698	28460099	.	.	.	.	.	.
chr7	28474212	28474613	chr7	28474183	28474268	(GA)n	Simple_repe	Simple_repeat
chr7	28474212	28474613	chr7	28474577	28474613	(TG)n	Simple_repe	Simple_repeat
chr7	28516178	28516579	.	.	.	.	.	.
chr7	28623353	28623754	.	.	.	.	.	.
chr7	28645404	28645805	.	.	.	.	.	.
chr7	28714278	28714679	.	.	.	.	.	.
chr7	28764019	28764420	.	.	.	.	.	.
chr7	28834914	28835315	.	.	.	.	.	.
chr7	28964355	28964756	.	.	.	.	.	.
chr7	29096986	29097387	.	.	.	.	.	.
chr7	29177750	29178151	.	.	.	.	.	.
chr7	29551527	29551928	.	.	.	.	.	.
chr7	30022900	30023301	chr7	30022789	30022915	B1_Mur4	SINE	Alu
chr7	30022900	30023301	chr7	30022930	30022952	(TAAA)n	Simple_repe	Simple_repeat
chr7	30033496	30033897	.	.	.	.	.	.
chr7	30088649	30089050	chr7	30088858	30088888	GC_rich	Low_comple	Low_complexity
chr7	30553354	30553755	.	.	.	.	.	.
chr7	30600792	30601193	.	.	.	.	.	.
chr7	30638511	30638912	chr7	30638786	30639049	MT2A	LTR	ERVL
chr7	30644760	30645161	chr7	30644798	30644914	GA-rich	Low_comple	Low_complexity
chr7	30693311	30693712	.	.	.	.	.	.
chr7	30768532	30768933	.	.	.	.	.	.
chr7	30836211	30836612	.	.	.	.	.	.
chr7	30857746	30858147	.	.	.	.	.	.
chr7	30875386	30875787	.	.	.	.	.	.
chr7	30879599	30880000	.	.	.	.	.	.
chr7	30906664	30907065	.	.	.	.	.	.
chr7	30954678	30955079	.	.	.	.	.	.
chr7	30981153	30981554	chr7	30981235	30981287	(TG)n	Simple_repe	Simple_repeat
chr7	31336912	31337313	.	.	.	.	.	.
chr7	31344712	31345113	.	.	.	.	.	.
chr7	31348115	31348516	.	.	.	.	.	.
chr7	31373775	31374176	chr7	31373794	31373824	(GGGGA)n	Simple_repe	Simple_repeat
chr7	31514358	31514759	.	.	.	.	.	.
chr7	35174609	35175010	chr7	35174675	35174716	(CGG)n	Simple_repe	Simple_repeat
chr7	36432370	36432771	.	.	.	.	.	.
chr7	48649007	48649408	.	.	.	.	.	.
chr7	48755068	48755469	.	.	.	.	.	.
chr7	49948010	49948411	.	.	.	.	.	.
chr7	50834874	50835275	.	.	.	.	.	.
chr7	50927137	50927538	.	.	.	.	.	.
chr7	51052148	51052549	.	.	.	.	.	.
chr7	51629153	51629554	.	.	.	.	.	.
chr7	51639789	51640190	.	.	.	.	.	.
chr7	51723127	51723528	.	.	.	.	.	.
chr7	51803943	51804344	.	.	.	.	.	.
chr7	52003647	52004048	.	.	.	.	.	.
chr7	52071530	52071931	chr7	52071792	52071937	(CGG)n	Simple_repe	Simple_repeat
chr7	52104114	52104515	.	.	.	.	.	.
chr7	52125286	52125687	.	.	.	.	.	.
chr7	52241835	52242236	.	.	.	.	.	.
chr7	52252480	52252881	.	.	.	.	.	.
chr7	52271452	52271853	chr7	52271477	52271508	(CGGGG)n	Simple_repe	Simple_repeat
chr7	52308620	52309021	chr7	52308694	52308731	G-rich	Low_comple	Low_complexity
chr7	52317863	52318264	chr7	52318263	52318406	B1_Mur2	SINE	Alu
chr7	52347513	52347914	chr7	52347847	52347932	PB1D9	SINE	Alu
chr7	52378500	52378901	.	.	.	.	.	.
chr7	52409496	52409897	.	.	.	.	.	.
chr7	52417293	52417694	.	.	.	.	.	.

chr7	52650567	52650968	chr7	52650593	52650614	(A)n	Simple_repe	Simple_repeat
chr7	52721733	52722134	.	.	.	.	.	.
chr7	52765828	52766229	chr7	52766113	52766201	B1F2	SINE	Alu
chr7	52876692	52877093	chr7	52876648	52876778	B1F1	SINE	Alu
chr7	52876692	52877093	chr7	52876671	52876791	MT2B	LTR	ERVL
chr7	52878886	52879287	chr7	52879024	52879041	MT2B2	LTR	ERVL
chr7	52878886	52879287	chr7	52879041	52879159	PB1	SINE	Alu
chr7	52878886	52879287	chr7	52879175	52879300	B1_Mur1	SINE	Alu
chr7	52894123	52894524	.	.	.	.	.	.
chr7	52935278	52935679	chr7	52935224	52935467	Tigger7	DNA	MER2_type
chr7	52935278	52935679	chr7	52935494	52935617	RSINE1	SINE	B4
chr7	52935278	52935679	chr7	52935623	52935753	Tigger7	DNA	MER2_type
chr7	52956121	52956522	.	.	.	.	.	.
chr7	52973190	52973591	.	.	.	.	.	.
chr7	53086175	53086576	.	.	.	.	.	.
chr7	53175943	53176344	.	.	.	.	.	.
chr7	54263507	54263908	chr7	54263713	54263745	(CA)n	Simple_repe	Simple_repeat
chr7	57033530	57033931	chr7	57033890	57033921	GC_rich	Low_comple	Low_complexity
chr7	59271768	59272169	chr7	59271696	59271798	ORR1C1	LTR	MaLR
chr7	59271768	59272169	chr7	59271814	59272218	MTC	LTR	MaLR
chr7	66483918	66484319	.	.	.	.	.	.
chr7	69564888	69565289	.	.	.	.	.	.
chr7	71432137	71432538	.	.	.	.	.	.
chr7	71536946	71537347	.	.	.	.	.	.
chr7	73205215	73205616	.	.	.	.	.	.
chr7	85927762	85928163	.	.	.	.	.	.
chr7	86040691	86041092	.	.	.	.	.	.
chr7	86610982	86611383	chr7	86611304	86611377	tRNA-Arg-CG	tRNA	tRNA
chr7	87065370	87065771	.	.	.	.	.	.
chr7	87390899	87391300	.	.	.	.	.	.
chr7	87405850	87406251	chr7	87405777	87405854	PB1	SINE	Alu
chr7	87405850	87406251	chr7	87405891	87405968	ID4	SINE	ID
chr7	88005497	88005898	chr7	88005865	88005891	(CCGGG)n	Simple_repe	Simple_repeat
chr7	88907632	88908033	.	.	.	.	.	.
chr7	88933843	88934244	.	.	.	.	.	.
chr7	89796891	89797292	.	.	.	.	.	.
chr7	91236799	91237200	.	.	.	.	.	.
chr7	97089599	97090000	.	.	.	.	.	.
chr7	99709750	99710151	.	.	.	.	.	.
chr7	99889836	99890237	.	.	.	.	.	.
chr7	104480541	104480942	.	.	.	.	.	.
chr7	104548410	104548811	chr7	104548435	104548464	(CA)n	Simple_repe	Simple_repeat
chr7	104629287	104629688	.	.	.	.	.	.
chr7	104844940	104845341	.	.	.	.	.	.
chr7	105268984	105269385	.	.	.	.	.	.
chr7	105294963	105295364	chr7	105295062	105295202	PB1D7	SINE	Alu
chr7	105294963	105295364	chr7	105295110	105295281	ID_B1	SINE	B4
chr7	105294963	105295364	chr7	105295291	105295388	PB1D10	SINE	Alu
chr7	105804987	105805388	.	.	.	.	.	.
chr7	105851375	105851776	.	.	.	.	.	.
chr7	106632029	106632430	chr7	106632375	106632494	ID_B1	SINE	B4
chr7	107007305	107007706	chr7	107007286	107007385	(CCG)n	Simple_repe	Simple_repeat
chr7	107269838	107270239	.	.	.	.	.	.
chr7	107375576	107375977	chr7	107375503	107375600	MIRc	SINE	MIR
chr7	107520465	107520866	.	.	.	.	.	.
chr7	107663104	107663505	.	.	.	.	.	.
chr7	107731170	107731571	.	.	.	.	.	.
chr7	107854673	107855074	.	.	.	.	.	.
chr7	108811940	108812341	.	.	.	.	.	.
chr7	109044724	109045125	.	.	.	.	.	.
chr7	109082230	109082631	.	.	.	.	.	.
chr7	109213802	109214203	chr7	109214066	109214094	AT_rich	Low_comple	Low_complexity
chr7	109627831	109628232	.	.	.	.	.	.
chr7	112788809	112789210	.	.	.	.	.	.
chr7	112884804	112885205	chr7	112885147	112885193	(CGGGG)n	Simple_repe	Simple_repeat
chr7	112959644	112960045	.	.	.	.	.	.
chr7	117129789	117130190	.	.	.	.	.	.
chr7	117161534	117161935	chr7	117161516	117161539	(CAAAA)n	Simple_repe	Simple_repeat
chr7	117205030	117205431	.	.	.	.	.	.
chr7	118172248	118172649	.	.	.	.	.	.
chr7	118266140	118266541	.	.	.	.	.	.
chr7	123236542	123236943	.	.	.	.	.	.
chr7	123477546	123477947	.	.	.	.	.	.
chr7	125259489	125259890	.	.	.	.	.	.
chr7	125387004	125387405	.	.	.	.	.	.
chr7	125855781	125856182	chr7	125855777	125855820	(CAGA)n	Simple_repe	Simple_repeat
chr7	125855781	125856182	chr7	125856143	125856170	(GGA)n	Simple_repe	Simple_repeat
chr7	125999043	125999444	.	.	.	.	.	.
chr7	127778499	127778900	.	.	.	.	.	.
chr7	128061008	128061409	chr7	128061030	128061112	tRNA-Leu-CT	tRNA	tRNA
chr7	128061008	128061409	chr7	128061224	128061254	GC_rich	Low_comple	Low_complexity
chr7	128061008	128061409	chr7	128061394	128061420	GC_rich	Low_comple	Low_complexity
chr7	129210745	129211146	.	.	.	.	.	.
chr7	129245194	129245595	.	.	.	.	.	.
chr7	129276305	129276706	.	.	.	.	.	.
chr7	129302696	129303097	.	.	.	.	.	.
chr7	130267441	130267842	chr7	130267683	130267723	(CGG)n	Simple_repe	Simple_repeat
chr7	130521161	130521562	.	.	.	.	.	.
chr7	132587910	132588311	.	.	.	.	.	.
chr7	133520732	133521133	.	.	.	.	.	.
chr7	133540366	133540767	.	.	.	.	.	.
chr7	133630487	133630888	.	.	.	.	.	.
chr7	133709782	133710183	chr7	133710125	133710222	PB1D10	SINE	Alu
chr7	133792578	133792979	.	.	.	.	.	.
chr7	133924095	133924496	.	.	.	.	.	.

chr7	133935782	133936183	.	.	.	.	.	.
chr7	134005213	134005614	.	.	.	.	.	.
chr7	134339339	134339740	.	.	.	.	.	.
chr7	134655247	134655648	chr7	134655113	134655250	B1_Mur1	SINE	Alu
chr7	134655247	134655648	chr7	134655558	134655597	(TGG)n	Simple_repe	Simple_repeat
chr7	134856582	134856983	.	.	.	.	.	.
chr7	134888785	134889186	.	.	.	.	.	.
chr7	134985904	134986305	.	.	.	.	.	.
chr7	135020183	135020584	chr7	135020174	135020298	PB1D7	SINE	Alu
chr7	135039083	135039484	chr7	135039392	135039540	B1_Mus2	SINE	Alu
chr7	135047358	135047759	chr7	135047247	135047407	B2_Mm1t	SINE	B2
chr7	135055796	135056197	chr7	135055761	135055888	B1_Mur1	SINE	Alu
chr7	135381214	135381615	.	.	.	.	.	.
chr7	135605043	135605444	.	.	.	.	.	.
chr7	135888135	135888536	chr7	135888060	135888163	PB1D10	SINE	Alu
chr7	136735103	136735504	.	.	.	.	.	.
chr7	137662900	137663301	chr7	137662985	137663049	(CCG)n	Simple_repe	Simple_repeat
chr7	138009042	138009443	.	.	.	.	.	.
chr7	138703405	138703806	.	.	.	.	.	.
chr7	139802151	139802552	.	.	.	.	.	.
chr7	140044168	140044569	.	.	.	.	.	.
chr7	140050676	140051077	.	.	.	.	.	.
chr7	146037737	146038138	chr7	146038085	146038128	(CGG)n	Simple_repe	Simple_repeat
chr7	147323306	147323707	chr7	147323297	147323323	AT_rich	Low_comple	Low_complexity
chr7	148042017	148042418	.	.	.	.	.	.
chr7	148043055	148043456	chr7	148043055	148043094	(CACCC)n	Simple_repe	Simple_repeat
chr7	148068060	148068461	.	.	.	.	.	.
chr7	148305395	148305796	chr7	148305394	148305630	RLTR42	LTR	ERVK
chr7	148305395	148305796	chr7	148305630	148305694	MLT1J	LTR	MaLR
chr7	148316963	148317364	.	.	.	.	.	.
chr7	148414430	148414831	.	.	.	.	.	.
chr7	148513920	148514321	.	.	.	.	.	.
chr7	148577880	148578281	.	.	.	.	.	.
chr7	148633024	148633425	.	.	.	.	.	.
chr7	149246818	149247219	.	.	.	.	.	.
chr7	150255067	150255468	.	.	.	.	.	.
chr7	150785816	150786217	.	.	.	.	.	.
chr7	150969830	150970231	.	.	.	.	.	.
chr7	152100843	152101244	.	.	.	.	.	.
chr8	3492927	3493328	chr8	3493039	3493079	GC_rich	Low_comple	Low_complexity
chr8	3500249	3500650	.	.	.	.	.	.
chr8	3516629	3517030	.	.	.	.	.	.
chr8	3620335	3620736	chr8	3620701	3620850	B1_Mur2	SINE	Alu
chr8	3803130	3803531	chr8	3802776	3803137	RMER16-int	LTR	ERVK
chr8	3803130	3803531	chr8	3803130	3803194	MMVL30-int	LTR	ERV1
chr8	3803130	3803531	chr8	3803356	3803440	IAPEy-int	LTR	ERVK
chr8	4275750	4276151	.	.	.	.	.	.
chr8	4612872	4613273	chr8	4612755	4612915	RLTR13D3	LTR	ERVK
chr8	4779403	4779804	.	.	.	.	.	.
chr8	8690338	8690739	chr8	8690320	8690407	GC_rich	Low_comple	Low_complexity
chr8	11497354	11497755	.	.	.	.	.	.
chr8	11555576	11555977	.	.	.	.	.	.
chr8	12671923	12672324	.	.	.	.	.	.
chr8	13159001	13159402	chr8	13159058	13159091	G-rich	Low_comple	Low_complexity
chr8	13159001	13159402	chr8	13159390	13159411	GC_rich	Low_comple	Low_complexity
chr8	13287932	13288333	.	.	.	.	.	.
chr8	18594893	18595294	chr8	18594736	18594940	B3	SINE	B2
chr8	19730774	19731175	chr8	19730766	19730881	RSINE1	SINE	B4
chr8	19957499	19957900	chr8	19957494	19957589	RSINE1	SINE	B4
chr8	19957499	19957900	chr8	19957876	19957993	B3	SINE	B2
chr8	20020223	20020624	.	.	.	.	.	.
chr8	23170935	23171336	.	.	.	.	.	.
chr8	23296293	23296694	.	.	.	.	.	.
chr8	23521634	23522035	.	.	.	.	.	.
chr8	23917580	23917981	.	.	.	.	.	.
chr8	26628991	26629392	.	.	.	.	.	.
chr8	26712423	26712824	chr8	26712724	26712770	(CGG)n	Simple_repe	Simple_repeat
chr8	28135958	28136359	chr8	28136121	28136198	ID4	SINE	ID
chr8	28135958	28136359	chr8	28136233	28136368	B1F2	SINE	Alu
chr8	32260361	32260762	chr8	32260332	32260440	U13	snRNA	snRNA
chr8	32279043	32279444	.	.	.	.	.	.
chr8	34495917	34496318	.	.	.	.	.	.
chr8	34752035	34752436	.	.	.	.	.	.
chr8	34842160	34842561	chr8	34842475	34842503	GC_rich	Low_comple	Low_complexity
chr8	34842160	34842561	chr8	34842524	34842557	(CGTG)n	Simple_repe	Simple_repeat
chr8	36028630	36029031	.	.	.	.	.	.
chr8	41720213	41720614	chr8	41720381	41720478	PB1	SINE	Alu
chr8	42324622	42325023	.	.	.	.	.	.
chr8	47060606	47061007	.	.	.	.	.	.
chr8	47637008	47637409	.	.	.	.	.	.
chr8	48618656	48619057	.	.	.	.	.	.
chr8	48799141	48799542	.	.	.	.	.	.
chr8	59966550	59966951	.	.	.	.	.	.
chr8	63369016	63369417	.	.	.	.	.	.
chr8	63966294	63966695	chr8	63966265	63966358	PB1D7	SINE	Alu
chr8	67472339	67472740	.	.	.	.	.	.
chr8	69010300	69010701	.	.	.	.	.	.
chr8	70018455	70018856	.	.	.	.	.	.
chr8	72566514	72566915	chr8	72566540	72566582	(CCG)n	Simple_repe	Simple_repeat
chr8	72695993	72696394	chr8	72695934	72696044	B1_Mus1	SINE	Alu
chr8	72695993	72696394	chr8	72696044	72696100	(CA)n	Simple_repe	Simple_repeat
chr8	72806578	72806979	chr8	72806753	72806852	C-rich	Low_comple	Low_complexity
chr8	72806578	72806979	chr8	72806868	72806977	(CGGGG)n	Simple_repe	Simple_repeat
chr8	72826429	72826830	.	.	.	.	.	.
chr8	73051669	73052070	chr8	73051668	73051696	GC_rich	Low_comple	Low_complexity

chr8	73196877	73197278	chr8	73196780	73196916	B1_Mus1	SINE	Alu
chr8	73196877	73197278	chr8	73196916	73196939	(CAAAA)n	Simple_repe	Simple_repeat
chr8	73222458	73222859	.	.	.	.	.	.
chr8	73397448	73397849	.	.	.	.	.	.
chr8	73421296	73421697	.	.	.	.	.	.
chr8	73906509	73906910	.	.	.	.	.	.
chr8	73920553	73920954	.	.	.	.	.	.
chr8	73988494	73988895	.	.	.	.	.	.
chr8	73992694	73993095	chr8	73992642	73992736	PB1D7	SINE	Alu
chr8	74012317	74012718	.	.	.	.	.	.
chr8	74066528	74066929	.	.	.	.	.	.
chr8	74432177	74432578	.	.	.	.	.	.
chr8	74743378	74743779	chr8	74743280	74743388	B1F2	SINE	Alu
chr8	74967538	74967939	.	.	.	.	.	.
chr8	74998915	74999316	.	.	.	.	.	.
chr8	75071986	75072387	.	.	.	.	.	.
chr8	82163007	82163408	.	.	.	.	.	.
chr8	83404271	83404672	chr8	83404267	83404317	GC_rich	Low_comple	Low_complexity
chr8	83404271	83404672	chr8	83404510	83404539	GC_rich	Low_comple	Low_complexity
chr8	83538620	83539021	.	.	.	.	.	.
chr8	85856166	85856567	.	.	.	.	.	.
chr8	86090447	86090848	chr8	86090389	86090460	B4A	SINE	B4
chr8	86590213	86590614	.	.	.	.	.	.
chr8	86671645	86672046	.	.	.	.	.	.
chr8	87364371	87364772	.	.	.	.	.	.
chr8	87380655	87381056	chr8	87380561	87380657	PB1D10	SINE	Alu
chr8	87417114	87417515	.	.	.	.	.	.
chr8	87489859	87490260	chr8	87490241	87490358	ID_B1	SINE	B4
chr8	87550545	87550946	.	.	.	.	.	.
chr8	88016196	88016597	.	.	.	.	.	.
chr8	93593719	93594120	.	.	.	.	.	.
chr8	93837049	93837450	.	.	.	.	.	.
chr8	94879960	94880361	.	.	.	.	.	.
chr8	96560867	96561268	.	.	.	.	.	.
chr8	96738218	96738619	chr8	96738336	96738364	GC_rich	Low_comple	Low_complexity
chr8	97578778	97579179	chr8	97578790	97578863	MER63D	DNA	AcHobo
chr8	97578778	97579179	chr8	97578893	97578920	(TGG)n	Simple_repe	Simple_repeat
chr8	98157188	98157589	.	.	.	.	.	.
chr8	98331833	98332234	.	.	.	.	.	.
chr8	98377268	98377669	.	.	.	.	.	.
chr8	107165413	107165814	.	.	.	.	.	.
chr8	107849994	107850395	.	.	.	.	.	.
chr8	108160094	108160495	chr8	108160191	108160250	(CGCGG)n	Simple_repe	Simple_repeat
chr8	108160094	108160495	chr8	108160356	108160377	GC_rich	Low_comple	Low_complexity
chr8	108231956	108232357	.	.	.	.	.	.
chr8	108351097	108351498	.	.	.	.	.	.
chr8	108375769	108376170	chr8	108376106	108376140	AT_rich	Low_comple	Low_complexity
chr8	108375769	108376170	chr8	108376166	108376317	B3	SINE	B2
chr8	108378520	108378921	chr8	108378589	108378610	(GGGTG)n	Simple_repe	Simple_repeat
chr8	108384274	108384675	.	.	.	.	.	.
chr8	108404582	108404983	.	.	.	.	.	.
chr8	108583124	108583525	chr8	108583445	108583549	G-rich	Low_comple	Low_complexity
chr8	108734620	108735021	.	.	.	.	.	.
chr8	108861892	108862293	.	.	.	.	.	.
chr8	108938958	108939359	chr8	108938974	108939026	(CA)n	Simple_repe	Simple_repeat
chr8	109572359	109572760	.	.	.	.	.	.
chr8	109580440	109580841	.	.	.	.	.	.
chr8	109620311	109620712	chr8	109620680	109620792	PB1D9	SINE	Alu
chr8	109927000	109927401	.	.	.	.	.	.
chr8	110112204	110112605	chr8	110112512	110112548	(TTTTTG)n	Simple_repe	Simple_repeat
chr8	112089328	112089729	.	.	.	.	.	.
chr8	112231127	112231528	chr8	112231304	112231422	B1_Mm	SINE	Alu
chr8	112231127	112231528	chr8	112231445	112231554	PB1D10	SINE	Alu
chr8	112302252	112302653	.	.	.	.	.	.
chr8	112740122	112740523	chr8	112740032	112740219	Lx8	LINE	L1
chr8	112740122	112740523	chr8	112740422	112740815	L1ME2	LINE	L1
chr8	113370696	113371097	.	.	.	.	.	.
chr8	113426181	113426582	chr8	113426538	113426586	(TTTG)n	Simple_repe	Simple_repeat
chr8	113443400	113443801	.	.	.	.	.	.
chr8	113557470	113557871	.	.	.	.	.	.
chr8	113579962	113580363	.	.	.	.	.	.
chr8	114045966	114046367	.	.	.	.	.	.
chr8	114167107	114167508	.	.	.	.	.	.
chr8	114255868	114256269	chr8	114255907	114255930	GC_rich	Low_comple	Low_complexity
chr8	114378123	114378524	chr8	114378443	114378860	MER82	DNA	MER2_type
chr8	114516025	114516426	.	.	.	.	.	.
chr8	114535039	114535440	.	.	.	.	.	.
chr8	116963130	116963531	chr8	116962964	116963169	RMER30	DNA	MER1_type
chr8	119502747	119503148	.	.	.	.	.	.
chr8	121868156	121868557	.	.	.	.	.	.
chr8	122082510	122082911	.	.	.	.	.	.
chr8	122625132	122625533	.	.	.	.	.	.
chr8	123191942	123192343	chr8	123192030	123192099	(CCCCG)n	Simple_repe	Simple_repeat
chr8	124473866	124474267	.	.	.	.	.	.
chr8	125589112	125589513	chr8	125589450	125589485	GC_rich	Low_comple	Low_complexity
chr8	125626071	125626472	.	.	.	.	.	.
chr8	127245774	127246175	.	.	.	.	.	.
chr8	128946908	128947309	.	.	.	.	.	.
chr8	129494822	129495223	.	.	.	.	.	.
chr9	3037996	3038397	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3335252	3335653	chr9	3334707	3335338	Lx9	LINE	L1
chr9	7184302	7184703	.	.	.	.	.	.
chr9	7836876	7837277	.	.	.	.	.	.
chr9	13553420	13553821	.	.	.	.	.	.
chr9	14304848	14305249	chr9	14304967	14304987	(A)n	Simple_repe	Simple_repeat

chr9	15084203	15084604	chr9	15084535	15084576	(TTTG)n	Simple_repe	Simple_repeat
chr9	18096339	18096740	.	.	.	.	.	.
chr9	19426218	19426619	chr9	19426199	19426243	HAL1-3A_ME	LINE	L1
chr9	19426218	19426619	chr9	19426456	19426596	LTR33C	LTR	ERVL
chr9	20189395	20189796	.	.	.	.	.	.
chr9	20264296	20264697	.	.	.	.	.	.
chr9	20692478	20692879	.	.	.	.	.	.
chr9	20877792	20878193	chr9	20878109	20878172	B3	SINE	B2
chr9	20896235	20896636	.	.	.	.	.	.
chr9	21300894	21301295	chr9	21301271	21301330	(TG)n	Simple_repe	Simple_repeat
chr9	21397105	21397506	.	.	.	.	.	.
chr9	22215648	22216049	.	.	.	.	.	.
chr9	22279920	22280321	.	.	.	.	.	.
chr9	25059856	25060257	chr9	25059863	25059890	(A)n	Simple_repe	Simple_repeat
chr9	26807008	26807409	.	.	.	.	.	.
chr9	30234408	30234809	.	.	.	.	.	.
chr9	30837774	30838175	chr9	30837949	30837972	GC_rich	Low_comple	Low_complexity
chr9	30837774	30838175	chr9	30838036	30838067	(CCCG)n	Simple_repe	Simple_repeat
chr9	34983472	34983873	.	.	.	.	.	.
chr9	35366805	35367206	.	.	.	.	.	.
chr9	36604833	36605234	.	.	.	.	.	.
chr9	42280123	42280524	.	.	.	.	.	.
chr9	44142262	44142663	chr9	44142153	44142299	B1_Mus1	SINE	Alu
chr9	44215537	44215938	.	.	.	.	.	.
chr9	44225963	44226364	.	.	.	.	.	.
chr9	44580786	44581187	.	.	.	.	.	.
chr9	44728633	44729034	.	.	.	.	.	.
chr9	45636639	45637040	.	.	.	.	.	.
chr9	45646412	45646813	chr9	45646394	45646437	(TAAA)n	Simple_repe	Simple_repeat
chr9	45761831	45762232	.	.	.	.	.	.
chr9	48288600	48289001	.	.	.	.	.	.
chr9	48302739	48303140	.	.	.	.	.	.
chr9	48863479	48863880	.	.	.	.	.	.
chr9	50336647	50337048	.	.	.	.	.	.
chr9	50411711	50412112	.	.	.	.	.	.
chr9	53212501	53212902	chr9	53212420	53212770	RLTR15	LTR	ERVK
chr9	56008636	56009037	.	.	.	.	.	.
chr9	56266228	56266629	.	.	.	.	.	.
chr9	56798428	56798829	.	.	.	.	.	.
chr9	56978295	56978696	chr9	56978293	56978347	ID	SINE	ID
chr9	56995791	56996192	.	.	.	.	.	.
chr9	57005889	57006290	.	.	.	.	.	.
chr9	57287779	57288180	chr9	57288083	57288217	L1MEe	LINE	L1
chr9	57400402	57400803	chr9	57400733	57400879	L2a	LINE	L2
chr9	57758566	57758967	chr9	57758960	57759085	MIRb	SINE	MIR
chr9	58158914	58159315	chr9	58158919	58159066	B1_Mm	SINE	Alu
chr9	58301756	58302157	.	.	.	.	.	.
chr9	62659630	62660031	.	.	.	.	.	.
chr9	63225549	63225950	.	.	.	.	.	.
chr9	63246999	63247400	.	.	.	.	.	.
chr9	64585440	64585841	.	.	.	.	.	.
chr9	65062273	65062674	chr9	65062186	65062364	B3A	SINE	B2
chr9	65062273	65062674	chr9	65062213	65062376	RSINE1	SINE	B4
chr9	65524080	65524481	chr9	65523928	65524125	B3	SINE	B2
chr9	65676350	65676751	.	.	.	.	.	.
chr9	65732705	65733106	.	.	.	.	.	.
chr9	65756527	65756928	chr9	65756819	65756870	CT-rich	Low_comple	Low_complexity
chr9	65907596	65907997	.	.	.	.	.	.
chr9	65974221	65974622	.	.	.	.	.	.
chr9	66767424	66767825	.	.	.	.	.	.
chr9	69837088	69837489	.	.	.	.	.	.
chr9	69860170	69860571	chr9	69860471	69860517	GC_rich	Low_comple	Low_complexity
chr9	70054815	70055216	.	.	.	.	.	.
chr9	72122430	72122831	chr9	72122766	72122802	(TCC)n	Simple_repe	Simple_repeat
chr9	72378043	72378444	.	.	.	.	.	.
chr9	72833095	72833496	.	.	.	.	.	.
chr9	72961026	72961427	chr9	72961098	72961151	(CTG)n	Simple_repe	Simple_repeat
chr9	74885227	74885628	.	.	.	.	.	.
chr9	74918755	74919156	chr9	74918973	74918997	(CGG)n	Simple_repe	Simple_repeat
chr9	75162940	75163341	chr9	75162954	75162978	(TTTTG)n	Simple_repe	Simple_repeat
chr9	75162940	75163341	chr9	75162984	75163056	LTR16E1	LTR	ERVL
chr9	75407325	75407726	chr9	75407684	75407711	(T)n	Simple_repe	Simple_repeat
chr9	77956718	77957119	.	.	.	.	.	.
chr9	78023386	78023787	chr9	78023108	78023440	7SK	RNA	RNA
chr9	78329308	78329709	.	.	.	.	.	.
chr9	82723340	82723741	.	.	.	.	.	.
chr9	83334530	83334931	.	.	.	.	.	.
chr9	85642842	85643243	.	.	.	.	.	.
chr9	86360613	86361014	.	.	.	.	.	.
chr9	87150220	87150621	.	.	.	.	.	.
chr9	88333798	88334199	.	.	.	.	.	.
chr9	88442657	88443058	.	.	.	.	.	.
chr9	89599564	89599965	.	.	.	.	.	.
chr9	90009431	90009832	.	.	.	.	.	.
chr9	90165465	90165866	chr9	90165449	90165622	C-rich	Low_comple	Low_complexity
chr9	90165465	90165866	chr9	90165565	90165694	(CCGCG)n	Simple_repe	Simple_repeat
chr9	95412184	95412585	.	.	.	.	.	.
chr9	97011492	97011893	.	.	.	.	.	.
chr9	98501910	98502311	chr9	98502186	98502246	B4	SINE	B4
chr9	99468985	99469386	chr9	99469089	99469112	GC_rich	Low_comple	Low_complexity
chr9	103104279	103104680	chr9	103104620	103104697	Lx8	LINE	L1
chr9	103207219	103207620	chr9	103207586	103207667	GC_rich	Low_comple	Low_complexity
chr9	105297438	105297839	.	.	.	.	.	.
chr9	106062205	106062606	.	.	.	.	.	.
chr9	106073028	106073429	.	.	.	.	.	.

chr9	106183140	106183541	.	.	.	.	.	.
chr9	106331605	106332006	chr9	106331572	106331667	PB1D10	SINE	Alu
chr9	106723893	106724294	.	.	.	.	.	.
chr9	106793505	106793906	.	.	.	.	.	.
chr9	107436037	107436438	chr9	107436348	107436387	GC_rich	Low_comple	Low_complexity
chr9	107444040	107444441	.	.	.	.	.	.
chr9	107465238	107465639	.	.	.	.	.	.
chr9	107489750	107490151	.	.	.	.	.	.
chr9	107673194	107673595	.	.	.	.	.	.
chr9	107774979	107775380	.	.	.	.	.	.
chr9	107790262	107790663	.	.	.	.	.	.
chr9	107853065	107853466	.	.	.	.	.	.
chr9	108192551	108192952	.	.	.	.	.	.
chr9	108208314	108208715	chr9	108208698	108208755	(CCCG)n	Simple_repe	Simple_repeat
chr9	108362629	108363030	.	.	.	.	.	.
chr9	108551530	108551931	chr9	108551585	108551628	(CAGGC)n	Simple_repe	Simple_repeat
chr9	108984760	108985161	.	.	.	.	.	.
chr9	109777601	109778002	chr9	109777677	109777714	(A)n	Simple_repe	Simple_repeat
chr9	110019753	110020154	.	.	.	.	.	.
chr9	110207755	110208156	.	.	.	.	.	.
chr9	110235621	110236022	chr9	110235885	110235907	GC_rich	Low_comple	Low_complexity
chr9	110310606	110311007	.	.	.	.	.	.
chr9	111020395	111020796	.	.	.	.	.	.
chr9	111174034	111174435	.	.	.	.	.	.
chr9	113839840	113840241	chr9	113840194	113840273	G-rich	Low_comple	Low_complexity
chr9	114549230	114549631	.	.	.	.	.	.
chr9	114842983	114843384	.	.	.	.	.	.
chr9	117949345	117949746	.	.	.	.	.	.
chr9	119353777	119354178	.	.	.	.	.	.
chr9	121905003	121905404	.	.	.	.	.	.
chr9	122795729	122796130	.	.	.	.	.	.
chr9	123760972	123761373	.	.	.	.	.	.
chrX	7182352	7182753	.	.	.	.	.	.
chrX	7273980	7274381	chrX	7273970	7274095	B3	SINE	B2
chrX	7305420	7305821	.	.	.	.	.	.
chrX	7418955	7419356	chrX	7419299	7419340	GC_rich	Low_comple	Low_complexity
chrX	7709046	7709447	.	.	.	.	.	.
chrX	7829343	7829744	.	.	.	.	.	.
chrX	12250512	12250913	.	.	.	.	.	.
chrX	17149335	17149736	chrX	17149618	17149680	T-rich	Low_comple	Low_complexity
chrX	20235199	20235600	.	.	.	.	.	.
chrX	20265846	20266247	chrX	20265863	20265905	GC_rich	Low_comple	Low_complexity
chrX	34650342	34650743	chrX	34650735	34650884	B1_Mus1	SINE	Alu
chrX	35954205	35954606	.	.	.	.	.	.
chrX	35987873	35988274	.	.	.	.	.	.
chrX	39264919	39265320	.	.	.	.	.	.
chrX	45947588	45947989	chrX	45947569	45947644	GA-rich	Low_comple	Low_complexity
chrX	45976678	45977079	chrX	45977028	45977080	(CCGGG)n	Simple_repe	Simple_repeat
chrX	46048072	46048473	.	.	.	.	.	.
chrX	46641412	46641813	.	.	.	.	.	.
chrX	50723457	50723858	.	.	.	.	.	.
chrX	51100691	51101092	.	.	.	.	.	.
chrX	53599292	53599693	.	.	.	.	.	.
chrX	53851030	53851431	.	.	.	.	.	.
chrX	57657864	57658265	.	.	.	.	.	.
chrX	68467777	68468178	chrX	68467797	68467825	(T)n	Simple_repe	Simple_repeat
chrX	68617738	68618139	.	.	.	.	.	.
chrX	68746370	68746771	.	.	.	.	.	.
chrX	71674804	71675205	chrX	71674730	71674833	PB1D9	SINE	Alu
chrX	92853654	92854055	.	.	.	.	.	.
chrX	93152230	93152631	chrX	93152611	93152636	(T)n	Simple_repe	Simple_repeat
chrX	94571818	94572219	.	.	.	.	.	.
chrX	96086163	96086564	.	.	.	.	.	.
chrX	97689391	97689792	.	.	.	.	.	.
chrX	98417802	98418203	chrX	98417880	98417916	(CACG)n	Simple_repe	Simple_repeat
chrX	98449229	98449630	.	.	.	.	.	.
chrX	98727693	98728094	.	.	.	.	.	.
chrX	98835145	98835546	.	.	.	.	.	.
chrX	99314610	99315011	.	.	.	.	.	.
chrX	99700552	99700953	.	.	.	.	.	.
chrX	101608994	101609395	chrX	101609390	101609486	MER53	DNA	hAT
chrX	102265327	102265728	.	.	.	.	.	.
chrX	103210775	103211176	.	.	.	.	.	.
chrX	110298986	110299387	.	.	.	.	.	.
chrX	132420233	132420634	.	.	.	.	.	.
chrX	132705700	132706101	chrX	132705736	132705800	C-rich	Low_comple	Low_complexity
chrX	133276049	133276450	.	.	.	.	.	.
chrX	136219251	136219652	.	.	.	.	.	.
chrX	136532938	136533339	.	.	.	.	.	.
chrX	137491178	137491579	.	.	.	.	.	.
chrX	147778177	147778578	.	.	.	.	.	.
chrX	147955453	147955854	.	.	.	.	.	.
chrX	148450784	148451185	.	.	.	.	.	.
chrX	148803147	148803548	.	.	.	.	.	.
chrX	155970375	155970776	chrX	155970687	155970742	(CGG)n	Simple_repe	Simple_repeat
chrX	159267388	159267789	.	.	.	.	.	.
chrX	159339414	159339815	chrX	159339442	159339494	GA-rich	Low_comple	Low_complexity
chrX	160396402	160396803	.	.	.	.	.	.
chrX	161418412	161418813	chrX	161418802	161418914	PB1D7	SINE	Alu
chrX	163820673	163821074	chrX	163821063	163821325	Cheshire	DNA	MER1_type
chrX	165110403	165110804	.	.	.	.	.	.

