

HeLa cells

ZNF143 peaks <= 2kb from TSS			Repeats from repeatMasker (USCS) table					
Chromosome	Start	End	Chromosome	Start	End	repName	repClass	repFamily
chr1	762622	763023	chr1	762942	763009	G-rich	Low_complexity	Low_complexity
chr1	894412	894813	chr1	894684	894732	(CCCCG)n	Simple_repeat	Simple_repeat
chr1	1051396	1051797	chr1	1051521	1051549	GC_rich	Low_complexity	Low_complexity
chr1	1051396	1051797	chr1	1051615	1051653	GC_rich	Low_complexity	Low_complexity
chr1	1310613	1311014
chr1	1334717	1335118
chr1	1342523	1342924
chr1	1447147	1447548
chr1	1551000	1551401
chr1	2457466	2457867	chr1	2457796	2457883	C-rich	Low_complexity	Low_complexity
chr1	3566493	3566894	chr1	3566853	3567001	MER53	DNA	hAT
chr1	3663726	3664127	chr1	3663887	3663909	GC_rich	Low_complexity	Low_complexity
chr1	3712829	3713230
chr1	3773804	3774205
chr1	3816982	3817383
chr1	6259526	6259927
chr1	6662469	6662870
chr1	6673450	6673851	chr1	6673413	6673570	C-rich	Low_complexity	Low_complexity
chr1	6761695	6762096
chr1	10490577	10490978	chr1	10490722	10490748	GC_rich	Low_complexity	Low_complexity
chr1	10532444	10532845
chr1	10534799	10535200
chr1	11072978	11073379	chr1	11073269	11073572	L2c	LINE	L2
chr1	11866642	11867043
chr1	12040055	12040456
chr1	15852903	15853304	chr1	15852854	15852972	MIR3	SINE	MIR
chr1	16302363	16302764	chr1	16302758	16302980	MIRb	SINE	MIR
chr1	16940050	16940451
chr1	17338302	17338703	chr1	17338252	17338346	GC_rich	Low_complexity	Low_complexity
chr1	17338302	17338703	chr1	17338598	17338757	MIRb	SINE	MIR
chr1	17380354	17380755
chr1	19536690	19537091	chr1	19536672	19536740	(CCG)n	Simple_repeat	Simple_repeat
chr1	19577945	19578346
chr1	20834348	20834749
chr1	20987707	20988108
chr1	22109969	22110370
chr1	22778168	22778569
chr1	23345627	23346028	chr1	23345582	23345685	L2c	LINE	L2
chr1	23670660	23671061
chr1	23695189	23695590	chr1	23695435	23695462	GC_rich	Low_complexity	Low_complexity
chr1	24018062	24018463
chr1	24151695	24152096	chr1	24151967	24151990	GC_rich	Low_complexity	Low_complexity
chr1	24151695	24152096	chr1	24152043	24152111	L2b	LINE	L2
chr1	24285934	24286335
chr1	24648200	24648601
chr1	24969593	24969994
chr1	26146256	26146657
chr1	26232856	26233257
chr1	26324477	26324878
chr1	26633019	26633420	chr1	26633411	26633572	MIRb	SINE	MIR
chr1	27560645	27561046
chr1	27930529	27930930	chr1	27930528	27930633	C-rich	Low_complexity	Low_complexity
chr1	27930529	27930930	chr1	27930734	27930781	GC_rich	Low_complexity	Low_complexity
chr1	28157092	28157493
chr1	28414933	28415334
chr1	28585646	28586047
chr1	28695975	28696376
chr1	28832213	28832614	chr1	28831924	28832223	Alu5z6	SINE	Alu
chr1	28908267	28908668
chr1	28969671	28970072	chr1	28970067	28970230	MIRb	SINE	MIR
chr1	28974676	28975077
chr1	29063068	29063469	chr1	29063346	29063368	GC_rich	Low_complexity	Low_complexity
chr1	29508476	29508877	chr1	29508728	29508950	MIRb	SINE	MIR
chr1	31796978	31797079
chr1	32110076	32110477
chr1	32645047	32645448
chr1	32859828	32860229
chr1	33502359	33502760
chr1	33937981	33938382
chr1	35325215	35325616	chr1	35325578	35325668	L2c	LINE	L2
chr1	35497343	35497744	chr1	35497731	35497911	AluSx	SINE	Alu
chr1	35544760	35545161	chr1	35544620	35544780	MIR	SINE	MIR
chr1	36023056	36023457
chr1	36235627	36236028	chr1	36236021	36236132	(TA)n	Simple_repeat	Simple_repeat
chr1	36554177	36554578
chr1	36615005	36615406
chr1	36689751	36690152
chr1	36863355	36863756	chr1	36863630	36863946	L2a	LINE	L2
chr1	38019732	38020133	chr1	38020043	38020340	Alu5z6	SINE	Alu
chr1	38156075	38156476
chr1	38412534	38412935
chr1	38455530	38455931
chr1	38478049	38478450
chr1	40506263	40506664
chr1	40723551	40723952
chr1	40915477	40915878
chr1	40974187	40974588
chr1	40997026	40997427
chr1	42800695	42801096	chr1	42800686	42800723	GC_rich	Low_complexity	Low_complexity
chr1	43123883	43124284
chr1	43311922	43312323
chr1	43855348	43855749
chr1	44412191	44412592
chr1	44435312	44435713	chr1	44435051	44435336	AluJb	SINE	Alu
chr1	44440292	44440693
chr1	44678888	44679289	chr1	44678750	44678916	MIRb	SINE	MIR
chr1	44820835	44821236
chr1	44870623	44871024	chr1	44870837	44870898	(TG)n	Simple_repeat	Simple_repeat
chr1	45205160	45205561	chr1	45205152	45205246	MIRb	SINE	MIR
chr1	45241003	45241404	chr1	45240565	45241008	L2	LINE	L2
chr1	45452103	45452504	chr1	45452456	45452550	L2b	LINE	L2
chr1	45769391	45769792	chr1	45769777	45769798	GC_rich	Low_complexity	Low_complexity

repName count	repClass count	repFamily count
GC_rich	342	Low_complexity
C-rich	49	Simple_repeat
(CGG)n	43	SINE
MIRb	42	LINE
(CCG)n	40	LTR
G-rich	39	DNA
MIRc	29	rRNA
MIR3	27	Satellite
L2a	25	rRNA
(CGGGG)n	22	snRNA
(CCCCG)n	21	srrpRNA
MIR	20	rRNA
L2c	20	TcMar-Tigge
L2b	19	Satellite
AluJb	15	hAT-Blackjac
AluSx	12	rRNA
AluSx1	11	hAT-Tip100
(CA)n	11	snRNA
(TG)n	10	hAT
(T)n	9	srrpRNA
AluSp	9	
L2	7	
AluS2	7	
(TCC)n	7	
AluS2	7	
CT-rich	7	
FRAM	6	
(A)n	6	
AluJr	6	
MERSA	6	
AT_rich	6	
MLT1J	5	
(CAG)n	5	
(CGCGG)n	5	
AluY	5	
FLAM_C	5	
L3	4	
T-rich	4	
AluJo	4	
(CGGGG)n	4	
AluSc	4	
(CAGC)n	4	
AluS6	3	
(TCCC)n	3	
(CCCG)n	3	
(CCCCG)n	3	
(CTGGG)n	3	
AluSg	3	
(GGA)n	3	
SSU-rRNA_H	3	
MLT1J1	3	
(CTG)n	3	
AluSc8	3	
MERSB	2	
(GGCTG)n	2	
(CCTCG)n	2	
MER81	2	
GA-rich	2	
AluSq	2	
(GA)n	2	
L1M5	2	
(CGAGG)n	2	
(TCCC)n	2	
AluS3	2	
(CGT)n	2	
(TGAA)n	2	
L3b	2	
LTR41	2	
MER33	2	
MERSA1	2	
(TCCC)n	2	
A-rich	2	
(CCCCAG)n	2	
MERS3	1	
MER67A	1	
(TA)n	1	
(TGGG)n	1	
L1M1	1	
(TTTA)n	1	
(GCTG)n	1	
U2	1	
L1MA3	1	
(AGGGGG)n	1	
L1ME2z	1	
LTR34	1	
MER67C	1	
L1MEg	1	
MLT1D	1	
tRNA-Leu-CT	1	
X7C_LINE	1	
Zaphod3	1	
(CTCG)n	1	
FAM	1	
MER82	1	
AluYb8	1	
tRNA-Asn-AA	1	
L1MB7	1	
L1M4	1	
LTR10D	1	
CR1_Mam	1	
(TCCA)n	1	
BSR/Beta	1	