3T3 cells

Zfp143 peaks <= 2kb from TSS			Repeats from repeatMasker (USCS) table					
Chromosome	Start	End	Chromosome	Start	End	repName	repClass	repFamily
chr1	5005376	5005777	.	.	.	.	.	.
chr1	7387573	7387974	chr1	7387592	7387630	(TAAA)n	Simple_repe	Simple_repeat
chr1	7387573	7387974	chr1	7387642	7387678	AT_rich	Low_comple	Low_complexity
chr1	12634710	12635111	chr1	12634715	12634833	MIR	SINE	MIR
chr1	12634710	12635111	chr1	12634855	12634921	(GAATG)n	Simple_repe	Simple_repeat
chr1	12634710	12635111	chr1	12635016	12635189	Lx7	LINE	L1
chr1	16218359	16218760	.	.	.	.	.	.
chr1	20856925	20857326	chr1	20857046	20857137	RLTR15	LTR	ERVK
chr1	20856925	20857326	chr1	20857289	20857445	RLTR15	LTR	ERVK
chr1	24462372	24462773	chr1	24462413	24462564	MER31B	LTR	ERV1
chr1	24619754	24620155	.	.	.	.	.	.
chr1	24740719	24741120	chr1	24740747	24740864	L1ME1	LINE	L1
chr1	31387822	31388223	chr1	31387924	31388048	MLT1J	LTR	MaLR
chr1	31850821	31851222	chr1	31850716	31850863	B1_Mus1	SINE	Alu
chr1	31850821	31851222	chr1	31851105	31851207	MIR	SINE	MIR
chr1	34166348	34166749	chr1	34166346	34166493	B1_Mur2	SINE	Alu
chr1	34166348	34166749	chr1	34166504	34166535	(CAGA)n	Simple_repe	Simple_repeat
chr1	34166348	34166749	chr1	34166731	34166797	GA-rich	Low_comple	Low_complexity
chr1	34196913	34197314	.	.	.	.	.	.
chr1	36360465	36360866	chr1	36360759	36360799	MIR	SINE	MIR
chr1	36382825	36383226	chr1	36382982	36383088	MER117	DNA	MER1_type
chr1	36489936	36490337	chr1	36489846	36489950	RSINE1	SINE	B4
chr1	36489936	36490337	chr1	36490312	36490445	RSINE1	SINE	B4
chr1	39770929	39771330	.	.	.	.	.	.
chr1	39963746	39964147	.	.	.	.	.	.
chr1	40415579	40415980	.	.	.	.	.	.
chr1	40450203	40450604	chr1	40450599	40450840	MLT1B	LTR	MaLR
chr1	40714852	40715253	.	.	.	.	.	.
chr1	40789741	40790142	.	.	.	.	.	.
chr1	43204302	43204703	chr1	43204302	43204521	MER44B	DNA	MER2_type
chr1	43281035	43281436	chr1	43281041	43281112	Tigger7	DNA	MER2_type
chr1	43326465	43326866	chr1	43326814	43327482	L1Md_F3	LINE	L1
chr1	45684610	45685011	.	.	.	.	.	.
chr1	45894582	45894983	chr1	45894649	45894690	MLT1L	LTR	MaLR
chr1	48938216	48938617	.	.	.	.	.	.
chr1	51182732	51183133	.	.	.	.	.	.
chr1	51273975	51274376	.	.	.	.	.	.
chr1	51321900	51322301	chr1	51321901	51321960	A-rich	Low_comple	Low_complexity
chr1	51582702	51583103	chr1	51583033	51583063	AT_rich	Low_comple	Low_complexity
chr1	51725900	51726301	chr1	51725965	51726078	RLTR15	LTR	ERVK
chr1	51725900	51726301	chr1	51726181	51726360	RLTR15	LTR	ERVK
chr1	52170552	52170953	.	.	.	.	.	.
chr1	53894898	53895299	.	.	.	.	.	.
chr1	53902102	53902503	.	.	.	.	.	.
chr1	53997050	53997451	.	.	.	.	.	.
chr1	54987478	54987879	chr1	54987392	54987773	RMER10B	LTR	ERVL
chr1	55467456	55467857	.	.	.	.	.	.
chr1	56014680	56015081	.	.	.	.	.	.
chr1	57111482	57111883	chr1	57111144	57111555	MTC	LTR	MaLR
chr1	57111482	57111883	chr1	57111606	57111696	B1F	SINE	Alu
chr1	58314016	58314417	chr1	58314254	58314282	(CA)n	Simple_repe	Simple_repeat
chr1	58416349	58416750	.	.	.	.	.	.
chr1	58422683	58423084	chr1	58423026	58423156	B1_Mus2	SINE	Alu
chr1	58818314	58818715	.	.	.	.	.	.
chr1	58854253	58854654	.	.	.	.	.	.
chr1	59002984	59003385	.	.	.	.	.	.
chr1	59521714	59522115	.	.	.	.	.	.
chr1	59637080	59637481	.	.	.	.	.	.
chr1	60681070	60681471	chr1	60681007	60681337	RLTR15	LTR	ERVK
chr1	60681070	60681471	chr1	60681437	60681469	(CAAAAA)n	Simple_repe	Simple_repeat
chr1	60882662	60883063	.	.	.	.	.	.
chr1	62768422	62768823	chr1	62768811	62768849	(CA)n	Simple_repe	Simple_repeat
chr1	63822980	63823381	.	.	.	.	.	.
chr1	64272664	64273065	.	.	.	.	.	.
chr1	64347719	64348120	chr1	64348117	64348265	MIR3	SINE	MIR
chr1	65158623	65159024	.	.	.	.	.	.
chr1	65400711	65401112	chr1	65400590	65401107	RLTR19B	LTR	ERVK
chr1	65400711	65401112	chr1	65401107	65401243	B1_Mus1	SINE	Alu
chr1	65436186	65436587	chr1	65436342	65436407	MIR	SINE	MIR
chr1	65436186	65436587	chr1	65436547	65436567	(CA)n	Simple_repe	Simple_repeat
chr1	65436186	65436587	chr1	65436567	65436593	(CG)n	Simple_repe	Simple_repeat
chr1	71798946	71799347	chr1	71799313	71800188	RMER19B	LTR	ERVK
chr1	72081079	72081480	.	.	.	.	.	.
chr1	72117034	72117435	.	.	.	.	.	.
chr1	72230151	72230552	chr1	72230414	72230488	ID2	SINE	ID
chr1	72230151	72230552	chr1	72230496	72230699	B4A	SINE	B4
chr1	72272395	72272796	.	.	.	.	.	.
chr1	72283097	72283498	.	.	.	.	.	.
chr1	72290433	72290834	chr1	72290786	72290971	U2	snRNA	snRNA
chr1	72301249	72301650	chr1	72301581	72301768	U2	snRNA	snRNA
chr1	72348460	72348861	chr1	72348521	72348731	MLT1J	LTR	MaLR
chr1	72348460	72348861	chr1	72348802	72348830	AT_rich	Low_comple	Low_complexity
chr1	74075339	74075740	.	.	.	.	.	.
chr1	74223763	74224164	chr1	74224021	74224129	HAL1	LINE	L1
chr1	74433328	74433729	.	.	.	.	.	.
chr1	75241414	75241815	.	.	.	.	.	.
chr1	75289512	75289913	.	.	.	.	.	.
chr1	75556152	75556553	.	.	.	.	.	.
chr1	75650304	75650705	chr1	75650567	75650642	MER63D	DNA	AcHobo
chr1	77549396	77549797	.	.	.	.	.	.
chr1	78534108	78534509	.	.	.	.	.	.
chr1	82808242	82808643	.	.	.	.	.	.

repName	count
MLT1J	69
(TG)n	60
B3	54
(CA)n	52
ID_B1	49
RSINE1	42
RLTR15	39
B4A	38
MLT1J1	38
MIR	35
MIRb	35
B3A	34
AT_rich	32
MLT1J2	30
GSAT_MM	29
(GA)n	26
B1_Mus1	24
B1F	23
PB1D10	22
B2_Mm2	22
PB1	22
MIRc	21
RLTR42	21
PB1D7	20
(TC)n	20
B4	20
ID4	20
ORR1E	20
CT-rich	20
RLTR23	18
L2b	18
GA-rich	17
L2	17
B1_Mus2	16
RMER15	16
Lx8	15
L2a	15
LTR33B	14
B1_Mur2	13
L1M5	13
LSU-rRNA_H	13
MTEa	13
Lx9	13
(A)n	13
GC_rich	12
B1_Mur4	12
LTR33A	12
B1_Mur1	12
MTC	11
MIR3	11
ID4_	11
SYNREP_MM	11
Lx7	10
B2_Mm1a	10
URR1A	9
RMER10A	9
(T)n	9
(CAGA)n	8
L1MB8	8
PB1D9	8
(CATTC)n	8
B1F1	8
URR1B	8
MER20	8
L2c	8
L1Md_F2	8
L1M4	8
U2	7
ORR1C1	7
MER5B	7
7SLRNA	7
(CAAAA)n	7
RLTR44-int	7
MLT1A1	7
MLT2F	7
MTE2a	7
MTD	7
G-rich	7
L1MC3	7
L1ME1	6
Tigger7	6
MT2B	6
B1_Mm	6
U5	6
ZP3AR	6
ID	6
Lx5	6
MLT1N2	6
RMER17C	6
MER5A	5
Tigger5	5
ORR1B1	5

repClass	count
SINE	620
LTR	585
Simple_repe	335
LINE	258
DNA	109
Low_comple	100
Satellite	49
snRNA	19
rRNA	16
Unknown	9
srpRNA	7
tRNA	7
Other	5
scRNA	4

repFamily	count
Simple_repe	335
MaLR	287
Alu	197
L1	191
B4	149
ERVK	133
B2	125
ERVL	119
MIR	105
Low_comple	100
MER1_type	71
L2	58
Satellite	48
ERV1	40
ID	40
MER2_type	20
snRNA	19
rRNA	16
Unknown	9
srpRNA	7
tRNA	7
AcHobo	6
CR1	6
Tip100	5
Other	5
SINE	4
scRNA	4
RTE	3
Gypsy	3
Mariner	2
Tigger	2
Genie?	2
DNA	1
Gypsy?	1
TcMar	1
centr	1
MER1_type?	1

chr1	84878052	84878453	chr1	84877907	84878105	B3A	SINE	B2
chr1	84878052	84878453	chr1	84878153	84878375	RMER15	LTR	ERVL
chr1	84878052	84878453	chr1	84878405	84878505	GA-rich	Low_comple	Low_complexity
chr1	84961470	84961871	chr1	84961533	84961670	LTR33B	LTR	ERVL
chr1	84961470	84961871	chr1	84961830	84961923	MIRb	SINE	MIR
chr1	85087300	85087701	chr1	85086689	85087413	Lx4A	LINE	L1
chr1	85276827	85277228	.	.	.	.	.	.
chr1	87447450	87447851	chr1	87447551	87447688	LTR33B	LTR	ERVL
chr1	87447450	87447851	chr1	87447835	87447941	MIRb	SINE	MIR
chr1	87488738	87489139	chr1	87488600	87489243	Lx7	LINE	L1
chr1	87928723	87929124	.	.	.	.	.	.
chr1	88367174	88367575	.	.	.	.	.	.
chr1	88383898	88384299	chr1	88383997	88384045	GA-rich	Low_comple	Low_complexity
chr1	88524837	88525238	.	.	.	.	.	.
chr1	88531338	88531739	chr1	88531396	88531438	(CA)n	Simple_repe	Simple_repeat
chr1	88531338	88531739	chr1	88531444	88531567	MLT1J2	LTR	MaLR
chr1	88531338	88531739	chr1	88531599	88531732	MER34A1	LTR	ERV1
chr1	88956256	88956657	chr1	88956453	88956740	Lx8	LINE	L1
chr1	89382984	89383385	.	.	.	.	.	.
chr1	89450199	89450600	chr1	89450589	89450601	B4A	SINE	B4
chr1	90371251	90371652	.	.	.	.	.	.
chr1	90422736	90423137	.	.	.	.	.	.
chr1	91947807	91948208	.	.	.	.	.	.
chr1	92122631	92123032	chr1	92122817	92122894	MER103	DNA	DNA
chr1	92122631	92123032	chr1	92122944	92123060	MER5A	DNA	MER1_type
chr1	92131227	92131628	.	.	.	.	.	.
chr1	92731405	92731806	.	.	.	.	.	.
chr1	93474519	93474920	.	.	.	.	.	.
chr1	93852756	93853157	chr1	93853084	93853281	URR1A	DNA	MER1_type
chr1	94609094	94609495	.	.	.	.	.	.
chr1	95025263	95025664	.	.	.	.	.	.
chr1	95080586	95080987	.	.	.	.	.	.
chr1	95628330	95628731	.	.	.	.	.	.
chr1	108292034	108292435	.	.	.	.	.	.
chr1	108526020	108526421	chr1	108525919	108526087	L3b	LINE	CR1
chr1	115194359	115194760	.	.	.	.	.	.
chr1	120873037	120873438	.	.	.	.	.	.
chr1	121022168	121022569	chr1	121022009	121022488	L1M5	LINE	L1
chr1	122032734	122033135	chr1	122033040	122033175	RSINE1	SINE	B4
chr1	122093760	122094161	.	.	.	.	.	.
chr1	122133625	122134026	.	.	.	.	.	.
chr1	122655378	122655779	chr1	122655233	122655472	B4A	SINE	B4
chr1	122655378	122655779	chr1	122655687	122655806	L2a	LINE	L2
chr1	124253591	124253992	chr1	124253703	124253912	LSU-rRNA_H	rRNA	rRNA
chr1	127347332	127347733	chr1	127347376	127347439	MER5A	DNA	MER1_type
chr1	127347332	127347733	chr1	127347474	127347649	Lx8	LINE	L1
chr1	127415609	127416010	chr1	127415525	127415636	MTEa	LTR	MaLR
chr1	129116149	129116550	.	.	.	.	.	.
chr1	129321525	129321926	.	.	.	.	.	.
chr1	133022577	133022978	.	.	.	.	.	.
chr1	133907219	133907620	chr1	133907496	133907818	L1MB8	LINE	L1
chr1	134252553	134252954	chr1	134252722	134252774	(TG)n	Simple_repe	Simple_repeat
chr1	134916720	134917121	chr1	134916802	134917183	RLTR23	LTR	ERV1
chr1	135808032	135808433	.	.	.	.	.	.
chr1	135820724	135821125	.	.	.	.	.	.
chr1	136715343	136715744	chr1	136715302	136715402	PB1D9	SINE	Alu
chr1	136715343	136715744	chr1	136715345	136715460	MT2B	LTR	ERVL
chr1	136715343	136715744	chr1	136715542	136715587	L1M5	LINE	L1
chr1	136806173	136806574	.	.	.	.	.	.
chr1	137050985	137051386	.	.	.	.	.	.
chr1	137388829	137389230	.	.	.	.	.	.
chr1	137490461	137490862	chr1	137490431	137490485	(GA)n	Simple_repe	Simple_repeat
chr1	137564920	137565321	.	.	.	.	.	.
chr1	137595912	137596313	.	.	.	.	.	.
chr1	137656224	137656625	.	.	.	.	.	.
chr1	137684397	137684798	chr1	137684640	137684698	(TG)n	Simple_repe	Simple_repeat
chr1	137748912	137749313	.	.	.	.	.	.
chr1	137758632	137759033	chr1	137758588	137758791	MIR	SINE	MIR
chr1	138225362	138225763	chr1	138225168	138225556	Lx8	LINE	L1
chr1	138225362	138225763	chr1	138225703	138225850	B1_Mm	SINE	Alu
chr1	138581763	138582164	.	.	.	.	.	.
chr1	138595131	138595532	chr1	138595263	138595368	PB1D7	SINE	Alu
chr1	138595131	138595532	chr1	138595269	138595394	MT2B2	LTR	ERVL
chr1	140391549	140391950	.	.	.	.	.	.
chr1	155198202	155198603	chr1	155198449	155198509	PB1D10	SINE	Alu
chr1	155198202	155198603	chr1	155198525	155198852	ORR1D2	LTR	MaLR
chr1	156903261	156903662	chr1	156902900	156903276	RMER10A	LTR	ERVL
chr1	156921903	156922304	.	.	.	.	.	.
chr1	159016283	159016684	chr1	159016669	159016690	(TGGGGG)n	Simple_repe	Simple_repeat
chr1	160783351	160783752	.	.	.	.	.	.
chr1	163664885	163665286	chr1	163664988	163665009	AT_rich	Low_comple	Low_complexity
chr1	163968044	163968445	.	.	.	.	.	.
chr1	166191680	166192081	chr1	166191665	166191746	MIR	SINE	MIR
chr1	166347781	166348182	chr1	166347989	166348028	LTR33B	LTR	ERVL
chr1	166347781	166348182	chr1	166348028	166348076	MLT1J1	LTR	MaLR
chr1	166347781	166348182	chr1	166348082	166348132	L2b	LINE	L2
chr1	167658124	167658525	chr1	167658074	167658187	MLT1J	LTR	MaLR
chr1	167658124	167658525	chr1	167658311	167658443	MLT1J	LTR	MaLR
chr1	167658124	167658525	chr1	167658518	167658638	MIRc	SINE	MIR
chr1	168980967	168981368	chr1	168981039	168981209	(CTATT)n	Simple_repe	Simple_repeat
chr1	169172191	169172592	chr1	169172109	169172404	MTC	LTR	MaLR
chr1	169172191	169172592	chr1	169172442	169172584	MIR	SINE	MIR
chr1	170514370	170514771	chr1	170514723	170514769	(TG)n	Simple_repe	Simple_repeat
chr1	170528211	170528612	.	.	.	.	.	.
chr1	174458784	174459185	.	.	.	.	.	.

MER121	5
B2_Mm1t	5
B1F2	5
B1_Mur3	5
T-rich	5
RLTR11A2	5
(TTTG)n	5
(CAAA)n	5
MTEb	5
(GAATG)n	4
MLT1L	4
RMER19B	4
MT2B2	4
ORR1D2	4
MT2A	4
(CAA)n	4
ORR1D1	4
MER2	4
MER58B	4
MLT1F	4
MLT1C	4
(TATG)n	4
LTR33	4
RLTR11A	4
L1M2	4
RLTR33	4
Lx6	4
RMER30	4
L1_Mur2	4
MLT1K	4
MTE2b	4
L1MB7	4
LTR33A_	4
RLTR28	4
L1Md_A	4
RLTR42-int	4
L1MC1	4
MER3	4
MLT1B	3
RMER10B	3
(CG)n	3
ID2	3
MER63D	3
L3b	3
RMER6A	3
MTB_Mm	3
MIRm	3
(CAGAGA)n	3
L1MA8	3
MER21B	3
L1MC	3
MLT1D	3
(GAAA)n	3
L1MC4	3
(TTTC)n	3
L4	3
L1MA6	3
(TCC)n	3
L1MB5	3
L1_Mus1	3
(TTTA)n	3
L1MEc	3
(CGGG)n	3
(GGGTG)n	3
MLT1H	3
(TCTG)n	3
L1MB2	3
MER58A	3
L1MB3	3
RMER1B	3
(CCCCCA)n	3
(G)n	3
L1MC4a	3
C-rich	3
MLT2C2	3
(GGAA)n	3
LTR33C	3
L1Md_F3	2
HAL1	2
Lx4A	2
5S	2
L1_Mm	2
(GGGA)n	2
LTR16A	2
ERVL-E-int	2
Lx	2
MLT2E	2
MER115	2
(CATATA)n	2
RMER4B	2
(CGGGG)n	2
AmnSINE1	2
MARNA	2
Charlie25	2
U1	2

chr1	179913083	179913484	chr1	179913090	179913207	RLTR5_Mm	LTR	ERV1
chr1	182363860	182364261	.	.	.	.	.	.
chr1	184002103	184002504	.	.	.	.	.	.
chr1	184688892	184689293	chr1	184689036	184689210	MLT1J1	LTR	MaLR
chr1	185729144	185729545	.	.	.	.	.	.
chr1	185745108	185745509	.	.	.	.	.	.
chr1	191540110	191540511	chr1	191539949	191540167	ID_B1	SINE	B4
chr1	193098466	193098867	chr1	193098572	193098706	MLT1L	LTR	MaLR
chr1	193098466	193098867	chr1	193098726	193098764	5S	rRNA	rRNA
chr1	194571407	194571808	chr1	194571764	194571881	U5	snRNA	snRNA
chr1	197067725	197068126	.	.	.	.	.	.
chr10	5315043	5315444	.	.	.	.	.	.
chr10	5570670	5571071	.	.	.	.	.	.
chr10	8112630	8113031	chr10	8112989	8113195	B3A	SINE	B2
chr10	12594728	12595129	.	.	.	.	.	.
chr10	13460321	13460722	.	.	.	.	.	.
chr10	19130696	19131097	chr10	19130835	19130911	MLT1J	LTR	MaLR
chr10	19130696	19131097	chr10	19131008	19131146	L2	LINE	L2
chr10	19635029	19635430	.	.	.	.	.	.
chr10	21308298	21308699	chr10	21308431	21308520	(GAATG)n	Simple_repe	Simple_repeat
chr10	21308298	21308699	chr10	21308533	21308565	(CA)n	Simple_repe	Simple_repeat
chr10	21308298	21308699	chr10	21308565	21308631	(GA)n	Simple_repe	Simple_repeat
chr10	21720305	21720706	.	.	.	.	.	.
chr10	21862370	21862771	chr10	21862398	21862535	B1_Mus1	SINE	Alu
chr10	21889287	21889688	chr10	21889447	21889552	Lx9	LINE	L1
chr10	21889287	21889688	chr10	21889564	21889685	B1_Mur2	SINE	Alu
chr10	22836551	22836952	.	.	.	.	.	.
chr10	24485122	24485523	.	.	.	.	.	.
chr10	24719607	24720008	.	.	.	.	.	.
chr10	27832928	27833329	.	.	.	.	.	.
chr10	36983386	36983787	chr10	36983462	36983623	(CATTC)n	Simple_repe	Simple_repeat
chr10	36983386	36983787	chr10	36983740	36983761	AT_rich	Low_comple	Low_complexity
chr10	39932265	39932666	chr10	39932624	39932646	(CAGA)n	Simple_repe	Simple_repeat
chr10	41586033	41586434	chr10	41585956	41586159	ORR1C1	LTR	MaLR
chr10	43172108	43172509	.	.	.	.	.	.
chr10	43409688	43410089	.	.	.	.	.	.
chr10	43958531	43958932	.	.	.	.	.	.
chr10	52478390	52478791	.	.	.	.	.	.
chr10	54382608	54383009	.	.	.	.	.	.
chr10	56502120	56502521	chr10	56501593	56502154	L1_Mm	LINE	L1
chr10	58332552	58332953	chr10	58332616	58332816	Tigger5	DNA	MER2_type
chr10	58893685	58894086	.	.	.	.	.	.
chr10	59372268	59372669	chr10	59372648	59372768	(GGGA)n	Simple_repe	Simple_repeat
chr10	59672125	59672526	chr10	59672503	59672641	MIRb	SINE	MIR
chr10	60041288	60041689	chr10	60041370	60041412	(GA)n	Simple_repe	Simple_repeat
chr10	60041288	60041689	chr10	60041428	60041668	ZP3AR	Satellite	Satellite
chr10	60279557	60279958	.	.	.	.	.	.
chr10	60984950	60985351	chr10	60984893	60985092	L1Md_F3	LINE	L1
chr10	60984950	60985351	chr10	60985117	60985234	PB1D9	SINE	Alu
chr10	60984950	60985351	chr10	60985251	60985470	B3A	SINE	B2
chr10	61018105	61018506	chr10	61018336	61018454	ID_B1	SINE	B4
chr10	61099753	61100154	chr10	61099684	61099792	RMER6A	LTR	ERVK
chr10	61099753	61100154	chr10	61099906	61100209	MLT1L	LTR	MaLR
chr10	61222696	61223097	chr10	61223026	61223390	MTB_Mm	LTR	MaLR
chr10	62585258	62585659	chr10	62585259	62585310	MER5B	DNA	MER1_type
chr10	62606127	62606528	chr10	62606107	62606258	ID_B1	SINE	B4
chr10	62606127	62606528	chr10	62606259	62606538	MLT1J	LTR	MaLR
chr10	65817693	65818094	chr10	65817583	65817891	LTR16A	LTR	ERVL
chr10	66327167	66327568	.	.	.	.	.	.
chr10	66384136	66384537	.	.	.	.	.	.
chr10	67073432	67073833	chr10	67073639	67073731	MIRm	SINE	MIR
chr10	67073432	67073833	chr10	67073811	67073871	MIR	SINE	MIR
chr10	67210149	67210550	.	.	.	.	.	.
chr10	67929835	67930236	.	.	.	.	.	.
chr10	68247565	68247966	chr10	68247640	68247994	RLTR15	LTR	ERVK
chr10	69042263	69042664	.	.	.	.	.	.
chr10	69351228	69351629	.	.	.	.	.	.
chr10	69657782	69658183	chr10	69657742	69657810	(TC)n	Simple_repe	Simple_repeat
chr10	69657782	69658183	chr10	69657810	69657838	(CA)n	Simple_repe	Simple_repeat
chr10	69657782	69658183	chr10	69657838	69658012	7SLRNA	srpRNA	srpRNA
chr10	69657782	69658183	chr10	69658177	69658333	MT2B	LTR	ERVL
chr10	70609282	70609683	chr10	70609253	70609346	PB1D10	SINE	Alu
chr10	74715071	74715472	.	.	.	.	.	.
chr10	75096495	75096896	chr10	75096674	75096726	MLT1J1	LTR	MaLR
chr10	75096495	75096896	chr10	75096796	75096825	GC_rich	Low_comple	Low_complexity
chr10	75299963	75300364	.	.	.	.	.	.
chr10	76365843	76366244	chr10	76366060	76366084	(CA)n	Simple_repe	Simple_repeat
chr10	76664663	76665064	.	.	.	.	.	.
chr10	77745064	77745465	.	.	.	.	.	.
chr10	77800939	77801340	chr10	77801332	77801532	B4	SINE	B4
chr10	77933928	77934329	.	.	.	.	.	.
chr10	79095772	79096173	.	.	.	.	.	.
chr10	79124588	79124989	chr10	79124852	79124892	(CA)n	Simple_repe	Simple_repeat
chr10	79618750	79619151	chr10	79618771	79618892	PB1D10	SINE	Alu
chr10	79624475	79624876	chr10	79624818	79624891	ID4	SINE	ID
chr10	80461513	80461914	chr10	80461466	80461530	RSINE1	SINE	B4
chr10	80461513	80461914	chr10	80461530	80461556	(TTTTA)n	Simple_repe	Simple_repeat
chr10	80461513	80461914	chr10	80461619	80461641	(T)n	Simple_repe	Simple_repeat
chr10	80499950	80500351	.	.	.	.	.	.
chr10	80887489	80887890	chr10	80887520	80887559	GA-rich	Low_comple	Low_complexity
chr10	80887489	80887890	chr10	80887846	80887866	(CAGAGA)n	Simple_repe	Simple_repeat
chr10	81014368	81014769	.	.	.	.	.	.
chr10	81033621	81034022	.	.	.	.	.	.
chr10	82615116	82615517	.	.	.	.	.	.
chr10	82640742	82641143	chr10	82641013	82641510	MT2A	LTR	ERVL

MER5A1	2
(TCCC)n	2
tRNA-Arg-AG	2
(C)n	2
(CAGCC)n	2
(TGGA)n	2
MLT1H2	2
L1_Mus3	2
U6	2
MamRep605	2
MYSERV6-int	2
tRNA-Ala-GC	2
RCHARR1	2
MLT2B1	2
L1MD3	2
(TATATG)n	2
MER119	2
L1_Mur3	2
RMER6B	2
Charlie1	2
polypurine	2
YREP_Mm	2
LFSINE_Vert	2
(CTGGGG)n	2
RLTR1B	2
(CACTC)n	2
ORR1C2	2
Charlie9	2
(CAG)n	2
(TCCA)n	2
MTA_Mm	2
Zaphod	2
RMER1C	2
LTR88c	2
L1ME3A	2
RLTR18	2
RLTR12B	2
ORR1A2	2
IAPLTR1_Mm	2
(TTA)n	2
L1M3	2
L3	2
MLT1I	2
LTR78	2
RMER20B	2
(CCAA)n	2
ERVL-int	2
L1_Rod	2
(TTTTG)n	2
MamGypLTR	2
RMER5	2
(CCG)n	2
RLTR6-int	2
L1_Mus4	2
(TAAA)n	1
MER31B	1
MER117	1
MER44B	1
A-rich	1
(CAAAAA)n	1
RLTR19B	1
MER34A1	1
MER103	1
(TGGGGG)n	1
(CTATT)n	1
RLTR5_Mm	1
(TTTTA)n	1
LTR48B	1
L1MEg	1
(GGA)n	1
L1MEe	1
U8	1
MLT1D-int	1
tRNA-Cys-TG	1
(CACG)n	1
(TAGG)n	1
Arthur1B	1
ORR1A4	1
Charlie1a	1
RLTR19	1
(TGG)n	1
MLT1E3	1
L1MC5	1
LTR16B1	1
LTR37A	1
(AATAG)n	1
(GAGAA)n	1
(TTTTC)n	1
RLTR20A2	1
Charlie2b	1
Lx2	1
RLTR20B3	1
LTR88b	1
(CGGAA)n	1
MER94	1

chr10	82816938	82817339	.	.	.	.	.	.	
chr10	83859949	83860350	.	.	.	.	.	.	
chr10	85562908	85563309	.	.	.	.	.	.	
chr10	85566841	85567242	.	.	.	.	.	.	
chr10	85733451	85733852	.	.	.	.	.	.	
chr10	85839081	85839482	chr10	85839217	85839383	MLT1J2	LTR	MaLR	
chr10	85839081	85839482	chr10	85839382	85839496	B4A	SINE	B4	
chr10	88921549	88921950	chr10	88921807	88921913	B1F1	SINE	Alu	
chr10	88921549	88921950	chr10	88921919	88922394	Lx9	LINE	L1	
chr10	90427652	90428053	chr10	90428029	90428096	ID	SINE	ID	
chr10	90621241	90621642	.	.	.	.	.	.	
chr10	90650952	90651353	chr10	90650983	90651029	(CAA)n	Simple_repe	Simple_repeat	
chr10	90650952	90651353	chr10	90651252	90651398	B1_Mur4	SINE	Alu	
chr10	92601462	92601863	chr10	92601714	92601772	(CA)n	Simple_repe	Simple_repeat	
chr10	92866189	92866590	chr10	92866169	92866489	RLTR15	LTR	ERVK	
chr10	92866189	92866590	chr10	92866489	92866604	Tigger5	DNA	MER2_type	
chr10	92884731	92885132	chr10	92884516	92884737	B3	SINE	B2	
chr10	92884731	92885132	chr10	92884743	92885066	L1MA8	LINE	L1	
chr10	92884731	92885132	chr10	92885077	92885257	B3	SINE	B2	
chr10	94628689	94629090	.	.	.	.	.	.	
chr10	94849170	94849571	chr10	94849006	94849281	B4A	SINE	B4	
chr10	94849170	94849571	chr10	94849281	94849401	MLT1J	LTR	MaLR	
chr10	94849170	94849571	chr10	94849425	94849756	MTEa	LTR	MaLR	
chr10	94971297	94971698	chr10	94971306	94971388	URR1B	DNA	MER1_type	
chr10	95690075	95690476	.	.	.	.	.	.	
chr10	96090814	96091215	.	.	.	.	.	.	
chr10	97971237	97971638	.	.	.	.	.	.	
chr10	98544199	98544600	chr10	98544389	98544453	ERVL-E-int	LTR	ERVL	
chr10	109646747	109647148	chr10	109646878	109647072	B3	SINE	B2	
chr10	109646747	109647148	chr10	109647076	109647295	Lx	LINE	L1	
chr10	110564492	110564893	chr10	110564616	110564789	MIR	SINE	MIR	
chr10	110953885	110954286	.	.	.	.	.	.	
chr10	111007753	111008154	.	.	.	.	.	.	
chr10	115201126	115201527	chr10	115201320	115201466	B1_Mus2	SINE	Alu	
chr10	116170368	116170769	.	.	.	.	.	.	
chr10	116187881	116188282	chr10	116187856	116187889	(T)n	Simple_repe	Simple_repeat	
chr10	116433326	116433727	.	.	.	.	.	.	
chr10	117154603	117155004	chr10	117154459	117154638	B2_Mm2	SINE	B2	
chr10	117421851	117422252	.	.	.	.	.	.	
chr10	117567061	117567462	chr10	117567207	117567353	MLT2E	LTR	ERVL	
chr10	118842653	118843054	.	.	.	.	.	.	
chr10	119100955	119101356	chr10	119101038	119101135	ID_B1	SINE	B4	
chr10	119100955	119101356	chr10	119101171	119101277	ID_B1	SINE	B4	
chr10	120053541	120053942	.	.	.	.	.	.	
chr10	120073184	120073585	.	.	.	.	.	.	
chr10	121382434	121382835	.	.	.	.	.	.	
chr10	121475603	121476004	chr10	121475790	121475837	MLT1J	LTR	MaLR	
chr10	122252070	122252471	.	.	.	.	.	.	
chr10	122350467	122350868	.	.	.	.	.	.	
chr10	126342844	126343245	.	.	.	.	.	.	
chr10	126365644	126366045	.	.	.	.	.	.	
chr10	127068319	127068720	chr10	127068291	127068361	ID4	SINE	ID	
chr10	127068319	127068720	chr10	127068379	127068706	ORR1D1	LTR	MaLR	
chr10	127926505	127926906	.	.	.	.	.	.	
chr11	3000267	3000668	chr11	3000013	3002238	GSAT_MM	Satellite	Satellite	
chr11	3718340	3718741	chr11	3718533	3718759	RLTR42	LTR	ERVK	
chr11	4082080	4082481	.	.	.	.	.	.	
chr11	7137803	7138204	.	.	.	.	.	.	
chr11	11972294	11972695	.	.	.	.	.	.	
chr11	16446400	16446801	.	.	.	.	.	.	
chr11	16491518	16491919	.	.	.	.	.	.	
chr11	20369369	20369770	.	.	.	.	.	.	
chr11	20377529	20377930	.	.	.	.	.	.	
chr11	20508359	20508760	.	.	.	.	.	.	
chr11	20796331	20796732	.	.	.	.	.	.	
chr11	22381984	22382385	chr11	22382014	22382133	LTR48B	LTR	ERV1	
chr11	22381984	22382385	chr11	22382145	22382270	RLTR42	LTR	ERVK	
chr11	22381984	22382385	chr11	22382270	22382292	(CAAAA)n	Simple_repe	Simple_repeat	
chr11	22381984	22382385	chr11	22382292	22382374	RLTR42	LTR	ERVK	
chr11	22593425	22593826	.	.	.	.	.	.	
chr11	22619736	22620137	.	.	.	.	.	.	
chr11	24999973	25000374	chr11	25000022	25000201	(CATTC)n	Simple_repe	Simple_repeat	
chr11	28806245	28806646	.	.	.	.	.	.	
chr11	29579989	29580390	chr11	29579859	29580268	RLTR23	LTR	ERV1	
chr11	29579989	29580390	chr11	29580268	29580400	Lx9	LINE	L1	
chr11	29784283	29784684	chr11	29784455	29784761	L1M5	LINE	L1	
chr11	31535618	31536019	chr11	31535674	31535763	RLTR42	LTR	ERVK	
chr11	31535618	31536019	chr11	31535683	31535847	MLT1J1	LTR	MaLR	
chr11	31535618	31536019	chr11	31535802	31535861	RLTR42	LTR	ERVK	
chr11	31535618	31536019	chr11	31535925	31536126	MER115	DNA	Tip100	
chr11	31576695	31577096	chr11	31576890	31577011	MLT1J	LTR	MaLR	
chr11	31707370	31707771	chr11	31707087	31707381	MER2	DNA	MER2_type	
chr11	32304686	32305087	chr11	32305066	32305525	MER21B	LTR	ERV1	
chr11	32662863	32663264	chr11	32662778	32662949	MIRb	SINE	MIR	
chr11	32662863	32663264	chr11	32663029	32663454	ORR1B1	LTR	MaLR	
chr11	33998519	33998920	.	.	.	.	.	.	
chr11	34444641	34445042	chr11	34444489	34444700	RLTR44-int	LTR	ERVK	
chr11	34444641	34445042	chr11	34444710	34444923	RLTR44-int	LTR	ERVK	
chr11	34444641	34445042	chr11	34444926	34445121	RLTR44-int	LTR	ERVK	
chr11	34495214	34495615	chr11	34495124	34495331	RLTR44-int	LTR	ERVK	
chr11	34495214	34495615	chr11	34495306	34495523	RLTR44-int	LTR	ERVK	
chr11	34495214	34495615	chr11	34495523	34495577	RLTR44-int	LTR	ERVK	
chr11	34495214	34495615	chr11	34495578	34495794	RLTR44-int	LTR	ERVK	
chr11	34879384	34879785	.	.	.	.	.	.	
chr11	34928083	34928484	chr11	34928205	34928349	MLT1J2	LTR	MaLR	

L1MCa	1
(GGAGA)n	1
Charlie21a	1
(TGAA)n	1
RMER4A	1
Tigger16a	1
LTR31	1
LTR83	1
Tigger15a	1
MTB	1
LTR79	1
MT2_Mm	1
MER77	1
(CAT)n	1
LTR40b	1
MER63B	1
(ACTG)n	1
MLT1H2-int	1
LTR40a	1
(TTCA)n	1
L1MEf	1
RMER6D	1
RLTR16	1
(CTG)n	1
ERVL-B4-int	1
HAL1-3A_ME	1
RLTR40	1
L1Md_T	1
polypyrimidi	1
MLT2B3	1
Charlie5	1
RLTR19A	1
(AGGGGG)n	1
MURVY-LTR	1
(CGTG)n	1
L1ME2	1
MER44D	1
LTR50	1
MYSERV16_I	1
LTR16A1	1
LTR16C	1
L1ME3	1
(ATG)n	1
tRNA-Tyr-TA	1
MER2B	1
L1MD	1
MLT2C1	1
RLTR13D5	1
MER72	1
ORR1B2	1
MLT1A	1
(TTAGGG)n	1
RMER6C	1
CENSAT_MC	1
Tigger6b	1
(CAGGG)n	1
(CAGG)n	1
MER33	1
L1MC2	1
MurERV4-int	1
(GAAAA)n	1
FLAM_A	1
CR1_Mam	1
RMER12	1
(TTCTC)n	1
(CATG)n	1
MTE-int	1
RLTR10-int	1
(CATCC)n	1
BLACKJACK	1
Tigger16b	1
MamGypLTR	1
RLTR20A	1
MER97c	1
(TCCG)n	1
(TCTCTG)n	1
RMER13A	1
L1MDb	1
U4	1
LTR16E2	1
(CGG)n	1
(CGCGG)n	1
MER46C	1
(CCCGG)n	1
RLTR18B	1
(TAGA)n	1
SSU-rRNA_H	1
L1MCc	1
HY3	1
HY1	1
MTE2b-int	1
(GGCTG)n	1
RLTR28B	1
Charlie17a	1
MLT1J1-int	1

chr11	34928083	34928484	chr11	34928364	34928425	MIR	SINE	MIR
chr11	34980841	34981242	.	.	.	.	.	.
chr11	35063533	35063934	chr11	35063590	35063702	MLT1A1	LTR	MaLR
chr11	35192889	35193290	chr11	35193043	35193162	MLT1J1	LTR	MaLR
chr11	35192889	35193290	chr11	35193183	35193330	MER58B	DNA	MER1_type
chr11	35287325	35287726	.	.	.	.	.	.
chr11	35651230	35651631	chr11	35651323	35651428	B3A	SINE	B2
chr11	35651230	35651631	chr11	35651436	35651633	B3	SINE	B2
chr11	40260504	40260905	chr11	40260635	40260678	(TG)n	Simple_repea	Simple_repeat
chr11	41445950	41446351	chr11	41445779	41446070	(CATATA)n	Simple_repea	Simple_repeat
chr11	41445950	41446351	chr11	41446107	41446276	(CA)n	Simple_repea	Simple_repeat
chr11	45609159	45609560	.	.	.	.	.	.
chr11	45697027	45697428	.	.	.	.	.	.
chr11	45886396	45886797	chr11	45886430	45886616	MER121	Unknown	Unknown
chr11	49311170	49311571	chr11	49311322	49311392	ID4_	SINE	ID
chr11	49624765	49625166	.	.	.	.	.	.
chr11	49802877	49803278	.	.	.	.	.	.
chr11	50065692	50066093	chr11	50065570	50065981	RLTR23	LTR	ERV1
chr11	50487927	50488328	.	.	.	.	.	.
chr11	51033743	51034144	chr11	51033723	51034017	RLTR15	LTR	ERVK
chr11	51033743	51034144	chr11	51034099	51034232	B1_Mur2	SINE	Alu
chr11	51429079	51429480	.	.	.	.	.	.
chr11	51618651	51619052	chr11	51618464	51618659	B2_Mm2	SINE	B2
chr11	51618651	51619052	chr11	51618710	51618762	B3A	SINE	B2
chr11	51618651	51619052	chr11	51618815	51619077	RLTR42	LTR	ERVK
chr11	51729191	51729592	.	.	.	.	.	.
chr11	51753962	51754363	.	.	.	.	.	.
chr11	51885268	51885669	chr11	51885279	51885469	RMER4B	LTR	ERVK
chr11	52382318	52382719	chr11	52382265	52382374	MIRb	SINE	MIR
chr11	52382318	52382719	chr11	52382436	52382577	LTR33A	LTR	ERVL
chr11	52539505	52539906	chr11	52539640	52539834	B3	SINE	B2
chr11	53122438	53122839	chr11	53122435	53122468	(CAGAGA)n	Simple_repea	Simple_repeat
chr11	53610294	53610695	.	.	.	.	.	.
chr11	53617042	53617443	chr11	53617043	53617097	MER5B	DNA	MER1_type
chr11	53617042	53617443	chr11	53617107	53617308	ID_B1	SINE	B4
chr11	53617042	53617443	chr11	53617359	53617552	L1M5	LINE	L1
chr11	53875369	53875770	.	.	.	.	.	.
chr11	53953436	53953837	chr11	53953418	53953526	L1MEg	LINE	L1
chr11	53953436	53953837	chr11	53953644	53953820	B2_Mm1t	SINE	B2
chr11	53953436	53953837	chr11	53953822	53953880	(GGA)n	Simple_repea	Simple_repeat
chr11	54037674	54038075	chr11	54037752	54037961	MIRc	SINE	MIR
chr11	56904696	56905097	.	.	.	.	.	.
chr11	58148286	58148687	.	.	.	.	.	.
chr11	59272464	59272865	.	.	.	.	.	.
chr11	59859854	59860255	.	.	.	.	.	.
chr11	59928654	59929055	chr11	59928786	59928814	(CGGGG)n	Simple_repea	Simple_repeat
chr11	60904653	60905054	.	.	.	.	.	.
chr11	61410876	61411277	chr11	61410962	61410987	AmnSINE1	SINE	SINE
chr11	61410876	61411277	chr11	61410987	61411027	5S	rRNA	rRNA
chr11	61770037	61770438	chr11	61769911	61770046	B1_Mur4	SINE	Alu
chr11	61819025	61819426	.	.	.	.	.	.
chr11	61836579	61836980	.	.	.	.	.	.
chr11	61840687	61841088	.	.	.	.	.	.
chr11	62057328	62057729	.	.	.	.	.	.
chr11	62544890	62545291	.	.	.	.	.	.
chr11	62780094	62780495	.	.	.	.	.	.
chr11	67328891	67329292	.	.	.	.	.	.
chr11	67340214	67340615	chr11	67340506	67340540	(CAGA)n	Simple_repea	Simple_repeat
chr11	67371306	67371707	chr11	67371132	67371342	L1MEe	LINE	L1
chr11	68413754	68414155	chr11	68413608	68414005	MLT2F	LTR	ERVL
chr11	68886600	68887001	chr11	68886927	68887064	U8	snRNA	snRNA
chr11	69142015	69142416	.	.	.	.	.	.
chr11	69148286	69148687	chr11	69148143	69148350	MARNA	DNA	Mariner
chr11	69148286	69148687	chr11	69148685	69148765	ORR1E	LTR	MaLR
chr11	69230981	69231382	.	.	.	.	.	.
chr11	69256893	69257294	chr11	69256858	69256918	(CA)n	Simple_repea	Simple_repeat
chr11	69256893	69257294	chr11	69256918	69256964	B1F2	SINE	Alu
chr11	69441749	69442150	chr11	69441936	69442278	MER21B	LTR	ERV1
chr11	69523295	69523696	chr11	69523647	69523792	RSINE1	SINE	B4
chr11	69834190	69834591	.	.	.	.	.	.
chr11	71897301	71897702	chr11	71897580	71897693	L1MC	LINE	L1
chr11	72661793	72662194	.	.	.	.	.	.
chr11	73094810	73095211	.	.	.	.	.	.
chr11	74661322	74661723	.	.	.	.	.	.
chr11	74868000	74868401	chr11	74868375	74868509	ID_B1	SINE	B4
chr11	75333327	75333728	chr11	75333214	75333360	B1_Mus1	SINE	Alu
chr11	75333327	75333728	chr11	75333594	75333660	MIR3	SINE	MIR
chr11	75377735	75378136	.	.	.	.	.	.
chr11	76098970	76099371	chr11	76099290	76099362	ID	SINE	ID
chr11	76308796	76309197	.	.	.	.	.	.
chr11	76400968	76401369	.	.	.	.	.	.
chr11	76427770	76428171	chr11	76427890	76427969	ID4_	SINE	ID
chr11	76427770	76428171	chr11	76428059	76428220	MIRb	SINE	MIR
chr11	76998367	76998768	chr11	76998477	76998636	MER58B	DNA	MER1_type
chr11	77599255	77599656	.	.	.	.	.	.
chr11	78011377	78011778	chr11	78011323	78011424	PB1D9	SINE	Alu
chr11	78011377	78011778	chr11	78011538	78011687	B1_Mus1	SINE	Alu
chr11	78011377	78011778	chr11	78011693	78011733	(CAAAA)n	Simple_repea	Simple_repeat
chr11	78011377	78011778	chr11	78011742	78011877	B1_Mus1	SINE	Alu
chr11	78160892	78161293	.	.	.	.	.	.
chr11	78609139	78609540	chr11	78608947	78609154	B4A	SINE	B4
chr11	78609139	78609540	chr11	78609336	78609466	MLT1J	LTR	MaLR
chr11	78609139	78609540	chr11	78609507	78609539	AT_rich	Low_comple	Low_complexity
chr11	78884968	78885369	.	.	.	.	.	.
chr11	79001688	79002089	.	.	.	.	.	.

(TTCC)n	1
L1MA4A	1
4.5SRNA	1
ETnERV2-int	1
Lx2B	1
(CACCC)n	1
(TTG)n	1
tRNA-SeC(e)-	1
(CCGAA)n	1
RLTR25B	1
RMER2	1
RMER13B	1
L1Md_F	1
L1M6	1
BC1_Mm	1
LTR41B	1
L1MA4	1
(GGGAGA)n	1
MTEb-int	1
RLTR1	1
MMSAT4	1
RLTR30	1
MTEa-int	1
(TCCCC)n	1
(TCTA)n	1
RLTR20D	1

chr11	79009993	79010394	chr11	79010004	79010070	(TG)n	Simple_repe	Simple_repeat
chr11	79009993	79010394	chr11	79010073	79010219	B3	SINE	B2
chr11	79118833	79119234	chr11	79118882	79119061	MLT1F	LTR	MaLR
chr11	79226707	79227108	.	.	.	.	.	.
chr11	79552578	79552979	.	.	.	.	.	.
chr11	80442912	80443313	chr11	80442921	80443174	Charlie25	DNA	MER1_type
chr11	80442912	80443313	chr11	80443197	80443301	MIR	SINE	MIR
chr11	81820422	81820823	.	.	.	.	.	.
chr11	81825262	81825663	.	.	.	.	.	.
chr11	81845678	81846079	.	.	.	.	.	.
chr11	81852722	81853123	chr11	81852886	81853015	MLT1D-int	LTR	MaLR
chr11	81852722	81853123	chr11	81853025	81853102	MLT1D	LTR	MaLR
chr11	81880557	81880958	chr11	81880270	81880655	ERVL-E-int	LTR	ERVL
chr11	81952970	81953371	.	.	.	.	.	.
chr11	82425574	82425975	chr11	82425458	82425634	MER20	DNA	MER1_type
chr11	83084652	83085053	chr11	83084999	83085186	U2	snRNA	snRNA
chr11	83377288	83377689	.	.	.	.	.	.
chr11	83542552	83542953	.	.	.	.	.	.
chr11	85417158	85417559	chr11	85417068	85417165	L1M5	LINE	L1
chr11	85599836	85600237	chr11	85600152	85600267	B1F	SINE	Alu
chr11	86195089	86195490	.	.	.	.	.	.
chr11	86733819	86734220	.	.	.	.	.	.
chr11	87236023	87236424	chr11	87236368	87236533	U1	snRNA	snRNA
chr11	87256998	87257399	chr11	87257262	87257449	B2_Mm1a	SINE	B2
chr11	87262363	87262764	.	.	.	.	.	.
chr11	87994807	87995208	chr11	87995187	87995438	(TG)n	Simple_repe	Simple_repeat
chr11	88064101	88064502	chr11	88064307	88064438	L2a	LINE	L2
chr11	88064101	88064502	chr11	88064443	88064623	ID_B1	SINE	B4
chr11	88899949	88900350	.	.	.	.	.	.
chr11	89846723	89847124	.	.	.	.	.	.
chr11	90086185	90086586	.	.	.	.	.	.
chr11	93672966	93673367	chr11	93672887	93673064	L1M5	LINE	L1
chr11	93672966	93673367	chr11	93673092	93673216	MLT1J2	LTR	MaLR
chr11	93770152	93770553	.	.	.	.	.	.
chr11	94002841	94003242	chr11	94003025	94003191	L2a	LINE	L2
chr11	94002841	94003242	chr11	94003233	94003277	(GAAA)n	Simple_repe	Simple_repeat
chr11	94021691	94022092	.	.	.	.	.	.
chr11	94138206	94138607	.	.	.	.	.	.
chr11	94197808	94198209	chr11	94197862	94198055	B3	SINE	B2
chr11	94197808	94198209	chr11	94198055	94198390	L1MC4	LINE	L1
chr11	94580609	94581010	chr11	94580936	94581191	B4A	SINE	B4
chr11	94789324	94789725	.	.	.	.	.	.
chr11	95265138	95265539	chr11	95264989	95265242	L2	LINE	L2
chr11	95368348	95368749	.	.	.	.	.	.
chr11	95640690	95641091	chr11	95640733	95640799	B1_Mus1	SINE	Alu
chr11	95640690	95641091	chr11	95640801	95641005	URR1A	DNA	MER1_type
chr11	95640690	95641091	chr11	95641007	95641072	B1_Mur2	SINE	Alu
chr11	95879373	95879774	.	.	.	.	.	.
chr11	96121711	96122112	.	.	.	.	.	.
chr11	96244840	96245241	chr11	96244892	96244992	B3	SINE	B2
chr11	96341983	96342384	chr11	96341791	96341999	RLTR15	LTR	ERVK
chr11	96341983	96342384	chr11	96342110	96342220	RLTR15	LTR	ERVK
chr11	96780309	96780710	.	.	.	.	.	.
chr11	96868501	96868902	chr11	96868575	96868633	L2a	LINE	L2
chr11	97068279	97068680	.	.	.	.	.	.
chr11	97171444	97171845	chr11	97171463	97171519	MIR	SINE	MIR
chr11	97261655	97262056	.	.	.	.	.	.
chr11	97448795	97449196	chr11	97448743	97448864	MT2B	LTR	ERVL
chr11	97448795	97449196	chr11	97448761	97448895	B1_Mur4	SINE	Alu
chr11	97448795	97449196	chr11	97448895	97448979	(GA)n	Simple_repe	Simple_repeat
chr11	97521319	97521720	.	.	.	.	.	.
chr11	97781763	97782164	chr11	97781828	97781972	MIRc	SINE	MIR
chr11	97793576	97793977	chr11	97793710	97793821	PB1	SINE	Alu
chr11	97793576	97793977	chr11	97793965	97794086	B1_Mur4	SINE	Alu
chr11	97850021	97850422	chr11	97850235	97850308	tRNA-Cys-TG	tRNA	tRNA
chr11	97906903	97907304	chr11	97906859	97906951	PB1D10	SINE	Alu
chr11	97906903	97907304	chr11	97906995	97907174	B3	SINE	B2
chr11	97906903	97907304	chr11	97907213	97907304	ID_B1	SINE	B4
chr11	97906903	97907304	chr11	97907301	97907319	B2_Mm2	SINE	B2
chr11	97918551	97918952	.	.	.	.	.	.
chr11	97923424	97923825	chr11	97923725	97923826	MIR3	SINE	MIR
chr11	98293079	98293480	.	.	.	.	.	.
chr11	98650192	98650593	chr11	98650528	98650569	(CA)n	Simple_repe	Simple_repeat
chr11	98927260	98927661	chr11	98927550	98927590	(TG)n	Simple_repe	Simple_repeat
chr11	98938049	98938450	.	.	.	.	.	.
chr11	99056835	99057236	.	.	.	.	.	.
chr11	100651053	100651454	chr11	100651128	100651241	MER5A1	DNA	MER1_type
chr11	100821939	100822340	.	.	.	.	.	.
chr11	100841267	100841668	.	.	.	.	.	.
chr11	100864297	100864698	.	.	.	.	.	.
chr11	101062344	101062745	.	.	.	.	.	.
chr11	101148541	101148942	.	.	.	.	.	.
chr11	101199560	101199961	chr11	101199529	101199590	CT-rich	Low_comple	Low_complexity
chr11	101465801	101466202	chr11	101466163	101466350	U2	snRNA	snRNA
chr11	101502690	101503091	chr11	101503061	101503248	U2	snRNA	snRNA
chr11	101507214	101507615	chr11	101507057	101507244	U2	snRNA	snRNA
chr11	101519181	101519582	chr11	101519090	101519202	PB1D7	SINE	Alu
chr11	101519181	101519582	chr11	101519551	101519738	U2	snRNA	snRNA
chr11	101548461	101548862	chr11	101548305	101548556	L2c	LINE	L2
chr11	101708751	101709152	chr11	101708958	101709115	MLT1J	LTR	MaLR
chr11	102106401	102106802	chr11	102106701	102106740	(CACG)n	Simple_repe	Simple_repeat
chr11	102170372	102170773	.	.	.	.	.	.
chr11	102326877	102327278	.	.	.	.	.	.
chr11	102505086	102505487	chr11	102505057	102505141	PB1D10	SINE	Alu
chr11	102672417	102672818	.	.	.	.	.	.

chr11	102751396	102751797	.	.	.	.	.	.
chr11	102864523	102864924	.	.	.	.	.	.
chr11	103035601	103036002	.	.	.	.	.	.
chr11	103107591	103107992	.	.	.	.	.	.
chr11	103153346	103153747	.	.	.	.	.	.
chr11	103625064	103625465	.	.	.	.	.	.
chr11	103758331	103758732	.	.	.	.	.	.
chr11	103781907	103782308	chr11	103782235	103782261	AT_rich	Low_complex	Low_complexity
chr11	103781907	103782308	chr11	103782296	103782359	B3	SINE	B2
chr11	103845262	103845663	.	.	.	.	.	.
chr11	103878833	103879234	.	.	.	.	.	.
chr11	103896486	103896887	.	.	.	.	.	.
chr11	104022445	104022846	.	.	.	.	.	.
chr11	104057060	104057461	chr11	104056979	104057079	MIRb	SINE	MIR
chr11	104150645	104151046	.	.	.	.	.	.
chr11	104164844	104165245	.	.	.	.	.	.
chr11	104466211	104466612	chr11	104466146	104466250	L1MC4	LINE	L1
chr11	104466211	104466612	chr11	104466395	104466609	ORR1D1	LTR	MaLR
chr11	104472910	104473311	chr11	104473134	104473161	(TG)n	Simple_repea	Simple_repeat
chr11	104487317	104487718	.	.	.	.	.	.
chr11	104981980	104982381	chr11	104982026	104982247	RMER15	LTR	ERVL
chr11	105021319	105021720	chr11	105021207	105021349	B1_Mur3	SINE	Alu
chr11	105021319	105021720	chr11	105021640	105021723	(TTTC)n	Simple_repea	Simple_repeat
chr11	105021319	105021720	chr11	105021437	105021640	RMER10B	LTR	ERVL
chr11	105172774	105173175	.	.	.	.	.	.
chr11	105270116	105270517	.	.	.	.	.	.
chr11	105301119	105301520	chr11	105301033	105301357	Tigger7	DNA	MER2_type
chr11	105301119	105301520	chr11	105301465	105301782	MTE2a	LTR	MaLR
chr11	105392111	105392512	.	.	.	.	.	.
chr11	105684578	105684979	.	.	.	.	.	.
chr11	105814755	105815156	chr11	105815107	105815214	B1F	SINE	Alu
chr11	105922718	105923119	chr11	105922641	105922744	PB1D9	SINE	Alu
chr11	105922718	105923119	chr11	105922770	105922917	L1MB8	LINE	L1
chr11	105922718	105923119	chr11	105922919	105923095	MTD	LTR	MaLR
chr11	105922718	105923119	chr11	105923095	105923158	(TCCC)n	Simple_repea	Simple_repeat
chr11	106248331	106248732	chr11	106248405	106248608	RLTR15	LTR	ERVK
chr11	106254461	106254862	chr11	106254294	106254502	B2_Mm2	SINE	B2
chr11	106336562	106336963	.	.	.	.	.	.
chr11	106341611	106342012	chr11	106341865	106342108	MARNA	DNA	Mariner
chr11	106417031	106417432	.	.	.	.	.	.
chr11	106449985	106450386	.	.	.	.	.	.
chr11	106509547	106509948	chr11	106509480	106509664	MTEa	LTR	MaLR
chr11	106527704	106528105	chr11	106527778	106527926	MER20	DNA	MER1_type
chr11	106527704	106528105	chr11	106527939	106528017	ID4	SINE	ID
chr11	106569151	106569552	.	.	.	.	.	.
chr11	106791765	106792166	.	.	.	.	.	.
chr11	106874012	106874413	chr11	106874181	106874249	tRNA-Arg-AG	tRNA	tRNA
chr11	106974418	106974819	.	.	.	.	.	.
chr11	107018820	107019221	chr11	107019163	107019261	MIRc	SINE	MIR
chr11	107645485	107645886	chr11	107645736	107645876	(TAGG)n	Simple_repea	Simple_repeat
chr11	107934067	107934468	.	.	.	.	.	.
chr11	108011612	108012013	.	.	.	.	.	.
chr11	108076796	108077197	.	.	.	.	.	.
chr11	108873100	108873501	chr11	108872959	108873436	LSU-rRNA_Hs	rRNA	rRNA
chr11	109533195	109533596	chr11	109533502	109533622	B4A	SINE	B4
chr11	109533195	109533596	chr11	109533519	109533626	PB1D10	SINE	Alu
chr11	109598634	109599035	.	.	.	.	.	.
chr11	109678147	109678548	chr11	109678111	109678151	ID	SINE	ID
chr11	109678147	109678548	chr11	109678178	109678285	PB1D10	SINE	Alu
chr11	109721466	109721867	.	.	.	.	.	.
chr11	109755681	109756082	chr11	109755463	109755935	RLTR23	LTR	ERV1
chr11	109755681	109756082	chr11	109755965	109756162	MLT1C	LTR	MaLR
chr11	110266950	110267351	.	.	.	.	.	.
chr11	110372725	110373126	.	.	.	.	.	.
chr11	110456413	110456814	.	.	.	.	.	.
chr11	110464378	110464779	chr11	110464409	110464653	L2	LINE	L2
chr11	110577888	110578289	chr11	110577863	110577985	MTEa	LTR	MaLR
chr11	110577888	110578289	chr11	110578067	110578301	MTEa	LTR	MaLR
chr11	110742259	110742660	.	.	.	.	.	.
chr11	110796991	110797392	chr11	110796981	110797029	(CAGAGA)n	Simple_repea	Simple_repeat
chr11	110796991	110797392	chr11	110797375	110797477	L1MA8	LINE	L1
chr11	110804215	110804616	.	.	.	.	.	.
chr11	111549712	111550113	chr11	111549697	111549817	RSINE1	SINE	B4
chr11	112476966	112477367	chr11	112477106	112477327	L2	LINE	L2
chr11	112711854	112712255	chr11	112711897	112712000	L4	LINE	RTE
chr11	112862320	112862721	chr11	112862288	112862331	(CA)n	Simple_repea	Simple_repeat
chr11	112862320	112862721	chr11	112862675	112862916	MER20	DNA	MER1_type
chr11	112888079	112888480	.	.	.	.	.	.
chr11	112924473	112924874	.	.	.	.	.	.
chr11	113158526	113158927	chr11	113158851	113159068	ID_B1	SINE	B4
chr11	113194037	113194438	chr11	113193859	113194210	RMER10A	LTR	ERVL
chr11	113478766	113479167	.	.	.	.	.	.
chr11	115034333	115034734	chr11	115034415	115034628	URR1B	DNA	MER1_type
chr11	115034333	115034734	chr11	115034723	115034743	(C)n	Simple_repea	Simple_repeat
chr11	115152333	115152734	chr11	115152086	115152348	B4A	SINE	B4
chr11	115152333	115152734	chr11	115152638	115152665	(CAGA)n	Simple_repea	Simple_repeat
chr11	115274388	115274789	chr11	115274375	115274396	AT_rich	Low_complex	Low_complexity
chr11	115274388	115274789	chr11	115274618	115274690	tRNA-Arg-AG	tRNA	tRNA
chr11	115289059	115289460	.	.	.	.	.	.
chr11	115584024	115584425	.	.	.	.	.	.
chr11	115595299	115595700	.	.	.	.	.	.
chr11	115819278	115819679	chr11	115819646	115819704	(CAGCC)n	Simple_repea	Simple_repeat
chr11	115831549	115831950	chr11	115831899	115831939	B4A	SINE	B4
chr11	115866112	115866513	.	.	.	.	.	.
chr11	116037233	116037634	chr11	116037231	116037408	Lx5	LINE	L1

chr11	116037233	116037634	chr11	116037415	116037606	MTC	LTR	MaLR
chr11	116037233	116037634	chr11	116037607	116037797	B2_Mm1a	SINE	B2
chr11	116080003	116080404	.	.	.	.	.	.
chr11	116180714	116181115	.	.	.	.	.	.
chr11	116307397	116307798	.	.	.	.	.	.
chr11	116943145	116943546	chr11	116943412	116943587	URR1B	DNA	MER1_type
chr11	116970589	116970990	.	.	.	.	.	.
chr11	117037641	117038042	chr11	117037892	117038070	(TATG)n	Simple_repe	Simple_repeat
chr11	117069376	117069777	chr11	117069259	117069455	B4A	SINE	B4
chr11	117069376	117069777	chr11	117069593	117069908	Arthur1B	DNA	Tip100
chr11	117228270	117228671	chr11	117228279	117228601	MTEa	LTR	MaLR
chr11	117430023	117430424	chr11	117430389	117430533	B1_Mur1	SINE	Alu
chr11	117693314	117693715	chr11	117693281	117693369	RSINE1	SINE	B4
chr11	117693314	117693715	chr11	117693372	117693407	(CA)n	Simple_repe	Simple_repeat
chr11	117873907	117874308	chr11	117873886	117874013	ID_B1	SINE	B4
chr11	117994426	117994827	chr11	117994102	117994441	ORR1A4	LTR	MaLR
chr11	117994426	117994827	chr11	117994462	117994483	MLT1J	LTR	MaLR
chr11	117994426	117994827	chr11	117994483	117994535	(TG)n	Simple_repe	Simple_repeat
chr11	117994426	117994827	chr11	117994535	117994741	MLT1J	LTR	MaLR
chr11	118189010	118189411	chr11	118189356	118189394	(TGGA)n	Simple_repe	Simple_repeat
chr11	118299937	118300338	.	.	.	.	.	.
chr11	119717907	119718308	.	.	.	.	.	.
chr11	120091172	120091573	chr11	120091058	120091211	URR1A	DNA	MER1_type
chr11	120103478	120103879	.	.	.	.	.	.
chr11	120118276	120118677	.	.	.	.	.	.
chr11	120177404	120177805	.	.	.	.	.	.
chr11	120408754	120409155	chr11	120408908	120409120	RLTR42	LTR	ERVK
chr11	120909568	120909969	chr11	120909568	120909712	B1_Mur1	SINE	Alu
chr11	120915000	120915401	.	.	.	.	.	.
chr11	121700750	121701151	chr11	121700710	121701049	RLTR15	LTR	ERVK
chr12	3109848	3110249	chr12	3109871	3110121	GSAT_MM	Satellite	Satellite
chr12	3349469	3349870	chr12	3349426	3349490	(GA)n	Simple_repe	Simple_repeat
chr12	3349469	3349870	chr12	3349700	3349806	MIR3	SINE	MIR
chr12	3389318	3389719	chr12	3389135	3389336	B2_Mm2	SINE	B2
chr12	3389318	3389719	chr12	3389336	3389390	MIR3	SINE	MIR
chr12	3729750	3730151	.	.	.	.	.	.
chr12	4417554	4417955	chr12	4417678	4418528	L1MA6	LINE	L1
chr12	4499786	4500187	chr12	4500002	4500075	MLT1J1	LTR	MaLR
chr12	4499786	4500187	chr12	4500161	4500459	B4A	SINE	B4
chr12	5393444	5393845	chr12	5393613	5393649	MLT1J1	LTR	MaLR
chr12	5393444	5393845	chr12	5393672	5393794	MLT1J1	LTR	MaLR
chr12	5393444	5393845	chr12	5393821	5393891	(TCC)n	Simple_repe	Simple_repeat
chr12	8364068	8364469	chr12	8363519	8364087	L1MB5	LINE	L1
chr12	8386559	8386960	chr12	8386380	8386597	URR1A	DNA	MER1_type
chr12	8457197	8457598	.	.	.	.	.	.
chr12	8516521	8516922	.	.	.	.	.	.
chr12	8554122	8554523	.	.	.	.	.	.
chr12	8647406	8647807	chr12	8646110	8647444	L1_Mus1	LINE	L1
chr12	8647406	8647807	chr12	8647444	8647465	AT_rich	Low_comple	Low_complexity
chr12	8647406	8647807	chr12	8647478	8647516	(A)n	Simple_repe	Simple_repeat
chr12	9119090	9119491	chr12	9119407	9119500	LTR33	LTR	ERVL
chr12	9305910	9306311	.	.	.	.	.	.
chr12	9846865	9847266	.	.	.	.	.	.
chr12	9862857	9863258	.	.	.	.	.	.
chr12	10596314	10596715	.	.	.	.	.	.
chr12	15838752	15839153	.	.	.	.	.	.
chr12	15984912	15985313	chr12	15985127	15985181	LTR33B	LTR	ERVL
chr12	16018851	16019252	.	.	.	.	.	.
chr12	16365863	16366264	.	.	.	.	.	.
chr12	16484317	16484718	chr12	16484297	16484397	MLT1H2	LTR	MaLR
chr12	16532955	16533356	.	.	.	.	.	.
chr12	17227482	17227883	.	.	.	.	.	.
chr12	17246088	17246489	chr12	17246254	17246398	B1F	SINE	Alu
chr12	17516808	17517209	.	.	.	.	.	.
chr12	25840224	25840625	.	.	.	.	.	.
chr12	25866242	25866643	chr12	25866137	25866504	Charlie1a	DNA	MER1_type
chr12	25866242	25866643	chr12	25866527	25866709	ID_B1	SINE	B4
chr12	25929917	25930318	chr12	25929931	25929983	(TG)n	Simple_repe	Simple_repeat
chr12	25929917	25930318	chr12	25929993	25930040	(TC)n	Simple_repe	Simple_repeat
chr12	25929917	25930318	chr12	25930040	25930063	(TG)n	Simple_repe	Simple_repeat
chr12	29823814	29824215	.	.	.	.	.	.
chr12	29975792	29976193	.	.	.	.	.	.
chr12	30591914	30592315	.	.	.	.	.	.
chr12	30688467	30688868	.	.	.	.	.	.
chr12	31697124	31697525	.	.	.	.	.	.
chr12	31741375	31741776	chr12	31741210	31741703	RLTR19	LTR	ERVK
chr12	32700181	32700582	.	.	.	.	.	.
chr12	33174588	33174989	chr12	33174724	33174783	MLT1J	LTR	MaLR
chr12	33866933	33867334	.	.	.	.	.	.
chr12	35895012	35895413	chr12	35895277	35895518	L1_Mus3	LINE	L1
chr12	35930945	35931346	.	.	.	.	.	.
chr12	35976616	35977017	.	.	.	.	.	.
chr12	36559923	36560324	.	.	.	.	.	.
chr12	39570363	39570764	chr12	39570460	39570485	(CA)n	Simple_repe	Simple_repeat
chr12	39631096	39631497	.	.	.	.	.	.
chr12	39655604	39656005	.	.	.	.	.	.
chr12	40170268	40170669	chr12	40170474	40170591	RLTR11A	LTR	ERVK
chr12	45363451	45363852	chr12	45363422	45365080	Lx5	LINE	L1
chr12	53089524	53089925	chr12	53089420	53089569	B1_Mur1	SINE	Alu
chr12	53227629	53228030	.	.	.	.	.	.
chr12	53482648	53483049	.	.	.	.	.	.
chr12	53549003	53549404	chr12	53549133	53549219	MLT1L	LTR	MaLR
chr12	53705572	53705973	chr12	53705472	53705578	U6	snRNA	snRNA
chr12	53883834	53884235	.	.	.	.	.	.
chr12	53919513	53919914	.	.	.	.	.	.

chr12	55810836	55811237	chr12	55811002	55811060	GA-rich	Low_comple	Low_complexity
chr12	55839580	55839981	chr12	55839444	55839609	U1	snRNA	snRNA
chr12	55839580	55839981	chr12	55839843	55839901	CT-rich	Low_comple	Low_complexity
chr12	68160149	68160550	chr12	68160158	68160943	GSAT_MM	Satellite	Satellite
chr12	70563082	70563483	chr12	70563407	70563435	(TGG)n	Simple_repe	Simple_repeat
chr12	70638260	70638661	.	.	.	.	.	.
chr12	70754987	70755388	chr12	70754967	70755033	L1M5	LINE	L1
chr12	70754987	70755388	chr12	70755350	70755491	L1M5	LINE	L1
chr12	71725218	71725619	.	.	.	.	.	.
chr12	74877336	74877737	.	.	.	.	.	.
chr12	74891491	74891892	.	.	.	.	.	.
chr12	75417963	75418364	.	.	.	.	.	.
chr12	75905089	75905490	chr12	75904824	75905492	GSAT_MM	Satellite	Satellite
chr12	76802130	76802531	.	.	.	.	.	.
chr12	77568273	77568674	chr12	77568503	77568717	MER63D	DNA	AcHobo
chr12	78239682	78240083	.	.	.	.	.	.
chr12	78324636	78325037	chr12	78324622	78324647	(TTTA)n	Simple_repe	Simple_repeat
chr12	78324636	78325037	chr12	78324647	78324808	RSINE1	SINE	B4
chr12	78324636	78325037	chr12	78324808	78325100	L1MEc	LINE	L1
chr12	79071037	79071438	chr12	79070903	79071333	RLTR23	LTR	ERV1
chr12	79071037	79071438	chr12	79071333	79071411	B3A	SINE	B2
chr12	80594340	80594741	chr12	80594368	80594641	MLT1E3	LTR	MaLR
chr12	80594340	80594741	chr12	80594640	80594861	MamRep605	Unknown	Unknown
chr12	80654321	80654722	.	.	.	.	.	.
chr12	80660470	80660871	.	.	.	.	.	.
chr12	80713660	80714061	.	.	.	.	.	.
chr12	81918906	81919307	.	.	.	.	.	.
chr12	82849122	82849523	chr12	82849243	82849315	L1MC5	LINE	L1
chr12	82849122	82849523	chr12	82849431	82849536	GA-rich	Low_comple	Low_complexity
chr12	83072760	83073161	.	.	.	.	.	.
chr12	83256015	83256416	chr12	83256024	83256078	(TTTA)n	Simple_repe	Simple_repeat
chr12	84785294	84785695	chr12	84785479	84785545	MLT1J	LTR	MaLR
chr12	86671069	86671470	chr12	86671290	86671760	MT2A	LTR	ERVL
chr12	87341480	87341881	.	.	.	.	.	.
chr12	87510072	87510473	chr12	87509866	87510140	LTR16B1	LTR	ERVL
chr12	87670808	87671209	chr12	87670778	87670886	L1M2	LINE	L1
chr12	88142068	88142469	.	.	.	.	.	.
chr12	88174643	88175044	chr12	88175002	88175030	(A)n	Simple_repe	Simple_repeat
chr12	88229689	88230090	chr12	88229719	88229743	(CGGG)n	Simple_repe	Simple_repeat
chr12	88229689	88230090	chr12	88229949	88229974	(A)n	Simple_repe	Simple_repeat
chr12	88235279	88235680	chr12	88235362	88235408	G-rich	Low_comple	Low_complexity
chr12	88240468	88240869	.	.	.	.	.	.
chr12	88282070	88282471	.	.	.	.	.	.
chr12	99912792	99913193	.	.	.	.	.	.
chr12	101592234	101592635	chr12	101592568	101592869	LTR37A	LTR	ERV1
chr12	106221549	106221950	.	.	.	.	.	.
chr12	107137747	107138148	chr12	107137852	107138246	MLT1J	LTR	MaLR
chr12	107210798	107211199	chr12	107210983	107211195	MLT1J2	LTR	MaLR
chr12	107622058	107622459	.	.	.	.	.	.
chr12	109551617	109552018	chr12	109551506	109551717	LTR33A	LTR	ERVL
chr12	109631826	109632227	.	.	.	.	.	.
chr12	109642176	109642577	.	.	.	.	.	.
chr12	109996171	109996572	chr12	109996439	109996465	(TG)n	Simple_repe	Simple_repeat
chr12	110655818	110656219	.	.	.	.	.	.
chr12	110987956	110988357	.	.	.	.	.	.
chr12	112664397	112664798	.	.	.	.	.	.
chr12	113833719	113834120	.	.	.	.	.	.
chr13	3372147	3372548	chr13	3371784	3372149	RLTR33	LTR	ERVK
chr13	3372147	3372548	chr13	3372476	3372531	B1_Mur4	SINE	Alu
chr13	3372147	3372548	chr13	3372531	3372668	B1_Mus1	SINE	Alu
chr13	4318043	4318444	chr13	4317276	4318746	MYSERV6-int	LTR	ERVK
chr13	4770673	4771074	chr13	4771017	4771056	(GGGTG)n	Simple_repe	Simple_repeat
chr13	6403747	6404148	chr13	6403773	6403828	(TG)n	Simple_repe	Simple_repeat
chr13	6403747	6404148	chr13	6403879	6403989	GSAT_MM	Satellite	Satellite
chr13	6403747	6404148	chr13	6403994	6404093	B4	SINE	B4
chr13	14060980	14061381	chr13	14061373	14061642	MER63D	DNA	AcHobo
chr13	15898927	15899328	.	.	.	.	.	.
chr13	16579088	16579489	chr13	16579225	16579713	RLTR23	LTR	ERV1
chr13	16751358	16751759	.	.	.	.	.	.
chr13	21500246	21500647	.	.	.	.	.	.
chr13	23504423	23504824	chr13	23504809	23504882	tRNA-Ala-GC	tRNA	tRNA
chr13	23773552	23773953	.	.	.	.	.	.
chr13	27297781	27298182	chr13	27297891	27297986	(AATAG)n	Simple_repe	Simple_repeat
chr13	27297781	27298182	chr13	27297987	27298165	(GAGAA)n	Simple_repe	Simple_repeat
chr13	28403526	28403927	.	.	.	.	.	.
chr13	28549275	28549676	.	.	.	.	.	.
chr13	28724948	28725349	.	.	.	.	.	.
chr13	28891348	28891749	chr13	28891723	28891785	Lx5	LINE	L1
chr13	31465792	31466193	chr13	31465400	31465933	L1Md_F2	LINE	L1
chr13	31465792	31466193	chr13	31465977	31466049	LTR33A	LTR	ERVL
chr13	31724304	31724705	.	.	.	.	.	.
chr13	34303147	34303548	chr13	34303105	34303173	(TTTTC)n	Simple_repe	Simple_repeat
chr13	34303147	34303548	chr13	34303216	34303360	B1_Mur3	SINE	Alu
chr13	35258755	35259156	.	.	.	.	.	.
chr13	36808521	36808922	chr13	36808619	36808803	LTR33A	LTR	ERVL
chr13	37876066	37876467	.	.	.	.	.	.
chr13	38412198	38412599	.	.	.	.	.	.
chr13	39418111	39418512	.	.	.	.	.	.
chr13	39679359	39679760	chr13	39679484	39679730	RMER15	LTR	ERVL
chr13	39679359	39679760	chr13	39679739	39679824	RLTR20A2	LTR	ERVK
chr13	39944770	39945171	chr13	39944649	39944976	Tigger7	DNA	MER2_type
chr13	39944770	39945171	chr13	39945138	39945161	(GA)n	Simple_repe	Simple_repeat
chr13	40778964	40779365	.	.	.	.	.	.
chr13	40818356	40818757	chr13	40818398	40818444	(CGGGG)n	Simple_repe	Simple_repeat
chr13	41084963	41085364	chr13	41085096	41085200	PB1D10	SINE	Alu

chr13	41180949	41181350	chr13	41181033	41181173	B1F	SINE	Alu
chr13	41180949	41181350	chr13	41181184	41182050	Lx6	LINE	L1
chr13	44397422	44397823	.	.	.	.	.	.
chr13	45450235	45450636	chr13	45450211	45450291	RMER30	DNA	MER1_type
chr13	45450235	45450636	chr13	45450351	45450446	MLT1J2	LTR	MaLR
chr13	47357300	47357701	.	.	.	.	.	.
chr13	48586746	48587147	.	.	.	.	.	.
chr13	51303366	51303767	chr13	51303443	51303589	MLT1J1	LTR	MaLR
chr13	51546012	51546413	chr13	51545967	51546194	MTD	LTR	MaLR
chr13	51546012	51546413	chr13	51546288	51546489	MTE2a	LTR	MaLR
chr13	52807032	52807433	.	.	.	.	.	.
chr13	52924208	52924609	chr13	52924603	52924636	GA-rich	Low_comple	Low_complexity
chr13	52999504	52999905	chr13	52999443	52999846	Charlie2b	DNA	MER1_type
chr13	54965436	54965837	chr13	54965387	54965714	MLT1J	LTR	MaLR
chr13	54988735	54989136	.	.	.	.	.	.
chr13	55612356	55612757	.	.	.	.	.	.
chr13	55684567	55684968	chr13	55684563	55684976	RLTR15	LTR	ERVK
chr13	58869618	58870019	chr13	58869616	58869641	AT_rich	Low_comple	Low_complexity
chr13	58869618	58870019	chr13	58869645	58869850	7SLRNA	srpRNA	srpRNA
chr13	58869618	58870019	chr13	58869850	58870313	Lx2	LINE	L1
chr13	60152126	60152527	.	.	.	.	.	.
chr13	60529181	60529582	.	.	.	.	.	.
chr13	61577753	61578154	chr13	61577723	61578233	L1_Mur2	LINE	L1
chr13	64445548	64445949	.	.	.	.	.	.
chr13	65342626	65343027	.	.	.	.	.	.
chr13	67209409	67209810	.	.	.	.	.	.
chr13	67825069	67825470	.	.	.	.	.	.
chr13	70597920	70598321	.	.	.	.	.	.
chr13	70852186	70852587	.	.	.	.	.	.
chr13	70874916	70875317	.	.	.	.	.	.
chr13	71938494	71938895	.	.	.	.	.	.
chr13	74528112	74528513	.	.	.	.	.	.
chr13	74600325	74600726	.	.	.	.	.	.
chr13	74754606	74755007	.	.	.	.	.	.
chr13	75962372	75962773	.	.	.	.	.	.
chr13	77578082	77578483	chr13	77578053	77578114	T-rich	Low_comple	Low_complexity
chr13	77578082	77578483	chr13	77578170	77578318	GSAT_MM	Satellite	Satellite
chr13	80696443	80696844	.	.	.	.	.	.
chr13	81003509	81003910	.	.	.	.	.	.
chr13	83269615	83270016	chr13	83269567	83269630	MIRb	SINE	MIR
chr13	89968037	89968438	chr13	89968381	89968540	MIR	SINE	MIR
chr13	94745643	94746044	.	.	.	.	.	.
chr13	94762331	94762732	chr13	94762620	94762737	MLT1H	LTR	MaLR
chr13	94922367	94922768	.	.	.	.	.	.
chr13	96403250	96403651	chr13	96403250	96403379	MER2	DNA	MER2_type
chr13	96403250	96403651	chr13	96403379	96403454	(CA)n	Simple_repe	Simple_repeat
chr13	96403250	96403651	chr13	96403463	96403567	PB1	SINE	Alu
chr13	96403250	96403651	chr13	96403580	96403700	MER2	DNA	MER2_type
chr13	96704669	96705070	chr13	96704733	96704983	RLTR15	LTR	ERVK
chr13	96704669	96705070	chr13	96705031	96705545	RCHARR1	DNA	MER1_type
chr13	97709549	97709950	.	.	.	.	.	.
chr13	97960328	97960729	chr13	97960498	97960589	LSU-rRNA_H	rRNA	rRNA
chr13	97974955	97975356	chr13	97974909	97975048	MLT1N2	LTR	MaLR
chr13	97974955	97975356	chr13	97975139	97975183	LTR33B	LTR	ERVL
chr13	98308470	98308871	.	.	.	.	.	.
chr13	98448472	98448873	chr13	98448613	98448887	MLT2B1	LTR	ERVL
chr13	99011301	99011702	chr13	99011521	99011872	MTEa	LTR	MaLR
chr13	99167464	99167865	chr13	99167539	99167740	MLT1J	LTR	MaLR
chr13	99223193	99223594	.	.	.	.	.	.
chr13	99832932	99833333	.	.	.	.	.	.
chr13	100560763	100561164	chr13	100560902	100560943	(CA)n	Simple_repe	Simple_repeat
chr13	100560763	100561164	chr13	100560982	100561031	(TG)n	Simple_repe	Simple_repeat
chr13	100560763	100561164	chr13	100561043	100561074	(TCTG)n	Simple_repe	Simple_repeat
chr13	101687471	101687872	chr13	101687388	101688093	Lx9	LINE	L1
chr13	101709549	101709950	.	.	.	.	.	.
chr13	104177023	104177424	.	.	.	.	.	.
chr13	105310147	105310548	chr13	105310310	105310724	RLTR23	LTR	ERV1
chr13	107824148	107824549	chr13	107824161	107824525	RLTR11A2	LTR	ERVK
chr13	108172814	108173215	chr13	108172559	108173002	L1MD3	LINE	L1
chr13	108172814	108173215	chr13	108173174	108173609	RLTR20B3	LTR	ERVK
chr13	108275766	108276167	.	.	.	.	.	.
chr13	111020306	111020707	.	.	.	.	.	.
chr13	111531185	111531586	chr13	111531145	111531424	ORR1D1	LTR	MaLR
chr13	113108402	113108803	.	.	.	.	.	.
chr13	113616215	113616616	chr13	113616304	113616455	(CATATA)n	Simple_repe	Simple_repeat
chr13	115237411	115237812	chr13	115237572	115237666	LTR88b	LTR	Gypsy?
chr13	115374816	115375217	.	.	.	.	.	.
chr14	9848455	9848856	chr14	9848211	9848583	RLTR23	LTR	ERV1
chr14	9848455	9848856	chr14	9848680	9848737	(CA)n	Simple_repe	Simple_repeat
chr14	15466535	15466936	chr14	15466606	15466639	(TTTG)n	Simple_repe	Simple_repeat
chr14	15466535	15466936	chr14	15466640	15466845	B3	SINE	B2
chr14	21020262	21020663	.	.	.	.	.	.
chr14	21066143	21066544	.	.	.	.	.	.
chr14	22131847	22132248	chr14	22132204	22132338	ID_B1	SINE	B4
chr14	22170906	22171307	.	.	.	.	.	.
chr14	23933718	23934119	.	.	.	.	.	.
chr14	25574255	25574656	chr14	25574334	25574411	B3A	SINE	B2
chr14	25574255	25574656	chr14	25574433	25574557	MLT1J	LTR	MaLR
chr14	26005771	26006172	.	.	.	.	.	.
chr14	26123878	26124279	chr14	26123937	26123968	(CAGA)n	Simple_repe	Simple_repeat
chr14	26180250	26180651	.	.	.	.	.	.
chr14	26295542	26295943	.	.	.	.	.	.
chr14	26595818	26596219	chr14	26596043	26596138	MLT1A1	LTR	MaLR
chr14	26595818	26596219	chr14	26596138	26596215	ID4_	SINE	ID
chr14	26595818	26596219	chr14	26596215	26596270	MLT1A1	LTR	MaLR