chr1	169763980	169764381
chr1	169862947	169863348
chr1	172412990	172413391
chr1	172501695	172502096
chr1	173683845	173684246
chr1	173793362	173793763
chr1	173837309	173837710
chr1	179846797	179847198
chr1	179851674	179852075
chr1	179923648	179924049	chr1	179923897	179923930	(CCG)n	Simple_repeat	Simple_repeat	
chr1	182758637	182759038
chr1	182991864	182992265	chr1	182992221	182992284	(TCCCC)n	Simple_repeat	Simple_repeat	
chr1	183441013	183441414
chr1	184020649	184021050
chr1	184724048	184724449
chr1	185126099	185126500
chr1	186344289	186344690
chr1	193028310	193028711
chr1	198125890	198126291	chr1	198126071	198126102	GC_rich	Low_complexity	Low_complexity	
chr1	198125890	198126291	chr1	198126250	198126271	GC_rich	Low_complexity	Low_complexity	
chr1	200378988	200379389	chr1	200379078	200379104	(CCG)n	Simple_repeat	Simple_repeat	
chr1	201924417	201924818
chr1	201979210	201979611
chr1	202310888	202311289
chr1	202317522	202317923
chr1	203764513	203764914	chr1	203764486	203764560	MIR	SINE	MIR	
chr1	203830547	203830948
chr1	205091197	205091598
chr1	205180686	205181087
chr1	205744425	205744826	chr1	205744671	205744734	X7C_LINE	LINE	CR1	
chr1	211848774	211849175
chr1	212588095	212588496
chr1	212965001	212965402
chr1	213188940	213189341	chr1	213189337	213189648	AluSq2	SINE	Alu	
chr1	213224343	213224744
chr1	222763076	222763477
chr1	224544309	224544710	chr1	224544218	224544338	FRAM	SINE	Alu	
chr1	225117075	225117476
chr1	226374209	226374610	chr1	226374242	226374284	(CGG)n	Simple_repeat	Simple_repeat	
chr1	226496688	226497089	chr1	226496938	226497081	GC_rich	Low_complexity	Low_complexity	
chr1	227922899	227923300
chr1	228270166	228270567
chr1	231114537	231114938	chr1	231114538	231114563	(CAG)n	Simple_repeat	Simple_repeat	
chr1	231663912	231664313
chr1	233431271	233431672	chr1	233431324	233431361	(CCG)n	Simple_repeat	Simple_repeat	
chr1	233431271	233431672	chr1	233431600	233431759	T-rich	Low_complexity	Low_complexity	
chr1	234859844	234860245	chr1	234859855	234859926	GA-rich	Low_complexity	Low_complexity	
chr1	235491546	235491947
chr1	235667719	235668120
chr1	236445132	236445533
chr1	236958255	236958656	chr1	236958136	236958290	MIRc	SINE	MIR	
chr1	241682990	241683391
chr1	242011048	242011449	chr1	242010931	242011088	MER67A	LTR	ERV1	
chr1	243419065	243419466
chr1	244615379	244615780
chr1	244815865	244816266
chr1	246729360	246729761
chr1	247095333	247095734	chr1	247095541	247095572	GC_rich	Low_complexity	Low_complexity	
chr1	249153208	249153609
chr10	5708452	5708853	chr10	5708548	5708635	G-rich	Low_complexity	Low_complexity	
chr10	5931798	5932199
chr10	6130786	6131187	chr10	6130903	6130985	SUBTEL_sa	Satellite	Satellite	
chr10	12237847	12238248
chr10	13389810	13390211	chr10	13389863	13389910	GC_rich	Low_complexity	Low_complexity	
chr10	13389810	13390211	chr10	13389972	13389995	GC_rich	Low_complexity	Low_complexity	
chr10	13389810	13390211	chr10	13390112	13390137	(CGG)n	Simple_repeat	Simple_repeat	
chr10	13389810	13390211	chr10	13390137	13390233	GC_rich	Low_complexity	Low_complexity	
chr10	14880143	14880544
chr10	17685899	17686300
chr10	21814654	21815055
chr10	22605132	22605533	chr10	22605176	22605284	GC_rich	Low_complexity	Low_complexity	
chr10	26986290	26986691	chr10	26986684	26986723	GC_rich	Low_complexity	Low_complexity	
chr10	27149813	27150214
chr10	27443138	27443539	chr10	27443491	27443668	AluSx1	SINE	Alu	
chr10	27530846	27531247
chr10	27792922	27793323
chr10	29698242	29698643
chr10	32635904	32636305
chr10	35625055	35625456	chr10	35625355	35625428	G-rich	Low_complexity	Low_complexity	
chr10	38265432	38265833	chr10	38265455	38265485	GC_rich	Low_complexity	Low_complexity	
chr10	38299304	38299705
chr10	38383047	38383448
chr10	43048158	43048559
chr10	43133944	43134345
chr10	43277920	43278321
chr10	44069836	44070237
chr10	44101644	44102045
chr10	44144176	44144577
chr10	46168307	46168708	chr10	46168675	46168737	MIRb	SINE	MIR	
chr10	58120815	58121216
chr10	60094472	60094873	chr10	60094487	60094527	MIRc	SINE	MIR	
chr10	60094472	60094873	chr10	60094679	60094701	GC_rich	Low_complexity	Low_complexity	
chr10	60145007	60145408
chr10	64564081	64564482
chr10	69597800	69598201
chr10	74114175	74114576
chr10	74385697	74386098
chr10	74870015	74870416
chr10	75012264	75012665	chr10	75012648	75012865	L2b	LINE	L2	
chr10	75255638	75256039
chr10	75503599	75504000	chr10	75503560	75503655	MIR	SINE	MIR	
chr10	75541633	75542034
chr10	75544883	75545284
chr10	76817418	76817819	chr10	76817573	76817624	MLT1J	LTR	ERVL-MaLR	
chr10	76817418	76817819	chr10	76817671	76817956	MLT1J	LTR	ERVL-MaLR	

chr11	59382586	59382987	chr11	59382931	59383151 (CCG)n	Simple_repeat	Simple_repeat
chr11	60673924	60674325	chr11	60674278	60674344 MER5A	DNA	hAT-Charlie
chr11	60681178	60681579
chr11	61100391	61100792
chr11	61129266	61129667
chr11	61560008	61560409
chr11	61584277	61584678
chr11	61891032	61891433
chr11	62358873	62359274
chr11	62413880	62414281
chr11	62438969	62439370
chr11	62495695	62496096
chr11	62538925	62539326	chr11	62538897	62538926 (CCG)n	Simple_repeat	Simple_repeat
chr11	62609009	62609410	chr11	62609095	62609281 U2	snRNA	snRNA
chr11	62623244	62623645
chr11	63439031	63439432	chr11	63438998	63439041 (CGAGG)n	Simple_repeat	Simple_repeat
chr11	63536139	63536540	chr11	63536094	63536219 (CGCG)n	Simple_repeat	Simple_repeat
chr11	63536139	63536540	chr11	63536444	63536481 GC_rich	Low_complexity	Low_complexity
chr11	63741874	63742275
chr11	63753744	63754145
chr11	63933438	63933839
chr11	64014812	64015213
chr11	64073441	64073842
chr11	64569954	64570355	chr11	64570170	64570216 MIR	SINE	MIR
chr11	64577897	64578298
chr11	64691884	64692285
chr11	64808278	64808679
chr11	64863396	64863797
chr11	64884975	64885376
chr11	65083980	65084381	chr11	65084012	65084179 MIRb	SINE	MIR
chr11	65382618	65383019
chr11	65479341	65479742
chr11	65488087	65488488	chr11	65488426	65488572 C-rich	Low_complexity	Low_complexity
chr11	65625575	65625976
chr11	65728887	65729288	chr11	65729283	65729454 (CGG)n	Simple_repeat	Simple_repeat
chr11	65769513	65769914
chr11	65819454	65819855
chr11	66025051	66025452
chr11	66035720	66036121	chr11	66035712	66035804 MIRc	SINE	MIR
chr11	66112393	66112794
chr11	66138701	66139102
chr11	66206329	66206730
chr11	66726322	66726723	chr11	66726469	66726546 MIRb	SINE	MIR
chr11	66726322	66726723	chr11	66726619	66727294 LTR34	LTR	ERV1
chr11	67085065	67085466
chr11	67195644	67196045	chr11	67195984	67196016 GC_rich	Low_complexity	Low_complexity
chr11	67374064	67374465
chr11	68671154	68671555
chr11	69489939	69490340
chr11	71639515	71639916
chr11	71791563	71791964
chr11	71823513	71823914
chr11	72145457	72145858	chr11	72145851	72146154 AluSx1	SINE	Alu
chr11	72433176	72433577	chr11	72433196	72433241 (GA)n	Simple_repeat	Simple_repeat
chr11	72433176	72433577	chr11	72433241	72433295 (TG)n	Simple_repeat	Simple_repeat
chr11	72504943	72505344
chr11	73309433	73309834	chr11	73309555	73309616 (TC)n	Simple_repeat	Simple_repeat
chr11	73358372	73358773
chr11	73498957	73499358	chr11	73499301	73499383 MIR3	SINE	MIR
chr11	73661827	73662228
chr11	73881856	73882257
chr11	74109658	74110059
chr11	74303390	74303791	chr11	74303252	74303479 MER44A	DNA	TcMar-Tigger
chr11	74660036	74660437
chr11	75110283	75110684	chr11	75110251	75110398 MIR3	SINE	MIR
chr11	76091981	76092382	chr11	76091935	76092020 GC_rich	Low_complexity	Low_complexity
chr11	76155764	76156165
chr11	77348663	77349064	chr11	77349049	77349602 LTR8	LTR	ERV1
chr11	77531690	77532091	chr11	77531732	77531758 (CCG)n	Simple_repeat	Simple_repeat
chr11	77705940	77706341
chr11	77790752	77791153
chr11	77899581	77899982
chr11	82782822	82783223
chr11	82996902	82997303
chr11	85339418	85339819
chr11	86012992	86013393	chr11	86012849	86013059 MIRc	SINE	MIR
chr11	93394557	93394958	chr11	93394269	93394611 AluJb	SINE	Alu
chr11	93517289	93517690
chr11	94706524	94706925
chr11	95657054	95657455
chr11	105892962	105893363
chr11	107436268	107436669
chr11	111957411	111957812
chr11	113644334	113644735
chr11	113746442	113746843
chr11	114309926	114310327
chr11	117186805	117187206	chr11	117186840	117186865 GC_rich	Low_complexity	Low_complexity
chr11	117186805	117187206	chr11	117187189	117187468 L2b	LINE	L2
chr11	117198289	117198690	chr11	117198184	117198317 AluSx	SINE	Alu
chr11	118868650	118869051
chr11	118888893	118889294
chr11	120894573	120894974
chr11	125439053	125439454
chr11	125772935	125773336
chr11	130786193	130786594
chr11	134123140	134123541
chr12	498619	499020	chr12	498714	498756 (CGAGG)n	Simple_repeat	Simple_repeat
chr12	510452	510853
chr12	861353	861754	chr12	861365	861407 polypyrimidi	Low_complexity	Low_complexity
chr12	1058669	1059070
chr12	1099967	1100368	chr12	1100100	1100133 (TG)n	Simple_repeat	Simple_repeat
chr12	1099967	1100368	chr12	1100231	1100259 GC_rich	Low_complexity	Low_complexity
chr12	1099967	1100368	chr12	1100305	1100351 GC_rich	Low_complexity	Low_complexity
chr12	1799842	1800243	chr12	1800161	1800228 (CGG)n	Simple_repeat	Simple_repeat
chr12	2904883	2905284	chr12	2905026	2905075 GC_rich	Low_complexity	Low_complexity