chr14	30224091	30224492	chr14	30224291	30224379	MLT1J2	LTR	MaLR
chr14	30456399	30456800	chr14	30456378	30456439	(CA)n	Simple_repe	Simple_repeat
chr14	30456399	30456800	chr14	30456547	30456701	MLT1J2	LTR	MaLR
chr14	31694650	31695051	chr14	31694595	31694784	B3	SINE	B2
chr14	32475474	32475875	chr14	32475818	32475892	MER5B	DNA	MER1_type
chr14	32776782	32777183	.	.	.	.	.	.
chr14	33667219	33667620	chr14	33667057	33667335	B4A	SINE	B4
chr14	33667219	33667620	chr14	33667340	33667458	PB1	SINE	Alu
chr14	34060920	34061321	chr14	34061277	34061334	(TATATG)n	Simple_repe	Simple_repeat
chr14	47256000	47256401	.	.	.	.	.	.
chr14	47970686	47971087	chr14	47970766	47970858	MTEa	LTR	MaLR
chr14	47970686	47971087	chr14	47970880	47971046	B3A	SINE	B2
chr14	47970686	47971087	chr14	47971046	47971097	B1_Mus1	SINE	Alu
chr14	48058616	48059017	chr14	48058783	48058883	MLT2F	LTR	ERVL
chr14	48058616	48059017	chr14	48058982	48059175	B2_Mm1a	SINE	B2
chr14	48564285	48564686	chr14	48564177	48564324	B1_Mus2	SINE	Alu
chr14	48564285	48564686	chr14	48564324	48564337	(CAAA)n	Simple_repe	Simple_repeat
chr14	48611714	48612115	.	.	.	.	.	.
chr14	57910477	57910878	.	.	.	.	.	.
chr14	60232976	60233377	chr14	60232917	60233108	B2_Mm1a	SINE	B2
chr14	60232976	60233377	chr14	60233108	60233204	PB1	SINE	Alu
chr14	62267467	62267868	.	.	.	.	.	.
chr14	63751209	63751610	.	.	.	.	.	.
chr14	63996771	63997172	chr14	63996876	63996981	MLT1J	LTR	MaLR
chr14	64512332	64512733	.	.	.	.	.	.
chr14	65245909	65246310	chr14	65246133	65246313	L1MB2	LINE	L1
chr14	65768799	65769200	.	.	.	.	.	.
chr14	67057402	67057803	chr14	67057728	67057897	L1MC3	LINE	L1
chr14	71528532	71528933	.	.	.	.	.	.
chr14	73924648	73925049	.	.	.	.	.	.
chr14	75444980	75445381	.	.	.	.	.	.
chr14	76234076	76234477	.	.	.	.	.	.
chr14	78644626	78645027	chr14	78644577	78644728	MER119	DNA	MER1_type
chr14	78644626	78645027	chr14	78644753	78644876	MLT1J2	LTR	MaLR
chr14	79581491	79581892	.	.	.	.	.	.
chr14	86909084	86909485	.	.	.	.	.	.
chr14	104736008	104736409	chr14	104735912	104736135	Lx8	LINE	L1
chr14	104736008	104736409	chr14	104736139	104736301	(CGGAA)n	Simple_repe	Simple_repeat
chr14	104736008	104736409	chr14	104736301	104737357	L1_Mur3	LINE	L1
chr14	105727888	105728289	.	.	.	.	.	.
chr14	118329835	118330236	.	.	.	.	.	.
chr14	118398096	118398497	chr14	118398147	118398257	MLT1C	LTR	MaLR
chr14	118398096	118398497	chr14	118398450	118399480	(GA)n	Simple_repe	Simple_repeat
chr14	121231517	121231918	.	.	.	.	.	.
chr14	122223841	122224242	.	.	.	.	.	.
chr14	123572381	123572782	chr14	123572459	123572500	(TG)n	Simple_repe	Simple_repeat
chr14	123572381	123572782	chr14	123572510	123572714	B4A	SINE	B4
chr15	3657594	3657995	.	.	.	.	.	.
chr15	3849203	3849604	.	.	.	.	.	.
chr15	5445169	5445570	.	.	.	.	.	.
chr15	5815719	5816120	chr15	5814775	5815910	Lx9	LINE	L1
chr15	6585488	6585889	chr15	6585614	6585810	MIRb	SINE	MIR
chr15	7700401	7700802	.	.	.	.	.	.
chr15	7828113	7828514	chr15	7828500	7828525	AT_rich	Low_comple	Low_complexity
chr15	7881595	7881996	.	.	.	.	.	.
chr15	10688614	10689015	.	.	.	.	.	.
chr15	11014662	11015063	.	.	.	.	.	.
chr15	11454283	11454684	chr15	11454595	11454625	AT_rich	Low_comple	Low_complexity
chr15	12041152	12041553	chr15	12041377	12041508	L2a	LINE	L2
chr15	12573529	12573930	chr15	12572096	12577029	Lx5	LINE	L1
chr15	16284636	16285037	chr15	16284653	16284759	RMER6A	LTR	ERVK
chr15	16284636	16285037	chr15	16284759	16285119	RLTR23	LTR	ERV1
chr15	23511622	23512023	.	.	.	.	.	.
chr15	25507119	25507520	.	.	.	.	.	.
chr15	25582745	25583146	.	.	.	.	.	.
chr15	25844743	25845144	.	.	.	.	.	.
chr15	27162531	27162932	.	.	.	.	.	.
chr15	27348263	27348664	chr15	27347853	27348293	MTE2a	LTR	MaLR
chr15	27779668	27780069	chr15	27779535	27779818	MTC	LTR	MaLR
chr15	27780545	27780946	.	.	.	.	.	.
chr15	27927284	27927685	chr15	27927609	27927742	MER94	DNA	AcHobo
chr15	31021902	31022303	.	.	.	.	.	.
chr15	31117266	31117667	chr15	31117666	31117700	(T)n	Simple_repe	Simple_repeat
chr15	32258359	32258760	.	.	.	.	.	.
chr15	32485950	32486351	.	.	.	.	.	.
chr15	32930199	32930600	.	.	.	.	.	.
chr15	33836910	33837311	.	.	.	.	.	.
chr15	34145374	34145775	.	.	.	.	.	.
chr15	34342285	34342686	.	.	.	.	.	.
chr15	35139373	35139774	chr15	35139235	35139694	RMER6B	LTR	ERVK
chr15	35139373	35139774	chr15	35139694	35139837	(TG)n	Simple_repe	Simple_repeat
chr15	36625346	36625747	chr15	36625387	36625629	MLT1J	LTR	MaLR
chr15	36784505	36784906	chr15	36784405	36784513	L1MCa	LINE	L1
chr15	36795446	36795847	chr15	36795777	36796145	ORR1B1	LTR	MaLR
chr15	36814678	36815079	.	.	.	.	.	.
chr15	38127181	38127582	.	.	.	.	.	.
chr15	38174601	38175002	chr15	38174900	38175056	L2	LINE	L2
chr15	38174601	38175002	chr15	38174715	38174890	MLT1J1	LTR	MaLR
chr15	38400331	38400732	.	.	.	.	.	.
chr15	47698082	47698483	chr15	47698202	47698699	RLTR23	LTR	ERV1
chr15	50231688	50232089	chr15	50232034	50232223	MIRc	SINE	MIR
chr15	50524241	50524642	.	.	.	.	.	.
chr15	50529772	50530173	.	.	.	.	.	.
chr15	50828731	50829132	.	.	.	.	.	.
chr15	52512908	52513309	chr15	52512768	52513112	ORR1C1	LTR	MaLR

chr15	52512908	52513309	chr15	52513113	52513891	L1M2	LINE	L1
chr15	52759912	52760313	.	.	.	.	.	.
chr15	52970264	52970665	.	.	.	.	.	.
chr15	53520614	53521015	.	.	.	.	.	.
chr15	54009082	54009483	chr15	54009446	54009639	LTR33	LTR	ERVL
chr15	54218405	54218806	.	.	.	.	.	.
chr15	54685900	54686301	.	.	.	.	.	.
chr15	56596873	56597274	chr15	56597252	56597392	(GGAGA)n	Simple_repea	Simple_repeat
chr15	56673088	56673489	.	.	.	.	.	.
chr15	57399637	57400038	.	.	.	.	.	.
chr15	57555227	57555628	chr15	57555227	57555429	MLT1J1	LTR	MaLR
chr15	58311795	58312196	chr15	58311814	58312217	Charlie21a	DNA	MER1_type
chr15	59343039	59343440	chr15	59343230	59343282	L2a	LINE	L2
chr15	59343039	59343440	chr15	59343421	59343519	MIRc	SINE	MIR
chr15	59355607	59356008	.	.	.	.	.	.
chr15	59372474	59372875	chr15	59372450	59372544	B3A	SINE	B2
chr15	59403413	59403814	.	.	.	.	.	.
chr15	59428244	59428645	.	.	.	.	.	.
chr15	59559798	59560199	.	.	.	.	.	.
chr15	59591271	59591672	.	.	.	.	.	.
chr15	59654696	59655097	chr15	59655096	59655177	GA-rich	Low_comple	Low_complexity
chr15	59659983	59660384	chr15	59660325	59660434	MIR3	SINE	MIR
chr15	60158618	60159019	chr15	60158466	60158843	LTR16A	LTR	ERVL
chr15	61021238	61021639	chr15	61021190	61021317	MER121	Unknown	Unknown
chr15	61073382	61073783	chr15	61073301	61073601	MLT1J2	LTR	MaLR
chr15	61439822	61440223	.	.	.	.	.	.
chr15	61486511	61486912	chr15	61486477	61486560	L2a	LINE	L2
chr15	61486511	61486912	chr15	61486568	61486599	(TGAA)n	Simple_repea	Simple_repeat
chr15	61830331	61830732	.	.	.	.	.	.
chr15	61875094	61875495	.	.	.	.	.	.
chr15	61880911	61881312	chr15	61880686	61880942	L1ME1	LINE	L1
chr15	61910840	61911241	.	.	.	.	.	.
chr15	61970665	61971066	.	.	.	.	.	.
chr15	62118874	62119275	.	.	.	.	.	.
chr15	62159785	62160186	.	.	.	.	.	.
chr15	62530140	62530541	chr15	62530139	62530172	CT-rich	Low_comple	Low_complexity
chr15	63389391	63389792	chr15	63389305	63389472	RMER4A	LTR	ERVK
chr15	64197104	64197505	chr15	64197235	64197389	MLT1J2	LTR	MaLR
chr15	64208796	64209197	.	.	.	.	.	.
chr15	64308587	64308988	chr15	64308791	64309210	L1MB8	LINE	L1
chr15	66638796	66639197	chr15	66638734	66638975	Tigger16a	DNA	Tigger
chr15	66830071	66830472	.	.	.	.	.	.
chr15	67612188	67612589	chr15	67612411	67612571	B4	SINE	B4
chr15	68107279	68107680	.	.	.	.	.	.
chr15	71317822	71318223	chr15	71317991	71318424	LTR31	LTR	ERV1
chr15	72834459	72834860	chr15	72834571	72834646	L2b	LINE	L2
chr15	73265277	73265678	.	.	.	.	.	.
chr15	74489416	74489817	.	.	.	.	.	.
chr15	74532418	74532819	.	.	.	.	.	.
chr15	74749876	74750277	chr15	74749802	74749977	L1_Mus3	LINE	L1
chr15	74749876	74750277	chr15	74749978	74750114	LTR83	LTR	ERVL
chr15	74917030	74917431	chr15	74917381	74917476	RLTR11A	LTR	ERVK
chr15	75681214	75681615	chr15	75681024	75681217	B2_Mm1t	SINE	B2
chr15	76034474	76034875	.	.	.	.	.	.
chr15	76051174	76051575	chr15	76051162	76051378	B3A	SINE	B2
chr15	76051174	76051575	chr15	76051472	76051577	PB1	SINE	Alu
chr15	76059806	76060207	chr15	76060000	76060021	GC_rich	Low_comple	Low_complexity
chr15	76925603	76926004	.	.	.	.	.	.
chr15	77166764	77167165	.	.	.	.	.	.
chr15	77571873	77572274	chr15	77572009	77572116	ID_B1	SINE	B4
chr15	77733386	77733787	chr15	77733427	77733575	RSINE1	SINE	B4
chr15	77752031	77752432	chr15	77751927	77752118	B2_Mm1a	SINE	B2
chr15	77764178	77764579	.	.	.	.	.	.
chr15	77978992	77979393	chr15	77978958	77979107	MER58A	DNA	MER1_type
chr15	77978992	77979393	chr15	77979119	77979313	MLT1J2	LTR	MaLR
chr15	78280094	78280495	.	.	.	.	.	.
chr15	78412220	78412621	.	.	.	.	.	.
chr15	78678900	78679301	chr15	78678847	78678948	B1_Mur2	SINE	Alu
chr15	78819044	78819445	chr15	78819307	78819403	MIR3	SINE	MIR
chr15	79111732	79112133	.	.	.	.	.	.
chr15	79294951	79295352	chr15	79295197	79295334	MIR	SINE	MIR
chr15	79643992	79644393	.	.	.	.	.	.
chr15	80180842	80181243	.	.	.	.	.	.
chr15	80244771	80245172	.	.	.	.	.	.
chr15	80266321	80266722	chr15	80266469	80266585	ORR1E	LTR	MaLR
chr15	80917448	80917849	.	.	.	.	.	.
chr15	81047539	81047940	.	.	.	.	.	.
chr15	81077882	81078283	chr15	81077690	81077929	B4A	SINE	B4
chr15	81077882	81078283	chr15	81077981	81078129	RSINE1	SINE	B4
chr15	81094697	81095098	.	.	.	.	.	.
chr15	81344662	81345063	.	.	.	.	.	.
chr15	81686439	81686840	.	.	.	.	.	.
chr15	82987849	82988250	chr15	82988154	82988340	RMER15	LTR	ERVL
chr15	83046151	83046552	.	.	.	.	.	.
chr15	83053526	83053927	chr15	83053218	83053631	MTD	LTR	MaLR
chr15	83112812	83113213	chr15	83112609	83112814	B3	SINE	B2
chr15	83112812	83113213	chr15	83112818	83112978	B4A	SINE	B4
chr15	83112812	83113213	chr15	83112981	83113202	RLTR42	LTR	ERVK
chr15	84020292	84020693	chr15	84020489	84020705	RLTR42	LTR	ERVK
chr15	85484534	85484935	.	.	.	.	.	.
chr15	85528779	85529180	chr15	85528728	85528880	RLTR15	LTR	ERVK
chr15	85528779	85529180	chr15	85528970	85529137	RLTR15	LTR	ERVK
chr15	85897915	85898316	chr15	85897836	85897943	Tigger15a	DNA	TcMar
chr15	85897915	85898316	chr15	85897954	85898031	G-rich	Low_comple	Low_complexity
chr15	85897915	85898316	chr15	85898214	85898260	(CA)n	Simple_repea	Simple_repeat

chr15	85910280	85910681	.	.	.	.	.	.
chr15	85920475	85920876	.	.	.	.	.	.
chr15	88632812	88633213	.	.	.	.	.	.
chr15	88684683	88685084	chr15	88685031	88685083	G-rich	Low_comple	Low_complexity
chr15	90454714	90455115	chr15	90455010	90455101	L2	LINE	L2
chr15	91238894	91239295	.	.	.	.	.	.
chr15	91445595	91445996	chr15	91445437	91445832	MTB	LTR	MaLR
chr15	91445595	91445996	chr15	91445959	91446002	(TG)n	Simple_repe	Simple_repeat
chr15	91521032	91521433	.	.	.	.	.	.
chr15	91533629	91534030	.	.	.	.	.	.
chr15	94125160	94125561	chr15	94125229	94125408	RLTR15	LTR	ERVK
chr15	94125160	94125561	chr15	94125432	94125553	RLTR15	LTR	ERVK
chr15	94847121	94847522	.	.	.	.	.	.
chr15	95633101	95633502	.	.	.	.	.	.
chr15	95654306	95654707	.	.	.	.	.	.
chr15	96337492	96337893	chr15	96337661	96337760	RLTR15	LTR	ERVK
chr15	97417678	97418079	chr15	97417532	97417725	B2_Mm2	SINE	B2
chr15	97417678	97418079	chr15	97417725	97417838	L1_Mur3	LINE	L1
chr15	97417678	97418079	chr15	97417838	97417984	7SLRNA	srpRNA	srpRNA
chr15	97523834	97524235	chr15	97524042	97524197	LTR79	LTR	ERVL
chr15	97581015	97581416	.	.	.	.	.	.
chr15	97655763	97656164	.	.	.	.	.	.
chr15	97744724	97745125	.	.	.	.	.	.
chr15	97928942	97929343	chr15	97928854	97929112	RLTR15	LTR	ERVK
chr15	97928942	97929343	chr15	97929147	97929237	RLTR15	LTR	ERVK
chr15	97986328	97986729	chr15	97986267	97986394	B1_Mur2	SINE	Alu
chr15	97986328	97986729	chr15	97986435	97986877	RLTR23	LTR	ERV1
chr15	98343135	98343536	chr15	98343123	98343157	MT2A	LTR	ERVL
chr15	98410501	98410902	chr15	98410510	98410554	(CA)n	Simple_repe	Simple_repeat
chr15	98697745	98698146	.	.	.	.	.	.
chr15	98823461	98823862	.	.	.	.	.	.
chr15	99163350	99163751	.	.	.	.	.	.
chr15	99232023	99232424	chr15	99232340	99232361	AT_rich	Low_comple	Low_complexity
chr15	99378232	99378633	chr15	99378376	99378473	L1M2	LINE	L1
chr15	99384213	99384614	chr15	99384051	99384254	ID_B1	SINE	B4
chr15	99384213	99384614	chr15	99384254	99384284	Charlie1	DNA	MER1_type
chr15	99384213	99384614	chr15	99384284	99384358	ID4_	SINE	ID
chr15	99384213	99384614	chr15	99384358	99384564	Charlie1	DNA	MER1_type
chr15	99416150	99416551	.	.	.	.	.	.
chr15	99919947	99920348	.	.	.	.	.	.
chr15	100292177	100292578	.	.	.	.	.	.
chr15	100909177	100909578	chr15	100909561	100909590	(TG)n	Simple_repe	Simple_repeat
chr15	100912971	100913372	chr15	100913296	100913437	PB1	SINE	Alu
chr15	101151616	101152017	chr15	101151814	101151951	MIR	SINE	MIR
chr15	101151616	101152017	chr15	101151993	101152044	polypurine	Low_comple	Low_complexity
chr15	101212280	101212681	.	.	.	.	.	.
chr15	101285704	101286105	.	.	.	.	.	.
chr15	101800976	101801377	chr15	101800943	101801011	(TC)n	Simple_repe	Simple_repeat
chr15	102033872	102034273	chr15	102034199	102034376	(CGGG)n	Simple_repe	Simple_repeat
chr15	102207651	102208052	.	.	.	.	.	.
chr15	102402502	102402903	.	.	.	.	.	.
chr15	102669418	102669819	.	.	.	.	.	.
chr15	103051855	103052256	chr15	103052096	103052127	(TG)n	Simple_repe	Simple_repeat
chr15	103051855	103052256	chr15	103052143	103052229	B4A	SINE	B4
chr15	103051855	103052256	chr15	103052209	103052244	B1_Mus2	SINE	Alu
chr15	103137562	103137963	.	.	.	.	.	.
chr15	103188783	103189184	chr15	103188895	103189071	MIR	SINE	MIR
chr15	103200861	103201262	.	.	.	.	.	.
chr16	3699347	3699748	.	.	.	.	.	.
chr16	8823809	8824210	chr16	8823726	8824032	MLT1J	LTR	MaLR
chr16	8823809	8824210	chr16	8824043	8824234	B3	SINE	B2
chr16	10443805	10444206	chr16	10443674	10443820	YREP_Mm	Unknown	Unknown
chr16	10443805	10444206	chr16	10443836	10443935	PB1D7	SINE	Alu
chr16	10754616	10755017	.	.	.	.	.	.
chr16	10850320	10850721	.	.	.	.	.	.
chr16	10857432	10857833	chr16	10857658	10857770	L1MB8	LINE	L1
chr16	10857432	10857833	chr16	10857791	10857815	(GGGA)n	Simple_repe	Simple_repeat
chr16	10975036	10975437	chr16	10975160	10975376	GSAT_MM	Satellite	Satellite
chr16	11305641	11306042	.	.	.	.	.	.
chr16	11330462	11330863	chr16	11330823	11330957	B1_Mur2	SINE	Alu
chr16	13372073	13372474	.	.	.	.	.	.
chr16	14303748	14304149	chr16	14304040	14304152	PB1D7	SINE	Alu
chr16	14350896	14351297	chr16	14350823	14351073	L1MB3	LINE	L1
chr16	14350896	14351297	chr16	14351113	14351280	L2	LINE	L2
chr16	14451527	14451928	chr16	14451731	14451812	PB1D10	SINE	Alu
chr16	15294459	15294860	chr16	15294799	15295001	B3	SINE	B2
chr16	16104383	16104784	chr16	16104334	16104418	RMER1B	Other	Other
chr16	16104383	16104784	chr16	16104422	16105068	RMER1B	Other	Other
chr16	18789171	18789572	chr16	18788932	18789206	B4A	SINE	B4
chr16	18789171	18789572	chr16	18789291	18789494	B3	SINE	B2
chr16	21333254	21333655	.	.	.	.	.	.
chr16	21778351	21778752	chr16	21778438	21778864	MLT1J	LTR	MaLR
chr16	21827438	21827839	chr16	21827668	21827713	(TG)n	Simple_repe	Simple_repeat
chr16	21827438	21827839	chr16	21827728	21827849	L2a	LINE	L2
chr16	21976256	21976657	.	.	.	.	.	.
chr16	22182348	22182749	.	.	.	.	.	.
chr16	22389664	22390065	.	.	.	.	.	.
chr16	23272924	23273325	.	.	.	.	.	.
chr16	24428088	24428489	.	.	.	.	.	.
chr16	24933918	24934319	.	.	.	.	.	.
chr16	25043363	25043764	chr16	25043709	25043763	(TC)n	Simple_repe	Simple_repeat
chr16	25485095	25485496	.	.	.	.	.	.
chr16	25942215	25942616	.	.	.	.	.	.
chr16	26211645	26212046	chr16	26211543	26212012	Lx8	LINE	L1
chr16	26211645	26212046	chr16	26212012	26212506	MT2_Mm	LTR	ERVL

chr16	30442489	30442890	chr16	30442506	30442554	L2c	LINE	L2
chr16	30500303	30500704	chr16	30500196	30500328	B1_Mur2	SINE	Alu
chr16	30513728	30514129	.	.	.	.	.	.
chr16	30737223	30737624	chr16	30737550	30737663	MIRc	SINE	MIR
chr16	30876945	30877346	chr16	30876915	30877081	RSINE1	SINE	B4
chr16	31526733	31527134	.	.	.	.	.	.
chr16	31589575	31589976	.	.	.	.	.	.
chr16	31598522	31598923	.	.	.	.	.	.
chr16	32542350	32542751	chr16	32542409	32542556	B1_Mur2	SINE	Alu
chr16	32542350	32542751	chr16	32542604	32542875	MLT1K	LTR	MaLR
chr16	32858849	32859250	chr16	32859079	32859210	B1F	SINE	Alu
chr16	33736853	33737254	chr16	33736666	33737203	MER77	LTR	ERVL
chr16	33869758	33870159	chr16	33869622	33869777	RSINE1	SINE	B4
chr16	33869758	33870159	chr16	33869777	33869823	(CAT)n	Simple_repea	Simple_repeat
chr16	33869758	33870159	chr16	33869831	33870027	B3	SINE	B2
chr16	33869758	33870159	chr16	33870073	33870149	RSINE1	SINE	B4
chr16	34490568	34490969	.	.	.	.	.	.
chr16	34528815	34529216	.	.	.	.	.	.
chr16	36874828	36875229	.	.	.	.	.	.
chr16	37814403	37814804	chr16	37814700	37814760	(TG)n	Simple_repea	Simple_repeat
chr16	41686562	41686963	.	.	.	.	.	.
chr16	42897375	42897776	.	.	.	.	.	.
chr16	43363051	43363452	chr16	43363087	43363222	LFSINE_Vert	SINE	SINE
chr16	43574186	43574587	.	.	.	.	.	.
chr16	44392296	44392697	.	.	.	.	.	.
chr16	45837980	45838381	.	.	.	.	.	.
chr16	51681420	51681821	chr16	51681358	51681557	B2_Mm2	SINE	B2
chr16	51681420	51681821	chr16	51681557	51681892	MTE2b	LTR	MaLR
chr16	55218686	55219087	chr16	55218864	55219015	MLT1J	LTR	MaLR
chr16	57391529	57391930	chr16	57391225	57391786	LSU-rRNA_Hs	rRNA	rRNA
chr16	57391529	57391930	chr16	57391786	57391910	RSINE1	SINE	B4
chr16	65451293	65451694	chr16	65451493	65451697	L2	LINE	L2
chr16	72804444	72804845	chr16	72804440	72804768	L1_Mur2	LINE	L1
chr16	75542432	75542833	chr16	75542558	75542741	B3	SINE	B2
chr16	77643234	77643635	.	.	.	.	.	.
chr16	81439484	81439885	.	.	.	.	.	.
chr16	91200026	91200427	chr16	91199994	91200343	RLTR15	LTR	ERVK
chr16	91200026	91200427	chr16	91200350	91200480	ID_B1	SINE	B4
chr16	91200026	91200427	chr16	91200378	91200486	B1F	SINE	Alu
chr16	91200026	91200427	chr16	91200404	91200498	MT2B2	LTR	ERVL
chr16	91534719	91535120	chr16	91534694	91534729	(TG)n	Simple_repea	Simple_repeat
chr16	91942857	91943258	chr16	91943001	91943092	ID4	SINE	ID
chr16	91942857	91943258	chr16	91943134	91943252	PB1D9	SINE	Alu
chr16	92022196	92022597	chr16	92022485	92022584	MLT1B	LTR	MaLR
chr16	92022196	92022597	chr16	92022584	92022653	(CTGGGG)n	Simple_repea	Simple_repeat
chr16	92620943	92621344	.	.	.	.	.	.
chr16	92864376	92864777	.	.	.	.	.	.
chr16	92905899	92906300	chr16	92905852	92906346	RCHARR1	DNA	MER1_type
chr16	93263517	93263918	.	.	.	.	.	.
chr16	93293153	93293554	chr16	93293420	93293750	LTR40b	LTR	ERVL
chr16	93918872	93919273	chr16	93918870	93918931	(CA)n	Simple_repea	Simple_repeat
chr16	95658251	95658652	chr16	95658264	95658305	(GA)n	Simple_repea	Simple_repeat
chr16	95898235	95898636	chr16	95898399	95898488	MLT1J1	LTR	MaLR
chr16	95898235	95898636	chr16	95898562	95898698	MLT1J1	LTR	MaLR
chr16	95987780	95988181	.	.	.	.	.	.
chr16	97528633	97529034	chr16	97528418	97528641	RLTR1B	LTR	ERV1
chr17	3200337	3200738	.	.	.	.	.	.
chr17	4626300	4626701	chr17	4626173	4626353	(CATTC)n	Simple_repea	Simple_repeat
chr17	4626300	4626701	chr17	4626353	4626388	(CACTC)n	Simple_repea	Simple_repeat
chr17	4626300	4626701	chr17	4626388	4626598	(CATTC)n	Satellite	Satellite
chr17	5138717	5139118	.	.	.	.	.	.
chr17	5189657	5190058	.	.	.	.	.	.
chr17	5782767	5783168	chr17	5782828	5782851	(TG)n	Simple_repea	Simple_repeat
chr17	5782767	5783168	chr17	5782851	5782893	(GA)n	Simple_repea	Simple_repeat
chr17	5782767	5783168	chr17	5782905	5783067	RLTR15	LTR	ERVK
chr17	5782767	5783168	chr17	5783084	5783126	(CAGA)n	Simple_repea	Simple_repeat
chr17	5782767	5783168	chr17	5783162	5783327	RLTR15	LTR	ERVK
chr17	5805960	5806361	.	.	.	.	.	.
chr17	5978704	5979105	chr17	5978922	5979046	MER63B	DNA	AcHobo
chr17	5994611	5995012	.	.	.	.	.	.
chr17	6016439	6016840	chr17	6016490	6016523	(ACTG)n	Simple_repea	Simple_repeat
chr17	6016439	6016840	chr17	6016804	6016946	RSINE1	SINE	B4
chr17	6128088	6128489	chr17	6127906	6128364	RLTR23	LTR	ERV1
chr17	9049163	9049564	chr17	9049368	9049473	L4	LINE	RTE
chr17	9049163	9049564	chr17	9049526	9049567	(CCCCCA)n	Simple_repea	Simple_repeat
chr17	12402440	12402841	.	.	.	.	.	.
chr17	12468689	12469090	chr17	12468716	12468757	L2b	LINE	L2
chr17	12984378	12984779	chr17	12984365	12984442	B1F	SINE	Alu
chr17	12984378	12984779	chr17	12984389	12984448	B4A	SINE	B4
chr17	14474660	14475061	.	.	.	.	.	.
chr17	14683117	14683518	.	.	.	.	.	.
chr17	14747903	14748304	.	.	.	.	.	.
chr17	14855805	14856206	.	.	.	.	.	.
chr17	16727450	16727851	chr17	16727150	16727641	MLT1H2-int	LTR	MaLR
chr17	16727450	16727851	chr17	16727715	16727796	MLT1H2	LTR	MaLR
chr17	16727450	16727851	chr17	16727816	16727997	B3	SINE	B2
chr17	17929546	17929947	chr17	17929555	17929922	Lx8	LINE	L1
chr17	17929546	17929947	chr17	17929941	17930145	B4A	SINE	B4
chr17	17974814	17975215	.	.	.	.	.	.
chr17	21575789	21576190	chr17	21575562	21576191	RMER19B	LTR	ERVK
chr17	21653731	21654132	.	.	.	.	.	.
chr17	24098524	24098925	chr17	24098702	24098817	PB1D7	SINE	Alu
chr17	24137248	24137649	chr17	24137376	24137424	L2a	LINE	L2
chr17	24171909	24172310	chr17	24171884	24171951	B3A	SINE	B2
chr17	24992737	24993138	.	.	.	.	.	.

chr17	25779119	25779520	chr17	25779431	25779577	B1_Mus1	SINE	Alu
chr17	26122632	26123033	.	.	.	.	.	.
chr17	26507943	26508344	.	.	.	.	.	.
chr17	26651615	26652016	.	.	.	.	.	.
chr17	26721492	26721893	.	.	.	.	.	.
chr17	26742510	26742911	chr17	26742814	26742991	L2b	LINE	L2
chr17	26997630	26998031	.	.	.	.	.	.
chr17	27024938	27025339	chr17	27025171	27025254	B3A	SINE	B2
chr17	27175275	27175676	.	.	.	.	.	.
chr17	27178004	27178405	chr17	27178019	27178052	(G)n	Simple_repea	Simple_repeat
chr17	27178004	27178405	chr17	27178321	27178420	ID_B1	SINE	B4
chr17	27220570	27220971	.	.	.	.	.	.
chr17	27268396	27268797	.	.	.	.	.	.
chr17	27278896	27279297	chr17	27278920	27278966	GA-rich	Low_comple	Low_complexity
chr17	27441666	27442067	.	.	.	.	.	.
chr17	27678212	27678613	chr17	27678123	27678265	ORR1C2	LTR	MaLR
chr17	27678212	27678613	chr17	27678324	27678441	MLT1J	LTR	MaLR
chr17	27678212	27678613	chr17	27678470	27678596	LTR40a	LTR	ERVL
chr17	27684158	27684559	chr17	27684080	27684180	ID_B1	SINE	B4
chr17	27936974	27937375	.	.	.	.	.	.
chr17	28373558	28373959	chr17	28373817	28373840	(TG)n	Simple_repea	Simple_repeat
chr17	28902985	28903386	chr17	28903002	28903095	MIR	SINE	MIR
chr17	28902985	28903386	chr17	28903200	28903272	CT-rich	Low_comple	Low_complexity
chr17	29003853	29004254	chr17	29003871	29004112	MLT1J	LTR	MaLR
chr17	29003853	29004254	chr17	29004147	29004209	ID4_	SINE	ID
chr17	29021101	29021502	chr17	29020892	29021148	MTE2a	LTR	MaLR
chr17	29021101	29021502	chr17	29021248	29021309	LTR33A	LTR	ERVL
chr17	29021101	29021502	chr17	29021410	29021502	PB1D10	SINE	Alu
chr17	29305880	29306281	.	.	.	.	.	.
chr17	29479986	29480387	chr17	29480301	29480467	RSINE1	SINE	B4
chr17	29980364	29980765	chr17	29980266	29980429	B3	SINE	B2
chr17	29980364	29980765	chr17	29980460	29980573	MLT1J	LTR	MaLR
chr17	31615532	31615933	chr17	31615374	31615569	B2_Mm2	SINE	B2
chr17	32029778	32030179	.	.	.	.	.	.
chr17	32201940	32202341	chr17	32202259	32202385	B1_Mur1	SINE	Alu
chr17	33925742	33926143	chr17	33925769	33926177	L1MC4	LINE	L1
chr17	34002345	34002746	chr17	34002656	34002789	RMER17C	LTR	ERVK
chr17	34792443	34792844	.	.	.	.	.	.
chr17	35438856	35439257	.	.	.	.	.	.
chr17	35834570	35834971	.	.	.	.	.	.
chr17	35950144	35950545	.	.	.	.	.	.
chr17	36007495	36007896	.	.	.	.	.	.
chr17	36368149	36368550	chr17	36368068	36368205	B1_Mus2	SINE	Alu
chr17	39980112	39980513	.	.	.	.	.	.
chr17	42356787	42357188	chr17	42356352	42356884	Lx7	LINE	L1
chr17	44854914	44855315	.	.	.	.	.	.
chr17	45817447	45817848	.	.	.	.	.	.
chr17	45832107	45832508	.	.	.	.	.	.
chr17	45889584	45889985	.	.	.	.	.	.
chr17	45935988	45936389	chr17	45936326	45936394	(TTCA)n	Simple_repea	Simple_repeat
chr17	45987871	45988272	.	.	.	.	.	.
chr17	46620376	46620777	.	.	.	.	.	.
chr17	46650281	46650682	chr17	46650187	46650337	B1_Mus1	SINE	Alu
chr17	46650281	46650682	chr17	46650603	46650630	(TGGA)n	Simple_repea	Simple_repeat
chr17	46828270	46828671	chr17	46828163	46828297	MT2B	LTR	ERVL
chr17	46828270	46828671	chr17	46828278	46828329	PB1	SINE	Alu
chr17	46828270	46828671	chr17	46828364	46828586	URR1B	DNA	MER1_type
chr17	46828270	46828671	chr17	46828590	46828751	B2_Mm2	SINE	B2
chr17	47013223	47013624	chr17	47013147	47013549	MT2B	LTR	ERVL
chr17	47016874	47017275	chr17	47016907	47017124	ORR1E	LTR	MaLR
chr17	47016874	47017275	chr17	47017210	47017314	B1_Mur1	SINE	Alu
chr17	47069914	47070315	chr17	47069668	47070348	RMER6A	LTR	ERVK
chr17	47131986	47132387	.	.	.	.	.	.
chr17	47978917	47979318	.	.	.	.	.	.
chr17	48495000	48495401	.	.	.	.	.	.
chr17	53542240	53542641	chr17	53542594	53542643	(CAGA)n	Simple_repea	Simple_repeat
chr17	56277230	56277631	.	.	.	.	.	.
chr17	56405281	56405682	chr17	56405237	56405419	B2_Mm2	SINE	B2
chr17	56405281	56405682	chr17	56405436	56405578	RSINE1	SINE	B4
chr17	56408543	56408944	chr17	56408600	56408643	B1_Mus2	SINE	Alu
chr17	56408543	56408944	chr17	56408686	56408752	MLT1J	LTR	MaLR
chr17	56584776	56585177	chr17	56584751	56584883	L1MEf	LINE	L1
chr17	56646507	56646908	chr17	56646478	56646520	(TG)n	Simple_repea	Simple_repeat
chr17	56646507	56646908	chr17	56646520	56646539	(CG)n	Simple_repea	Simple_repeat
chr17	57261277	57261678	.	.	.	.	.	.
chr17	64054389	64054790	.	.	.	.	.	.
chr17	64062124	64062525	.	.	.	.	.	.
chr17	64087576	64087977	chr17	64087458	64087586	RMER6D	LTR	ERVK
chr17	64087576	64087977	chr17	64087608	64088045	RLTR23	LTR	ERV1
chr17	65907596	65907997	.	.	.	.	.	.
chr17	66070695	66071096	.	.	.	.	.	.
chr17	66859661	66860062	chr17	66859876	66859907	(TG)n	Simple_repea	Simple_repeat
chr17	68536998	68537399	.	.	.	.	.	.
chr17	69770974	69771375	chr17	69769883	69771061	L1M4	LINE	L1
chr17	69770974	69771375	chr17	69771200	69771262	L1M4	LINE	L1
chr17	69770974	69771375	chr17	69771262	69771442	B3A	SINE	B2
chr17	71071634	71072035	.	.	.	.	.	.
chr17	71078340	71078741	chr17	71078388	71078741	Tigger7	DNA	MER2_type
chr17	71087445	71087846	.	.	.	.	.	.
chr17	71096064	71096465	chr17	71096247	71096341	Charlie9	DNA	MER1_type
chr17	71186159	71186560	chr17	71186088	71186541	Tigger7	DNA	MER2_type
chr17	71514366	71514767	.	.	.	.	.	.
chr17	72009005	72009406	.	.	.	.	.	.
chr17	73424620	73425021	chr17	73424292	73425577	L1MB7	LINE	L1
chr17	73543952	73544353	.	.	.	.	.	.

chr17	73602586	73602987	chr17	73602763	73602836	L1MC4a	LINE	L1
chr17	74438605	74439006	chr17	74438923	74439023	RLTR16	LTR	ERVK
chr17	75454477	75454878	.	.	.	.	.	.
chr17	75510422	75510823	.	.	.	.	.	.
chr17	80100216	80100617	chr17	80100464	80100798	MER58B	DNA	MER1_type
chr17	80145426	80145827	chr17	80145718	80145777	MIRb	SINE	MIR
chr17	80331963	80332364	.	.	.	.	.	.
chr17	82776524	82776925	chr17	82776515	82776901	RMER19B	LTR	ERVK
chr17	82776524	82776925	chr17	82776901	82776935	(CTG)n	Simple_repea	Simple_repeat
chr17	84272039	84272440	.	.	.	.	.	.
chr17	84289058	84289459	.	.	.	.	.	.
chr17	84301911	84302312	.	.	.	.	.	.
chr17	84378370	84378771	.	.	.	.	.	.
chr17	84389780	84390181	chr17	84389696	84389835	MIRb	SINE	MIR
chr17	84425357	84425758	chr17	84425362	84425386	GC_rich	Low_comple	Low_complexity
chr17	84438820	84439221	chr17	84438803	84438885	ORR1E	LTR	MaLR
chr17	84438820	84439221	chr17	84439102	84439163	ORR1E	LTR	MaLR
chr17	84438820	84439221	chr17	84439188	84439360	B3A	SINE	B2
chr17	84443989	84444390	.	.	.	.	.	.
chr17	84483158	84483559	chr17	84483148	84483185	(TG)n	Simple_repea	Simple_repeat
chr17	84483158	84483559	chr17	84483214	84483344	RSINE1	SINE	B4
chr17	84509272	84509673	.	.	.	.	.	.
chr17	84548141	84548542	.	.	.	.	.	.
chr17	87560543	87560944	chr17	87560749	87560953	L1ME1	LINE	L1
chr17	87606169	87606570	chr17	87606337	87606367	(CA)n	Simple_repea	Simple_repeat
chr17	87636436	87636837	chr17	87636820	87636951	MER5B	DNA	MER1_type
chr17	87647579	87647980	chr17	87647337	87647662	RLTR11A2	LTR	ERVK
chr17	87647579	87647980	chr17	87647789	87648125	RLTR11A2	LTR	ERVK
chr17	87701767	87702168	.	.	.	.	.	.
chr17	87970794	87971195	chr17	87970822	87970916	MIRb	SINE	MIR
chr17	88136483	88136884	chr17	88136492	88136633	B3	SINE	B2
chr17	88136483	88136884	chr17	88136637	88136757	LTR33B	LTR	ERVL
chr17	88250731	88251132	.	.	.	.	.	.
chr17	88594650	88595051	chr17	88594316	88595094	ERVL-B4-int	LTR	ERVL
chr17	88661864	88662265	chr17	88661444	88661983	L1MB2	LINE	L1
chr17	88861989	88862390	.	.	.	.	.	.
chr17	88908513	88908914	.	.	.	.	.	.
chr18	3005632	3006033	chr18	3005757	3005881	RLTR11A	LTR	ERVK
chr18	3005632	3006033	chr18	3006013	3006125	(GAAA)n	Simple_repea	Simple_repeat
chr18	4522959	4523360	.	.	.	.	.	.
chr18	5510158	5510559	.	.	.	.	.	.
chr18	13107617	13108018	.	.	.	.	.	.
chr18	13114104	13114505	chr18	13114099	13114169	(CAG)n	Simple_repea	Simple_repeat
chr18	14416620	14417021	.	.	.	.	.	.
chr18	22516816	22517217	chr18	22517189	22517259	(GA)n	Simple_repea	Simple_repeat
chr18	35911706	35912107	.	.	.	.	.	.
chr18	36574665	36575066	chr18	36574875	36575047	B3A	SINE	B2
chr18	38227492	38227893	chr18	38227855	38227920	GA-rich	Low_comple	Low_complexity
chr18	38376463	38376864	.	.	.	.	.	.
chr18	38414542	38414943	chr18	38414323	38414689	MLT1J	LTR	MaLR
chr18	39826082	39826483	chr18	39826218	39826272	(TG)n	Simple_repea	Simple_repeat
chr18	40467694	40468095	chr18	40468091	40468224	HAL1-3A_ME	LINE	L1
chr18	44632166	44632567	chr18	44632000	44632181	B3A	SINE	B2
chr18	45215530	45215931	chr18	45215525	45215562	MTC	LTR	MaLR
chr18	45215530	45215931	chr18	45215562	45218559	L1_Mus1	LINE	L1
chr18	56099050	56099451	chr18	56099124	56099300	GSAT_MM	Satellite	Satellite
chr18	57947546	57947947	chr18	57947381	57947568	B3A	SINE	B2
chr18	61051069	61051470	.	.	.	.	.	.
chr18	61169854	61170255	.	.	.	.	.	.
chr18	61383874	61384275	.	.	.	.	.	.
chr18	61801107	61801508	chr18	61801042	61801159	MLT1D	LTR	MaLR
chr18	65151187	65151588	chr18	65151252	65151459	MLT1J2	LTR	MaLR
chr18	65151187	65151588	chr18	65151504	65151637	B1_Mur2	SINE	Alu
chr18	65586952	65587353	chr18	65587122	65587481	7SLRNA	srpRNA	srpRNA
chr18	66047585	66047986	chr18	66047702	66047887	MLT1N2	LTR	MaLR
chr18	70152022	70152423	.	.	.	.	.	.
chr18	77293649	77294050	chr18	77293968	77294027	CT-rich	Low_comple	Low_complexity
chr18	77469955	77470356	chr18	77470102	77470179	LTR33B	LTR	ERVL
chr18	77469955	77470356	chr18	77470278	77470321	AT_rich	Low_comple	Low_complexity
chr18	79459569	79459970	chr18	79459681	79459828	LTR33B	LTR	ERVL
chr18	79459569	79459970	chr18	79459877	79460132	ORR1D2	LTR	MaLR
chr18	80579357	80579758	.	.	.	.	.	.
chr18	80731097	80731498	.	.	.	.	.	.
chr18	81894585	81894986	chr18	81894625	81894860	RMER15	LTR	ERVL
chr18	81941510	81941911	.	.	.	.	.	.
chr18	82662173	82662574	chr18	82662370	82662494	MLT1J	LTR	MaLR
chr18	82662173	82662574	chr18	82662530	82662677	(TC)n	Simple_repea	Simple_repeat
chr18	85050496	85050897	chr18	85050415	85050601	B3	SINE	B2
chr18	85050496	85050897	chr18	85050666	85050737	ID4	SINE	ID
chr18	85050496	85050897	chr18	85050737	85050848	B4	SINE	B4
chr18	88923271	88923672	chr18	88923135	88923345	RLTR40	LTR	ERVK
chr19	3333985	3334386	chr19	3333796	3334068	B4A	SINE	B4
chr19	3376915	3377316	chr19	3376806	3377013	B3	SINE	B2
chr19	4046005	4046406	chr19	4046250	4046375	L1M5	LINE	L1
chr19	4121079	4121480	.	.	.	.	.	.
chr19	4244716	4245117	chr19	4244279	4244769	RMER4B	LTR	ERVK
chr19	4257497	4257898	.	.	.	.	.	.
chr19	4309806	4310207	chr19	4309790	4309811	(A)n	Simple_repea	Simple_repeat
chr19	4309806	4310207	chr19	4310171	4310368	B2_Mm1a	SINE	B2
chr19	4333738	4334139	.	.	.	.	.	.
chr19	5013326	5013727	chr19	5013267	5013505	MTEa	LTR	MaLR
chr19	5061854	5062255	chr19	5061820	5061982	(TCCA)n	Simple_repea	Simple_repeat
chr19	5345565	5345966	chr19	5345937	5345991	L2b	LINE	L2
chr19	5431985	5432386	.	.	.	.	.	.
chr19	5572433	5572834	chr19	5572594	5572711	RMER15	LTR	ERVL

chr19	5743616	5744017	.	.	.	.	.	.	
chr19	5749477	5749878	chr19	5749460	5749506	(TG)n	Simple_repea	Simple_repeat	
chr19	5749477	5749878	chr19	5749743	5749951	MIRb	SINE	MIR	
chr19	5786957	5787358	chr19	5786994	5787151	B2_Mm2	SINE	B2	
chr19	5786957	5787358	chr19	5787158	5787366	B3	SINE	B2	
chr19	5794694	5795095	chr19	5794384	5794789	MTA_Mm	LTR	MaLR	
chr19	5945131	5945532	.	.	.	.	.	.	
chr19	5956201	5956602	.	.	.	.	.	.	
chr19	6297632	6298033	.	.	.	.	.	.	
chr19	6452177	6452578	chr19	6452566	6452633	(TC)n	Simple_repea	Simple_repeat	
chr19	6476895	6477296	chr19	6476829	6477000	B3	SINE	B2	
chr19	6476895	6477296	chr19	6477002	6477169	L1MB3	LINE	L1	
chr19	6519476	6519877	.	.	.	.	.	.	
chr19	6525383	6525784	chr19	6525330	6525402	MLT1J1	LTR	MaLR	
chr19	6525383	6525784	chr19	6525549	6525628	MLT1J1	LTR	MaLR	
chr19	6525383	6525784	chr19	6525663	6525809	B1_Mus1	SINE	Alu	
chr19	6529573	6529974	.	.	.	.	.	.	
chr19	6925967	6926368	chr19	6925956	6926103	B4	SINE	B4	
chr19	6925967	6926368	chr19	6925976	6926104	B1_Mus1	SINE	Alu	
chr19	6925967	6926368	chr19	6926104	6926152	GA-rich	Low_comple	Low_complexity	
chr19	7025212	7025613	.	.	.	.	.	.	
chr19	7163591	7163992	.	.	.	.	.	.	
chr19	7376351	7376752	chr19	7376718	7376749	AT_rich	Low_comple	Low_complexity	
chr19	9057843	9058244	.	.	.	.	.	.	
chr19	9135720	9136121	.	.	.	.	.	.	
chr19	9985882	9986283	chr19	9986242	9986444	URR1A	DNA	MER1_type	
chr19	10029142	10029543	.	.	.	.	.	.	
chr19	10052807	10053208	chr19	10053167	10053218	(CA)n	Simple_repea	Simple_repeat	
chr19	10184519	10184920	chr19	10184361	10184533	B4A	SINE	B4	
chr19	10184519	10184920	chr19	10184787	10185063	L1Md_T	LINE	L1	
chr19	10340943	10341344	.	.	.	.	.	.	
chr19	10354230	10354631	chr19	10354588	10354715	RSINE1	SINE	B4	
chr19	10636476	10636877	chr19	10636790	10636812	(TTTG)n	Simple_repea	Simple_repeat	
chr19	11060381	11060782	.	.	.	.	.	.	
chr19	14316633	14317034	chr19	14316788	14316873	LTR33B	LTR	ERVL	
chr19	16446422	16446823	.	.	.	.	.	.	
chr19	16667837	16668238	chr19	16667845	16668009	MER58A	DNA	MER1_type	
chr19	16667837	16668238	chr19	16668071	16668420	MLT1J2	LTR	MaLR	
chr19	17214841	17215242	.	.	.	.	.	.	
chr19	17331405	17331806	.	.	.	.	.	.	
chr19	18736189	18736590	chr19	18736576	18736612	polypyrimidi	Low_comple	Low_complexity	
chr19	18840918	18841319	chr19	18840772	18841114	ORR1E	LTR	MaLR	
chr19	18964657	18965058	.	.	.	.	.	.	
chr19	19321638	19322039	chr19	19322003	19322106	MIR	SINE	MIR	
chr19	21415036	21415437	chr19	21415234	21415463	MLT1K	LTR	MaLR	
chr19	21894078	21894479	chr19	21893993	21894109	PB1D9	SINE	Alu	
chr19	21894078	21894479	chr19	21894305	21894445	B4A	SINE	B4	
chr19	21937981	21938382	.	.	.	.	.	.	
chr19	22064729	22065130	.	.	.	.	.	.	
chr19	22991897	22992298	chr19	22991817	22991899	MIRc	SINE	MIR	
chr19	22991897	22992298	chr19	22992071	22992302	URR1B	DNA	MER1_type	
chr19	23109794	23110195	.	.	.	.	.	.	
chr19	23128951	23129352	chr19	23128921	23129115	ID_B1	SINE	B4	
chr19	23210090	23210491	.	.	.	.	.	.	
chr19	23431748	23432149	chr19	23431912	23432083	GSAT_MM	Satellite	Satellite	
chr19	23564222	23564623	chr19	23564067	23564501	Zaphod	DNA	Tip100	
chr19	24271843	24272244	chr19	24272211	24272383	B3A	SINE	B2	
chr19	24358723	24359124	chr19	24358589	24358725	Lx8	LINE	L1	
chr19	24358723	24359124	chr19	24358874	24359032	MER20	DNA	MER1_type	
chr19	24375469	24375870	chr19	24375678	24375866	MLT1C	LTR	MaLR	
chr19	24400129	24400530	chr19	24400106	24400167	ID4_	SINE	ID	
chr19	24795043	24795444	.	.	.	.	.	.	
chr19	27426274	27426675	chr19	27425905	27426472	MLT2B3	LTR	ERVL	
chr19	27426274	27426675	chr19	27426472	27426631	Charlie5	DNA	MER1_type	
chr19	27426274	27426675	chr19	27426651	27426707	(TATG)n	Simple_repea	Simple_repeat	
chr19	28358158	28358559	chr19	28358506	28358890	MER121	Unknown	Unknown	
chr19	28723314	28723715	chr19	28723657	28724263	MER119	DNA	MER1_type	
chr19	28888195	28888596	.	.	.	.	.	.	
chr19	29715570	29715971	.	.	.	.	.	.	
chr19	29731525	29731926	chr19	29731878	29732093	B3	SINE	B2	
chr19	29924424	29924825	chr19	29924308	29924568	B4A	SINE	B4	
chr19	29991829	29992230	.	.	.	.	.	.	
chr19	30181982	30182383	.	.	.	.	.	.	
chr19	30392247	30392648	chr19	30392347	30392510	RLTR15	LTR	ERVK	
chr19	33099892	33100293	chr19	33100214	33100552	GA-rich	Low_comple	Low_complexity	
chr19	36203713	36204114	.	.	.	.	.	.	
chr19	36571541	36571942	.	.	.	.	.	.	
chr19	36740121	36740522	.	.	.	.	.	.	
chr19	37252355	37252756	.	.	.	.	.	.	
chr19	37563367	37563768	.	.	.	.	.	.	
chr19	37582429	37582830	chr19	37582521	37582660	B1_Mur1	SINE	Alu	
chr19	38034535	38034936	.	.	.	.	.	.	
chr19	38099694	38100095	chr19	38099679	38099763	MIR	SINE	MIR	
chr19	38099694	38100095	chr19	38099909	38099942	(G)n	Simple_repea	Simple_repeat	
chr19	38333026	38333427	.	.	.	.	.	.	
chr19	41368792	41369193	chr19	41368868	41369081	RLTR15	LTR	ERVK	
chr19	41931880	41932281	.	.	.	.	.	.	
chr19	42091252	42091653	.	.	.	.	.	.	
chr19	43991064	43991465	.	.	.	.	.	.	
chr19	44096051	44096452	.	.	.	.	.	.	
chr19	44300200	44300601	chr19	44300220	44300712	RLTR19A	LTR	ERVK	
chr19	44355316	44355717	.	.	.	.	.	.	
chr19	44386450	44386851	.	.	.	.	.	.	
chr19	45129696	45130097	.	.	.	.	.	.	
chr19	45557958	45558359	chr19	45557958	45558036	T-rich	Low_comple	Low_complexity	

chr19	45557958	45558359	chr19	45558052	45558198	B1F	SINE	Alu
chr19	45557958	45558359	chr19	45558352	45558512	RSINE1	SINE	B4
chr19	45724307	45724708	chr19	45724315	45724431	B1_Mus1	SINE	Alu
chr19	45724307	45724708	chr19	45724562	45724744	B2_Mm2	SINE	B2
chr19	46089038	46089439	chr19	46088987	46089148	B3A	SINE	B2
chr19	46089038	46089439	chr19	46089134	46089188	B1F	SINE	Alu
chr19	47291160	47291561	chr19	47290993	47291181	B2_Mm1a	SINE	B2
chr19	47291160	47291561	chr19	47291181	47291223	ID_B1	SINE	B4
chr19	47291160	47291561	chr19	47291365	47291449	ID_B1	SINE	B4
chr19	47291160	47291561	chr19	47291529	47291634	B3	SINE	B2
chr19	47338833	47339234	chr19	47339120	47339248	MIR3	SINE	MIR
chr19	47403577	47403978	chr19	47403728	47404092	RMER1C	Other	Other
chr19	47421214	47421615	.	.	.	.	.	.
chr19	47583189	47583590	.	.	.	.	.	.
chr19	47960975	47961376	chr19	47961050	47961093	(AGGGGG)n	Simple_repe	Simple_repeat
chr19	47960975	47961376	chr19	47961096	47961142	(GAAA)n	Simple_repe	Simple_repeat
chr19	53141337	53141738	.	.	.	.	.	.
chr19	53495515	53495916	.	.	.	.	.	.
chr19	53626663	53627064	.	.	.	.	.	.
chr19	53629564	53629965	.	.	.	.	.	.
chr19	53653465	53653866	chr19	53653444	53653498	RSINE1	SINE	B4
chr19	53653465	53653866	chr19	53653755	53653876	B1F	SINE	Alu
chr19	53806161	53806562	chr19	53806220	53806277	(CA)n	Simple_repe	Simple_repeat
chr19	53875054	53875455	chr19	53875009	53875082	(TG)n	Simple_repe	Simple_repeat
chr19	54244944	54245345	.	.	.	.	.	.
chr19	55514933	55515334	chr19	55515025	55515234	B3A	SINE	B2
chr19	55788450	55788851	.	.	.	.	.	.
chr19	56096803	56097204	.	.	.	.	.	.
chr19	56295213	56295614	.	.	.	.	.	.
chr19	57347789	57348190	chr19	57347930	57347988	RMER15	LTR	ERVL
chr19	57432825	57433226	chr19	57432807	57433136	ORR1E	LTR	MaLR
chr19	58179052	58179453	.	.	.	.	.	.
chr19	58598180	58598581	chr19	58598338	58598377	(TG)n	Simple_repe	Simple_repeat
chr19	58598180	58598581	chr19	58598387	58598490	RSINE1	SINE	B4
chr19	58625069	58625470	.	.	.	.	.	.
chr19	59053146	59053547	.	.	.	.	.	.
chr19	59920179	59920580	chr19	59920122	59920193	CT-rich	Low_comple	Low_complexity
chr19	59974135	59974536	chr19	59974124	59974200	G-rich	Low_comple	Low_complexity
chr19	60539904	60540305	.	.	.	.	.	.
chr19	60571725	60572126	chr19	60571744	60571968	RMER15	LTR	ERVL
chr19	61275481	61275882	chr19	61275773	61276286	MURVY-LTR	LTR	ERV1
chr19	61299605	61300006	chr19	61299855	61299963	RLTR11A2	LTR	ERVK
chr19	61299605	61300006	chr19	61299983	61300082	B2_Mm2	SINE	B2
chr19	61340134	61340535	chr19	61339804	61340389	RLTR33	LTR	ERVK
chr19	61340134	61340535	chr19	61340397	61340442	(CAGA)n	Simple_repe	Simple_repeat
chr19	61340134	61340535	chr19	61340445	61340495	(CA)n	Simple_repe	Simple_repeat
chr19	61341249	61341650	chr19	61341556	61341667	RLTR11A2	LTR	ERVK
chr2	3370381	3370782	.	.	.	.	.	.
chr2	3463775	3464176	chr2	3463879	3463981	MIR	SINE	MIR
chr2	4181730	4182131	.	.	.	.	.	.
chr2	4366832	4367233	.	.	.	.	.	.
chr2	5300182	5300583	chr2	5300087	5300422	LSU-rRNA_H	rRNA	rRNA
chr2	5300182	5300583	chr2	5300465	5300700	B4	SINE	B4
chr2	6141216	6141617	chr2	6141080	6141241	RMER1B	Other	Other
chr2	6300781	6301182	chr2	6300734	6300917	MIR	SINE	MIR
chr2	7036936	7037337	.	.	.	.	.	.
chr2	8675864	8676265	.	.	.	.	.	.
chr2	10171869	10172270	.	.	.	.	.	.
chr2	12686073	12686474	chr2	12686168	12686194	(TG)n	Simple_repe	Simple_repeat
chr2	12686073	12686474	chr2	12686194	12686240	(GA)n	Simple_repe	Simple_repeat
chr2	16604536	16604937	chr2	16604694	16604892	7SLRNA	srpRNA	srpRNA
chr2	16604536	16604937	chr2	16604893	16604936	(CAAA)n	Simple_repe	Simple_repeat
chr2	19501662	19502063	.	.	.	.	.	.
chr2	22600198	22600599	chr2	22600039	22600528	LSU-rRNA_H	rRNA	rRNA
chr2	22600198	22600599	chr2	22600594	22600665	LSU-rRNA_H	rRNA	rRNA
chr2	22667002	22667403	.	.	.	.	.	.
chr2	25999831	26000232	.	.	.	.	.	.
chr2	26349858	26350259	chr2	26349725	26349991	B4A	SINE	B4
chr2	26349858	26350259	chr2	26350004	26350052	(CA)n	Simple_repe	Simple_repeat
chr2	27297883	27298284	chr2	27297709	27297925	C-rich	Low_comple	Low_complexity
chr2	27395517	27395918	.	.	.	.	.	.
chr2	27630121	27630522	.	.	.	.	.	.
chr2	27691636	27692037	.	.	.	.	.	.
chr2	29526097	29526498	chr2	29525960	29526141	B3A	SINE	B2
chr2	29526097	29526498	chr2	29526142	29526189	B1_Mus2	SINE	Alu
chr2	30297228	30297629	.	.	.	.	.	.
chr2	30327309	30327710	chr2	30327587	30327608	GC_rich	Low_comple	Low_complexity
chr2	30327309	30327710	chr2	30327615	30327671	G-rich	Low_comple	Low_complexity
chr2	30351294	30351695	.	.	.	.	.	.
chr2	30409298	30409699	chr2	30409422	30409590	MLT1J1	LTR	MaLR
chr2	30446368	30446769	chr2	30446223	30446372	B1_Mur3	SINE	Alu
chr2	30446368	30446769	chr2	30446505	30446764	MLT1J2	LTR	MaLR
chr2	30457051	30457452	chr2	30457186	30457610	MLT1F	LTR	MaLR
chr2	30555248	30555649	chr2	30555342	30555541	MLT1J	LTR	MaLR
chr2	30572851	30573252	chr2	30572898	30573266	MER115	DNA	Tip100
chr2	30638800	30639201	chr2	30638945	30639087	MLT1J	LTR	MaLR
chr2	30638800	30639201	chr2	30639100	30639122	(CA)n	Simple_repe	Simple_repeat
chr2	30638800	30639201	chr2	30639122	30639156	GC_rich	Low_comple	Low_complexity
chr2	30754990	30755391	chr2	30755390	30755515	B1F1	SINE	Alu
chr2	31094870	31095271	chr2	31094870	31094937	(CGTG)n	Simple_repe	Simple_repeat
chr2	31094870	31095271	chr2	31094972	31095245	MTEa	LTR	MaLR
chr2	31112084	31112485	.	.	.	.	.	.
chr2	31153342	31153743	chr2	31153529	31153619	MLT1J	LTR	MaLR
chr2	31322955	31323356	chr2	31323085	31323255	ID_B1	SINE	B4
chr2	31322955	31323356	chr2	31323255	31323318	(CAGCC)n	Simple_repe	Simple_repeat

chr2	31322955	31323356	chr2	31323326	31323526	L1MC	LINE	L1
chr2	31405947	31406348	chr2	31406092	31406361	MLT1J2	LTR	MaLR
chr2	31626299	31626700	.	.	.	.	.	.
chr2	32198636	32199037	.	.	.	.	.	.
chr2	32713242	32713643	chr2	32713492	32713538	(TC)n	Simple_repea	Simple_repeat
chr2	32713242	32713643	chr2	32713538	32713625	B1_Mm	SINE	Alu
chr2	32718803	32719204	chr2	32718923	32719257	L1ME2	LINE	L1
chr2	32718803	32719204	chr2	32718651	32718866	ID_B1	SINE	B4
chr2	32736507	32736908	.	.	.	.	.	.
chr2	32822443	32822844	.	.	.	.	.	.
chr2	33010195	33010596	.	.	.	.	.	.
chr2	33539641	33540042	chr2	33539554	33539756	ID_B1	SINE	B4
chr2	33539641	33540042	chr2	33539759	33539895	PB1	SINE	Alu
chr2	33841930	33842331	chr2	33841952	33841992	(CCCCCA)n	Simple_repea	Simple_repeat
chr2	34262197	34262598	.	.	.	.	.	.
chr2	34657502	34657903	chr2	34657380	34657528	B1_Mus1	SINE	Alu
chr2	35090542	35090943	chr2	35090857	35090912	L2c	LINE	L2
chr2	35334060	35334461	chr2	35333997	35334147	B1F	SINE	Alu
chr2	35334060	35334461	chr2	35334289	35334365	(GA)n	Simple_repea	Simple_repeat
chr2	36080120	36080521	chr2	36080239	36080343	MLT1J2	LTR	MaLR
chr2	36103436	36103837	chr2	36103210	36103851	MER44D	DNA	MER2_type
chr2	36114898	36115299	.	.	.	.	.	.
chr2	38273458	38273859	chr2	38273439	38273630	ID_B1	SINE	B4
chr2	38273458	38273859	chr2	38273842	38273853	B1_Mur4	SINE	Alu
chr2	38273458	38273859	chr2	38273853	38273880	(TTTG)n	Simple_repea	Simple_repeat
chr2	38401725	38402126	.	.	.	.	.	.
chr2	38781787	38782188	chr2	38781878	38781914	GC_rich	Low_comple	Low_complexity
chr2	38781787	38782188	chr2	38782102	38782134	AT_rich	Low_comple	Low_complexity
chr2	38842097	38842498	.	.	.	.	.	.
chr2	44824690	44825091	.	.	.	.	.	.
chr2	44832614	44833015	.	.	.	.	.	.
chr2	46298431	46298832	.	.	.	.	.	.
chr2	49589505	49589906	.	.	.	.	.	.
chr2	50542762	50543163	.	.	.	.	.	.
chr2	59438976	59439377	chr2	59439036	59439233	LTR50	LTR	ERVL
chr2	59535213	59535614	.	.	.	.	.	.
chr2	60526942	60527343	chr2	60526898	60526949	(TG)n	Simple_repea	Simple_repeat
chr2	60538027	60538428	.	.	.	.	.	.
chr2	60778442	60778843	.	.	.	.	.	.
chr2	64877996	64878397	chr2	64877953	64878000	(GA)n	Simple_repea	Simple_repeat
chr2	64877996	64878397	chr2	64878000	64878231	RLTR23	LTR	ERV1
chr2	65240141	65240542	chr2	65240214	65240555	RLTR15	LTR	ERVK
chr2	65321507	65321908	.	.	.	.	.	.
chr2	65560596	65560997	chr2	65560879	65560905	(CAAA)n	Simple_repea	Simple_repeat
chr2	65862127	65862528	.	.	.	.	.	.
chr2	68753811	68754212	chr2	68753819	68754069	RLTR42	LTR	ERVK
chr2	68821520	68821921	chr2	68821687	68821898	ID_B1	SINE	B4
chr2	71337347	71337748	.	.	.	.	.	.
chr2	71380605	71381006	chr2	71380857	71380901	(TG)n	Simple_repea	Simple_repeat
chr2	71427212	71427613	.	.	.	.	.	.
chr2	71481942	71482343	chr2	71481813	71481980	L1MB3	LINE	L1
chr2	71481942	71482343	chr2	71481985	71482007	AT_rich	Low_comple	Low_complexity
chr2	71481942	71482343	chr2	71482245	71482301	(CA)n	Simple_repea	Simple_repeat
chr2	71916040	71916441	chr2	71915905	71916115	ID_B1	SINE	B4
chr2	72719610	72720011	chr2	72719914	72720056	MYSERV16_I	LTR	ERVK
chr2	72833629	72834030	chr2	72833765	72833886	LTR88c	LTR	Genie?
chr2	73423476	73423877	chr2	73423566	73423989	RMER10B	LTR	ERVL
chr2	73431150	73431551	.	.	.	.	.	.
chr2	74129412	74129813	chr2	74129350	74129508	MIRb	SINE	MIR
chr2	74129412	74129813	chr2	74129650	74129876	MLT1J2	LTR	MaLR
chr2	75601137	75601538	chr2	75601097	75601252	L1ME3A	LINE	L1
chr2	75606232	75606633	chr2	75606162	75606342	L1MB8	LINE	L1
chr2	81040597	81040998	chr2	81039863	81040866	Lx8	LINE	L1
chr2	84305052	84305453	.	.	.	.	.	.
chr2	84322056	84322457	chr2	84321951	84322220	RLTR18	LTR	ERVK
chr2	84322056	84322457	chr2	84322205	84322221	RLTR42	LTR	ERVK
chr2	84322056	84322457	chr2	84322221	84322245	(CA)n	Simple_repea	Simple_repeat
chr2	84322056	84322457	chr2	84322245	84322299	RLTR42	LTR	ERVK
chr2	84322056	84322457	chr2	84322400	84322436	AT_rich	Low_comple	Low_complexity
chr2	84660099	84660500	.	.	.	.	.	.
chr2	84700116	84700517	.	.	.	.	.	.
chr2	84729560	84729961	chr2	84729667	84729749	L2c	LINE	L2
chr2	90519353	90519754	.	.	.	.	.	.
chr2	91357428	91357829	chr2	91357450	91357502	ID4	SINE	ID
chr2	91892930	91893331	chr2	91893151	91893771	RLTR18	LTR	ERVK
chr2	94018935	94019336	.	.	.	.	.	.
chr2	98502712	98503113	chr2	98502625	98502983	SYNREP_MM	Satellite	Satellite
chr2	98502712	98503113	chr2	98502984	98503150	GSAT_MM	Satellite	Satellite
chr2	98503853	98504254	chr2	98503798	98504248	GSAT_MM	Satellite	Satellite
chr2	98506960	98507361	chr2	98506701	98507489	GSAT_MM	Satellite	Satellite
chr2	102822068	102822469	chr2	102822047	102822424	Lx8	LINE	L1
chr2	103510263	103510664	chr2	103510220	103510426	MIRb	SINE	MIR
chr2	103527181	103527582	.	.	.	.	.	.
chr2	105939838	105940239	chr2	105939800	105940161	RLTR12B	LTR	ERVK
chr2	109799298	109799699	.	.	.	.	.	.
chr2	112043094	112043495	chr2	112042399	112044116	Lx9	LINE	L1
chr2	112283686	112284087	.	.	.	.	.	.
chr2	113494831	113495232	.	.	.	.	.	.
chr2	113678784	113679185	.	.	.	.	.	.
chr2	113726219	113726620	.	.	.	.	.	.
chr2	116844879	116845280	.	.	.	.	.	.
chr2	117272655	117273056	.	.	.	.	.	.
chr2	117664043	117664444	.	.	.	.	.	.
chr2	120958681	120959082	chr2	120958998	120959167	RSINE1	SINE	B4
chr2	121401527	121401928	.	.	.	.	.	.

chr2	121447135	121447536	.	.	.	.	.	.	
chr2	121454078	121454479	.	.	.	.	.	.	
chr2	121997975	121998376	chr2	121997946	121998094	B1_Mur3	SINE	Alu	
chr2	121997975	121998376	chr2	121998223	121998391	(CA)n	Simple_repea	Simple_repeat	
chr2	122153776	122154177	chr2	122154042	122154262	MIRb	SINE	MIR	
chr2	122204296	122204697	.	.	.	.	.	.	
chr2	122507398	122507799	.	.	.	.	.	.	
chr2	122530307	122530708	.	.	.	.	.	.	
chr2	122534871	122535272	chr2	122534973	122535175	B3	SINE	B2	
chr2	122534871	122535272	chr2	122535193	122535294	PB1	SINE	Alu	
chr2	124431052	124431453	.	.	.	.	.	.	
chr2	124566447	124566848	chr2	124566421	124566563	MLT1H	LTR	MaLR	
chr2	125127941	125128342	chr2	125127924	125128083	MER5A	DNA	MER1_type	
chr2	126057328	126057729	chr2	126057386	126057411	AT_rich	Low_comple	Low_complexity	
chr2	126057328	126057729	chr2	126057422	126057832	Lx5	LINE	L1	
chr2	126189154	126189555	.	.	.	.	.	.	
chr2	126962629	126963030	.	.	.	.	.	.	
chr2	127509219	127509620	.	.	.	.	.	.	
chr2	128066290	128066691	.	.	.	.	.	.	
chr2	131030203	131030604	.	.	.	.	.	.	
chr2	131212022	131212423	chr2	131211910	131212131	B4	SINE	B4	
chr2	131212022	131212423	chr2	131212415	131212498	MIRc	SINE	MIR	
chr2	131218547	131218948	chr2	131218269	131218565	ORR1A2	LTR	MaLR	
chr2	131910145	131910546	.	.	.	.	.	.	
chr2	132149343	132149744	chr2	132149159	132149470	MTE2a	LTR	MaLR	
chr2	132149343	132149744	chr2	132149725	132149758	(TC)n	Simple_repea	Simple_repeat	
chr2	132512408	132512809	.	.	.	.	.	.	
chr2	132697270	132697671	chr2	132697302	132697429	MIR	SINE	MIR	
chr2	132697270	132697671	chr2	132697442	132697617	MLT1J1	LTR	MaLR	
chr2	136746968	136747369	.	.	.	.	.	.	
chr2	137860593	137860994	chr2	137860821	137861191	IAPLTR1_Mm	LTR	ERVK	
chr2	137865880	137866281	chr2	137865654	137866024	IAPLTR1_Mm	LTR	ERVK	
chr2	137865880	137866281	chr2	137866024	137866149	LTR16A1	LTR	ERVL	
chr2	139925784	139926185	.	.	.	.	.	.	
chr2	143729503	143729904	chr2	143729778	143729960	ID_B1	SINE	B4	
chr2	143735008	143735409	chr2	143734834	143735262	RLTR23	LTR	ERV1	
chr2	143735008	143735409	chr2	143735262	143735308	ID	SINE	ID	
chr2	143998169	143998570	chr2	143998009	143998410	LTR33A	LTR	ERVL	
chr2	145669050	145669451	chr2	145668934	145669063	B1_Mur1	SINE	Alu	
chr2	145669050	145669451	chr2	145669306	145669568	L1MB8	LINE	L1	
chr2	145691981	145692382	chr2	145691994	145692056	ID4_	SINE	ID	
chr2	145691981	145692382	chr2	145692067	145692207	B1F1	SINE	Alu	
chr2	145691981	145692382	chr2	145692071	145692250	B4	SINE	B4	
chr2	147940313	147940714	chr2	147940340	147940371	(TTTC)n	Simple_repea	Simple_repeat	
chr2	147940313	147940714	chr2	147940490	147940872	LTR33A_	LTR	ERVL	
chr2	148347791	148348192	.	.	.	.	.	.	
chr2	151460630	151461031	.	.	.	.	.	.	
chr2	151518351	151518752	chr2	151517916	151518445	Lx8	LINE	L1	
chr2	151518351	151518752	chr2	151518474	151518717	MLT1J	LTR	MaLR	
chr2	151739822	151740223	.	.	.	.	.	.	
chr2	152152405	152152806	chr2	152152354	152152486	MT2B	LTR	ERVL	
chr2	152152405	152152806	chr2	152152395	152152523	B1_Mur1	SINE	Alu	
chr2	152152405	152152806	chr2	152152536	152152711	B3	SINE	B2	
chr2	152152405	152152806	chr2	152152769	152152911	ORR1E	LTR	MaLR	
chr2	152618143	152618544	.	.	.	.	.	.	
chr2	152631717	152632118	chr2	152631556	152631864	L2b	LINE	L2	
chr2	152752600	152753001	.	.	.	.	.	.	
chr2	153657580	153657981	.	.	.	.	.	.	
chr2	154210070	154210471	chr2	154210292	154210470	MLT1J	LTR	MaLR	
chr2	154546680	154547081	chr2	154546997	154547095	B1_Mm	SINE	Alu	
chr2	154561749	154562150	chr2	154561896	154562158	LTR16C	LTR	ERVL	
chr2	154568720	154569121	chr2	154568496	154568937	RLTR28	LTR	ERVL	
chr2	155529278	155529679	chr2	155529649	155529725	ID4	SINE	ID	
chr2	155851225	155851626	chr2	155851417	155851557	L1MC4a	LINE	L1	
chr2	156104404	156104805	chr2	156104715	156104841	RSINE1	SINE	B4	
chr2	156279414	156279815	.	.	.	.	.	.	
chr2	156635291	156635692	chr2	156635283	156635387	PB1D10	SINE	Alu	
chr2	157071363	157071764	chr2	157071308	157071496	B2_Mm2	SINE	B2	
chr2	157378185	157378586	.	.	.	.	.	.	
chr2	158150521	158150922	chr2	158150667	158150783	LTR33A_	LTR	ERVL	
chr2	158150521	158150922	chr2	158150860	158150965	LTR33A_	LTR	ERVL	
chr2	160393554	160393955	chr2	160393273	160393598	L1ME3	LINE	L1	
chr2	160393554	160393955	chr2	160393604	160393852	MLT1J2	LTR	MaLR	
chr2	160393554	160393955	chr2	160393867	160393912	(ATG)n	Simple_repea	Simple_repeat	
chr2	161003206	161003607	.	.	.	.	.	.	
chr2	163562157	163562558	chr2	163562178	163562230	ID4	SINE	ID	
chr2	164280361	164280762	chr2	164280704	164280849	B1F1	SINE	Alu	
chr2	165089419	165089820	chr2	165089506	165089765	MLT1J	LTR	MaLR	
chr2	165245987	165246388	.	.	.	.	.	.	
chr2	165681177	165681578	.	.	.	.	.	.	
chr2	166000566	166000967	.	.	.	.	.	.	
chr2	166553667	166554068	chr2	166553794	166554080	MLT1J1	LTR	MaLR	
chr2	166612096	166612497	.	.	.	.	.	.	
chr2	167368575	167368976	.	.	.	.	.	.	
chr2	167395804	167396205	chr2	167396139	167396178	B4A	SINE	B4	
chr2	167395804	167396205	chr2	167396178	167396291	PB1D7	SINE	Alu	
chr2	167459838	167460239	.	.	.	.	.	.	
chr2	167533861	167534262	chr2	167533775	167533960	ID_B1	SINE	B4	
chr2	167564588	167564989	.	.	.	.	.	.	
chr2	167590671	167591072	.	.	.	.	.	.	
chr2	167602812	167603213	.	.	.	.	.	.	
chr2	167625562	167625963	chr2	167625586	167625785	MLT1J1	LTR	MaLR	
chr2	167625562	167625963	chr2	167625832	167625987	CT-rich	Low_comple	Low_complexity	
chr2	167776777	167777178	.	.	.	.	.	.	
chr2	168277269	168277670	.	.	.	.	.	.	