chr12	4758107	4758508
chr12	6602203	6602604
chr12	6641548	6641949 chr12	6641360	6641576 MER20	DNA		hAT-Charlie	
chr12	6772210	6772611
chr12	6798374	6798775
chr12	6961454	6961855
chr12	9102423	9102824
chr12	9217379	9217780 chr12	9217739	9217769 (C)n	Simple_repeat		Simple_repeat	
chr12	9217379	9217780 chr12	9217769	9219265 MER52D	LTR		ERV1	
chr12	11323977	11324378
chr12	12419868	12420269
chr12	12764525	12764926
chr12	12966061	12966462
chr12	13197111	13197512 chr12	13197068	13197165 MIRb	SINE		MIR	
chr12	22198925	22199326 chr12	22199102	22199144 GC_rich	Low_complexity		Low_complexity	
chr12	22777897	22778298
chr12	26111150	26111551 chr12	26111421	26111461 GC_rich	Low_complexity		Low_complexity	
chr12	26111150	26111551 chr12	26111483	26111515 GC_rich	Low_complexity		Low_complexity	
chr12	31811929	31812330 chr12	31811889	31811953 L2a	LINE		L2	
chr12	31811929	31812330 chr12	31812113	31812167 GC_rich	Low_complexity		Low_complexity	
chr12	31881956	31882357
chr12	32831910	32832311
chr12	32908616	32909017 chr12	32908991	32909118 MIR	SINE		MIR	
chr12	34175184	34175585 chr12	34175185	34175215 (T)n	Simple_repeat		Simple_repeat	
chr12	38710327	38710728
chr12	46384436	46384837
chr12	46663035	46663436
chr12	48099634	48100035
chr12	48499853	48500254
chr12	48551072	48551473
chr12	49110465	49110866
chr12	49245821	49246222
chr12	49449748	49450149
chr12	49961712	49962113
chr12	50135191	50135592
chr12	50505490	50505891
chr12	50794387	50794788
chr12	51441936	51442337
chr12	51477254	51477655
chr12	53574260	53574661 chr12	53574261	53574302 GC_rich	Low_complexity		Low_complexity	
chr12	53661806	53662207
chr12	53693300	53693701
chr12	53834882	53835283 chr12	53834780	53835035 L2	LINE		L2	
chr12	53834882	53835283 chr12	53835136	53835284 L2c	LINE		L2	
chr12	53845565	53845966 chr12	53845934	53845989 (CCCG)n	Simple_repeat		Simple_repeat	
chr12	53895126	53895527
chr12	54121199	54121600 chr12	54121569	54121804 MIRc	SINE		MIR	
chr12	54582703	54583104
chr12	56223238	56223639 chr12	56222948	56223260 AluSg	SINE		Alu	
chr12	56435508	56435909
chr12	56498062	56498463 chr12	56498343	56498423 (CTCG)n	Simple_repeat		Simple_repeat	
chr12	56509947	56510348 chr12	56509922	56510018 (GAAA)n	Simple_repeat		Simple_repeat	
chr12	56511754	56512155
chr12	56546126	56546527 chr12	56546465	56546507 (TG)n	Simple_repeat		Simple_repeat	
chr12	56660419	56660820 chr12	56660068	56660428 MLT2A2	LTR		ERV1	
chr12	56709954	56710355 chr12	56710333	56710616 AluSg7	SINE		Alu	
chr12	56727389	56727790
chr12	57081741	57082142
chr12	57118932	57119333
chr12	57146025	57146426
chr12	57623210	57623611
chr12	57881610	57882011 chr12	57881349	57881657 AluSx	SINE		Alu	
chr12	57916439	57916840 chr12	57916461	57916484 GC_rich	Low_complexity		Low_complexity	
chr12	57916439	57916840 chr12	57916495	57916567 (CGG)n	Simple_repeat		Simple_repeat	
chr12	57916439	57916840 chr12	57916812	57916973 C-rich	Low_complexity		Low_complexity	
chr12	57940869	57941270
chr12	58329755	58330156
chr12	62653921	62654322
chr12	62860403	62860804
chr12	64797850	64798251 chr12	64798189	64798213 GC_rich	Low_complexity		Low_complexity	
chr12	64797850	64798251 chr12	64798246	64798279 (CGG)n	Simple_repeat		Simple_repeat	
chr12	65672251	65672652 chr12	65672225	65672336 GA-rich	Low_complexity		Low_complexity	
chr12	65672251	65672652 chr12	65672341	65672389 GC_rich	Low_complexity		Low_complexity	
chr12	65672251	65672652 chr12	65672576	65672616 (TCTCCC)n	Simple_repeat		Simple_repeat	
chr12	66524340	66524741
chr12	66562966	66563367
chr12	67662439	67662840
chr12	69080529	69080930
chr12	69864001	69864402
chr12	70637003	70637404 chr12	70637293	70637316 GC_rich	Low_complexity		Low_complexity	
chr12	75905352	75905753 chr12	75905734	75905806 L2c	LINE		L2	
chr12	77157855	77158256
chr12	88429048	88429449
chr12	88535815	88536216
chr12	93835568	93835969
chr12	93861066	93861467 chr12	93860788	93861071 AluJr	SINE		Alu	
chr12	94656064	94656465 chr12	94655980	94656181 MIR3	SINE		MIR	
chr12	95467135	95467536
chr12	95611305	95611706
chr12	95867642	95868043
chr12	96252528	96252929
chr12	96429274	96429675
chr12	99038544	99038945
chr12	102455720	102456121
chr12	102513711	102514112
chr12	104323339	104323740
chr12	104350813	104351214
chr12	104359324	104359725
chr12	104458129	104458530
chr12	105501216	105501617
chr12	106639548	106639949 chr12	106639366	106639672 AluSx	SINE		Alu	
chr12	107167774	107168175
chr12	109490141	109490542 chr12	109490426	109490459 (CGG)n	Simple_repeat		Simple_repeat	
chr12	109531073	109531474
chr12	109915067	109915468

chr12	110151157	110151558	chr12	110151184	110151288	MIRb	SINE	MIR
chr12	111021055	111021456	chr12	111021084	111021105	GC_rich	Low_complexity	Low_complexity
chr12	111051724	111052125
chr12	112123639	112124040
chr12	112820133	112820534	chr12	112820131	112820164	(CCG)n	Simple_repeat	Simple_repeat
chr12	112847237	112847638	chr12	112847532	112847828	AluSx	SINE	Alu
chr12	117175668	117176069	chr12	117175719	117175742	GC_rich	Low_complexity	Low_complexity
chr12	117175668	117176069	chr12	117175809	117175830	GC_rich	Low_complexity	Low_complexity
chr12	118814061	118814462
chr12	120632332	120632733
chr12	120739956	120740357	chr12	120739891	120739957	L1MA3	LINE	L1
chr12	120907329	120907730	chr12	120907371	120907464	(CCG)n	Simple_repeat	Simple_repeat
chr12	120933518	120933919	chr12	120933730	120933783	LTR71B	LTR	ERV1
chr12	120971916	120972317	chr12	120972033	120972067	(CAA)n	Simple_repeat	Simple_repeat
chr12	120971916	120972317	chr12	120972297	120972319	GC_rich	Low_complexity	Low_complexity
chr12	121454151	121454552	chr12	121454465	121454589	MIR3	SINE	MIR
chr12	121790129	121790530
chr12	122326325	122326726	chr12	122326411	122326463	L2c	LINE	L2
chr12	122985404	122985805	chr12	122985739	122986030	AluJr	SINE	Alu
chr12	123011314	123011715
chr12	123868132	123868533	chr12	123867846	123868159	AluSp	SINE	Alu
chr12	124086398	124086799
chr12	124457109	124457510	chr12	124457130	124457227	GC_rich	Low_complexity	Low_complexity
chr12	124457109	124457510	chr12	124457305	124457371	GC_rich	Low_complexity	Low_complexity
chr12	133405331	133405732
chr12	133532718	133533119	chr12	133533114	133533291	AluJo	SINE	Alu
chr12	133562662	133563063
chr12	133613683	133614084	chr12	133613425	133613715	AluSx1	SINE	Alu
chr12	133656646	133657047
chr12	133706695	133707096
chr12	133757851	133758252	chr12	133757762	133757906	L1MEg	LINE	L1
chr13	21141181	21141582	chr13	21141177	21141271	C-rich	Low_complexity	Low_complexity
chr13	21476698	21477099	chr13	21477067	21477115	GC_rich	Low_complexity	Low_complexity
chr13	21750575	21750976
chr13	25496882	25497283
chr13	25875438	25875839
chr13	26796287	26796688
chr13	26827858	26828259
chr13	28712114	28712515
chr13	30424653	30425054	chr13	30424715	30424739	(CGG)n	Simple_repeat	Simple_repeat
chr13	30881084	30881485
chr13	31191780	31192181
chr13	31736322	31736723
chr13	33112798	33113199
chr13	41345177	41345578
chr13	41706798	41707199
chr13	41768532	41768933	chr13	41768887	41768988	AluJb	SINE	Alu
chr13	41837517	41837918
chr13	46038802	46039203	chr13	46039152	46039214	(CGG)n	Simple_repeat	Simple_repeat
chr13	47371266	47371667
chr13	50366894	50367295
chr13	50656012	50656413
chr13	52157806	52158207
chr13	53226723	53227124	chr13	53226990	53227074	(CGG)n	Simple_repeat	Simple_repeat
chr13	79980187	79980588
chr13	92001073	92001474	chr13	92001201	92001272	GC_rich	Low_complexity	Low_complexity
chr13	98085955	98086356	chr13	98086249	98086338	GC_rich	Low_complexity	Low_complexity
chr13	98085955	98086356	chr13	98086354	98086379	(CGG)n	Simple_repeat	Simple_repeat
chr13	100153367	100153768
chr13	101240891	101241292	chr13	101241070	101241092	GC_rich	Low_complexity	Low_complexity
chr13	103046726	103047127
chr13	103426028	103426429	chr13	103426148	103426191	GC_rich	Low_complexity	Low_complexity
chr13	103451241	103451642
chr13	107220275	107220676
chr13	111267718	111268119
chr13	111365090	111365491
chr13	111521975	111522376
chr13	111566850	111567251	chr13	111566861	111566892	GC_rich	Low_complexity	Low_complexity
chr13	113242279	113242680
chr13	113343958	113344359	chr13	113344180	113344280	G-rich	Low_complexity	Low_complexity
chr13	113862762	113863163	chr13	113863036	113863059	GC_rich	Low_complexity	Low_complexity
chr13	113951250	113951651
chr13	114103454	114103855
chr13	114144954	114145355
chr13	115079728	115080129	chr13	115079743	115079765	GC_rich	Low_complexity	Low_complexity
chr14	20811435	20811836
chr14	21457925	21458326	chr14	21457885	21457929	(CCCCG)n	Simple_repeat	Simple_repeat
chr14	21571625	21572026
chr14	23398650	23399051	chr14	23398909	23398982	tRNA-Arg-CG	tRNA	tRNA
chr14	23540555	23540956
chr14	23564572	23564973
chr14	23789962	23790363
chr14	24020837	24021238	chr14	24020861	24020935	(TCC)n	Simple_repeat	Simple_repeat
chr14	24025032	24025433
chr14	24657969	24658370
chr14	24701612	24702013
chr14	24911906	24912307
chr14	31091258	31091659	chr14	31091547	31091582	(CAG)n	Simple_repeat	Simple_repeat
chr14	31495506	31495907
chr14	32030429	32030830	chr14	32030275	32030481	MIRc	SINE	MIR
chr14	35183621	35184022
chr14	35451931	35452332
chr14	35591510	35591911
chr14	35761403	35761804
chr14	36295221	36295622
chr14	37641090	37641491
chr14	45431118	45431519
chr14	45722518	45722919
chr14	50052902	50053303	chr14	50053297	50053597	7SLRNA	srpRNA	srpRNA
chr14	50100999	50101400	chr14	50101150	50101171	GC_rich	Low_complexity	Low_complexity
chr14	51134925	51135326
chr14	53173785	53174186
chr14	54907904	54908305	chr14	54907870	54907911	GC_rich	Low_complexity	Low_complexity
chr14	54907904	54908305	chr14	54908290	54908784	L2c	LINE	L2
chr14	55878377	55878778

chr14	58711313	58711714	chr14	58711287	58711316	AT_rich	Low_complexity	Low_complexity
chr14	59655112	59655513
chr14	60558598	60558999
chr14	64108998	64109399
chr14	64970153	64970554
chr14	65453686	65454087
chr14	65569084	65569485	chr14	65569094	65569126	(AGGGGG)n	Simple_repeat	Simple_repeat
chr14	65569084	65569485	chr14	65569155	65569206	(CTCA)n	Simple_repeat	Simple_repeat
chr14	65569084	65569485	chr14	65569443	65569475	(G)n	Simple_repeat	Simple_repeat
chr14	68141381	68141782	chr14	68141589	68141622	GC_rich	Low_complexity	Low_complexity
chr14	68162330	68162731
chr14	68286246	68286647	chr14	68285962	68286274	AluY	SINE	Alu
chr14	69658050	69658451
chr14	69865178	69865579
chr14	70826273	70826674
chr14	70883622	70884023	chr14	70883994	70884623	MER67C	LTR	ERV1
chr14	73493798	73494199
chr14	73525034	73525435
chr14	73957519	73957920	chr14	73957679	73957702	GC_rich	Low_complexity	Low_complexity
chr14	74111415	74111816
chr14	75179609	75180010
chr14	75469434	75469835
chr14	75530382	75530783
chr14	75593574	75593975
chr14	75643170	75643571
chr14	77787105	77787506	chr14	77787168	77787292	(CGGGG)n	Simple_repeat	Simple_repeat
chr14	77923831	77924232
chr14	78174183	78174584
chr14	78227380	78227781
chr14	78266196	78266597
chr14	82000281	82000682
chr14	90797875	90798276	chr14	90797858	90797908	MIRc	SINE	MIR
chr14	90863087	90863488	chr14	90863467	90863492	(CAG)n	Simple_repeat	Simple_repeat
chr14	92506283	92506684
chr14	93214909	93215310	chr14	93215255	93215309	MER5B	DNA	hAT-Charlie
chr14	95623798	95624199
chr14	96000797	96001198
chr14	96968435	96968836
chr14	97263382	97263783
chr14	98444268	98444669
chr14	102430546	102430947	chr14	102430573	102430631	L2b	LINE	L2
chr14	102430546	102430947	chr14	102430761	102430795	GC_rich	Low_complexity	Low_complexity
chr14	102430546	102430947	chr14	102430828	102430862	GC_rich	Low_complexity	Low_complexity
chr14	102553767	102554168	chr14	102554102	102554186	CR1_Mam	LINE	CR1
chr14	102829163	102829564
chr14	103800130	103800531
chr14	103995247	103995648	chr14	103995177	103995320	FLAM_C	SINE	Alu
chr14	104095284	104095685	chr14	104095456	104095522	(CGGGG)n	Simple_repeat	Simple_repeat
chr14	104387714	104388115	chr14	104388046	104388159	MER81	DNA	hAT-Blackjack
chr14	104394423	104394824	chr14	104394641	104394665	GC_rich	Low_complexity	Low_complexity
chr14	105487531	105487932	chr14	105487626	105487670	(CCCCG)n	Simple_repeat	Simple_repeat
chr15	25684007	25684408	chr15	25684201	25684223	GC_rich	Low_complexity	Low_complexity
chr15	31195894	31196295
chr15	34393890	34394291
chr15	34502035	34502436	chr15	34501985	34502051	GC_rich	Low_complexity	Low_complexity
chr15	34502035	34502436	chr15	34502265	34502291	GC_rich	Low_complexity	Low_complexity
chr15	34630137	34630538
chr15	352621806	35262207
chr15	35280363	35280764
chr15	36871332	36871733
chr15	38746159	38746560	chr15	38746130	38746179	AT_rich	Low_complexity	Low_complexity
chr15	40452969	40453370
chr15	40986742	40987143	chr15	40987101	40987186	FAM	SINE	Alu
chr15	41099512	41099913	chr15	41099900	41099938	G-rich	Low_complexity	Low_complexity
chr15	41408694	41409095
chr15	41694497	41694898
chr15	41836259	41836660	chr15	41836645	41836947	AluX1	SINE	Alu
chr15	43213065	43213466
chr15	44067609	44068010
chr15	44093020	44093421	chr15	44093173	44093266	L1ME5	LINE	L1
chr15	44116749	44117150
chr15	45694271	45694672
chr15	48623458	48623859
chr15	49447650	49448051	chr15	49447645	49447667	GC_rich	Low_complexity	Low_complexity
chr15	49913027	49913428
chr15	50647167	50647568
chr15	50716392	50716793
chr15	52043541	52043942	chr15	52043754	52043785	GC_rich	Low_complexity	Low_complexity
chr15	52121605	52122006
chr15	52821151	52821552	chr15	52821102	52821162	(CGGGG)n	Simple_repeat	Simple_repeat
chr15	52821151	52821552	chr15	52821256	52821329	(CCG)n	Simple_repeat	Simple_repeat
chr15	52861208	52861609
chr15	55488910	55489311
chr15	55700375	55700776
chr15	57025624	57026025	chr15	57025627	57025651	GC_rich	Low_complexity	Low_complexity
chr15	57025624	57026025	chr15	57025689	57025725	(GGA)n	Simple_repeat	Simple_repeat
chr15	59949533	59949934
chr15	59981290	59981691	chr15	59981563	59981611	(CGG)n	Simple_repeat	Simple_repeat
chr15	63481417	63481818
chr15	64386014	64386415
chr15	64455331	64455732
chr15	64648229	64648630	chr15	64648291	64648347	G-rich	Low_complexity	Low_complexity
chr15	64679830	64680231
chr15	64995403	64995804	chr15	64995425	64995464	(CCG)n	Simple_repeat	Simple_repeat
chr15	65477788	65478189
chr15	65809817	65810218
chr15	65903256	65903657
chr15	66161537	66161938	chr15	66161732	66161753	GC_rich	Low_complexity	Low_complexity
chr15	67834747	67835148	chr15	67834873	67834895	GC_rich	Low_complexity	Low_complexity
chr15	67834747	67835148	chr15	67835059	67835096	(CCG)n	Simple_repeat	Simple_repeat
chr15	68569436	68569837	chr15	68569392	68569469	L2a	LINE	L2
chr15	69744174	69744575	chr15	69744493	69744688	MIRb	SINE	MIR
chr15	72668227	72668628
chr15	74611018	74611419
chr15	74753347	74753748	chr15	74753217	74753364	MIRb	SINE	MIR