chr2	168284097	168284498	.	.	.	.	.	.
chr2	168343063	168343464	chr2	168342876	168343102	ID_B1	SINE	B4
chr2	169983253	169983654	chr2	169983320	169983406	(TC)n	Simple_repe	Simple_repeat
chr2	173107142	173107543	chr2	173107489	173107551	MIR	SINE	MIR
chr2	174168122	174168523	chr2	174168187	174168223	(CAA)n	Simple_repe	Simple_repeat
chr2	179458134	179458535	.	.	.	.	.	.
chr2	180345627	180346028	.	.	.	.	.	.
chr2	181652225	181652626	chr2	181652116	181652258	B1_Mus1	SINE	Alu
chr2	181652225	181652626	chr2	181652260	181652322	(TTA)n	Simple_repe	Simple_repeat
chr2	181653277	181653678	chr2	181653643	181653796	B1_Mus1	SINE	Alu
chr2	181665258	181665659	chr2	181665064	181665654	RLTR33	LTR	ERVK
chr3	5860461	5860862	chr3	5860318	5860822	LSU-rRNA_H	rRNA	rRNA
chr3	5860461	5860862	chr3	5860823	5862537	L1Md_A	LINE	L1
chr3	8246332	8246733	.	.	.	.	.	.
chr3	8270048	8270449	.	.	.	.	.	.
chr3	8971646	8972047	chr3	8971690	8971774	MLT1J1	LTR	MaLR
chr3	8971646	8972047	chr3	8971813	8971880	MLT1J1	LTR	MaLR
chr3	8971646	8972047	chr3	8971866	8971996	MLT1J1	LTR	MaLR
chr3	14902408	14902809	chr3	14902788	14902904	Lx9	LINE	L1
chr3	19329714	19330115	.	.	.	.	.	.
chr3	19528796	19529197	chr3	19528781	19528870	tRNA-Tyr-TA	tRNA	tRNA
chr3	19528796	19529197	chr3	19528994	19529067	tRNA-Ala-GC	tRNA	tRNA
chr3	21721601	21722002	chr3	21721788	21721874	ID4	SINE	ID
chr3	21834818	21835219	.	.	.	.	.	.
chr3	21851894	21852295	.	.	.	.	.	.
chr3	28242647	28243048	.	.	.	.	.	.
chr3	28422046	28422447	chr3	28421873	28422124	B4	SINE	B4
chr3	34178980	34179381	chr3	34178971	34178998	AT_rich	Low_comple	Low_complexity
chr3	34178980	34179381	chr3	34179118	34179216	RLTR15	LTR	ERVK
chr3	34431393	34431794	.	.	.	.	.	.
chr3	35570734	35571135	chr3	35570708	35571018	RLTR15	LTR	ERVK
chr3	35570734	35571135	chr3	35571031	35572064	Lx9	LINE	L1
chr3	35579276	35579677	chr3	35579389	35579702	(TG)n	Simple_repe	Simple_repeat
chr3	36348271	36348672	.	.	.	.	.	.
chr3	36439657	36440058	.	.	.	.	.	.
chr3	37027169	37027570	.	.	.	.	.	.
chr3	37259774	37260175	.	.	.	.	.	.
chr3	37773800	37774201	chr3	37774104	37774155	(CA)n	Simple_repe	Simple_repeat
chr3	37773800	37774201	chr3	37774168	37774276	(GA)n	Simple_repe	Simple_repeat
chr3	38154040	38154441	chr3	38153951	38154249	L1MB5	LINE	L1
chr3	38154040	38154441	chr3	38154394	38154452	SYNREP_MM	Satellite	Satellite
chr3	39901759	39902160	chr3	39901928	39901986	PB1	SINE	Alu
chr3	39901759	39902160	chr3	39901986	39902037	ID_B1	SINE	B4
chr3	39901759	39902160	chr3	39902048	39902138	B1F	SINE	Alu
chr3	39901759	39902160	chr3	39902156	39902491	ORR1B1	LTR	MaLR
chr3	40397847	40398248	chr3	40397471	40397920	L1M3	LINE	L1
chr3	40397847	40398248	chr3	40398110	40398131	(TTTG)n	Simple_repe	Simple_repeat
chr3	40397847	40398248	chr3	40398137	40398207	ID4	SINE	ID
chr3	40397847	40398248	chr3	40398217	40398948	RMER1C	Other	Other
chr3	41088784	41089185	.	.	.	.	.	.
chr3	48898308	48898709	.	.	.	.	.	.
chr3	49837172	49837573	.	.	.	.	.	.
chr3	50895409	50895810	chr3	50895648	50896020	L3	LINE	CR1
chr3	51856237	51856638	.	.	.	.	.	.
chr3	51984368	51984769	chr3	51984144	51984409	B4A	SINE	B4
chr3	52314299	52314700	.	.	.	.	.	.
chr3	52800610	52801011	.	.	.	.	.	.
chr3	52912493	52912894	.	.	.	.	.	.
chr3	52954907	52955308	.	.	.	.	.	.
chr3	54284171	54284572	.	.	.	.	.	.
chr3	54899764	54900165	chr3	54899492	54899791	RLTR42-int	LTR	ERVK
chr3	54899764	54900165	chr3	54899920	54899994	RLTR42	LTR	ERVK
chr3	54899764	54900165	chr3	54900143	54900227	MER2B	DNA	MER2_type
chr3	55375675	55376076	.	.	.	.	.	.
chr3	56379277	56379678	chr3	56379320	56379354	(TC)n	Simple_repe	Simple_repeat
chr3	56379277	56379678	chr3	56379356	56379673	GSAT_MM	Satellite	Satellite
chr3	56379277	56379678	chr3	56379673	56379735	(TC)n	Simple_repe	Simple_repeat
chr3	57098975	57099376	.	.	.	.	.	.
chr3	57308040	57308441	.	.	.	.	.	.
chr3	58883282	58883683	chr3	58882927	58883287	ORR1E	LTR	MaLR
chr3	59214618	59215019	chr3	59213766	59216252	L1Md_F2	LINE	L1
chr3	60331945	60332346	.	.	.	.	.	.
chr3	60393410	60393811	.	.	.	.	.	.
chr3	63243679	63244080	chr3	63244011	63244134	ID_B1	SINE	B4
chr3	64768955	64769356	chr3	64769038	64769236	MLT1J1	LTR	MaLR
chr3	65100936	65101337	.	.	.	.	.	.
chr3	65726439	65726840	.	.	.	.	.	.
chr3	65883789	65884190	chr3	65883800	65883887	PB1D10	SINE	Alu
chr3	65883789	65884190	chr3	65884156	65884335	(TG)n	Simple_repe	Simple_repeat
chr3	65885424	65885825	.	.	.	.	.	.
chr3	66012829	66013230	.	.	.	.	.	.
chr3	66113235	66113636	chr3	66113132	66113274	L1MD	LINE	L1
chr3	66113235	66113636	chr3	66113354	66113464	L1M4	LINE	L1
chr3	66113235	66113636	chr3	66113600	66113710	L1M4	LINE	L1
chr3	67294072	67294473	.	.	.	.	.	.
chr3	67357215	67357616	chr3	67357403	67357446	RLTR42	LTR	ERVK
chr3	68312488	68312889	.	.	.	.	.	.
chr3	69009536	69009937	.	.	.	.	.	.
chr3	69057023	69057424	.	.	.	.	.	.
chr3	69244696	69245097	.	.	.	.	.	.
chr3	69908682	69909083	.	.	.	.	.	.
chr3	70300833	70301234	.	.	.	.	.	.
chr3	79346496	79346897	.	.	.	.	.	.
chr3	79654551	79654952	.	.	.	.	.	.
chr3	80862141	80862542	.	.	.	.	.	.

chr3	80967966	80968367	.	.	.	.	.	.	.
chr3	82079377	82079778	.	.	.	.	.	.	.
chr3	82940316	82940717	.	.	.	.	.	.	.
chr3	84066847	84067248	chr3	84067056	84067234	(TATG)n	Simple_repe	Simple_repeat
chr3	84097492	84097893	chr3	84097441	84097575	B1_Mus2	SINE	Alu
chr3	84097492	84097893	chr3	84097651	84097714	ID4	SINE	ID
chr3	84097492	84097893	chr3	84097719	84097855	ZP3AR	Satellite	Satellite
chr3	84122646	84123047	chr3	84122538	84122797	MLT2C2	LTR	ERVL
chr3	84122646	84123047	chr3	84122797	84122880	ID4_	SINE	ID
chr3	84122646	84123047	chr3	84122880	84123011	MLT2C2	LTR	ERVL
chr3	84128809	84129210	chr3	84128967	84129225	ORR1E	LTR	MaLR
chr3	84233195	84233596	.	.	.	.	.	.
chr3	84451598	84451999	chr3	84451455	84451651	L3b	LINE	CR1
chr3	84451598	84451999	chr3	84451859	84451897	MER5B	DNA	MER1_type
chr3	84451598	84451999	chr3	84451987	84452133	B1_Mus2	SINE	Alu
chr3	85728311	85728712	.	.	.	.	.	.
chr3	85860580	85860981	chr3	85860483	85860671	B3A	SINE	B2
chr3	85860580	85860981	chr3	85860936	85861034	MLT2C1	LTR	ERVL
chr3	87714811	87715212	chr3	87715167	87715362	B3	SINE	B2
chr3	87937265	87937666	.	.	.	.	.	.
chr3	87981512	87981913	.	.	.	.	.	.
chr3	88014047	88014448	.	.	.	.	.	.
chr3	88024771	88025172	.	.	.	.	.	.
chr3	88268345	88268746	chr3	88268495	88268687	L2	LINE	L2
chr3	88292301	88292702	.	.	.	.	.	.
chr3	88428947	88429348	.	.	.	.	.	.
chr3	89003768	89004169	chr3	89003714	89003791	(GGAA)n	Simple_repe	Simple_repeat
chr3	89003768	89004169	chr3	89003801	89003857	GA-rich	Low_comple	Low_complexity
chr3	89120981	89121382	chr3	89121167	89121245	(TC)n	Simple_repe	Simple_repeat
chr3	89192714	89193115	.	.	.	.	.	.
chr3	89253496	89253897	chr3	89253878	89254019	B1_Mus1	SINE	Alu
chr3	89991754	89992155	chr3	89991751	89991843	L1M3	LINE	L1
chr3	89991754	89992155	chr3	89991892	89991952	ID_B1	SINE	B4
chr3	89991754	89992155	chr3	89991952	89992354	MTC	LTR	MaLR
chr3	90353640	90354041	chr3	90353637	90353729	PB1D7	SINE	Alu
chr3	90353640	90354041	chr3	90353961	90354009	B3	SINE	B2
chr3	90353640	90354041	chr3	90354010	90354101	L2	LINE	L2
chr3	90391566	90391967	chr3	90391652	90391676	(CG)n	Simple_repe	Simple_repeat
chr3	90391566	90391967	chr3	90391676	90391720	(CA)n	Simple_repe	Simple_repeat
chr3	90391566	90391967	chr3	90391881	90392217	MTB_Mm	LTR	MaLR
chr3	93341192	93341593	chr3	93341502	93341524	(TG)n	Simple_repe	Simple_repeat
chr3	93341192	93341593	chr3	93341577	93341816	RMER6B	LTR	ERVK
chr3	93372582	93372983	.	.	.	.	.	.
chr3	94452996	94453397	.	.	.	.	.	.
chr3	95050564	95050965	chr3	95050556	95050624	RSINE1	SINE	B4
chr3	95050564	95050965	chr3	95050907	95051038	B1F	SINE	Alu
chr3	95097587	95097988	chr3	95097757	95097924	MLT1I	LTR	MaLR
chr3	95211697	95212098	chr3	95211745	95211964	Charlie25	DNA	MER1_type
chr3	95211697	95212098	chr3	95211984	95212089	B3	SINE	B2
chr3	95478775	95479176	chr3	95478685	95479062	RMER10A	LTR	ERVL
chr3	96380148	96380549	.	.	.	.	.	.
chr3	97438335	97438736	chr3	97438234	97438444	B4	SINE	B4
chr3	97438335	97438736	chr3	97438444	97438621	B2_Mm2	SINE	B2
chr3	97438335	97438736	chr3	97438621	97438679	B4	SINE	B4
chr3	97438335	97438736	chr3	97438718	97439028	L1MC	LINE	L1
chr3	97702254	97702655	chr3	97702303	97702343	(TC)n	Simple_repe	Simple_repeat
chr3	98031091	98031492	chr3	98031089	98031298	MIR	SINE	MIR
chr3	98120929	98121330	chr3	98120859	98120955	PB1D7	SINE	Alu
chr3	98193248	98193649	chr3	98193315	98193380	L1MC1	LINE	L1
chr3	98193248	98193649	chr3	98193384	98193497	MLT1J	LTR	MaLR
chr3	98193248	98193649	chr3	98193522	98195764	RLTR42-int	LTR	ERVK
chr3	99784917	99785318	chr3	99785017	99785317	GSAT_MM	Satellite	Satellite
chr3	101010084	101010485	chr3	101009857	101010206	RLTR13D5	LTR	ERVK
chr3	101010084	101010485	chr3	101010271	101010343	LTR33A	LTR	ERVL
chr3	101010084	101010485	chr3	101010280	101010356	MLT1J	LTR	MaLR
chr3	102505773	102506174	.	.	.	.	.	.
chr3	103177901	103178302	chr3	103178069	103178263	B3	SINE	B2
chr3	103486400	103486801	.	.	.	.	.	.
chr3	103487548	103487949	.	.	.	.	.	.
chr3	103520954	103521355	chr3	103520996	103521040	(CA)n	Simple_repe	Simple_repeat
chr3	103563518	103563919	.	.	.	.	.	.
chr3	104156766	104157167	.	.	.	.	.	.
chr3	104164297	104164698	chr3	104164390	104164438	L2a	LINE	L2
chr3	104231289	104231690	chr3	104231294	104231464	RMER10A	LTR	ERVL
chr3	104231289	104231690	chr3	104231464	104231553	PB1	SINE	Alu
chr3	104231289	104231690	chr3	104231553	104231703	GA-rich	Low_comple	Low_complexity
chr3	104345027	104345428	chr3	104345004	104345029	(A)n	Simple_repe	Simple_repeat
chr3	107579225	107579626	.	.	.	.	.	.
chr3	107632949	107633350	chr3	107632931	107632998	PB1D7	SINE	Alu
chr3	107742399	107742800	chr3	107742751	107742842	L3	LINE	CR1
chr3	108573674	108574075	.	.	.	.	.	.
chr3	108813973	108814374	.	.	.	.	.	.
chr3	109851060	109851461	.	.	.	.	.	.
chr3	115815987	115816388	.	.	.	.	.	.
chr3	116139674	116140075	chr3	116139868	116140068	MER72	LTR	ERV1
chr3	116469825	116470226	chr3	116469840	116469978	B1_Mus2	SINE	Alu
chr3	116469825	116470226	chr3	116469978	116470021	(CAAAA)n	Simple_repe	Simple_repeat
chr3	116469825	116470226	chr3	116470139	116470257	B1_Mus1	SINE	Alu
chr3	116551057	116551458	chr3	116551433	116551494	(TCTG)n	Simple_repe	Simple_repeat
chr3	116741434	116741835	.	.	.	.	.	.
chr3	116790581	116790982	chr3	116790546	116790694	ORR1B2	LTR	MaLR
chr3	119619141	119619542	chr3	119619061	119619249	RMER30	DNA	MER1_type
chr3	119619141	119619542	chr3	119619293	119619469	B3	SINE	B2
chr3	119619141	119619542	chr3	119619499	119619624	MIR	SINE	MIR
chr3	120119502	120119903	.	.	.	.	.	.

chr3	121279221	121279622	chr3	121279231	121279389	ID_B1	SINE	B4
chr3	121352938	121353339	chr3	121352957	121353053	MIR	SINE	MIR
chr3	121399958	121400359	chr3	121400251	121400421	LTR78	LTR	ERV1
chr3	121471825	121472226	.	.	.	.	.	.
chr3	121791185	121791586	.	.	.	.	.	.
chr3	121824996	121825397	.	.	.	.	.	.
chr3	122051621	122052022	.	.	.	.	.	.
chr3	122212450	122212851	chr3	122212644	122212745	MIRb	SINE	MIR
chr3	122825591	122825992	.	.	.	.	.	.
chr3	123355860	123356261	.	.	.	.	.	.
chr3	126273650	126274051	.	.	.	.	.	.
chr3	126534366	126534767	.	.	.	.	.	.
chr3	126671669	126672070	.	.	.	.	.	.
chr3	126766537	126766938	.	.	.	.	.	.
chr3	129001278	129001679	.	.	.	.	.	.
chr3	129607558	129607959	chr3	129607468	129607572	PB1	SINE	Alu
chr3	129607558	129607959	chr3	129607585	129607715	MER3	DNA	MER1_type
chr3	129640816	129641217	.	.	.	.	.	.
chr3	129652081	129652482	chr3	129651973	129652084	L1MA8	LINE	L1
chr3	129652081	129652482	chr3	129652363	129652688	MLT1A	LTR	MaLR
chr3	130288486	130288887	.	.	.	.	.	.
chr3	130590412	130590813	chr3	130590363	130590820	L1MC3	LINE	L1
chr3	131509777	131510178	chr3	131509698	131509887	L1MC1	LINE	L1
chr3	131509777	131510178	chr3	131510048	131510340	L1MC1	LINE	L1
chr3	131558027	131558428	chr3	131557785	131558283	MLT2F	LTR	ERVL
chr3	132534423	132534824	.	.	.	.	.	.
chr3	133263846	133264247	.	.	.	.	.	.
chr3	133271973	133272374	chr3	133272017	133272198	MLT2E	LTR	ERVL
chr3	133271973	133272374	chr3	133272341	133272392	(TC)n	Simple_repea	Simple_repeat
chr3	135171207	135171608	.	.	.	.	.	.
chr3	135185101	135185502	chr3	135185398	135185444	(GA)n	Simple_repea	Simple_repeat
chr3	135291566	135291967	.	.	.	.	.	.
chr3	135829653	135830054	.	.	.	.	.	.
chr3	136114339	136114740	.	.	.	.	.	.
chr3	136303780	136304181	.	.	.	.	.	.
chr3	138179087	138179488	chr3	138178870	138179158	B4A	SINE	B4
chr3	138423563	138423964	.	.	.	.	.	.
chr3	144265822	144266223	chr3	144266203	144266393	B3A	SINE	B2
chr3	144332394	144332795	.	.	.	.	.	.
chr3	144931056	144931457	chr3	144931029	144931203	Lx9	LINE	L1
chr3	144931056	144931457	chr3	144931205	144931321	LTR78	LTR	ERV1
chr3	144931056	144931457	chr3	144931376	144931497	MIRb	SINE	MIR
chr3	145348012	145348413	.	.	.	.	.	.
chr3	145368420	145368821	chr3	145368720	145368752	(TG)n	Simple_repea	Simple_repeat
chr3	145368420	145368821	chr3	145368752	145368818	(CA)n	Simple_repea	Simple_repeat
chr3	146564238	146564639	.	.	.	.	.	.
chr3	146776716	146777117	.	.	.	.	.	.
chr3	147465552	147465953	.	.	.	.	.	.
chr3	148715485	148715886	chr3	148715436	148715898	(TTAGGG)n	Simple_repea	Simple_repeat
chr3	151071079	151071480	.	.	.	.	.	.
chr3	151168482	151168883	.	.	.	.	.	.
chr3	151641143	151641544	.	.	.	.	.	.
chr3	151703490	151703891	.	.	.	.	.	.
chr3	151785637	151786038	chr3	151785579	151785734	ID_B1	SINE	B4
chr3	151785637	151786038	chr3	151785734	151785787	ORR1C1	LTR	MaLR
chr3	151785637	151786038	chr3	151785787	151786134	ORR1C1	LTR	MaLR
chr3	151971615	151972016	chr3	151971879	151971979	RSINE1	SINE	B4
chr3	151971615	151972016	chr3	151972006	151972133	B1_Mur2	SINE	Alu
chr3	152231632	152232033	.	.	.	.	.	.
chr3	152786582	152786983	chr3	152786703	152786882	(CATTC)n	Simple_repea	Simple_repeat
chr3	153647414	153647815	chr3	153647525	153647801	RMER20B	LTR	ERVK
chr3	153953187	153953588	chr3	153953212	153953276	(GA)n	Simple_repea	Simple_repeat
chr3	153953187	153953588	chr3	153953551	153953678	RSINE1	SINE	B4
chr3	154741003	154741404	chr3	154740938	154741339	RMER6C	LTR	ERVK
chr3	154741003	154741404	chr3	154741385	154741496	RLTR33	LTR	ERVK
chr3	157725109	157725510	.	.	.	.	.	.
chr4	3010773	3011174	.	.	.	.	.	.
chr4	3017259	3017660	chr4	3016701	3018331	GSAT_MM	Satellite	Satellite
chr4	8426084	8426485	chr4	8425968	8426087	B1F	SINE	Alu
chr4	10284788	10285189	chr4	10284824	10285070	L2c	LINE	L2
chr4	14598595	14598996	chr4	14598692	14599033	RLTR15	LTR	ERVK
chr4	28103922	28104323	chr4	28103933	28103988	CENSAT_MC	Satellite	centr
chr4	28103922	28104323	chr4	28103949	28104365	SYNREP_MM	Satellite	Satellite
chr4	32028460	32028861	chr4	32028630	32028828	LTR88c	LTR	Genie?
chr4	32028460	32028861	chr4	32028856	32029132	Lx7	LINE	L1
chr4	41300362	41300763	chr4	41300402	41300491	B1F2	SINE	Alu
chr4	41300362	41300763	chr4	41300624	41300746	L1M5	LINE	L1
chr4	43052098	43052499	.	.	.	.	.	.
chr4	43490972	43491373	chr4	43491055	43491090	(CCAA)n	Simple_repea	Simple_repeat
chr4	46214365	46214766	chr4	46214481	46214597	PB1D10	SINE	Alu
chr4	53208859	53209260	.	.	.	.	.	.
chr4	54942521	54942922	chr4	54942624	54942752	PB1D9	SINE	Alu
chr4	54942521	54942922	chr4	54942771	54942880	PB1D7	SINE	Alu
chr4	54942521	54942922	chr4	54942880	54942988	(GGAA)n	Simple_repea	Simple_repeat
chr4	55115450	55115851	chr4	55115732	55116156	MTE2a	LTR	MaLR
chr4	55266634	55267035	.	.	.	.	.	.
chr4	55338773	55339174	chr4	55338856	55339031	B2_Mm2	SINE	B2
chr4	55338773	55339174	chr4	55339078	55339116	B2_Mm2	SINE	B2
chr4	55338773	55339174	chr4	55339168	55339309	RSINE1	SINE	B4
chr4	55720718	55721119	.	.	.	.	.	.
chr4	55734598	55734999	.	.	.	.	.	.
chr4	56117426	56117827	chr4	56117465	56117696	MLT1J2	LTR	MaLR
chr4	56117426	56117827	chr4	56117740	56117879	L2c	LINE	L2
chr4	56173347	56173748	.	.	.	.	.	.
chr4	56336208	56336609	chr4	56336100	56336303	Tigger6b	DNA	MER2_type

chr4	56386638	56387039	.	.	.	.	.	.
chr4	56406793	56407194	.	.	.	.	.	.
chr4	56432422	56432823	chr4	56431997	56432674	MamRep605	Unknown	Unknown
chr4	56546160	56546561	.	.	.	.	.	.
chr4	56698093	56698494	chr4	56698072	56698095	(A)n	Simple_repe	Simple_repeat
chr4	56698093	56698494	chr4	56698098	56698133	(CAGGG)n	Simple_repe	Simple_repeat
chr4	56698093	56698494	chr4	56698341	56698549	MIRb	SINE	MIR
chr4	56850521	56850922	.	.	.	.	.	.
chr4	57166341	57166742	chr4	57166341	57166473	MIRb	SINE	MIR
chr4	57166341	57166742	chr4	57166695	57166719	(CAGG)n	Simple_repe	Simple_repeat
chr4	57307928	57308329	.	.	.	.	.	.
chr4	57556624	57557025	.	.	.	.	.	.
chr4	57744065	57744466	.	.	.	.	.	.
chr4	57811236	57811637	chr4	57811402	57811415	B4A	SINE	B4
chr4	57811236	57811637	chr4	57811415	57811513	PB1D10	SINE	Alu
chr4	57811236	57811637	chr4	57811513	57812075	RLTR28	LTR	ERVL
chr4	57852391	57852792	chr4	57852538	57852658	B4A	SINE	B4
chr4	57878899	57879300	.	.	.	.	.	.
chr4	57977046	57977447	chr4	57976988	57977103	PB1D10	SINE	Alu
chr4	58045533	58045934	.	.	.	.	.	.
chr4	58343731	58344132	.	.	.	.	.	.
chr4	58371968	58372369	chr4	58372358	58372437	MIRb	SINE	MIR
chr4	58414998	58415399	.	.	.	.	.	.
chr4	59813021	59813422	chr4	59813110	59813161	(CA)n	Simple_repe	Simple_repeat
chr4	59813021	59813422	chr4	59813402	59813456	L4	LINE	RTE
chr4	59820402	59820803	chr4	59820474	59820663	MLT1F	LTR	MaLR
chr4	59820402	59820803	chr4	59820663	59820850	MLT1F	LTR	MaLR
chr4	62059976	62060377	chr4	62060007	62060123	PB1D7	SINE	Alu
chr4	62059976	62060377	chr4	62060354	62060443	PB1D7	SINE	Alu
chr4	62393787	62394188	.	.	.	.	.	.
chr4	62424994	62425395	chr4	62424940	62425075	B1_Mus2	SINE	Alu
chr4	62729854	62730255	.	.	.	.	.	.
chr4	62984419	62984820	.	.	.	.	.	.
chr4	63070773	63071174	.	.	.	.	.	.
chr4	63182829	63183230	chr4	63182727	63182857	L1M5	LINE	L1
chr4	63191457	63191858	.	.	.	.	.	.
chr4	63329352	63329753	.	.	.	.	.	.
chr4	63335942	63336343	.	.	.	.	.	.
chr4	63446510	63446911	chr4	63446686	63446743	MIRm	SINE	MIR
chr4	63737498	63737899	.	.	.	.	.	.
chr4	63985315	63985716	.	.	.	.	.	.
chr4	63999529	63999930	.	.	.	.	.	.
chr4	64158749	64159150	chr4	64158708	64159112	SYNREP_MM	Satellite	Satellite
chr4	64158749	64159150	chr4	64159104	64159171	Lx6	LINE	L1
chr4	64562059	64562460	.	.	.	.	.	.
chr4	64903827	64904228	.	.	.	.	.	.
chr4	64927994	64928395	.	.	.	.	.	.
chr4	65138197	65138598	.	.	.	.	.	.
chr4	66555639	66556040	chr4	66555679	66555699	(T)n	Simple_repe	Simple_repeat
chr4	66608781	66609182	chr4	66608968	66609088	MIRb	SINE	MIR
chr4	67683975	67684376	.	.	.	.	.	.
chr4	68196866	68197267	.	.	.	.	.	.
chr4	68326289	68326690	.	.	.	.	.	.
chr4	68381900	68382301	chr4	68382096	68382550	MT2A	LTR	ERVL
chr4	70039048	70039449	chr4	70039150	70039288	GSAT_MM	Satellite	Satellite
chr4	70792946	70793347	chr4	70793216	70793371	MER3	DNA	MER1_type
chr4	80617580	80617981	.	.	.	.	.	.
chr4	81680871	81681272	chr4	81680956	81680987	(CA)n	Simple_repe	Simple_repeat
chr4	82948692	82949093	.	.	.	.	.	.
chr4	82954823	82955224	chr4	82954585	82955002	MTC	LTR	MaLR
chr4	83026309	83026710	chr4	83026255	83026393	MER5B	DNA	MER1_type
chr4	83026309	83026710	chr4	83026570	83026680	ORR1E	LTR	MaLR
chr4	83026309	83026710	chr4	83026680	83026809	B1_Mur4	SINE	Alu
chr4	84169052	84169453	.	.	.	.	.	.
chr4	84387281	84387682	.	.	.	.	.	.
chr4	87080827	87081228	chr4	87080758	87080845	MIRc	SINE	MIR
chr4	87080827	87081228	chr4	87081015	87081158	MER58A	DNA	MER1_type
chr4	87484720	87485121	chr4	87484865	87484934	Charlie9	DNA	MER1_type
chr4	87859739	87860140	chr4	87859675	87859782	MER33	DNA	MER1_type
chr4	87859739	87860140	chr4	87859796	87860069	RMER15	LTR	ERVL
chr4	88605556	88605957	.	.	.	.	.	.
chr4	88668407	88668808	chr4	88668383	88668433	L1Md_F2	LINE	L1
chr4	89127132	89127533	chr4	89127072	89127213	MIRb	SINE	MIR
chr4	89127132	89127533	chr4	89127219	89127283	Lx9	LINE	L1
chr4	89127132	89127533	chr4	89127283	89127465	(GA)n	Simple_repe	Simple_repeat
chr4	89127132	89127533	chr4	89127532	89127571	AT_rich	Low_comple	Low_complexity
chr4	89153655	89154056	.	.	.	.	.	.
chr4	89181641	89182042	.	.	.	.	.	.
chr4	91223649	91224050	.	.	.	.	.	.
chr4	94668154	94668555	.	.	.	.	.	.
chr4	94702044	94702445	chr4	94702198	94702241	L2b	LINE	L2
chr4	94771940	94772341	.	.	.	.	.	.
chr4	94870184	94870585	chr4	94870325	94870397	MLT1A1	LTR	MaLR
chr4	94984441	94984842	.	.	.	.	.	.
chr4	95083775	95084176	.	.	.	.	.	.
chr4	95093259	95093660	.	.	.	.	.	.
chr4	97572484	97572885	.	.	.	.	.	.
chr4	97670738	97671139	.	.	.	.	.	.
chr4	98369135	98369536	.	.	.	.	.	.
chr4	98418520	98418921	chr4	98418664	98418771	MLT1J	LTR	MaLR
chr4	98758063	98758464	chr4	98758043	98758321	L1MC2	LINE	L1
chr4	98758063	98758464	chr4	98758321	98758601	MTD	LTR	MaLR
chr4	99946508	99946909	.	.	.	.	.	.
chr4	100263457	100263858	.	.	.	.	.	.
chr4	100875383	100875784	.	.	.	.	.	.

chr4	100978771	100979172	chr4	100978712	100978826	RSINE1	SINE	B4
chr4	101042352	101042753	chr4	101042148	101042359	L1ME1	LINE	L1
chr4	101042352	101042753	chr4	101042381	101042394	RSINE1	SINE	B4
chr4	101042352	101042753	chr4	101042394	101042444	(GA)n	Simple_repe	Simple_repeat
chr4	101042352	101042753	chr4	101042444	101042590	RSINE1	SINE	B4
chr4	101042352	101042753	chr4	101042700	101042840	L1ME1	LINE	L1
chr4	101242634	101243035	chr4	101242781	101242867	MLT1J	LTR	MaLR
chr4	101912212	101912613	.	.	.	.	.	.
chr4	102559446	102559847	chr4	102559592	102559809	MIR	SINE	MIR
chr4	102937757	102938158	.	.	.	.	.	.
chr4	104963950	104964351	chr4	104963993	104964018	(A)n	Simple_repe	Simple_repeat
chr4	104963950	104964351	chr4	104964233	104964330	MIRc	SINE	MIR
chr4	105123444	105123845	chr4	105123448	105123545	B1F2	SINE	Alu
chr4	105241943	105242344	chr4	105241888	105242070	MIR	SINE	MIR
chr4	105283508	105283909	.	.	.	.	.	.
chr4	105313430	105313831	.	.	.	.	.	.
chr4	105378722	105379123	.	.	.	.	.	.
chr4	106202354	106202755	.	.	.	.	.	.
chr4	106286771	106287172	chr4	106286603	106286791	MIRb	SINE	MIR
chr4	106500203	106500604	.	.	.	.	.	.
chr4	106512495	106512896	chr4	106512768	106512818	GC_rich	Low_comple	Low_complexity
chr4	106781071	106781472	.	.	.	.	.	.
chr4	106836568	106836969	.	.	.	.	.	.
chr4	106958117	106958518	chr4	106958010	106958148	B1_Mus2	SINE	Alu
chr4	106958117	106958518	chr4	106958320	106958373	RSINE1	SINE	B4
chr4	106958117	106958518	chr4	106958425	106958534	PB1D10	SINE	Alu
chr4	107125745	107126146	chr4	107125814	107125837	GC_rich	Low_comple	Low_complexity
chr4	107140889	107141290	.	.	.	.	.	.
chr4	107196313	107196714	.	.	.	.	.	.
chr4	107537522	107537923	chr4	107537778	107538130	MTC	LTR	MaLR
chr4	107657027	107657428	chr4	107657035	107657133	MER121	Unknown	Unknown
chr4	107657027	107657428	chr4	107657156	107657199	(TG)n	Simple_repe	Simple_repeat
chr4	107730772	107731173	chr4	107730673	107731031	MTEb	LTR	MaLR
chr4	107730772	107731173	chr4	107731031	107731322	L1MB5	LINE	L1
chr4	107743796	107744197	.	.	.	.	.	.
chr4	108632405	108632806	.	.	.	.	.	.
chr4	108886566	108886967	chr4	108886571	108886702	URR1B	DNA	MER1_type
chr4	108886566	108886967	chr4	108886866	108887118	MLT1A1	LTR	MaLR
chr4	109154118	109154519	.	.	.	.	.	.
chr4	109755544	109755945	chr4	109755564	109755675	PB1D7	SINE	Alu
chr4	111318309	111318710	chr4	111318444	111318499	(CA)n	Simple_repe	Simple_repeat
chr4	111318309	111318710	chr4	111318500	111318667	MER20	DNA	MER1_type
chr4	113608599	113609000	chr4	113608337	113609221	MurERV4-int	LTR	ERVK
chr4	113971744	113972145	.	.	.	.	.	.
chr4	113972909	113973310	chr4	113972925	113973110	L1MA6	LINE	L1
chr4	114018323	114018724	.	.	.	.	.	.
chr4	114032347	114032748	.	.	.	.	.	.
chr4	115595359	115595760	chr4	115595682	115595748	MIRb	SINE	MIR
chr4	115657571	115657972	chr4	115657532	115657681	L1ME1	LINE	L1
chr4	115657571	115657972	chr4	115657681	115658016	ORR1E	LTR	MaLR
chr4	115973450	115973851	.	.	.	.	.	.
chr4	116050590	116050991	.	.	.	.	.	.
chr4	116340837	116341238	chr4	116341195	116341258	PB1D10	SINE	Alu
chr4	116793045	116793446	.	.	.	.	.	.
chr4	116862175	116862576	chr4	116862192	116862226	(GAAAA)n	Simple_repe	Simple_repeat
chr4	116862175	116862576	chr4	116862546	116862663	U5	snRNA	snRNA
chr4	116874758	116875159	chr4	116874559	116874769	Lx8	LINE	L1
chr4	116874758	116875159	chr4	116875132	116875249	U5	snRNA	snRNA
chr4	116883086	116883487	chr4	116883448	116883565	U5	snRNA	snRNA
chr4	116891139	116891540	.	.	.	.	.	.
chr4	116961911	116962312	chr4	116961886	116961914	GC_rich	Low_comple	Low_complexity
chr4	116961911	116962312	chr4	116962092	116962127	(CTGGGG)n	Simple_repe	Simple_repeat
chr4	117459675	117460076	chr4	117459605	117459694	FLAM_A	SINE	Alu
chr4	117459675	117460076	chr4	117459747	117459778	(CCCCCA)n	Simple_repe	Simple_repeat
chr4	117606600	117607001	chr4	117606983	117607361	L2	LINE	L2
chr4	117689007	117689408	chr4	117688935	117689028	MIRb	SINE	MIR
chr4	117734509	117734910	chr4	117734636	117734787	CR1_Mam	LINE	CR1
chr4	118020503	118020904	chr4	118020788	118020998	LTR33	LTR	ERVL
chr4	118220658	118221059	chr4	118220677	118220860	G-rich	Low_comple	Low_complexity
chr4	118220658	118221059	chr4	118220896	118221083	G-rich	Low_comple	Low_complexity
chr4	118798073	118798474	chr4	118798051	118798166	CT-rich	Low_comple	Low_complexity
chr4	118819403	118819804	chr4	118819367	118820521	ERVL-int	LTR	ERVL
chr4	119335572	119335973	chr4	119335490	119335716	MLT2C2	LTR	ERVL
chr4	119335572	119335973	chr4	119335719	119336000	L2a	LINE	L2
chr4	119458918	119459319	chr4	119459262	119459378	(TCC)n	Simple_repe	Simple_repeat
chr4	119605232	119605633	chr4	119605217	119605243	(TG)n	Simple_repe	Simple_repeat
chr4	119740174	119740575	.	.	.	.	.	.
chr4	119898063	119898464	.	.	.	.	.	.
chr4	120053241	120053642	.	.	.	.	.	.
chr4	120160975	120161376	.	.	.	.	.	.
chr4	120189981	120190382	.	.	.	.	.	.
chr4	120498137	120498538	.	.	.	.	.	.
chr4	122485393	122485794	chr4	122484561	122486220	Lx6	LINE	L1
chr4	122914743	122915144	chr4	122914832	122914980	MIR3	SINE	MIR
chr4	123480773	123481174	chr4	123480732	123480805	B1F	SINE	Alu
chr4	123480773	123481174	chr4	123480896	123480938	(TG)n	Simple_repe	Simple_repeat
chr4	123685941	123686342	chr4	123686107	123686232	MLT2F	LTR	ERVL
chr4	124179023	124179424	chr4	124178945	124179054	B1_Mur1	SINE	Alu
chr4	124179023	124179424	chr4	124179183	124179295	LTR33C	LTR	ERVL
chr4	124179023	124179424	chr4	124179371	124179635	MLT2F	LTR	ERVL
chr4	124386453	124386854	chr4	124386717	124386791	PB1D7	SINE	Alu
chr4	124386453	124386854	chr4	124386837	124386883	(TG)n	Simple_repe	Simple_repeat
chr4	124428463	124428864	.	.	.	.	.	.
chr4	124800552	124800953	.	.	.	.	.	.
chr4	124808749	124809150	.	.	.	.	.	.