chr15	74908096	74908497	chr15	74908259	74908285	(CGG)n	Simple_repeat	Simple_repeat
chr15	75182167	75182568	chr15	75181678	75182250	L2a	LINE	L2
chr15	75315653	75316054	chr15	75315646	75315669	(A)n	Simple_repeat	Simple_repeat
chr15	75639716	75640117
chr15	75918057	75918458
chr15	77712847	77713248
chr15	78369927	78370328	chr15	78369908	78370079	C-rich	Low_complexity	Low_complexity
chr15	78369927	78370328	chr15	78370130	78370153	GC_rich	Low_complexity	Low_complexity
chr15	78369927	78370328	chr15	78370248	78370367	L1ME2z	LINE	L1
chr15	79164946	79165347	chr15	79165058	79165097	GC_rich	Low_complexity	Low_complexity
chr15	79164946	79165347	chr15	79165133	79165170	GC_rich	Low_complexity	Low_complexity
chr15	82554867	82555268	chr15	82555046	82555074	GC_rich	Low_complexity	Low_complexity
chr15	85143927	85144328	chr15	85143883	85143982	MIR3	SINE	MIR
chr15	85174432	85174833
chr15	85259203	85259604
chr15	89010413	89010814
chr15	89877933	89878334	chr15	89878303	89878376	tRNA-Arg-CG	tRNA	tRNA
chr15	90437095	90437496
chr15	90895180	90895581
chr15	93447294	93447695	chr15	93447518	93447541	GC_rich	Low_complexity	Low_complexity
chr15	100273201	100273602
chr15	101142648	101143049
chr15	101835247	101835648
chr15	102192513	102192914	chr15	102192585	102192609	GC_rich	Low_complexity	Low_complexity
chr16	279287	279688	chr16	279682	279815	MIR	SINE	MIR
chr16	577411	577812	chr16	577734	577785	GC_rich	Low_complexity	Low_complexity
chr16	577411	577812	chr16	577806	577865	GC_rich	Low_complexity	Low_complexity
chr16	686227	686628
chr16	734161	734562	chr16	734118	734256	C-rich	Low_complexity	Low_complexity
chr16	1401692	1402093
chr16	1524941	1525342
chr16	2009290	2009691	chr16	2009282	2009394	L2a	LINE	L2
chr16	2009290	2009691	chr16	2009420	2009474	GC_rich	Low_complexity	Low_complexity
chr16	2021826	2022227
chr16	2034006	2034407	chr16	2033987	2034113	C-rich	Low_complexity	Low_complexity
chr16	2034006	2034407	chr16	2034317	2034342	GC_rich	Low_complexity	Low_complexity
chr16	2097682	2098083	chr16	2098032	2098067	GC_rich	Low_complexity	Low_complexity
chr16	2205488	2205889	chr16	2205825	2205860	GC_rich	Low_complexity	Low_complexity
chr16	2255819	2256220	chr16	2255831	2255973	MIRc	SINE	MIR
chr16	2653229	2653630
chr16	2732315	2732716	chr16	2732577	2732619	GC_rich	Low_complexity	Low_complexity
chr16	2802169	2802570
chr16	2827196	2827597	chr16	2827187	2827373	(CCCCG)n	Simple_repeat	Simple_repeat
chr16	3074113	3074514
chr16	3162341	3162742
chr16	3184759	3185160	chr16	3185099	3185140	(CGGGGG)n	Simple_repeat	Simple_repeat
chr16	3285149	3285550	chr16	3285518	3285929	C-rich	Low_complexity	Low_complexity
chr16	3314385	3314786
chr16	3332712	3333113	chr16	3333095	3333220	MER5A	DNA	hAT-Charlie
chr16	3450867	3451268
chr16	4321716	4322117	chr16	4321999	4322020	GC_rich	Low_complexity	Low_complexity
chr16	4321716	4322117	chr16	4322039	4322078	GC_rich	Low_complexity	Low_complexity
chr16	4475365	4475766
chr16	4588430	4588831	chr16	4588562	4588594	GC_rich	Low_complexity	Low_complexity
chr16	4664754	4665155	chr16	4664975	4665006	GC_rich	Low_complexity	Low_complexity
chr16	4674520	4674921
chr16	4784102	4784503
chr16	4817058	4817459	chr16	4817412	4817449	MLT1D	LTR	ERV1-MaLR
chr16	4817058	4817459	chr16	4817449	4817717	AluSp	SINE	Alu
chr16	4818688	4819089	chr16	4819034	4819113	MIRb	SINE	MIR
chr16	4897115	4897516
chr16	8891417	8891818
chr16	9183837	9184238	chr16	9183784	9184125	L2a	LINE	L2
chr16	11038147	11038548
chr16	11679548	11679949
chr16	12009775	12010176
chr16	12070286	12070687	chr16	12070548	12070574	GC_rich	Low_complexity	Low_complexity
chr16	12070286	12070687	chr16	12070600	12070648	(CGG)n	Simple_repeat	Simple_repeat
chr16	14013865	14014266
chr16	15149887	15150288	chr16	15149882	15149952	(CCCCG)n	Simple_repeat	Simple_repeat
chr16	15736941	15737342	chr16	15736869	15737028	C-rich	Low_complexity	Low_complexity
chr16	15736941	15737342	chr16	15737119	15737147	GC_rich	Low_complexity	Low_complexity
chr16	15981911	15982312	chr16	15981682	15981950	AluJr	SINE	Alu
chr16	15981911	15982312	chr16	15981965	15982044	MIRb	SINE	MIR
chr16	18801474	18801875	chr16	18801872	18802161	AluSc	SINE	Alu
chr16	18812717	18813118
chr16	18937597	18937998
chr16	19534934	19535335
chr16	19729345	19729746
chr16	20817543	20817944
chr16	21513419	21513820
chr16	21964504	21964905
chr16	22019151	22019552	chr16	22019443	22019555	GC_rich	Low_complexity	Low_complexity
chr16	22308487	22308888	chr16	22308460	22308542	tRNA-Leu-CT	tRNA	tRNA
chr16	22448174	22448575	chr16	22448562	22448622	CT-rich	Low_complexity	Low_complexity
chr16	23160658	23161059	chr16	23160615	23160661	GC_rich	Low_complexity	Low_complexity
chr16	23160658	23161059	chr16	23160740	23160775	GC_rich	Low_complexity	Low_complexity
chr16	23160658	23161059	chr16	23160808	23160830	GC_rich	Low_complexity	Low_complexity
chr16	23568807	23569208	chr16	23569094	23569125	GC_rich	Low_complexity	Low_complexity
chr16	23607413	23607814
chr16	23652548	23652949
chr16	23689882	23690283
chr16	24740638	24741039	chr16	24740622	24740642	(T)n	Simple_repeat	Simple_repeat
chr16	24740638	24741039	chr16	24740989	24741044	(CGG)n	Simple_repeat	Simple_repeat
chr16	25042644	25043045	chr16	25042654	25042726	MIRb	SINE	MIR
chr16	25122727	25123128
chr16	25268839	25269240	chr16	25269202	25269265	GC_rich	Low_complexity	Low_complexity
chr16	28565026	28565427	chr16	28565040	28565062	(TTTA)n	Simple_repeat	Simple_repeat
chr16	28857708	28858109
chr16	28874577	28874978	chr16	28874569	28874615	C-rich	Low_complexity	Low_complexity
chr16	28891054	28891455
chr16	28961785	28962186	chr16	28961637	28961906	AluSz	SINE	Alu
chr16	30007277	30007678
chr16	30103107	30103508
chr16	30198333	30198734

chr16	30366401	30366802
chr16	30546055	30546456
chr16	30569531	30569932
chr16	30596860	30597261	chr16	30596901	30596930	GC_rich	Low_complexity	Low_complexity	
chr16	30709193	30709594	chr16	30709505	30709533	(TGG)n	Simple_repeat	Simple_repeat	
chr16	30797807	30798208	chr16	30797923	30797947	GC_rich	Low_complexity	Low_complexity	
chr16	30797807	30798208	chr16	30798141	30798226	C-rich	Low_complexity	Low_complexity	
chr16	30908313	30908714
chr16	30933750	30934151
chr16	31045514	31045915	chr16	31045867	31046036	MIR3	SINE	MIR	
chr16	31085430	31085831	chr16	31085809	31085870	C-rich	Low_complexity	Low_complexity	
chr16	31106082	31106483	chr16	31106370	31106675	AluX	SINE	Alu	
chr16	31119475	31119876
chr16	31128789	31129190
chr16	31453964	31454365
chr16	31470491	31470892
chr16	33963043	33963444	chr16	33962496	33964361	SSU-rRNA_Hi	rRNA	rRNA	
chr16	46917960	46918361	chr16	46918263	46918295	GC_rich	Low_complexity	Low_complexity	
chr16	47007423	47007824
chr16	53468102	53468503	chr16	53468357	53468399	GC_rich	Low_complexity	Low_complexity	
chr16	53737693	53738094
chr16	54963033	54963434
chr16	56485215	56485616
chr16	56763827	56764228	chr16	56763919	56763971	C-rich	Low_complexity	Low_complexity	
chr16	57728511	57728912	chr16	57728411	57728544	FLAM_C	SINE	Alu	
chr16	58426548	58426949
chr16	58718495	58718896
chr16	67260751	67261152
chr16	67313224	67313625	chr16	67313195	67313233	GC_rich	Low_complexity	Low_complexity	
chr16	67313224	67313625	chr16	67313361	67313396	GC_rich	Low_complexity	Low_complexity	
chr16	67596071	67596472	chr16	67596329	67596401	C-rich	Low_complexity	Low_complexity	
chr16	67700500	67700901	chr16	67700398	67700577	C-rich	Low_complexity	Low_complexity	
chr16	67840446	67840847
chr16	67875704	67876105
chr16	67880513	67880914
chr16	68118817	68119218	chr16	68119096	68119119	GC_rich	Low_complexity	Low_complexity	
chr16	68344652	68345053
chr16	68482481	68482882	chr16	68482876	68482911	MIR3	SINE	MIR	
chr16	68572915	68573316
chr16	69364324	69364725
chr16	69419746	69420147	chr16	69419758	69419794	GC_rich	Low_complexity	Low_complexity	
chr16	69419746	69420147	chr16	69420113	69420423	AluSp	SINE	Alu	
chr16	69458348	69458749
chr16	70285682	70286083
chr16	70473063	70473464	chr16	70473003	70473083	C-rich	Low_complexity	Low_complexity	
chr16	70488190	70488591
chr16	72127638	72128039
chr16	74330478	74330879
chr16	75019013	75019414	chr16	75019372	75019656	AluSq2	SINE	Alu	
chr16	75182116	75182517
chr16	75467292	75467693	chr16	75467576	75468022	MER82	DNA	TcMar-Tigger	
chr16	75657040	75657441	chr16	75657418	75657541	AluX	SINE	Alu	
chr16	75681433	75681834
chr16	78133041	78133442
chr16	83841367	83841768
chr16	85045018	85045419
chr16	85833077	85833478	chr16	85833379	85833416	GC_rich	Low_complexity	Low_complexity	
chr16	87984455	87984856
chr16	89387246	89387647
chr16	89626880	89627281	chr16	89627277	89627313	GC_rich	Low_complexity	Low_complexity	
chr16	89753104	89753505	chr16	89753335	89753371	GC_rich	Low_complexity	Low_complexity	
chr16	90039043	90039444	chr16	90039246	90039283	GC_rich	Low_complexity	Low_complexity	
chr17	617967	618368
chr17	655248	655649
chr17	685379	685780
chr17	900078	900479
chr17	1359411	1359812	chr17	1359439	1359483	GC_rich	Low_complexity	Low_complexity	
chr17	1419969	1420370
chr17	1619665	1620066
chr17	1732967	1733368
chr17	2239555	2239956
chr17	2614872	2615273	chr17	2614795	2614890	C-rich	Low_complexity	Low_complexity	
chr17	3116917	3117318	chr17	3116832	3117051	MLT1J1	LTR	ERV1-MaLR	
chr17	3116917	3117318	chr17	3117076	3117185	MLT1J1	LTR	ERV1-MaLR	
chr17	3116917	3117318	chr17	3117225	3117409	L2	LINE	L2	
chr17	3539751	3540152
chr17	3571943	3572344
chr17	4634412	4634813	chr17	4634205	4634481	AluX1	SINE	Alu	
chr17	4699207	4699608	chr17	4698992	4699233	AluSg	SINE	Alu	
chr17	4843181	4843582
chr17	5323226	5323627	chr17	5323248	5323312	L2	LINE	L2	
chr17	5372153	5372554	chr17	5372496	5372810	AluSp	SINE	Alu	
chr17	5389900	5390301
chr17	6543940	6544341
chr17	6554756	6555157
chr17	6915709	6916110
chr17	7122942	7123343
chr17	7142851	7143252	chr17	7142819	7142880	CT-rich	Low_complexity	Low_complexity	
chr17	7155577	7155978
chr17	7212053	7212454
chr17	7218505	7218906	chr17	7218461	7218518	GC_rich	Low_complexity	Low_complexity	
chr17	7218505	7218906	chr17	7218569	7218599	GC_rich	Low_complexity	Low_complexity	
chr17	7338426	7338827
chr17	7387444	7387845
chr17	7591422	7591823	chr17	7591167	7591442	L2a	LINE	L2	
chr17	7760432	7760833
chr17	8286465	8286866
chr17	12692560	12692961
chr17	15587428	15587829	chr17	15587665	15587716	AluYb8	SINE	Alu	
chr17	15587428	15587829	chr17	15587755	15588052	AluX1	SINE	Alu	
chr17	15602789	15603190
chr17	16120332	16120733
chr17	16284187	16284588
chr17	16342058	16342459	chr17	16341933	16342115	MIRb	SINE	MIR	
chr17	16557008	16557409