chr4	124955139	124955540	chr4	124955034	124955394	MLT1J	LTR	MaLR
chr4	125091584	125091985	chr4	125091850	125091870	(T)n	Simple_repe	Simple_repeat
chr4	125091584	125091985	chr4	125091543	125091850	MLT1J1	LTR	MaLR
chr4	125787992	125788393	.	.	.	.	.	.
chr4	125809205	125809606	chr4	125809594	125809711	MIR3	SINE	MIR
chr4	125827485	125827886	.	.	.	.	.	.
chr4	125904302	125904703	.	.	.	.	.	.
chr4	127001936	127002337	.	.	.	.	.	.
chr4	127048787	127049188	chr4	127048696	127048853	RMER30	DNA	MER1_type
chr4	127079821	127080222	chr4	127080005	127080072	MLT1J1	LTR	MaLR
chr4	127872081	127872482	.	.	.	.	.	.
chr4	128105338	128105739	chr4	128105404	128105445	ID4	SINE	ID
chr4	128105338	128105739	chr4	128105442	128105844	MTD	LTR	MaLR
chr4	128488640	128489041	chr4	128488579	128488881	MLT1J1	LTR	MaLR
chr4	128517126	128517527	.	.	.	.	.	.
chr4	128587826	128588227	chr4	128587953	128588067	LTR33B	LTR	ERVL
chr4	128688808	128689209	chr4	128689041	128689067	(A)n	Simple_repe	Simple_repeat
chr4	128713249	128713650	chr4	128713450	128713595	MER5A	DNA	MER1_type
chr4	128745291	128745692	.	.	.	.	.	.
chr4	128940731	128941132	.	.	.	.	.	.
chr4	129133351	129133752	chr4	129133269	129133679	RLTR15	LTR	ERVK
chr4	129472532	129472933	.	.	.	.	.	.
chr4	129727710	129728111	chr4	129727631	129727740	RMER12	LTR	ERVK
chr4	130346068	130346469	.	.	.	.	.	.
chr4	130415389	130415790	chr4	130415480	130415623	LTR33B	LTR	ERVL
chr4	130752071	130752472	chr4	130752203	130752375	MLT1J	LTR	MaLR
chr4	130796332	130796733	chr4	130796479	130796631	MLT1J1	LTR	MaLR
chr4	135696327	135696728	.	.	.	.	.	.
chr4	136789543	136789944	chr4	136789714	136789793	MLT1J2	LTR	MaLR
chr4	136790307	136790708	chr4	136790469	136790655	MLT1J2	LTR	MaLR
chr4	136944129	136944530	.	.	.	.	.	.
chr4	137056805	137057206	chr4	137057198	137057326	YREP_Mm	Unknown	Unknown
chr4	137240702	137241103	.	.	.	.	.	.
chr4	137295034	137295435	chr4	137295202	137295314	MLT1J1	LTR	MaLR
chr4	138762590	138762991	chr4	138762584	138762721	ID_B1	SINE	B4
chr4	138762590	138762991	chr4	138762931	138763034	PB1D10	SINE	Alu
chr4	139959037	139959438	chr4	139959212	139959339	MLT1J1	LTR	MaLR
chr4	140111267	140111668	chr4	140111235	140111377	Tigger5	DNA	MER2_type
chr4	140111267	140111668	chr4	140111640	140111736	Tigger5	DNA	MER2_type
chr4	140835384	140835785	chr4	140835541	140835596	L2a	LINE	L2
chr4	140835384	140835785	chr4	140835633	140835704	L1Md_A	LINE	L1
chr4	140835384	140835785	chr4	140835737	140835789	CT-rich	Low_comple	Low_complexity
chr4	146023687	146024088	chr4	146023622	146024447	L1_Mur2	LINE	L1
chr4	146893069	146893470	chr4	146893288	146893337	B1_Mus1	SINE	Alu
chr4	146893069	146893470	chr4	146893337	146894069	Lx6	LINE	L1
chr4	148118195	148118596	.	.	.	.	.	.
chr4	148319688	148320089	.	.	.	.	.	.
chr4	149194712	149195113	.	.	.	.	.	.
chr4	149340659	149341060	.	.	.	.	.	.
chr4	149349934	149350335	chr4	149349910	149349952	(CAAAA)n	Simple_repe	Simple_repeat
chr4	149349934	149350335	chr4	149349958	149350125	ID_B1	SINE	B4
chr4	149349934	149350335	chr4	149350126	149350242	RMER17C	LTR	ERVK
chr4	149349934	149350335	chr4	149350242	149350420	(TTCTC)n	Simple_repe	Simple_repeat
chr4	149423048	149423449	.	.	.	.	.	.
chr4	150077533	150077934	.	.	.	.	.	.
chr4	150847144	150847545	chr4	150847371	150847410	L2c	LINE	L2
chr4	150847144	150847545	chr4	150847498	150847570	(CATG)n	Simple_repe	Simple_repeat
chr4	151769888	151770289	.	.	.	.	.	.
chr4	151785116	151785517	.	.	.	.	.	.
chr4	154282601	154283002	chr4	154282658	154282683	(T)n	Simple_repe	Simple_repeat
chr4	154282601	154283002	chr4	154282685	154282832	B1_Mm	SINE	Alu
chr4	154282601	154283002	chr4	154282929	154283175	RLTR12B	LTR	ERVK
chr4	154547525	154547926	.	.	.	.	.	.
chr5	4530166	4530567	.	.	.	.	.	.
chr5	4633719	4634120	chr5	4633491	4633926	MTE-int	LTR	MaLR
chr5	4633719	4634120	chr5	4634099	4634215	RLTR10-int	LTR	ERVK
chr5	5265216	5265617	.	.	.	.	.	.
chr5	5689091	5689492	chr5	5689437	5689578	MER5A1	DNA	MER1_type
chr5	8312268	8312669	chr5	8312407	8312559	MIRc	SINE	MIR
chr5	9068856	9069257	.	.	.	.	.	.
chr5	14733715	14734116	chr5	14733688	14733756	(TATATG)n	Simple_repe	Simple_repeat
chr5	14733715	14734116	chr5	14733767	14734084	L1_Rod	LINE	L1
chr5	14733715	14734116	chr5	14734094	14734764	L1M4	LINE	L1
chr5	14973397	14973798	.	.	.	.	.	.
chr5	15195756	15196157	.	.	.	.	.	.
chr5	17061857	17062258	.	.	.	.	.	.
chr5	19388570	19388971	chr5	19387674	19389671	L1Md_F2	LINE	L1
chr5	19762193	19762594	.	.	.	.	.	.
chr5	20650454	20650855	chr5	20650373	20650638	MLT1N2	LTR	MaLR
chr5	20650454	20650855	chr5	20650765	20650966	MIR	SINE	MIR
chr5	20680832	20681233	chr5	20680931	20680975	(CA)n	Simple_repe	Simple_repeat
chr5	20993156	20993557	.	.	.	.	.	.
chr5	22892773	22893174	.	.	.	.	.	.
chr5	23805509	23805910	chr5	23805548	23805587	(A)n	Simple_repe	Simple_repeat
chr5	23805509	23805910	chr5	23805695	23805763	ORR1C2	LTR	MaLR
chr5	23805509	23805910	chr5	23805809	23806004	MER20	DNA	MER1_type
chr5	23825874	23826275	.	.	.	.	.	.
chr5	23866389	23866790	.	.	.	.	.	.
chr5	23911230	23911631	.	.	.	.	.	.
chr5	24327339	24327740	chr5	24327718	24327753	(A)n	Simple_repe	Simple_repeat
chr5	25381743	25382144	chr5	25381880	25382050	(CATCC)n	Simple_repe	Simple_repeat
chr5	28369522	28369923	chr5	28369697	28369815	PB1D7	SINE	Alu
chr5	28369522	28369923	chr5	28369828	28369954	ID_B1	SINE	B4
chr5	30169242	30169643	.	.	.	.	.	.
chr5	31108318	31108719	chr5	31108099	31108348	L1M4	LINE	L1

chr5	31108318	31108719	chr5	31108348	31108403	(CA)n	Simple_repea	Simple_repeat
chr5	31218306	31218707	.	.	.	.	.	.
chr5	31230302	31230703	.	.	.	.	.	.
chr5	31302561	31302962	chr5	31302871	31302934	BLACKJACK	DNA	AcHobo
chr5	31302561	31302962	chr5	31302940	31303245	Lx8	LINE	L1
chr5	31878928	31879329	chr5	31879081	31879124	(TG)n	Simple_repea	Simple_repeat
chr5	31932302	31932703	chr5	31932244	31932331	(GA)n	Simple_repea	Simple_repeat
chr5	32049457	32049858	chr5	32049428	32049623	Lx9	LINE	L1
chr5	32049457	32049858	chr5	32049659	32050456	L1MEc	LINE	L1
chr5	32286760	32287161	.	.	.	.	.	.
chr5	32479251	32479652	chr5	32479190	32479374	MLT1B	LTR	MaLR
chr5	32479251	32479652	chr5	32479428	32479505	MIR	SINE	MIR
chr5	32479251	32479652	chr5	32479569	32479631	ID4	SINE	ID
chr5	32498301	32498702	chr5	32498282	32498396	L2b	LINE	L2
chr5	32498301	32498702	chr5	32498552	32498618	CT-rich	Low_comple	Low_complexity
chr5	32719304	32719705	chr5	32719527	32719626	Tigger16b	DNA	Tigger
chr5	32719304	32719705	chr5	32719636	32719671	(TTTG)n	Simple_repea	Simple_repeat
chr5	32719304	32719705	chr5	32719676	32719741	ID4_	SINE	ID
chr5	33068812	33069213	chr5	33068742	33068864	B1_Mur4	SINE	Alu
chr5	33071443	33071844	.	.	.	.	.	.
chr5	33076583	33076984	.	.	.	.	.	.
chr5	33088309	33088710	chr5	33088653	33088682	GC_rich	Low_comple	Low_complexity
chr5	33200493	33200894	chr5	33200682	33200728	RLTR42	LTR	ERVK
chr5	33200493	33200894	chr5	33200760	33200858	RLTR42-int	LTR	ERVK
chr5	33200493	33200894	chr5	33200858	33200924	T-rich	Low_comple	Low_complexity
chr5	33581617	33582018	.	.	.	.	.	.
chr5	34877656	34878057	.	.	.	.	.	.
chr5	34908688	34909089	chr5	34908644	34908729	L1ME3A	LINE	L1
chr5	34908688	34909089	chr5	34908768	34908978	MamGypLTR	LTR	Gypsy
chr5	34908688	34909089	chr5	34909032	34909233	B3	SINE	B2
chr5	35332191	35332592	.	.	.	.	.	.
chr5	36147861	36148262	chr5	36148209	36148286	L1MB8	LINE	L1
chr5	36699437	36699838	.	.	.	.	.	.
chr5	37113660	37114061	.	.	.	.	.	.
chr5	37682239	37682640	.	.	.	.	.	.
chr5	38945104	38945505	.	.	.	.	.	.
chr5	53046211	53046612	chr5	53046325	53046444	PB1	SINE	Alu
chr5	53046211	53046612	chr5	53046380	53046459	B4A	SINE	B4
chr5	53762841	53763242	.	.	.	.	.	.
chr5	53772645	53773046	.	.	.	.	.	.
chr5	53821345	53821746	.	.	.	.	.	.
chr5	53848621	53849022	.	.	.	.	.	.
chr5	53871077	53871478	.	.	.	.	.	.
chr5	53882077	53882478	chr5	53882406	53882503	CT-rich	Low_comple	Low_complexity
chr5	53934223	53934624	chr5	53933944	53934357	RMER10A	LTR	ERVL
chr5	54362497	54362898	chr5	54362871	54362907	(CAA)n	Simple_repea	Simple_repeat
chr5	58990940	58991341	chr5	58990633	58991539	Lx7	LINE	L1
chr5	64925639	64926040	chr5	64925227	64925710	RLTR20A	LTR	ERVK
chr5	64925639	64926040	chr5	64925714	64925977	MER97c	DNA	MER1_type?
chr5	64925639	64926040	chr5	64925981	64926115	B1F	SINE	Alu
chr5	65258464	65258865	.	.	.	.	.	.
chr5	65792857	65793258	.	.	.	.	.	.
chr5	65849033	65849434	chr5	65849262	65849356	L2	LINE	L2
chr5	66323653	66324054	chr5	66323754	66324166	MLT1J	LTR	MaLR
chr5	66437537	66437938	.	.	.	.	.	.
chr5	66936744	66937145	.	.	.	.	.	.
chr5	67585281	67585682	chr5	67585358	67585399	(CA)n	Simple_repea	Simple_repeat
chr5	67585281	67585682	chr5	67585453	67585614	MLT1J	LTR	MaLR
chr5	72641369	72641770	.	.	.	.	.	.
chr5	73116666	73117067	.	.	.	.	.	.
chr5	73247058	73247459	.	.	.	.	.	.
chr5	73735764	73736165	.	.	.	.	.	.
chr5	73792553	73792954	chr5	73792411	73792618	MTEb	LTR	MaLR
chr5	73792553	73792954	chr5	73792837	73793478	L1MB8	LINE	L1
chr5	74438950	74439351	chr5	74438899	74439249	RMER15	LTR	ERVL
chr5	74438950	74439351	chr5	74439249	74439440	B2_Mm2	SINE	B2
chr5	74888695	74889096	.	.	.	.	.	.
chr5	75149801	75150202	chr5	75150034	75150175	B1F1	SINE	Alu
chr5	75188317	75188718	.	.	.	.	.	.
chr5	75442664	75443065	.	.	.	.	.	.
chr5	76775083	76775484	.	.	.	.	.	.
chr5	76818666	76819067	.	.	.	.	.	.
chr5	77017920	77018321	chr5	77017959	77018009	GC_rich	Low_comple	Low_complexity
chr5	77017920	77018321	chr5	77018094	77018120	(TCCG)n	Simple_repea	Simple_repeat
chr5	77796659	77797060	.	.	.	.	.	.
chr5	81112817	81113218	chr5	81113074	81113541	RMER15	LTR	ERVL
chr5	86196165	86196566	chr5	86196323	86196574	B4A	SINE	B4
chr5	86196165	86196566	chr5	86196174	86196240	AT_rich	Low_comple	Low_complexity
chr5	89412076	89412477	chr5	89411741	89412153	MTB_Mm	LTR	MaLR
chr5	89906462	89906863	chr5	89906402	89906571	L2a	LINE	L2
chr5	89965045	89965446	chr5	89965211	89965418	7SLRNA	srpRNA	srpRNA
chr5	89965045	89965446	chr5	89965433	89965478	(TG)n	Simple_repea	Simple_repeat
chr5	89971497	89971898	chr5	89971663	89971691	(A)n	Simple_repea	Simple_repeat
chr5	90812087	90812488	chr5	90812186	90812269	L2b	LINE	L2
chr5	91040298	91040699	.	.	.	.	.	.
chr5	91090441	91090842	chr5	91090652	91090801	MIRb	SINE	MIR
chr5	91118866	91119267	.	.	.	.	.	.
chr5	91305057	91305458	.	.	.	.	.	.
chr5	91539027	91539428	.	.	.	.	.	.
chr5	91749353	91749754	chr5	91749666	91749874	URR1A	DNA	MER1_type
chr5	92649571	92649972	chr5	92649841	92649901	(TG)n	Simple_repea	Simple_repeat
chr5	93724687	93725088	chr5	93724836	93725105	MTE2b	LTR	MaLR
chr5	97384340	97384741	.	.	.	.	.	.
chr5	99319558	99319959	chr5	99319573	99319611	(GA)n	Simple_repea	Simple_repeat
chr5	99319558	99319959	chr5	99319666	99319823	MIR	SINE	MIR

chr5	99327048	99327449	chr5	99327351	99327452	L2c	LINE	L2
chr5	100996232	100996633	chr5	100996211	100996268	(TCTCTG)n	Simple_repea	Simple_repeat
chr5	100996232	100996633	chr5	100996269	100996295	(TG)n	Simple_repea	Simple_repeat
chr5	100996232	100996633	chr5	100996307	100996391	Lx8	LINE	L1
chr5	101051829	101052230	chr5	101051852	101051881	AT_rich	Low_comple	Low_complexity
chr5	101051829	101052230	chr5	101052090	101052294	MTEa	LTR	MaLR
chr5	102802713	102803114	chr5	102802861	102802929	MLT1J	LTR	MaLR
chr5	102802713	102803114	chr5	102802862	102802939	LTR33B	LTR	ERVL
chr5	103422784	103423185	chr5	103422901	103423073	B3	SINE	B2
chr5	104203743	104204144	.	.	.	.	.	.
chr5	104484192	104484593	chr5	104484130	104484394	B4A	SINE	B4
chr5	104803296	104803697	chr5	104803294	104803377	MIRc	SINE	MIR
chr5	104809622	104810023	chr5	104809933	104809964	AT_rich	Low_comple	Low_complexity
chr5	104861852	104862253	.	.	.	.	.	.
chr5	105000418	105000819	chr5	105000283	105000589	RMER13A	LTR	ERVK
chr5	105929312	105929713	chr5	105929708	105929934	MER21B	LTR	ERV1
chr5	106208343	106208744	chr5	106208706	106208804	L1MC4a	LINE	L1
chr5	107420500	107420901	.	.	.	.	.	.
chr5	107456524	107456925	chr5	107456467	107456799	RLTR15	LTR	ERVK
chr5	107456524	107456925	chr5	107456815	107456937	B3A	SINE	B2
chr5	107508269	107508670	.	.	.	.	.	.
chr5	107516198	107516599	.	.	.	.	.	.
chr5	107553393	107553794	chr5	107553199	107553411	B3	SINE	B2
chr5	107553393	107553794	chr5	107553436	107553475	ID	SINE	ID
chr5	107586508	107586909	.	.	.	.	.	.
chr5	107625155	107625556	chr5	107625553	107625592	(GA)n	Simple_repea	Simple_repeat
chr5	107630085	107630486	chr5	107630073	107630362	ORR1E	LTR	MaLR
chr5	107630085	107630486	chr5	107630364	107630495	RSINE1	SINE	B4
chr5	108429942	108430343	chr5	108430031	108430080	RSINE1	SINE	B4
chr5	108429942	108430343	chr5	108430097	108430122	(A)n	Simple_repea	Simple_repeat
chr5	108429942	108430343	chr5	108430301	108430385	RLTR42	LTR	ERVK
chr5	109151020	109151421	chr5	109150990	109151185	B4A	SINE	B4
chr5	110922854	110923255	chr5	110923169	110923283	CT-rich	Low_comple	Low_complexity
chr5	110993946	110994347	.	.	.	.	.	.
chr5	111657351	111657752	.	.	.	.	.	.
chr5	111676986	111677387	chr5	111676947	111677205	L1MDb	LINE	L1
chr5	111918059	111918460	chr5	111918033	111918282	MLT1J2	LTR	MaLR
chr5	112228565	112228966	.	.	.	.	.	.
chr5	112309143	112309544	chr5	112309322	112309419	MIRc	SINE	MIR
chr5	112319765	112320166	chr5	112319453	112319773	(TCCA)n	Simple_repea	Simple_repeat
chr5	112422951	112423352	chr5	112423060	112423190	MLT1J	LTR	MaLR
chr5	112669827	112670228	.	.	.	.	.	.
chr5	113700093	113700494	chr5	113699918	113700100	B3A	SINE	B2
chr5	113700093	113700494	chr5	113700252	113700370	MLT1K	LTR	MaLR
chr5	114263644	114264045	chr5	114263624	114263701	B4	SINE	B4
chr5	114263644	114264045	chr5	114263746	114263927	B3A	SINE	B2
chr5	114263644	114264045	chr5	114263950	114264157	B3	SINE	B2
chr5	114622939	114623340	chr5	114622859	114622987	B1_Mus2	SINE	Alu
chr5	114622939	114623340	chr5	114622987	114623015	(CAAA)n	Simple_repea	Simple_repeat
chr5	114622939	114623340	chr5	114623089	114623185	MT2B2	LTR	ERVL
chr5	114622939	114623340	chr5	114623114	114623206	PB1D10	SINE	Alu
chr5	114622939	114623340	chr5	114623215	114623296	L1_Mus1	LINE	L1
chr5	114622939	114623340	chr5	114623300	114623486	B2_Mm1a	SINE	B2
chr5	115939161	115939562	chr5	115939467	115939611	U4	snRNA	snRNA
chr5	115984821	115985222	.	.	.	.	.	.
chr5	116804497	116804898	chr5	116804718	116804812	MLT1A1	LTR	MaLR
chr5	116821474	116821875	chr5	116821346	116821744	MLT1J1	LTR	MaLR
chr5	116821474	116821875	chr5	116821810	116822065	L2	LINE	L2
chr5	116837522	116837923	chr5	116837299	116837589	B4	SINE	B4
chr5	116896567	116896968	.	.	.	.	.	.
chr5	117608459	117608860	chr5	117608459	117608502	(TG)n	Simple_repea	Simple_repeat
chr5	118399347	118399748	chr5	118399342	118399525	LTR16E2	LTR	ERVL
chr5	118863372	118863773	chr5	118863239	118863377	Lx9	LINE	L1
chr5	118863372	118863773	chr5	118863525	118863686	MLT1J1	LTR	MaLR
chr5	118906828	118907229	chr5	118906598	118906944	ORR1E	LTR	MaLR
chr5	118906828	118907229	chr5	118907032	118907204	URR1A	DNA	MER1_type
chr5	118909088	118909489	chr5	118909268	118909464	RMER17C	LTR	ERVK
chr5	118915204	118915605	chr5	118915447	118915474	(TG)n	Simple_repea	Simple_repeat
chr5	118928223	118928624	chr5	118928553	118928579	(TTTTG)n	Simple_repea	Simple_repeat
chr5	119062962	119063363	.	.	.	.	.	.
chr5	119114025	119114426	.	.	.	.	.	.
chr5	119666055	119666456	chr5	119666076	119666096	(GGGTG)n	Simple_repea	Simple_repeat
chr5	119666055	119666456	chr5	119666099	119666339	LTR33A	LTR	ERVL
chr5	120398482	120398883	chr5	120398631	120398721	MLT1J	LTR	MaLR
chr5	120428403	120428804	.	.	.	.	.	.
chr5	120747940	120748341	chr5	120747692	120747953	MIRb	SINE	MIR
chr5	121511692	121512093	chr5	121511648	121511704	(GA)n	Simple_repea	Simple_repeat
chr5	121511692	121512093	chr5	121511704	121511858	ORR1D1	LTR	MaLR
chr5	121511692	121512093	chr5	121511858	121512040	MLT1J	LTR	MaLR
chr5	121669985	121670386	chr5	121670286	121670312	(CGG)n	Simple_repea	Simple_repeat
chr5	121669985	121670386	chr5	121670356	121670424	(CGCGG)n	Simple_repea	Simple_repeat
chr5	122504401	122504802	chr5	122504549	122504733	LTR33	LTR	ERVL
chr5	122585499	122585900	chr5	122585595	122585638	CT-rich	Low_comple	Low_complexity
chr5	122596317	122596718	.	.	.	.	.	.
chr5	122754037	122754438	.	.	.	.	.	.
chr5	123220797	123221198	chr5	123221030	123221065	(TCCC)n	Simple_repea	Simple_repeat
chr5	123507999	123508400	chr5	123508350	123508451	PB1D7	SINE	Alu
chr5	124442085	124442486	.	.	.	.	.	.
chr5	124456988	124457389	.	.	.	.	.	.
chr5	124496970	124497371	chr5	124497043	124497267	L2b	LINE	L2
chr5	124496970	124497371	chr5	124497352	124497455	L1MC3	LINE	L1
chr5	124621755	124622156	chr5	124621761	124621951	MER46C	DNA	MER2_type
chr5	124621755	124622156	chr5	124622140	124622184	(CA)n	Simple_repea	Simple_repeat
chr5	124899550	124899951	chr5	124899519	124900090	L1MB7	LINE	L1
chr5	125552221	125552622	.	.	.	.	.	.

chr5	125561882	125562283	chr5	125561904	125561943	(CCCGG)n	Simple_repe	Simple_repeat
chr5	125726079	125726480	.	.	.	.	.	.
chr5	125752013	125752414	.	.	.	.	.	.
chr5	125764348	125764749	chr5	125764533	125764601	MLT1J2	LTR	MaLR
chr5	125873494	125873895	.	.	.	.	.	.
chr5	129623245	129623646	chr5	129622192	129623880	Lx8	LINE	L1
chr5	131995427	131995828	chr5	131995440	131995520	CT-rich	Low_comple	Low_complexity
chr5	131995427	131995828	chr5	131995562	131995660	B1F1	SINE	Alu
chr5	131995427	131995828	chr5	131995676	131995803	B1F1	SINE	Alu
chr5	135170904	135171305	chr5	135170628	135170923	L2	LINE	L2
chr5	135170904	135171305	chr5	135171084	135171148	RMER15	LTR	ERVL
chr5	135170904	135171305	chr5	135171153	135171330	RLTR18B	LTR	ERVK
chr5	135393934	135394335	chr5	135393948	135394070	MLT1J2	LTR	MaLR
chr5	135998215	135998616	.	.	.	.	.	.
chr5	136186727	136187128	chr5	136187116	136187242	B1_Mur4	SINE	Alu
chr5	136269460	136269861	chr5	136269554	136269706	B4	SINE	B4
chr5	136525835	136526236	chr5	136525728	136525915	ZP3AR	Satellite	Satellite
chr5	136525835	136526236	chr5	136526118	136526238	RSINE1	SINE	B4
chr5	136527480	136527881	.	.	.	.	.	.
chr5	136570553	136570954	.	.	.	.	.	.
chr5	136584932	136585333	chr5	136585166	136585326	B3	SINE	B2
chr5	137488478	137488879	chr5	137488471	137488561	MIRb	SINE	MIR
chr5	137488478	137488879	chr5	137488740	137488776	(TC)n	Simple_repe	Simple_repeat
chr5	137488478	137488879	chr5	137488776	137488908	B1_Mur4	SINE	Alu
chr5	137491849	137492250	chr5	137491856	137491959	MTEb	LTR	MaLR
chr5	137491849	137492250	chr5	137492133	137492190	ID4_	SINE	ID
chr5	137491849	137492250	chr5	137492198	137492240	(CA)n	Simple_repe	Simple_repeat
chr5	137491849	137492250	chr5	137492242	137492280	GA-rich	Low_comple	Low_complexity
chr5	137578812	137579213	.	.	.	.	.	.
chr5	137779469	137779870	chr5	137779431	137779512	(TAGA)n	Simple_repe	Simple_repeat
chr5	137779469	137779870	chr5	137779771	137779794	AT_rich	Low_comple	Low_complexity
chr5	138426967	138427368	chr5	138426803	138427009	URR1A	DNA	MER1_type
chr5	138426967	138427368	chr5	138427269	138427291	AT_rich	Low_comple	Low_complexity
chr5	139201090	139201491	.	.	.	.	.	.
chr5	139465438	139465839	.	.	.	.	.	.
chr5	139936380	139936781	chr5	139936752	139936861	ID_B1	SINE	B4
chr5	142843276	142843677	.	.	.	.	.	.
chr5	142921657	142922058	chr5	142921967	142922071	ZP3AR	Satellite	Satellite
chr5	143585123	143585524	.	.	.	.	.	.
chr5	143682355	143682756	chr5	143682281	143682364	(GGAA)n	Simple_repe	Simple_repeat
chr5	143697275	143697676	chr5	143697201	143697348	B1_Mur1	SINE	Alu
chr5	143697275	143697676	chr5	143697436	143697563	LTR33B	LTR	ERVL
chr5	144236360	144236761	chr5	144236363	144236474	RSINE1	SINE	B4
chr5	144322549	144322950	.	.	.	.	.	.
chr5	145659435	145659836	.	.	.	.	.	.
chr5	146041703	146042104	.	.	.	.	.	.
chr5	147072556	147072957	chr5	147072553	147072941	LSU-rRNA_H	rRNA	rRNA
chr5	147072556	147072957	chr5	147072941	147072973	(A)n	Simple_repe	Simple_repeat
chr5	150115783	150116184	.	.	.	.	.	.
chr5	150123104	150123505	.	.	.	.	.	.
chr5	150142877	150143278	.	.	.	.	.	.
chr5	150155729	150156130	.	.	.	.	.	.
chr5	152005485	152005886	.	.	.	.	.	.
chr5	152054263	152054664	.	.	.	.	.	.
chr6	3151300	3151701	chr6	3150778	3151677	SSU-rRNA_H	rRNA	rRNA
chr6	3695661	3696062	.	.	.	.	.	.
chr6	4369085	4369486	.	.	.	.	.	.
chr6	4382164	4382565	.	.	.	.	.	.
chr6	6647625	6648026	.	.	.	.	.	.
chr6	8122063	8122464	.	.	.	.	.	.
chr6	8445973	8446374	.	.	.	.	.	.
chr6	12382382	12382783	chr6	12382339	12382673	ORR1E	LTR	MaLR
chr6	12382382	12382783	chr6	12382722	12382980	L1Md_F2	LINE	L1
chr6	12552186	12552587	.	.	.	.	.	.
chr6	12971508	12971909	chr6	12971747	12971886	LFSINE_Vert	SINE	SINE
chr6	13633610	13634011	chr6	13633861	13634084	RMER15	LTR	ERVL
chr6	16560841	16561242	chr6	16561227	16561331	L2	LINE	L2
chr6	16571137	16571538	.	.	.	.	.	.
chr6	17022776	17023177	.	.	.	.	.	.
chr6	17122059	17122460	.	.	.	.	.	.
chr6	17196788	17197189	chr6	17196316	17197527	Lx7	LINE	L1
chr6	17303826	17304227	chr6	17303611	17303827	MamGypLTR	LTR	Gypsy
chr6	17303826	17304227	chr6	17303934	17304096	MamGypLTR	LTR	Gypsy
chr6	17411394	17411795	.	.	.	.	.	.
chr6	17428833	17429234	chr6	17429133	17429242	PB1D10	SINE	Alu
chr6	17826577	17826978	chr6	17826815	17826871	MIR3	SINE	MIR
chr6	22230202	22230603	.	.	.	.	.	.
chr6	24577717	24578118	chr6	24577552	24577786	B2_Mm1t	SINE	B2
chr6	29380731	29381132	.	.	.	.	.	.
chr6	30754705	30755106	.	.	.	.	.	.
chr6	31008313	31008714	chr6	31008257	31008439	HAL1	LINE	L1
chr6	31008313	31008714	chr6	31008473	31008564	LTR33C	LTR	ERVL
chr6	31050319	31050720	.	.	.	.	.	.
chr6	31140945	31141346	chr6	31141102	31141196	LTR33C	LTR	ERVL
chr6	32454260	32454661	.	.	.	.	.	.
chr6	32745529	32745930	chr6	32745498	32745565	(GA)n	Simple_repe	Simple_repeat
chr6	32885557	32885958	chr6	32885727	32885910	Tigger5	DNA	MER2_type
chr6	34033504	34033905	.	.	.	.	.	.
chr6	34293339	34293740	.	.	.	.	.	.
chr6	34746870	34747271	chr6	34746146	34747121	L1MCc	LINE	L1
chr6	37233319	37233720	.	.	.	.	.	.
chr6	38037284	38037685	chr6	38037386	38037735	RLTR15	LTR	ERVK
chr6	39284258	39284659	chr6	39284487	39284612	B1F	SINE	Alu
chr6	39784612	39785013	chr6	39784499	39784624	ORR1D2	LTR	MaLR
chr6	39784612	39785013	chr6	39784688	39784967	RLTR15	LTR	ERVK

chr6	42331722	42332123	.	.	.	.	.	.
chr6	43293580	43293981	chr6	43293760	43293805	GSAT_MM	Satellite	Satellite
chr6	47586705	47587106	.	.	.	.	.	.
chr6	47601061	47601462	chr6	47601044	47601135	(CAA)n	Simple_repe	Simple_repeat
chr6	47731240	47731641	chr6	47731622	47731723	HY3	scRNA	scRNA
chr6	47738137	47738538	chr6	47738068	47738179	HY1	scRNA	scRNA
chr6	48071185	48071586	chr6	48071013	48071196	B2_Mm1a	SINE	B2
chr6	48071185	48071586	chr6	48071395	48071442	B3A	SINE	B2
chr6	48491551	48491952	.	.	.	.	.	.
chr6	49046353	49046754	.	.	.	.	.	.
chr6	50204857	50205258	chr6	50205207	50205304	PB1D7	SINE	Alu
chr6	51201412	51201813	chr6	51200510	51201465	MYSERV6-int	LTR	ERVK
chr6	51201412	51201813	chr6	51201465	51201626	RLTR15	LTR	ERVK
chr6	51201412	51201813	chr6	51201637	51201897	RLTR15	LTR	ERVK
chr6	55215095	55215496	chr6	55215078	55215187	L2b	LINE	L2
chr6	55308674	55309075	.	.	.	.	.	.
chr6	55333942	55334343	.	.	.	.	.	.
chr6	56754637	56755038	chr6	56754453	56754662	ORR1C1	LTR	MaLR
chr6	56754637	56755038	chr6	56754719	56754969	MTE2b	LTR	MaLR
chr6	56754637	56755038	chr6	56754971	56755288	MTE2b-int	LTR	MaLR
chr6	60637039	60637440	chr6	60637216	60637324	GSAT_MM	Satellite	Satellite
chr6	63848163	63848564	chr6	63848365	63848575	B3	SINE	B2
chr6	67118272	67118673	chr6	67118509	67118686	RLTR42	LTR	ERVK
chr6	69466162	69466563	chr6	69466309	69466332	ID	SINE	ID
chr6	69466162	69466563	chr6	69466332	69466546	7SLRNA	srpRNA	srpRNA
chr6	72006586	72006987	chr6	72006880	72007226	MTE2b	LTR	MaLR
chr6	72166571	72166972	.	.	.	.	.	.
chr6	72280125	72280526	chr6	72280051	72280202	B1_Mm	SINE	Alu
chr6	72280125	72280526	chr6	72280202	72280239	B3	SINE	B2
chr6	72280125	72280526	chr6	72280297	72280409	PB1D10	SINE	Alu
chr6	72280125	72280526	chr6	72280437	72280541	B4A	SINE	B4
chr6	72462451	72462852	.	.	.	.	.	.
chr6	72488696	72489097	.	.	.	.	.	.
chr6	72605344	72605745	.	.	.	.	.	.
chr6	72693620	72694021	.	.	.	.	.	.
chr6	82946622	82947023	chr6	82946524	82946773	ORR1D2	LTR	MaLR
chr6	82964719	82965120	.	.	.	.	.	.
chr6	83081226	83081627	chr6	83081199	83081331	RSINE1	SINE	B4
chr6	83081226	83081627	chr6	83081339	83081390	(TCTG)n	Simple_repe	Simple_repeat
chr6	83228885	83229286	chr6	83228516	83228886	MTE2a	LTR	MaLR
chr6	83228885	83229286	chr6	83229000	83229170	B3A	SINE	B2
chr6	83228885	83229286	chr6	83229269	83229524	MER2	DNA	MER2_type
chr6	86756481	86756882	chr6	86756865	86756896	(TG)n	Simple_repe	Simple_repeat
chr6	88074540	88074941	.	.	.	.	.	.
chr6	88890538	88890939	.	.	.	.	.	.
chr6	88913915	88914316	chr6	88913843	88914030	RSINE1	SINE	B4
chr6	88913915	88914316	chr6	88914033	88914191	B4A	SINE	B4
chr6	89018344	89018745	chr6	89018744	89018795	(GA)n	Simple_repe	Simple_repeat
chr6	89037877	89038278	.	.	.	.	.	.
chr6	91151839	91152240	chr6	91151844	91151987	L2b	LINE	L2
chr6	91151839	91152240	chr6	91151991	91152138	L1M5	LINE	L1
chr6	91157530	91157931	chr6	91157915	91157956	MIRc	SINE	MIR
chr6	91257995	91258396	chr6	91258004	91258244	MLT1A1	LTR	MaLR
chr6	91438876	91439277	.	.	.	.	.	.
chr6	91567154	91567555	chr6	91567327	91567480	MLT1J2	LTR	MaLR
chr6	92191195	92191596	chr6	92191341	92191411	MLT1J	LTR	MaLR
chr6	92240773	92241174	chr6	92240841	92241004	RLTR42-int	LTR	ERVK
chr6	92414055	92414456	.	.	.	.	.	.
chr6	93207496	93207897	.	.	.	.	.	.
chr6	94175042	94175443	chr6	94174857	94175116	B4	SINE	B4
chr6	94698419	94698820	chr6	94698676	94698751	CT-rich	Low_comple	Low_complexity
chr6	97307599	97308000	chr6	97307542	97307735	B2_Mm1t	SINE	B2
chr6	97307599	97308000	chr6	97307748	97307827	RLTR11A	LTR	ERVK
chr6	97307599	97308000	chr6	97307840	97308074	L1Md_A	LINE	L1
chr6	97776527	97776928	.	.	.	.	.	.
chr6	97874236	97874637	chr6	97874219	97874261	(CAAAA)n	Simple_repe	Simple_repeat
chr6	97902817	97903218	.	.	.	.	.	.
chr6	99167724	99168125	chr6	99168002	99168026	(GGCTG)n	Simple_repe	Simple_repeat
chr6	99167724	99168125	chr6	99168027	99168338	B4	SINE	B4
chr6	99334950	99335351	chr6	99335103	99335248	MER20	DNA	MER1_type
chr6	99396746	99397147	.	.	.	.	.	.
chr6	100456159	100456560	chr6	100456308	100456416	PB1	SINE	Alu
chr6	100456159	100456560	chr6	100456474	100456709	B4	SINE	B4
chr6	100750524	100750925	.	.	.	.	.	.
chr6	103598956	103599357	chr6	103598482	103598957	L1Md_F2	LINE	L1
chr6	103598956	103599357	chr6	103599041	103599288	SYNREP_MM	Satellite	Satellite
chr6	108486958	108487359	chr6	108487291	108487319	(CA)n	Simple_repe	Simple_repeat
chr6	112721030	112721431	chr6	112720901	112721101	URR1A	DNA	MER1_type
chr6	112838856	112839257	.	.	.	.	.	.
chr6	112950874	112951275	.	.	.	.	.	.
chr6	113640406	113640807	chr6	113640240	113640677	RLTR28B	LTR	ERVL
chr6	114816011	114816412	.	.	.	.	.	.
chr6	115234263	115234664	.	.	.	.	.	.
chr6	115694507	115694908	chr6	115694635	115694719	MLT1J	LTR	MaLR
chr6	115694507	115694908	chr6	115694796	115695118	(TG)n	Simple_repe	Simple_repeat
chr6	116216415	116216816	chr6	116216781	116216904	L1MC1	LINE	L1
chr6	117829058	117829459	chr6	117828919	117829067	RMER5	LTR	ERV1
chr6	118934188	118934589	chr6	118934359	118934477	MER121	Unknown	Unknown
chr6	119291441	119291842	chr6	119291576	119291677	MLT1J	LTR	MaLR
chr6	119338683	119339084	chr6	119338661	119338687	(CCG)n	Simple_repe	Simple_repeat
chr6	119338683	119339084	chr6	119338711	119338744	(CCG)n	Simple_repe	Simple_repeat
chr6	119346252	119346653	.	.	.	.	.	.
chr6	120140913	120141314	.	.	.	.	.	.
chr6	120544443	120544844	chr6	120544437	120544507	B4	SINE	B4
chr6	120544443	120544844	chr6	120544603	120544707	PB1	SINE	Alu

chr6	120544443	120544844	chr6	120544837	120545028	B3	SINE	B2
chr6	121072647	121073048	chr6	121072748	121072881	Charlie17a	DNA	MER1_type
chr6	121123600	121124001	chr6	121123949	121124018	MIRc	SINE	MIR
chr6	121451221	121451622	chr6	121451381	121451495	MLT1J1	LTR	MaLR
chr6	122760625	122761026	.	.	.	.	.	.
chr6	124374215	124374616	chr6	124374170	124374321	MLT1J1-int	LTR	MaLR
chr6	124374215	124374616	chr6	124374345	124374560	MLT1J1	LTR	MaLR
chr6	124374215	124374616	chr6	124374574	124374706	B4A	SINE	B4
chr6	124755512	124755913	.	.	.	.	.	.
chr6	125522231	125522632	chr6	125521636	125522341	L1Md_A	LINE	L1
chr6	125522231	125522632	chr6	125522626	125522723	MTD	LTR	MaLR
chr6	125567861	125568262	chr6	125567987	125568017	AT_rich	Low_comple	Low_complexity
chr6	125567861	125568262	chr6	125568024	125568141	PB1	SINE	Alu
chr6	125567861	125568262	chr6	125568164	125568222	(TG)n	Simple_repe	Simple_repeat
chr6	125826906	125827307	chr6	125826928	125827013	(CATTC)n	Simple_repe	Simple_repeat
chr6	125826906	125827307	chr6	125827015	125827195	(CACTC)n	Simple_repe	Simple_repeat
chr6	125826906	125827307	chr6	125827197	125827282	(CATTC)n	Simple_repe	Simple_repeat
chr6	125826906	125827307	chr6	125827281	125827349	(TTCC)n	Simple_repe	Simple_repeat
chr6	126300942	126301343	chr6	126301036	126301275	L1MA4A	LINE	L1
chr6	126437251	126437652	.	.	.	.	.	.
chr6	127821536	127821937	chr6	127821910	127822067	MLT1J	LTR	MaLR
chr6	127869462	127869863	.	.	.	.	.	.
chr6	127996762	127997163	.	.	.	.	.	.
chr6	128246465	128246866	.	.	.	.	.	.
chr6	128792999	128793400	chr6	128793304	128793398	4.5SRNA	scRNA	scRNA
chr6	129206158	129206559	chr6	129206342	129206415	ID4_	SINE	ID
chr6	131327385	131327786	chr6	131327484	131327622	B1F	SINE	Alu
chr6	132413602	132414003	chr6	132413697	132413824	(GAATG)n	Simple_repe	Simple_repeat
chr6	132413602	132414003	chr6	132413871	132413977	(GA)n	Simple_repe	Simple_repeat
chr6	132413602	132414003	chr6	132413977	132414872	ETnERV2-int	LTR	ERVK
chr6	134136351	134136752	.	.	.	.	.	.
chr6	134423260	134423661	chr6	134423154	134423369	Tigger7	DNA	MER2_type
chr6	135102463	135102864	chr6	135102502	135102550	(CA)n	Simple_repe	Simple_repeat
chr6	136417058	136417459	.	.	.	.	.	.
chr6	136914563	136914964	chr6	136914683	136914906	MTC	LTR	MaLR
chr6	136914563	136914964	chr6	136914907	136915007	CT-rich	Low_comple	Low_complexity
chr6	136950033	136950434	chr6	136950373	136950750	RMER10A	LTR	ERVL
chr6	137468502	137468903	.	.	.	.	.	.
chr6	137507391	137507792	chr6	137507546	137507621	AmnSINE1	SINE	SINE
chr6	137514436	137514837	.	.	.	.	.	.
chr6	137530987	137531388	.	.	.	.	.	.
chr6	141138282	141138683	.	.	.	.	.	.
chr6	142316099	142316500	.	.	.	.	.	.
chr6	142467721	142468122	chr6	142467919	142467989	ID4	SINE	ID
chr6	142467721	142468122	chr6	142468056	142468101	(TTA)n	Simple_repe	Simple_repeat
chr6	142467721	142468122	chr6	142468104	142469147	Lx2B	LINE	L1
chr6	142481274	142481675	chr6	142481639	142481683	CT-rich	Low_comple	Low_complexity
chr6	143100838	143101239	.	.	.	.	.	.
chr6	143483518	143483919	chr6	143483461	143483554	MIR	SINE	MIR
chr6	143483518	143483919	chr6	143483629	143483697	ID4	SINE	ID
chr6	143589204	143589605	.	.	.	.	.	.
chr6	143807109	143807510	chr6	143807452	143807572	B3A	SINE	B2
chr6	146353855	146354256	.	.	.	.	.	.
chr6	146634131	146634532	chr6	146634407	146634522	L2b	LINE	L2
chr6	147216872	147217273	.	.	.	.	.	.
chr6	147718538	147718939	chr6	147718632	147718722	B2_Mm2	SINE	B2
chr6	147718538	147718939	chr6	147718726	147718773	MLT1J	LTR	MaLR
chr6	147718538	147718939	chr6	147718875	147718977	RLTR42	LTR	ERVK
chr6	148084504	148084905	chr6	148084570	148084775	ERVL-int	LTR	ERVL
chr6	148689157	148689558	.	.	.	.	.	.
chr7	3134623	3135024	chr7	3134734	3134773	RMER10A	LTR	ERVL
chr7	3134623	3135024	chr7	3134949	3135362	RMER17C	LTR	ERVK
chr7	3314439	3314840	.	.	.	.	.	.
chr7	3331763	3332164	.	.	.	.	.	.
chr7	3452029	3452430	.	.	.	.	.	.
chr7	4049956	4050357	chr7	4049982	4050154	MIR	SINE	MIR
chr7	4049956	4050357	chr7	4050290	4050311	(CACCC)n	Simple_repe	Simple_repeat
chr7	4049956	4050357	chr7	4050309	4050392	CT-rich	Low_comple	Low_complexity
chr7	4515846	4516247	chr7	4516144	4516320	B3A	SINE	B2
chr7	6235185	6235586	.	.	.	.	.	.
chr7	6351174	6351575	.	.	.	.	.	.
chr7	6362750	6363151	.	.	.	.	.	.
chr7	7140766	7141167	chr7	7141084	7141119	(TTG)n	Simple_repe	Simple_repeat
chr7	7327226	7327627	chr7	7327531	7327636	B1F2	SINE	Alu
chr7	7327226	7327627	chr7	7327623	7327974	RMER10A	LTR	ERVL
chr7	9112095	9112496	chr7	9111754	9112105	RMER10A	LTR	ERVL
chr7	9112095	9112496	chr7	9112092	9112196	B1_Mur1	SINE	Alu
chr7	13534751	13535152	.	.	.	.	.	.
chr7	13547145	13547546	chr7	13547254	13547293	(T)n	Simple_repe	Simple_repeat
chr7	13547145	13547546	chr7	13547453	13547572	B1_Mus1	SINE	Alu
chr7	16614042	16614443	chr7	16614374	16614831	ZP3AR	Satellite	Satellite
chr7	16898387	16898788	chr7	16898585	16898724	MIRc	SINE	MIR
chr7	16991318	16991719	.	.	.	.	.	.
chr7	19552990	19553391	.	.	.	.	.	.
chr7	19716567	19716968	.	.	.	.	.	.
chr7	19881130	19881531	.	.	.	.	.	.
chr7	19886214	19886615	chr7	19886270	19886297	(CAAA)n	Simple_repe	Simple_repeat
chr7	19886214	19886615	chr7	19886592	19886678	tRNA-SeC(e)-	tRNA	tRNA
chr7	19902084	19902485	.	.	.	.	.	.
chr7	19912600	19913001	chr7	19912956	19913043	B1F	SINE	Alu
chr7	20011678	20012079	chr7	20011859	20011893	MLT1K	LTR	MaLR
chr7	20015037	20015438	.	.	.	.	.	.
chr7	20461283	20461684	chr7	20461426	20461509	MLT1J	LTR	MaLR
chr7	20461283	20461684	chr7	20461532	20461885	MLT1I	LTR	MaLR
chr7	20496516	20496917	chr7	20496403	20496630	L2a	LINE	L2

chr7	20518874	20519275	chr7	20519173	20519358	B2_Mm1a	SINE	B2
chr7	25172295	25172696	.	.	.	.	.	.
chr7	25385937	25386338	.	.	.	.	.	.
chr7	25393063	25393464	.	.	.	.	.	.
chr7	26052748	26053149	.	.	.	.	.	.
chr7	26566640	26567041	.	.	.	.	.	.
chr7	28589611	28590012	chr7	28589951	28590061	(TG)n	Simple_repea	Simple_repeat
chr7	28799032	28799433	.	.	.	.	.	.
chr7	29586506	29586907	chr7	29586665	29586706	(TG)n	Simple_repea	Simple_repeat
chr7	30092733	30093134	chr7	30092788	30092856	(TG)n	Simple_repea	Simple_repeat
chr7	30134877	30135278	chr7	30134875	30135041	L2a	LINE	L2
chr7	30134877	30135278	chr7	30135068	30135317	MLT1J2	LTR	MaLR
chr7	30168274	30168675	.	.	.	.	.	.
chr7	30242794	30243195	chr7	30242634	30242816	MIRb	SINE	MIR
chr7	30303482	30303883	.	.	.	.	.	.
chr7	30603772	30604173	.	.	.	.	.	.
chr7	30738937	30739338	.	.	.	.	.	.
chr7	31001722	31002123	.	.	.	.	.	.
chr7	31158518	31158919	.	.	.	.	.	.
chr7	31787669	31788070	.	.	.	.	.	.
chr7	31993090	31993491	chr7	31992997	31993143	B1_Mur4	SINE	Alu
chr7	31993090	31993491	chr7	31993165	31993219	(CCAA)n	Simple_repea	Simple_repeat
chr7	31993090	31993491	chr7	31993222	31993259	(CCGAA)n	Simple_repea	Simple_repeat
chr7	38961205	38961606	chr7	38961255	38961308	polypurine	Low_comple	Low_complexity
chr7	38961205	38961606	chr7	38961412	38962435	RLTR25B	LTR	ERVK
chr7	38961205	38961606	chr7	38961128	38961255	B1_Mur2	SINE	Alu
chr7	38985967	38986368	.	.	.	.	.	.
chr7	50508840	50509241	.	.	.	.	.	.
chr7	50538181	50538582	chr7	50538158	50538233	GA-rich	Low_comple	Low_complexity
chr7	51536360	51536761	chr7	51536446	51536582	MLT1J	LTR	MaLR
chr7	52701987	52702388	chr7	52702277	52702464	B2_Mm2	SINE	B2
chr7	52730668	52731069	.	.	.	.	.	.
chr7	52736747	52737148	chr7	52736635	52736772	B1_Mus2	SINE	Alu
chr7	52736747	52737148	chr7	52736772	52736793	(CAAAA)n	Simple_repea	Simple_repeat
chr7	52736747	52737148	chr7	52737076	52737107	(G)n	Simple_repea	Simple_repeat
chr7	52775102	52775503	.	.	.	.	.	.
chr7	52793680	52794081	.	.	.	.	.	.
chr7	52844406	52844807	.	.	.	.	.	.
chr7	52885729	52886130	.	.	.	.	.	.
chr7	53118235	53118636	chr7	53118081	53118325	MLT1J1	LTR	MaLR
chr7	53118235	53118636	chr7	53118571	53118585	MER3	DNA	MER1_type
chr7	53118235	53118636	chr7	53118585	53118757	MER3	DNA	MER1_type
chr7	53507180	53507581	chr7	53507072	53507260	URR1B	DNA	MER1_type
chr7	53645558	53645959	chr7	53645396	53645612	L1MB7	LINE	L1
chr7	53645558	53645959	chr7	53645612	53645653	(CAAAA)n	Simple_repea	Simple_repeat
chr7	53645558	53645959	chr7	53645653	53645975	L1MB7	LINE	L1
chr7	53857388	53857789	.	.	.	.	.	.
chr7	54218085	54218486	chr7	54217908	54218176	RLTR6-int	LTR	ERV1
chr7	54218085	54218486	chr7	54218212	54218247	(TC)n	Simple_repea	Simple_repeat
chr7	54218085	54218486	chr7	54218247	54218375	RLTR6-int	LTR	ERV1
chr7	54286704	54287105	chr7	54286729	54286954	URR1B	DNA	MER1_type
chr7	56503965	56504366	.	.	.	.	.	.
chr7	56533941	56534342	.	.	.	.	.	.
chr7	59074061	59074462	chr7	59073953	59074167	L1MC3	LINE	L1
chr7	59074061	59074462	chr7	59074461	59074596	(TC)n	Simple_repea	Simple_repeat
chr7	59234043	59234444	chr7	59234201	59234267	ID4	SINE	ID
chr7	71394631	71395032	.	.	.	.	.	.
chr7	71471932	71472333	chr7	71472113	71472253	RSINE1	SINE	B4
chr7	73263136	73263537	.	.	.	.	.	.
chr7	73383045	73383446	chr7	73382926	73383070	B1_Mm	SINE	Alu
chr7	73383045	73383446	chr7	73383070	73384119	Lx5	LINE	L1
chr7	77004912	77005313	chr7	77005067	77005164	LTR33B	LTR	ERVL
chr7	77411999	77412400	.	.	.	.	.	.
chr7	77778399	77778800	.	.	.	.	.	.
chr7	79255628	79256029	chr7	79256015	79256069	(TATG)n	Simple_repea	Simple_repeat
chr7	79835669	79836070	chr7	79835389	79835762	L1M2	LINE	L1
chr7	80682615	80683016	.	.	.	.	.	.
chr7	82262874	82263275	chr7	82263056	82263123	MLT1J	LTR	MaLR
chr7	86251018	86251419	.	.	.	.	.	.
chr7	86481542	86481943	chr7	86481828	86481948	ID_B1	SINE	B4
chr7	86733191	86733592	chr7	86733144	86733273	RSINE1	SINE	B4
chr7	86733191	86733592	chr7	86733315	86733483	MLT1J	LTR	MaLR
chr7	87158745	87159146	chr7	87159078	87159101	(T)n	Simple_repea	Simple_repeat
chr7	88028059	88028460	chr7	88028452	88028521	B3A	SINE	B2
chr7	88324141	88324542	chr7	88324034	88324238	ID_B1	SINE	B4
chr7	88324141	88324542	chr7	88324488	88324678	L1MC3	LINE	L1
chr7	89167318	89167719	chr7	89167351	89167372	AT_rich	Low_comple	Low_complexity
chr7	89167318	89167719	chr7	89167443	89167464	AT_rich	Low_comple	Low_complexity
chr7	89920151	89920552	.	.	.	.	.	.
chr7	90886325	90886726	chr7	90886316	90886380	L2b	LINE	L2
chr7	90886325	90886726	chr7	90886626	90886718	L2b	LINE	L2
chr7	91087428	91087829	chr7	91087302	91087543	B4A	SINE	B4
chr7	91614298	91614699	chr7	91614145	91614549	MTEa	LTR	MaLR
chr7	104594993	104595394	.	.	.	.	.	.
chr7	105564002	105564403	.	.	.	.	.	.
chr7	106453507	106453908	.	.	.	.	.	.
chr7	108458884	108459285	.	.	.	.	.	.
chr7	108575341	108575742	.	.	.	.	.	.
chr7	109408012	109408413	chr7	109407982	109408097	B1_Mus2	SINE	Alu
chr7	109408012	109408413	chr7	109408154	109408278	PB1	SINE	Alu
chr7	109408012	109408413	chr7	109408279	109408351	ID2	SINE	ID
chr7	109408012	109408413	chr7	109408351	109408659	L1MB2	LINE	L1
chr7	116690034	116690435	.	.	.	.	.	.
chr7	117324123	117324524	chr7	117324108	117324219	(TTTC)n	Simple_repea	Simple_repeat
chr7	117324123	117324524	chr7	117324219	117324401	B3A	SINE	B2

chr7	117324123	117324524	chr7	117324420	117324600	B3	SINE	B2
chr7	118510477	118510878	.	.	.	.	.	.
chr7	119441665	119442066	chr7	119442004	119442093	B4	SINE	B4
chr7	120292275	120292676	chr7	120292578	120292631	CT-rich	Low_comple	Low_complexity
chr7	121326906	121327307	chr7	121327051	121327404	L2	LINE	L2
chr7	125735563	125735964	.	.	.	.	.	.
chr7	126078792	126079193	.	.	.	.	.	.
chr7	130040635	130041036	chr7	130040279	130040657	RMER2	LTR	ERV1
chr7	130040635	130041036	chr7	130040788	130040928	MLT1J1	LTR	MaLR
chr7	130573833	130574234	chr7	130574157	130574267	MLT1D	LTR	MaLR
chr7	133898335	133898736	chr7	133898335	133898456	B1_Mur2	SINE	Alu
chr7	134623327	134623728	.	.	.	.	.	.
chr7	135175154	135175555	.	.	.	.	.	.
chr7	138379597	138379998	.	.	.	.	.	.
chr7	139921073	139921474	.	.	.	.	.	.
chr7	142797012	142797413	.	.	.	.	.	.
chr7	146862334	146862735	chr7	146862467	146862603	CT-rich	Low_comple	Low_complexity
chr7	146862334	146862735	chr7	146862603	146862692	MER20	DNA	MER1_type
chr7	147248915	147249316	chr7	147249288	147249362	(TG)n	Simple_repe	Simple_repeat
chr7	148211357	148211758	chr7	148211413	148211435	GC_rich	Low_comple	Low_complexity
chr7	148211357	148211758	chr7	148211502	148211560	RLTR42	LTR	ERVK
chr7	148211357	148211758	chr7	148211552	148211713	B3	SINE	B2
chr7	148282427	148282828	.	.	.	.	.	.
chr7	150554123	150554524	chr7	150554112	150554796	L1M4	LINE	L1
chr7	152094593	152094994	chr7	152094544	152094650	ID_B1	SINE	B4
chr7	152094593	152094994	chr7	152094650	152094669	PB1D7	SINE	Alu
chr7	152094593	152094994	chr7	152094754	152094828	MLT1J	LTR	MaLR
chr7	152094593	152094994	chr7	152094986	152095062	ORR1E	LTR	MaLR
chr8	3593496	3593897	chr8	3593830	3594334	RLTR28	LTR	ERVL
chr8	3672219	3672620	.	.	.	.	.	.
chr8	4677659	4678060	.	.	.	.	.	.
chr8	7814323	7814724	chr8	7814597	7814633	T-rich	Low_comple	Low_complexity
chr8	7814323	7814724	chr8	7814654	7814684	L1_Mur2	LINE	L1
chr8	7814323	7814724	chr8	7814684	7815114	L1_Mus4	LINE	L1
chr8	8274946	8275347	.	.	.	.	.	.
chr8	8328359	8328760	chr8	8328497	8328564	MIRm	SINE	MIR
chr8	8605606	8606007	.	.	.	.	.	.
chr8	10646550	10646951	.	.	.	.	.	.
chr8	10664789	10665190	.	.	.	.	.	.
chr8	10977779	10978180	.	.	.	.	.	.
chr8	11259885	11260286	.	.	.	.	.	.
chr8	11273492	11273893	.	.	.	.	.	.
chr8	11323088	11323489	.	.	.	.	.	.
chr8	11371331	11371732	.	.	.	.	.	.
chr8	11382427	11382828	.	.	.	.	.	.
chr8	11486059	11486460	chr8	11485939	11486103	L1M4	LINE	L1
chr8	11959439	11959840	chr8	11959605	11959664	RLTR42	LTR	ERVK
chr8	11959439	11959840	chr8	11959663	11959857	RLTR42	LTR	ERVK
chr8	13548833	13549234	.	.	.	.	.	.
chr8	13551048	13551449	.	.	.	.	.	.
chr8	13624744	13625145	.	.	.	.	.	.
chr8	14306740	14307141	.	.	.	.	.	.
chr8	14411635	14412036	chr8	14410472	14411678	Lx7	LINE	L1
chr8	14528613	14529014	.	.	.	.	.	.
chr8	14600551	14600952	chr8	14600502	14600740	MTEb	LTR	MaLR
chr8	14616491	14616892	.	.	.	.	.	.
chr8	14651358	14651759	.	.	.	.	.	.
chr8	14705663	14706064	chr8	14705950	14706325	ORR1B1	LTR	MaLR
chr8	15012917	15013318	.	.	.	.	.	.
chr8	18699089	18699490	.	.	.	.	.	.
chr8	19707320	19707721	chr8	19707699	19707836	MIRc	SINE	MIR
chr8	19761722	19762123	.	.	.	.	.	.
chr8	19762693	19763094	chr8	19762645	19763027	Lx4A	LINE	L1
chr8	19762693	19763094	chr8	19763030	19763532	RMER13B	LTR	ERVK
chr8	19784449	19784850	.	.	.	.	.	.
chr8	19927358	19927759	.	.	.	.	.	.
chr8	19938479	19938880	.	.	.	.	.	.
chr8	19953288	19953689	.	.	.	.	.	.
chr8	19962948	19963349	chr8	19963303	19963370	Lx	LINE	L1
chr8	19982744	19983145	chr8	19982654	19982794	B1_Mus1	SINE	Alu
chr8	20017351	20017752	chr8	20017473	20017599	MER5B	DNA	MER1_type
chr8	20032646	20033047	chr8	20032567	20036607	L1Md_F	LINE	L1
chr8	24205909	24206310	chr8	24205871	24205935	(TG)n	Simple_repe	Simple_repeat
chr8	24205909	24206310	chr8	24205947	24206277	GSAT_MM	Satellite	Satellite
chr8	26384580	26384981	chr8	26384486	26384626	B1_Mus1	SINE	Alu
chr8	26384580	26384981	chr8	26384677	26384942	Zaphod	DNA	Tip100
chr8	32631565	32631966	chr8	32631902	32631928	AT_rich	Low_comple	Low_complexity
chr8	32830912	32831313	.	.	.	.	.	.
chr8	32837944	32838345	.	.	.	.	.	.
chr8	33397051	33397452	.	.	.	.	.	.
chr8	34545682	34546083	.	.	.	.	.	.
chr8	35128187	35128588	chr8	35128035	35128224	B2_Mm2	SINE	B2
chr8	35128187	35128588	chr8	35128332	35128660	MLT1J	LTR	MaLR
chr8	35676163	35676564	.	.	.	.	.	.
chr8	47310812	47311213	chr8	47310999	47311084	L1MEc	LINE	L1
chr8	47310812	47311213	chr8	47311166	47311226	RMER5	LTR	ERV1
chr8	47772149	47772550	chr8	47772048	47772382	L1M6	LINE	L1
chr8	63820825	63821226	.	.	.	.	.	.
chr8	64070138	64070539	.	.	.	.	.	.
chr8	72372910	72373311	chr8	72373052	72373191	ZP3AR	Satellite	Satellite
chr8	72372910	72373311	chr8	72373230	72373305	ID_B1	SINE	B4
chr8	72372910	72373311	chr8	72373306	72373520	B3	SINE	B2
chr8	72985625	72986026	.	.	.	.	.	.
chr8	73028109	73028510	.	.	.	.	.	.
chr8	74033233	74033634	chr8	74033181	74033326	B1_Mus1	SINE	Alu

chr8	74669372	74669773	chr8	74669403	74669718	Lx8	LINE	L1
chr8	86528538	86528939	.	.	.	.	.	.
chr8	86661724	86662125	.	.	.	.	.	.
chr8	87025807	87026208	.	.	.	.	.	.
chr8	87266016	87266417	.	.	.	.	.	.
chr8	88126665	88127066	chr8	88126711	88126816	RLTR23	LTR	ERV1
chr8	88126665	88127066	chr8	88126839	88127069	RLTR23	LTR	ERV1
chr8	88130953	88131354	chr8	88130768	88130979	RLTR15	LTR	ERVK
chr8	88130953	88131354	chr8	88131035	88131236	RLTR15	LTR	ERVK
chr8	88130953	88131354	chr8	88131313	88131352	(TC)n	Simple_repe	Simple_repeat
chr8	89749590	89749991	chr8	89749753	89749856	MLT1J2	LTR	MaLR
chr8	89749590	89749991	chr8	89749919	89750032	MLT1J2	LTR	MaLR
chr8	94139838	94140239	.	.	.	.	.	.
chr8	94295312	94295713	chr8	94295466	94295583	MLT1J1	LTR	MaLR
chr8	94911622	94912023	chr8	94911759	94912105	LTR33A	LTR	ERVL
chr8	96375871	96376272	.	.	.	.	.	.
chr8	96718681	96719082	chr8	96718504	96718707	ID_B1	SINE	B4
chr8	96718681	96719082	chr8	96718711	96718796	L1MC3	LINE	L1
chr8	96718681	96719082	chr8	96718865	96718990	L1MC3	LINE	L1
chr8	107126574	107126975	.	.	.	.	.	.
chr8	108811316	108811717	.	.	.	.	.	.
chr8	109053731	109054132	chr8	109053804	109053892	BC1_Mm	scRNA	scRNA
chr8	109053731	109054132	chr8	109054079	109054210	MIRb	SINE	MIR
chr8	109135966	109136367	chr8	109135939	109136020	B1_Mus2	SINE	Alu
chr8	109135966	109136367	chr8	109136155	109136229	ID2	SINE	ID
chr8	109778936	109779337	.	.	.	.	.	.
chr8	110013669	110014070	.	.	.	.	.	.
chr8	113313061	113313462	.	.	.	.	.	.
chr8	114303621	114304022	.	.	.	.	.	.
chr8	117139997	117140398	chr8	117140156	117140303	C-rich	Low_comple	Low_complexity
chr8	117720765	117721166	chr8	117720754	117720892	MLT1H	LTR	MaLR
chr8	117720765	117721166	chr8	117720900	117721003	MLT1J1	LTR	MaLR
chr8	122233085	122233486	chr8	122233280	122233310	(CA)n	Simple_repe	Simple_repeat
chr8	122233085	122233486	chr8	122233311	122233362	(TC)n	Simple_repe	Simple_repeat
chr8	122740881	122741282	chr8	122740898	122741010	L2b	LINE	L2
chr8	123335853	123336254	chr8	123336014	123336099	MLT1J	LTR	MaLR
chr8	123451976	123452377	.	.	.	.	.	.
chr8	123657938	123658339	.	.	.	.	.	.
chr8	123700095	123700496	chr8	123700147	123700170	(TTTA)n	Simple_repe	Simple_repeat
chr8	123700095	123700496	chr8	123700268	123700419	MLT1J	LTR	MaLR
chr8	123711626	123712027	.	.	.	.	.	.
chr8	123738792	123739193	chr8	123738969	123739150	B3A	SINE	B2
chr8	124197812	124198213	chr8	124197800	124198104	MLT1J	LTR	MaLR
chr8	124514780	124515181	.	.	.	.	.	.
chr8	124668720	124669121	.	.	.	.	.	.
chr8	124697933	124698334	.	.	.	.	.	.
chr8	125430680	125431081	chr8	125430642	125430745	LTR41B	LTR	ERVL
chr8	126189949	126190350	.	.	.	.	.	.
chr8	126216064	126216465	.	.	.	.	.	.
chr8	126716721	126717122	.	.	.	.	.	.
chr8	126936507	126936908	.	.	.	.	.	.
chr8	127350538	127350939	.	.	.	.	.	.
chr8	127707844	127708245	.	.	.	.	.	.
chr8	127777573	127777974	chr8	127777253	127777577	ORR1A2	LTR	MaLR
chr8	127777573	127777974	chr8	127777577	127777716	ORR1E	LTR	MaLR
chr8	127810154	127810555	.	.	.	.	.	.
chr8	128791019	128791420	chr8	128790608	128791035	L1MA4	LINE	L1
chr8	128791019	128791420	chr8	128791393	128791504	PB1D10	SINE	Alu
chr8	129074894	129075295	.	.	.	.	.	.
chr8	129090621	129091022	.	.	.	.	.	.
chr8	129127172	129127573	.	.	.	.	.	.
chr8	129190240	129190641	chr8	129190207	129190251	(TG)n	Simple_repe	Simple_repeat
chr8	129190240	129190641	chr8	129190258	129190291	(GGGAGA)n	Simple_repe	Simple_repeat
chr8	129209275	129209676	.	.	.	.	.	.
chr8	129260029	129260430	.	.	.	.	.	.
chr8	129356478	129356879	.	.	.	.	.	.
chr8	129362834	129363235	chr8	129362965	129362992	(TG)n	Simple_repe	Simple_repeat
chr8	129373690	129374091	.	.	.	.	.	.
chr8	129376934	129377335	chr8	129377260	129377290	(GGGTG)n	Simple_repe	Simple_repeat
chr8	129443109	129443510	.	.	.	.	.	.
chr8	130762835	130763236	.	.	.	.	.	.
chr8	130796862	130797263	.	.	.	.	.	.
chr9	2999914	3000315	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3004618	3005019	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3015106	3015507	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3019153	3019554	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3026462	3026863	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3031831	3032232	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3035711	3036112	chr9	3000002	3038419	GSAT_MM	Satellite	Satellite
chr9	3258655	3259056	chr9	3258511	3258766	LSU-rRNA_H	rRNA	rRNA
chr9	3258655	3259056	chr9	3258789	3259525	LSU-rRNA_H	rRNA	rRNA
chr9	4376190	4376591	.	.	.	.	.	.
chr9	5264083	5264484	.	.	.	.	.	.
chr9	6434080	6434481	chr9	6434107	6434466	MTEb	LTR	MaLR
chr9	6434080	6434481	chr9	6434466	6434647	MTEb-int	LTR	MaLR
chr9	7594903	7595304	chr9	7594844	7595230	MTD	LTR	MaLR
chr9	11380615	11381016	chr9	11380316	11380894	RLTR1	LTR	ERV1
chr9	13291529	13291930	.	.	.	.	.	.
chr9	14446262	14446663	chr9	14446598	14446624	(TCC)n	Simple_repe	Simple_repeat
chr9	20556030	20556431	chr9	20556002	20556067	ORR1E	LTR	MaLR
chr9	20556030	20556431	chr9	20556239	20556468	LTR33A_	LTR	ERVL
chr9	20985701	20986102	chr9	20985609	20985733	B1F2	SINE	Alu
chr9	21519749	21520150	.	.	.	.	.	.
chr9	21533746	21534147	.	.	.	.	.	.
chr9	21608693	21609094	chr9	21608735	21608807	GA-rich	Low_comple	Low_complexity

chr9	21705922	21706323	chr9	21706070	21706137	LTR33A	LTR	ERVL
chr9	21705922	21706323	chr9	21706286	21706384	B3	SINE	B2
chr9	21727742	21728143	chr9	21727649	21727767	B1F	SINE	Alu
chr9	21727742	21728143	chr9	21727994	21728109	ID_B1	SINE	B4
chr9	21727742	21728143	chr9	21728113	21728177	T-rich	Low_comple	Low_complexity
chr9	24346342	24346743	chr9	24346317	24346416	RMER20B	LTR	ERVK
chr9	24346342	24346743	chr9	24346451	24346603	SYNREP_MM	Satellite	Satellite
chr9	24346342	24346743	chr9	24346658	24347870	Lx9	LINE	L1
chr9	31073641	31074042	chr9	31073647	31073754	MMSAT4	Satellite	Satellite
chr9	32517544	32517945	chr9	32517869	32517996	MIRc	SINE	MIR
chr9	32788424	32788825	chr9	32788484	32788700	MIR	SINE	MIR
chr9	34087416	34087817	.	.	.	.	.	.
chr9	34346268	34346669	.	.	.	.	.	.
chr9	34701629	34702030	chr9	34701710	34701843	MIRb	SINE	MIR
chr9	34777509	34777910	chr9	34777806	34777860	L3b	LINE	CR1
chr9	35112789	35113190	chr9	35112790	35113194	GSAT_MM	Satellite	Satellite
chr9	40204715	40205116	chr9	40204818	40204838	(CAG)n	Simple_repea	Simple_repeat
chr9	40564372	40564773	chr9	40564316	40564421	PB1	SINE	Alu
chr9	41283414	41283815	chr9	41283770	41283990	MIRc	SINE	MIR
chr9	41403900	41404301	.	.	.	.	.	.
chr9	42819165	42819566	chr9	42819387	42819519	RMER15	LTR	ERVL
chr9	42823538	42823939	.	.	.	.	.	.
chr9	43070018	43070419	.	.	.	.	.	.
chr9	43506394	43506795	chr9	43506257	43506421	L2b	LINE	L2
chr9	43605429	43605830	.	.	.	.	.	.
chr9	43753404	43753805	chr9	43753377	43753948	MLT1N2	LTR	MaLR
chr9	43866815	43867216	chr9	43867064	43867275	MLT1C	LTR	MaLR
chr9	44291681	44292082	.	.	.	.	.	.
chr9	44712982	44713383	.	.	.	.	.	.
chr9	47969852	47970253	chr9	47969880	47969963	MIRb	SINE	MIR
chr9	49300206	49300607	.	.	.	.	.	.
chr9	50388465	50388866	.	.	.	.	.	.
chr9	50866970	50867371	.	.	.	.	.	.
chr9	50913826	50914227	.	.	.	.	.	.
chr9	54416525	54416926	chr9	54416840	54416922	ID4	SINE	ID
chr9	54635708	54636109	chr9	54636083	54636213	ID_B1	SINE	B4
chr9	54649317	54649718	.	.	.	.	.	.
chr9	55209854	55210255	chr9	55209708	55210158	MTC	LTR	MaLR
chr9	56113398	56113799	chr9	56113352	56113488	Lx7	LINE	L1
chr9	56113398	56113799	chr9	56113485	56113572	Lx7	LINE	L1
chr9	56311362	56311763	.	.	.	.	.	.
chr9	56313075	56313476	.	.	.	.	.	.
chr9	56356852	56357253	chr9	56356977	56357057	L2b	LINE	L2
chr9	56720262	56720663	.	.	.	.	.	.
chr9	57275721	57276122	chr9	57276045	57276122	(CA)n	Simple_repea	Simple_repeat
chr9	57507522	57507923	chr9	57507397	57507526	B1F1	SINE	Alu
chr9	57507522	57507923	chr9	57507864	57507878	ID_B1	SINE	B4
chr9	57507522	57507923	chr9	57507878	57508003	B1_Mur1	SINE	Alu
chr9	57679232	57679633	.	.	.	.	.	.
chr9	57819911	57820312	chr9	57819929	57819977	ID4	SINE	ID
chr9	58062305	58062706	chr9	58062589	58062615	(TG)n	Simple_repea	Simple_repeat
chr9	58123118	58123519	chr9	58123320	58123424	L1MD3	LINE	L1
chr9	58128363	58128764	chr9	58128312	58128654	RLTR30	LTR	ERV1
chr9	58128363	58128764	chr9	58128683	58128843	B3	SINE	B2
chr9	58147183	58147584	.	.	.	.	.	.
chr9	58294228	58294629	chr9	58294342	58294504	MLT1J	LTR	MaLR
chr9	58294228	58294629	chr9	58294175	58294342	B2_Mm2	SINE	B2
chr9	58392551	58392952	chr9	58392707	58393067	MLT1J	LTR	MaLR
chr9	58928102	58928503	chr9	58928066	58928137	MTEa	LTR	MaLR
chr9	59037256	59037657	chr9	59037599	59037984	ORR1B1	LTR	MaLR
chr9	59432754	59433155	chr9	59432886	59433041	L2	LINE	L2
chr9	60925000	60925401	chr9	60924867	60925215	LTR33A	LTR	ERVL
chr9	62358335	62358736	chr9	62358532	62358603	MLT1J	LTR	MaLR
chr9	62407659	62408060	.	.	.	.	.	.
chr9	62456218	62456619	chr9	62456082	62456291	MLT2B1	LTR	ERVL
chr9	62456218	62456619	chr9	62456386	62456480	(GAATG)n	Simple_repea	Simple_repeat
chr9	62456218	62456619	chr9	62456499	62456817	MTC	LTR	MaLR
chr9	62472493	62472894	.	.	.	.	.	.
chr9	62474645	62475046	.	.	.	.	.	.
chr9	62676647	62677048	chr9	62677009	62677391	MTA_Mm	LTR	MaLR
chr9	62957033	62957434	chr9	62957304	62957411	MIR	SINE	MIR
chr9	62980708	62981109	chr9	62981089	62981196	U6	snRNA	snRNA
chr9	63504902	63505303	.	.	.	.	.	.
chr9	63550208	63550609	.	.	.	.	.	.
chr9	63566589	63566990	.	.	.	.	.	.
chr9	63591694	63592095	chr9	63591955	63592162	B3	SINE	B2
chr9	63651353	63651754	chr9	63651652	63651939	B4	SINE	B4
chr9	63657975	63658376	chr9	63657906	63658027	ID_B1	SINE	B4
chr9	63776971	63777372	chr9	63777095	63777214	MLT1J	LTR	MaLR
chr9	63789549	63789950	.	.	.	.	.	.
chr9	63838987	63839388	chr9	63838993	63839100	PB1D7	SINE	Alu
chr9	63978796	63979197	chr9	63978738	63978922	B3	SINE	B2
chr9	63978796	63979197	chr9	63978930	63979040	B1_Mur4	SINE	Alu
chr9	63978796	63979197	chr9	63979064	63979264	B3	SINE	B2
chr9	65044432	65044833	chr9	65044377	65044494	U5	snRNA	snRNA
chr9	65049592	65049993	chr9	65049532	65049648	U5	snRNA	snRNA
chr9	65398779	65399180	.	.	.	.	.	.
chr9	66448810	66449211	.	.	.	.	.	.
chr9	66836829	66837230	.	.	.	.	.	.
chr9	69144241	69144642	chr9	69144316	69144360	(TTTTG)n	Simple_repea	Simple_repeat
chr9	70089164	70089565	.	.	.	.	.	.
chr9	70096671	70097072	.	.	.	.	.	.
chr9	70653813	70654214	chr9	70653725	70653876	B1_Mur3	SINE	Alu
chr9	70653813	70654214	chr9	70653941	70654051	PB1	SINE	Alu
chr9	71746740	71747141	.	.	.	.	.	.

chr9	72257509	72257910	.	.	.	.	.	.
chr9	72487780	72488181	.	.	.	.	.	.
chr9	74942638	74943039	.	.	.	.	.	.
chr9	75151817	75152218	.	.	.	.	.	.
chr9	75283830	75284231	.	.	.	.	.	.
chr9	75857969	75858370	.	.	.	.	.	.
chr9	78368287	78368688	.	.	.	.	.	.
chr9	78471088	78471489	.	.	.	.	.	.
chr9	79458089	79458490	chr9	79458448	79458464	MT2B2	LTR	ERVL
chr9	79458089	79458490	chr9	79458464	79458549	B1F	SINE	Alu
chr9	83462530	83462931	chr9	83462671	83462926	L1MA6	LINE	L1
chr9	84288550	84288951	chr9	84288268	84288572	MER58B	DNA	MER1_type
chr9	84288550	84288951	chr9	84288614	84288889	MLT1J	LTR	MaLR
chr9	87359029	87359430	.	.	.	.	.	.
chr9	88136374	88136775	chr9	88136391	88136531	RSINE1	SINE	B4
chr9	89810665	89811066	chr9	89810670	89810752	ID4	SINE	ID
chr9	89810665	89811066	chr9	89810805	89810903	PB1	SINE	Alu
chr9	89810665	89811066	chr9	89811006	89811089	MIRb	SINE	MIR
chr9	92711433	92711834	chr9	92711377	92711752	RLTR15	LTR	ERVK
chr9	92711433	92711834	chr9	92711753	92712213	MTEa-int	LTR	MaLR
chr9	95604376	95604777	chr9	95604420	95604450	(TG)n	Simple_repea	Simple_repeat
chr9	95604376	95604777	chr9	95604547	95604642	MLT2F	LTR	ERVL
chr9	95604376	95604777	chr9	95604684	95604776	MLT2F	LTR	ERVL
chr9	96682514	96682915	.	.	.	.	.	.
chr9	96696024	96696425	chr9	96696356	96696376	(C)n	Simple_repea	Simple_repeat
chr9	96700753	96701154	chr9	96700909	96701124	RLTR23	LTR	ERV1
chr9	96700753	96701154	chr9	96701124	96701208	RMER17C	LTR	ERVK
chr9	96739248	96739649	chr9	96739137	96739364	RMER15	LTR	ERVL
chr9	99537179	99537580	chr9	99537151	99537235	ID4	SINE	ID
chr9	99537179	99537580	chr9	99537328	99537412	MLT1J	LTR	MaLR
chr9	100507776	100508177	chr9	100507650	100507962	ORR1E	LTR	MaLR
chr9	101748040	101748441	chr9	101748183	101748283	MLT1J1	LTR	MaLR
chr9	102410826	102411227	chr9	102410730	102410831	MLT1N2	LTR	MaLR
chr9	102410826	102411227	chr9	102410956	102411030	MLT1N2	LTR	MaLR
chr9	102674452	102674853	chr9	102674366	102674569	B3	SINE	B2
chr9	102674452	102674853	chr9	102674574	102674677	PB1	SINE	Alu
chr9	102896138	102896539	chr9	102895971	102896192	(CA)n	Simple_repea	Simple_repeat
chr9	102896138	102896539	chr9	102896502	102896669	MER5A	DNA	MER1_type
chr9	102975132	102975533	.	.	.	.	.	.
chr9	106256039	106256440	.	.	.	.	.	.
chr9	106280290	106280691	.	.	.	.	.	.
chr9	107166223	107166624	chr9	107166147	107166238	MIRc	SINE	MIR
chr9	108022992	108023393	.	.	.	.	.	.
chr9	108038541	108038942	chr9	108038481	108038669	B2_Mm1t	SINE	B2
chr9	108038541	108038942	chr9	108038675	108038885	B3	SINE	B2
chr9	108046952	108047353	chr9	108046982	108047116	ORR1C1	LTR	MaLR
chr9	108046952	108047353	chr9	108047119	108047155	ORR1C1	LTR	MaLR
chr9	108103528	108103929	.	.	.	.	.	.
chr9	110003365	110003766	.	.	.	.	.	.
chr9	110183622	110184023	chr9	110183041	110183750	RMER19B	LTR	ERVK
chr9	110183622	110184023	chr9	110183750	110183892	LSU-rRNA_Hs	rRNA	rRNA
chr9	110897092	110897493	chr9	110897383	110897576	RMER17C	LTR	ERVK
chr9	114409344	114409745	chr9	114409524	114409635	PB1D9	SINE	Alu
chr9	114409344	114409745	chr9	114409654	114409810	RSINE1	SINE	B4
chr9	115996965	115997366	.	.	.	.	.	.
chr9	117601629	117602030	chr9	117601701	117601861	RMER15	LTR	ERVL
chr9	119958475	119958876	chr9	119958419	119958618	B3	SINE	B2
chr9	119958475	119958876	chr9	119958625	119958712	RMER30	DNA	MER1_type
chr9	120095972	120096373	chr9	120096290	120096401	Lx7	LINE	L1
chr9	120685850	120686251	chr9	120686152	120686181	(T)n	Simple_repea	Simple_repeat
chr9	122346814	122347215	chr9	122346886	122347211	L1M5	LINE	L1
chr9	122557013	122557414	chr9	122557166	122557260	PB1	SINE	Alu
chr9	122557013	122557414	chr9	122557252	122557468	ID_B1	SINE	B4
chr9	123370905	123371306	chr9	123370909	123371305	LSU-rRNA_Hs	rRNA	rRNA
chr9	123782043	123782444	chr9	123781577	123782096	RLTR28	LTR	ERVL
chrX	11522331	11522732	chrX	11522301	11522448	B1F	SINE	Alu
chrX	11522331	11522732	chrX	11522477	11522704	LTR33A	LTR	ERVL
chrX	39371157	39371558	.	.	.	.	.	.
chrX	45696623	45697024	chrX	45696631	45696667	(TCCCC)n	Simple_repea	Simple_repeat
chrX	45696623	45697024	chrX	45696726	45696782	C-rich	Low_comple	Low_complexity
chrX	45696623	45697024	chrX	45696904	45696931	(CA)n	Simple_repea	Simple_repeat
chrX	45776859	45777260	.	.	.	.	.	.
chrX	65665704	65666105	chrX	65665684	65666015	RLTR1B	LTR	ERV1
chrX	65665704	65666105	chrX	65666015	65666183	L1_Mus4	LINE	L1
chrX	72912435	72912836	chrX	72909472	72912683	GSAT_MM	Satellite	Satellite
chrX	72912435	72912836	chrX	72912523	72912752	SYNREP_MM	Satellite	Satellite
chrX	72912435	72912836	chrX	72912747	72913319	GSAT_MM	Satellite	Satellite
chrX	72919558	72919959	.	.	.	.	.	.
chrX	73844091	73844492	chrX	73843904	73844466	SYNREP_MM	Satellite	Satellite
chrX	73844091	73844492	chrX	73844487	73844913	L1_Rod	LINE	L1
chrX	83006765	83007166	chrX	83006914	83006998	B3A	SINE	B2
chrX	83006765	83007166	chrX	83007003	83007050	(CA)n	Simple_repea	Simple_repeat
chrX	83006765	83007166	chrX	83007050	83007075	(GA)n	Simple_repea	Simple_repeat
chrX	83006765	83007166	chrX	83007145	83007259	PB1D7	SINE	Alu
chrX	84483524	84483925	chrX	84482926	84483682	L1_Mm	LINE	L1
chrX	84483524	84483925	chrX	84483759	84483877	L1Md_F2	LINE	L1
chrX	97934822	97935223	chrX	97935070	97935093	(CA)n	Simple_repea	Simple_repeat
chrX	97934822	97935223	chrX	97935126	97935172	(TC)n	Simple_repea	Simple_repeat
chrX	97934822	97935223	chrX	97935172	97935214	(CA)n	Simple_repea	Simple_repeat
chrX	100812241	100812642	chrX	100812270	100812325	(CGGG)n	Simple_repea	Simple_repeat
chrX	109484320	109484721	chrX	109484308	109484380	B3	SINE	B2
chrX	119944836	119945237	chrX	119944996	119945070	(CATTC)n	Simple_repea	Simple_repeat
chrX	119944836	119945237	chrX	119945077	119945199	(TCTA)n	Simple_repea	Simple_repeat
chrX	119944836	119945237	chrX	119945199	119945760	RLTR20D	LTR	ERVK
chrX	133572473	133572874	.	.	.	.	.	.

chrX	139099876	139100277	chrX	139099975	139100334	ORR1E	LTR	MaLR
chrX	139917400	139917801	chrX	139917547	139917652	SYNREP_MM	Satellite	Satellite
chrX	139917400	139917801	chrX	139917676	139918331	L1Md_F2	LINE	L1
chrX	139935704	139936105	.	.	.	.	.	.
chrX	140052696	140053097	chrX	140052478	140052703	MIRb	SINE	MIR
chrX	140052696	140053097	chrX	140052756	140052787	AT_rich	Low_comple	Low_complexity
chrX	158072300	158072701	chrX	158072407	158072705	MLT1J	LTR	MaLR
chrX	163083764	163084165	chrX	163083906	163083985	MLT1J2	LTR	MaLR
chrX	165561591	165561992	.	.	.	.	.	.
chrX	166424705	166425106	.	.	.	.	.	.
chrX	166438809	166439210	.	.	.	.	.	.
chrX	166444799	166445200	.	.	.	.	.	.
chrX	166446510	166446911	chrX	166446740	166446765	AT_rich	Low_comple	Low_complexity
chrY	2688238	2688639	chrY	2687752	2692209	SYNREP_MM	Satellite	Satellite
chrY	2765602	2766003	chrY	2761830	2766398	SYNREP_MM	Satellite	Satellite