chr17	17494862	17495263	
chr17	17942412	17942813	chr17	17942719	17942785	(TG)n	Simple_repeat	Simple_repeat
chr17	17990989	17991390
chr17	18128477	18128878	chr17	18128294	18128512	L2b	LINE	L2
chr17	18128477	18128878	chr17	18128449	18128525	MIR	SINE	MIR
chr17	18128477	18128878	chr17	18128830	18128973	GC_rich	Low_complexity	Low_complexity
chr17	18218174	18218575
chr17	18585376	18585777
chr17	19881016	19881417
chr17	21117393	21117794	chr17	21117623	21117651	GC_rich	Low_complexity	Low_complexity
chr17	21904676	21905077
chr17	22020520	22020921
chr17	26554581	26554982
chr17	26662375	26662776
chr17	26684346	26684747
chr17	27046708	27047109	chr17	27046650	27046811	AluY	SINE	Alu
chr17	27181826	27182227
chr17	27279228	27279629
chr17	27919900	27920301	chr17	27920228	27920310	GC_rich	Low_complexity	Low_complexity
chr17	28804133	28804534
chr17	30263568	30263969	chr17	30263309	30263605	AluSx3	SINE	Alu
chr17	30669005	30669406
chr17	30676954	30677355
chr17	30771247	30771648	chr17	30771498	30771563	(CGG)n	Simple_repeat	Simple_repeat
chr17	30771247	30771648	chr17	30771640	30771671	GC_rich	Low_complexity	Low_complexity
chr17	33905424	33905825
chr17	35969247	35969648
chr17	36003196	36003597
chr17	36349798	36350199	chr17	36349859	36349884	(TCCA)n	Simple_repeat	Simple_repeat
chr17	36452952	36453353
chr17	36858455	36858856	chr17	36858604	36858642	GC_rich	Low_complexity	Low_complexity
chr17	36858455	36858856	chr17	36858834	36858987	MIRb	SINE	MIR
chr17	36908650	36909051	chr17	36908591	36908653	L2a	LINE	L2
chr17	36981396	36981797
chr17	37009837	37010238
chr17	37123615	37124016
chr17	37617458	37617859
chr17	37844114	37844515
chr17	38083723	38084124	chr17	38084108	38084255	MIRc	SINE	MIR
chr17	38136850	38137251	chr17	38137239	38137260	GC_rich	Low_complexity	Low_complexity
chr17	38210542	38210943
chr17	38256834	38257235
chr17	38296564	38296965	chr17	38296570	38296683	(CA)n	Simple_repeat	Simple_repeat
chr17	38296564	38296965	chr17	38296869	38296939	(CGG)n	Simple_repeat	Simple_repeat
chr17	38443656	38444057	chr17	38443641	38443719	MIRb	SINE	MIR
chr17	39844831	39845232
chr17	40021508	40021909	chr17	40021579	40021621	(CCG)n	Simple_repeat	Simple_repeat
chr17	40021508	40021909	chr17	40021707	40021742	GC_rich	Low_complexity	Low_complexity
chr17	40075172	40075573	chr17	40075434	40075458	GC_rich	Low_complexity	Low_complexity
chr17	40117877	40118278	chr17	40117977	40118172	MIRb	SINE	MIR
chr17	40273235	40273636	chr17	40273157	40273304	(CTGGG)n	Simple_repeat	Simple_repeat
chr17	40306920	40307321	chr17	40307267	40307560	AluSx	SINE	Alu
chr17	40713982	40714383
chr17	40925259	40925660
chr17	40950572	40950973
chr17	41150205	41150606
chr17	41277917	41278318
chr17	41322495	41322896
chr17	41465998	41466399	chr17	41466224	41466581	L2c	LINE	L2
chr17	41561153	41561554
chr17	42092204	42092605	chr17	42092588	42092749	MIRb	SINE	MIR
chr17	42147804	42148205	chr17	42147815	42147857	(T)n	Simple_repeat	Simple_repeat
chr17	42264221	42264622
chr17	42275583	42275984
chr17	42580794	42581195	chr17	42581143	42581206	MIR	SINE	MIR
chr17	42766955	42767356	chr17	42767284	42767436	MIRb	SINE	MIR
chr17	43138346	43138747
chr17	43225544	43225945	chr17	43225855	43225962	G-rich	Low_complexity	Low_complexity
chr17	43238982	43239383
chr17	44271336	44271737	chr17	44271519	44271542	GC_rich	Low_complexity	Low_complexity
chr17	45266347	45266748
chr17	45401153	45401554	chr17	45401302	45401330	GC_rich	Low_complexity	Low_complexity
chr17	45569675	45570076
chr17	45726613	45727014	chr17	45726473	45726623	MIR3	SINE	MIR
chr17	45908722	45909123	chr17	45908379	45908775	L2b	LINE	L2
chr17	45918432	45918833
chr17	45973090	45973491
chr17	46124961	46125362
chr17	46178697	46179098	chr17	46179030	46179331	AluSx1	SINE	Alu
chr17	46184898	46185299
chr17	46908125	46908526	chr17	46907850	46908169	AluJb	SINE	Alu
chr17	46969572	46969973
chr17	47492211	47492612
chr17	47865762	47866163
chr17	48450345	48450746
chr17	48785080	48785481	chr17	48785030	48785110	GC_rich	Low_complexity	Low_complexity
chr17	48796743	48797144
chr17	49230678	49231079
chr17	53045799	53046200
chr17	56084777	56085178
chr17	56429370	56429771
chr17	57643332	57643733
chr17	57784622	57785023
chr17	58754504	58754905
chr17	61851011	61851412
chr17	61904501	61904902
chr17	61920348	61920749	chr17	61920720	61921017	AluSq2	SINE	Alu
chr17	62492723	62493124
chr17	62502267	62502668
chr17	65241038	65241439	chr17	65241115	65241166	GC_rich	Low_complexity	Low_complexity
chr17	65241038	65241439	chr17	65241351	65241414	C-rich	Low_complexity	Low_complexity
chr17	65713838	65714239
chr17	66031359	66031760	chr17	66031567	66031657	C-rich	Low_complexity	Low_complexity
chr17	66243778	66244179	chr17	66244120	66244204	(CGCGG)n	Simple_repeat	Simple_repeat
chr17	67410591	67410992

chr17	70588882	70589283	chr17	70588990	70589030	(CGGGG)n	Simple_repeat	Simple_repeat
chr17	73285473	73285874
chr17	73663152	73663553
chr17	73780567	73780968
chr17	73841380	73841781
chr17	73851406	73851807
chr17	73937010	73937411
chr17	74068495	74068896	chr17	74068483	74068548	(CCG)n	Simple_repeat	Simple_repeat
chr17	74553579	74553980	chr17	74553971	74554126	MIRc	SINE	MIR
chr17	74733821	74734222
chr17	76210099	76210500	chr17	76209828	76210125	AluSq2	SINE	Alu
chr17	77005709	77006110	chr17	77005640	77005737	G-rich	Low_complexity	Low_complexity
chr17	77005709	77006110	chr17	77005777	77005816	(GGCTG)n	Simple_repeat	Simple_repeat
chr17	77005709	77006110	chr17	77005946	77005996	T-rich	Low_complexity	Low_complexity
chr17	78518443	78518844
chr17	79670164	79670565
chr17	79829156	79829557	chr17	79829090	79829158	C-rich	Low_complexity	Low_complexity
chr17	79884385	79884786
chr17	79980905	79981306
chr17	80009586	80009987	chr17	80009722	80009749	GC_rich	Low_complexity	Low_complexity
chr17	80009586	80009987	chr17	80009852	80009889	GC_rich	Low_complexity	Low_complexity
chr17	80023585	80023986	chr17	80023551	80023661	GC_rich	Low_complexity	Low_complexity
chr17	80316861	80317262
chr17	80709665	80710066	chr17	80709486	80709744	(CCCCG)n	Simple_repeat	Simple_repeat
chr18	108030	108431	chr18	105673	111670	BSR/Beta	Satellite	Satellite
chr18	3447403	3447804
chr18	9102352	9102753
chr18	9475146	9475547
chr18	9913452	9913853
chr18	12948277	12948678
chr18	13726379	13726780	chr18	13726482	13726510	GC_rich	Low_complexity	Low_complexity
chr18	22006381	22006782
chr18	29522868	29523269	chr18	29523261	29523294	(CGGGGG)n	Simple_repeat	Simple_repeat
chr18	32870130	32870531
chr18	32923778	32924179	chr18	32923814	32923841	GC_rich	Low_complexity	Low_complexity
chr18	33552471	33552872
chr18	34408607	34409008	chr18	34408976	34409014	GC_rich	Low_complexity	Low_complexity
chr18	43684066	43684467
chr18	46065130	46065531	chr18	46065460	46065515	C-rich	Low_complexity	Low_complexity
chr18	46986877	46987278	chr18	46987202	46987515	AluSc	SINE	Alu
chr18	47018627	47019028
chr18	54305731	54306132	chr18	54305837	54305900	G-rich	Low_complexity	Low_complexity
chr18	54318666	54319067
chr18	56806786	56807187
chr18	57026278	57026679
chr18	60382108	60382509
chr18	61089587	61089988
chr18	67872969	67873370	chr18	67873236	67873258	GC_rich	Low_complexity	Low_complexity
chr18	71815483	71815884
chr18	77439292	77439693
chr19	507746	508147
chr19	531400	531801	chr19	531702	531730	GC_rich	Low_complexity	Low_complexity
chr19	531400	531801	chr19	531787	531835	(CGG)n	Simple_repeat	Simple_repeat
chr19	633428	633829	chr19	633799	633962	FRAM	SINE	Alu
chr19	892918	893319	chr19	892811	893001	C-rich	Low_complexity	Low_complexity
chr19	1021133	1021534	chr19	1021520	1021627	U6	snRNA	snRNA
chr19	1068116	1068517
chr19	1095352	1095753
chr19	1241473	1241874	chr19	1241387	1241531	FLAM_C	SINE	Alu
chr19	1241473	1241874	chr19	1241784	1241945	(CCG)n	Simple_repeat	Simple_repeat
chr19	1275206	1275607	chr19	1275561	1275605	(CTG)n	Simple_repeat	Simple_repeat
chr19	1383610	1384011	chr19	1383561	1383636	tRNA-Asn-AA	tRNA	tRNA
chr19	1407186	1407587	chr19	1407281	1407331	(CAGC)n	Simple_repeat	Simple_repeat
chr19	1407186	1407587	chr19	1407538	1407590	GC_rich	Low_complexity	Low_complexity
chr19	1490312	1490713
chr19	1592278	1592679	chr19	1592364	1592375	GC_rich	Low_complexity	Low_complexity
chr19	1592278	1592679	chr19	1592375	1592422	(CACG)n	Simple_repeat	Simple_repeat
chr19	1592278	1592679	chr19	1592422	1592465	GC_rich	Low_complexity	Low_complexity
chr19	1592278	1592679	chr19	1592648	1592732	(CCG)n	Simple_repeat	Simple_repeat
chr19	1905104	1905505
chr19	2236627	2237028
chr19	2269146	2269547
chr19	2328424	2328825
chr19	2427451	2427852
chr19	2456844	2457245	chr19	2456832	2456857	GC_rich	Low_complexity	Low_complexity
chr19	2456844	2457245	chr19	2456958	2456984	(CCGCG)n	Simple_repeat	Simple_repeat
chr19	2456844	2457245	chr19	2457083	2457134	MIR	SINE	MIR
chr19	2456844	2457245	chr19	2457200	2457228	L1MB7	LINE	L1
chr19	2456844	2457245	chr19	2457228	2457521	AluSz	SINE	Alu
chr19	2785331	2785732	chr19	2785542	2785605	(CGG)n	Simple_repeat	Simple_repeat
chr19	2819616	2820017
chr19	3185644	3186045	chr19	3185968	3186022	(CCG)n	Simple_repeat	Simple_repeat
chr19	3505902	3506303	chr19	3506252	3506289	GC_rich	Low_complexity	Low_complexity
chr19	3761523	3761924
chr19	3762441	3762842
chr19	4065843	4066244	chr19	4065794	4065942	GC_rich	Low_complexity	Low_complexity
chr19	4182322	4182723
chr19	4246767	4247168
chr19	4304355	4304756	chr19	4304377	4304480	MIRc	SINE	MIR
chr19	4304355	4304756	chr19	4304621	4304656	GC_rich	Low_complexity	Low_complexity
chr19	4304355	4304756	chr19	4304699	4304726	GC_rich	Low_complexity	Low_complexity
chr19	4723640	4724041	chr19	4723569	4723720	(CGGGG)n	Simple_repeat	Simple_repeat
chr19	4791412	4791813
chr19	5680458	5680859
chr19	5690070	5690471	chr19	5689983	5690079	MIR	SINE	MIR
chr19	5790464	5790865
chr19	5977877	5978278
chr19	6361339	6361740	chr19	6361050	6361347	AluSg4	SINE	Alu
chr19	6393033	6393434
chr19	6424674	6425075	chr19	6424661	6424688	GC_rich	Low_complexity	Low_complexity
chr19	6424674	6425075	chr19	6424755	6424776	(CGG)n	Simple_repeat	Simple_repeat
chr19	6737754	6738155
chr19	7580707	7581108	chr19	7580510	7580790	(CAGAGA)n	Simple_repeat	Simple_repeat
chr19	7580707	7581108	chr19	7580925	7580946	GC_rich	Low_complexity	Low_complexity
chr19	7580707	7581108	chr19	7581025	7581204	G-rich	Low_complexity	Low_complexity

chr19	7600352	7600753
chr19	8386083	8386484
chr19	9250807	9251208	chr19	9250588	9250889	L1MC4	LINE		L1
chr19	9250807	9251208	chr19	9250982	9251125	LTR33B	LTR		ERV1
chr19	9938364	9938765
chr19	10197113	10197514
chr19	10305580	10305981	chr19	10305934	10306060	MIRb	SINE		MIR
chr19	10363047	10363448
chr19	10399781	10400182
chr19	10443915	10444316
chr19	10811968	10812369
chr19	10827901	10828302
chr19	10947045	10947446	chr19	10947427	10947544	MIR	SINE		MIR
chr19	11639755	11640156
chr19	12780184	12780585
chr19	12834659	12835060
chr19	12845280	12845681	chr19	12845328	12845418	C-rich	Low_complexity		Low_complexity
chr19	12845280	12845681	chr19	12845669	12845980	AluSp	SINE		Alu
chr19	12917104	12917505
chr19	12992050	12992451
chr19	13056493	13056894	chr19	13056664	13056685	GC_rich	Low_complexity		Low_complexity
chr19	13056493	13056894	chr19	13056836	13056864	GC_rich	Low_complexity		Low_complexity
chr19	13105518	13105919	chr19	13105289	13105558	AluJb	SINE		Alu
chr19	13105518	13105919	chr19	13105623	13105801	(TG)n	Simple_repeat		Simple_repeat
chr19	13885012	13885413
chr19	14016794	14017195
chr19	14117321	14117722
chr19	14141840	14142241
chr19	14229031	14229432	chr19	14229098	14229127	GC_rich	Low_complexity		Low_complexity
chr19	14229031	14229432	chr19	14229348	14229443	MIR	SINE		MIR
chr19	14607978	14608379	chr19	14607882	14608004	L2b	LINE		L2
chr19	14682674	14683075
chr19	14800613	14801014	chr19	14800905	14800936	(CGCGG)n	Simple_repeat		Simple_repeat
chr19	15217791	15218192	chr19	15218137	15218197	(CGGGG)n	Simple_repeat		Simple_repeat
chr19	15490484	15490885
chr19	16606887	16607288
chr19	16738863	16739264	chr19	16738860	16738944	GC_rich	Low_complexity		Low_complexity
chr19	17378049	17378450
chr19	17416440	17416841
chr19	17419951	17420352	chr19	17419779	17420043	AluSq2	SINE		Alu
chr19	17516003	17516404
chr19	17530561	17530962
chr19	17970318	17970719	chr19	17970423	17970444	GC_rich	Low_complexity		Low_complexity
chr19	18043354	18043755
chr19	18304141	18304542
chr19	18334801	18335202	chr19	18334842	18334955	L2c	LINE		L2
chr19	18385705	18386106	chr19	18385665	18385740	L2c	LINE		L2
chr19	18385705	18386106	chr19	18386077	18386373	AluSz	SINE		Alu
chr19	18392402	18392803	chr19	18392303	18392413	GC_rich	Low_complexity		Low_complexity
chr19	18392402	18392803	chr19	18392633	18392674	GC_rich	Low_complexity		Low_complexity
chr19	18392402	18392803	chr19	18392738	18392806	GC_rich	Low_complexity		Low_complexity
chr19	18633274	18633675	chr19	18633631	18633798	AluJb	SINE		Alu
chr19	19030126	19030527
chr19	19249182	19249583
chr19	19431270	19431671	chr19	19431670	19431733	(CGG)n	Simple_repeat		Simple_repeat
chr19	19495916	19496317
chr19	19887120	19887521
chr19	28284699	28285100
chr19	34663100	34663501	chr19	34663338	34663379	(CCG)n	Simple_repeat		Simple_repeat
chr19	35168268	35168669
chr19	35224831	35225232
chr19	35263999	35264400
chr19	35417658	35418059
chr19	36036296	36036697	chr19	36036609	36036638	GC_rich	Low_complexity		Low_complexity
chr19	36208273	36208674
chr19	36236195	36236596
chr19	36239050	36239451	chr19	36239007	36239095	MIRb	SINE		MIR
chr19	36249013	36249414
chr19	36485902	36486303
chr19	36630646	36631047
chr19	36705412	36705813
chr19	36869900	36870301	chr19	36870008	36870036	GC_rich	Low_complexity		Low_complexity
chr19	36869900	36870301	chr19	36870290	36870592	AluJo	SINE		Alu
chr19	36909380	36909781
chr19	36980320	36980721
chr19	37019406	37019807
chr19	37064035	37064436
chr19	37157578	37157979
chr19	37178199	37178600
chr19	37341471	37341872	chr19	37341314	37341565	MER31B	LTR		ERV1
chr19	37569071	37569472
chr19	37825286	37825687
chr19	37861741	37862142
chr19	38085508	38085909
chr19	38210441	38210842
chr19	38270079	38270480
chr19	38397580	38397981
chr19	38714737	38715138	chr19	38714906	38714935	GC_rich	Low_complexity		Low_complexity
chr19	38714737	38715138	chr19	38715067	38715208	(CA)n	Simple_repeat		Simple_repeat
chr19	38720285	38720686	chr19	38720243	38720309	GC_rich	Low_complexity		Low_complexity
chr19	38720285	38720686	chr19	38720365	38720388	GC_rich	Low_complexity		Low_complexity
chr19	38720285	38720686	chr19	38720435	38720465	GC_rich	Low_complexity		Low_complexity
chr19	38754435	38754836	chr19	38754318	38754540	L2b	LINE		L2
chr19	38754435	38754836	chr19	38754550	38754638	L2b	LINE		L2
chr19	38754435	38754836	chr19	38754743	38754816	L2b	LINE		L2
chr19	39390220	39390621
chr19	39616467	39616868
chr19	39881550	39881951
chr19	39936021	39936422
chr19	40476821	40477222
chr19	40502753	40503154
chr19	40561962	40562363
chr19	40596673	40597074
chr19	40697095	40697496	chr19	40697115	40697136	GC_rich	Low_complexity		Low_complexity
chr19	40697095	40697496	chr19	40697418	40697519	GC_rich	Low_complexity		Low_complexity

chr19	40791381	40791782	chr19	40791705	40791850	MIR	SINE	MIR
chr19	40948988	40949389
chr19	41084361	41084762
chr19	41256883	41257284
chr19	42007357	42007758	chr19	42007381	42007780	L1PA12	LINE	L1
chr19	42388186	42388587	chr19	42388237	42388261	GC_rich	Low_complexity	Low_complexity
chr19	42463376	42463777	chr19	42463495	42463524	GC_rich	Low_complexity	Low_complexity
chr19	42746729	42747130
chr19	44123415	44123816
chr19	44145487	44145888	chr19	44145837	44145945	MIR3	SINE	MIR
chr19	44331227	44331628
chr19	44439271	44439672
chr19	44455113	44455514
chr19	44488070	44488471
chr19	44506832	44507233
chr19	44529230	44529631
chr19	44555846	44556247
chr19	44576060	44576461
chr19	44598250	44598651
chr19	44617256	44617657
chr19	44645476	44645877
chr19	44668923	44669324
chr19	44716449	44716850	chr19	44716519	44716544	(T)n	Simple_repeat	Simple_repeat
chr19	44763815	44764216	chr19	44763641	44763950	Alu5g	SINE	Alu
chr19	44809017	44809418
chr19	44860672	44861073
chr19	44905571	44905972
chr19	44952507	44952908
chr19	45004427	45004828
chr19	45393600	45394001
chr19	45908594	45908995	chr19	45908657	45908701	MIR3	SINE	MIR
chr19	46010480	46010881
chr19	46234043	46234444
chr19	46366379	46366780	chr19	46366371	46366391	(CCG)n	Simple_repeat	Simple_repeat
chr19	46389927	46390328
chr19	47287884	47288285
chr19	47354079	47354480	chr19	47354474	47354595	AluJr4	SINE	Alu
chr19	47551860	47552261	chr19	47552226	47552354	T-rich	Low_complexity	Low_complexity
chr19	47734889	47735290
chr19	48111235	48111636	chr19	48111147	48111244	L2a	LINE	L2
chr19	48111235	48111636	chr19	48111237	48111345	L2b	LINE	L2
chr19	48673604	48674005	chr19	48673959	48674123	(CGGG)n	Simple_repeat	Simple_repeat
chr19	48866270	48866671	chr19	48866264	48866383	MIRb	SINE	MIR
chr19	48948861	48949262
chr19	48965603	48966004
chr19	49122430	49122831
chr19	49148009	49148410	chr19	49148029	49148151	AluSq10	SINE	Alu
chr19	49248459	49248860
chr19	49403092	49403493	chr19	49403009	49403194	AluJr	SINE	Alu
chr19	49469019	49469420
chr19	49588724	49589125
chr19	49618176	49618577
chr19	49954473	49954874	chr19	49954278	49954585	AluY	SINE	Alu
chr19	49956539	49956940
chr19	50000478	50000879
chr19	50030835	50031236	chr19	50030541	50030854	AluSp	SINE	Alu
chr19	50030835	50031236	chr19	50030856	50030908	(TTTTG)n	Simple_repeat	Simple_repeat
chr19	50083724	50084125
chr19	50145068	50145469	chr19	50145441	50145471	(CCCCG)n	Simple_repeat	Simple_repeat
chr19	50168970	50169371
chr19	50179999	50180400
chr19	50314627	50315028	chr19	50315005	50315082	MSR1	Satellite	Satellite
chr19	50321274	50321675
chr19	50353757	50354158	chr19	50353911	50353939	GC_rich	Low_complexity	Low_complexity
chr19	50432476	50432877
chr19	50529048	50529449
chr19	50553963	50554364
chr19	50879413	50879814
chr19	50887390	50887791
chr19	50979554	50979955
chr19	51014348	51014749
chr19	51142386	51142787
chr19	51152787	51153188
chr19	51275616	51276017	chr19	51275421	51275751	AluJb	SINE	Alu
chr19	51275616	51276017	chr19	51275751	51275987	MLT1J	LTR	ERVL-MaLR
chr19	51275616	51276017	chr19	51275987	51276043	MLT1H	LTR	ERVL-MaLR
chr19	51611536	51611937
chr19	52074198	52074599
chr19	52097573	52097974
chr19	52193866	52194267	chr19	52193928	52194065	MIR3	SINE	MIR
chr19	52430169	52430570
chr19	52489908	52490309
chr19	54023953	54024354
chr19	54040721	54041122
chr19	54057086	54057487
chr19	54605905	54606306
chr19	54618548	54618949
chr19	54694205	54694606
chr19	55628973	55629374	chr19	55628968	55629001	GC_rich	Low_complexity	Low_complexity
chr19	55677262	55677663
chr19	55690348	55690749
chr19	55770127	55770528
chr19	55791334	55791735
chr19	55987670	55988071
chr19	56110791	56111192	chr19	56110899	56111010	C-rich	Low_complexity	Low_complexity
chr19	56632695	56633096
chr19	56652167	56652568
chr19	57106414	57106815	chr19	57106402	57106485	C-rich	Low_complexity	Low_complexity
chr19	57106414	57106815	chr19	57106532	57106566	(CTCGG)n	Simple_repeat	Simple_repeat
chr19	57751684	57752085
chr19	57791520	57791921
chr19	57862333	57862734
chr19	57874504	57874905	chr19	57874731	57874760	(CGTG)n	Simple_repeat	Simple_repeat
chr19	57900945	57901346
chr19	57922239	57922640

chr19	57946396	57946797
chr19	57988835	57989236
chr19	57998839	57999240	chr19	57998894	57998968 (CACCAT)n	Simple_repeat	Simple_repeat
chr19	58090157	58090558	chr19	58090540	58091091 MER4D1	LTR	ERV1
chr19	58110975	58111376
chr19	58125324	58125725
chr19	58144253	58144654	chr19	58144246	58144319 Tigger2b_Pri	DNA	TcMar-Tigger
chr19	58257891	58258292
chr19	58280724	58281125
chr19	58326178	58326579	chr19	58326499	58326647 FRAM	SINE	Alu
chr19	58360907	58361308	chr19	58361003	58361048 L2c	LINE	L2
chr19	58427851	58428252	chr19	58428178	58428500 AluY	SINE	Alu
chr19	58694510	58694911
chr19	58740017	58740418
chr19	58790109	58790510
chr19	58838125	58838526
chr19	58873632	58874033	chr19	58873697	58873771 (TGAA)n	Simple_repeat	Simple_repeat
chr19	58892240	58892641
chr19	58898391	58898792
chr19	58919769	58920170
chr19	58962720	58963121
chr19	58978086	58978487
chr19	58987205	58987606
chr19	59031082	59031483
chr19	59066162	59066563
chr19	59084310	59084711
chr19	59086562	59086963	chr19	59086262	59086572 AluYa5	SINE	Alu
chr2	3622602	3623003
chr2	9695790	9696191
chr2	11484538	11484939	chr2	11484590	11484626 GC_rich	Low_complexity	Low_complexity
chr2	11484538	11484939	chr2	11484660	11484827 (CCG)n	Simple_repeat	Simple_repeat
chr2	11484538	11484939	chr2	11484837	11484860 (CCCCG)n	Simple_repeat	Simple_repeat
chr2	11484538	11484939	chr2	11484868	11484956 CT-rich	Low_complexity	Low_complexity
chr2	18741773	18742174
chr2	21022658	21023059
chr2	24270227	24270628
chr2	24299030	24299431
chr2	25016063	25016464
chr2	26100203	26100604
chr2	26205448	26205849	chr2	26205443	26205518 G-rich	Low_complexity	Low_complexity
chr2	26568512	26568913
chr2	27070577	27070978	chr2	27070814	27070836 GC_rich	Low_complexity	Low_complexity
chr2	27255556	27255957	chr2	27255768	27255797 GC_rich	Low_complexity	Low_complexity
chr2	27255556	27255957	chr2	27255948	27255969 GC_rich	Low_complexity	Low_complexity
chr2	27579664	27580065
chr2	27593167	27593568
chr2	27603475	27603876	chr2	27603483	27603581 GC_rich	Low_complexity	Low_complexity
chr2	27886448	27886849
chr2	27994571	27994972	chr2	27994965	27995109 MIR3	SINE	MIR
chr2	28113050	28113451
chr2	32288290	32288691
chr2	32390610	32391011	chr2	32390572	32390673 MIRb	SINE	MIR
chr2	32852952	32853353
chr2	37193585	37193986	chr2	37193821	37193859 GC_rich	Low_complexity	Low_complexity
chr2	37193585	37193986	chr2	37193891	37193919 GC_rich	Low_complexity	Low_complexity
chr2	38152467	38152868
chr2	38892830	38893231
chr2	39005151	39005552
chr2	39102849	39103250
chr2	39187902	39188303
chr2	43823002	43823403
chr2	44000957	44001358	chr2	44000953	44000974 AT_rich	Low_complexity	Low_complexity
chr2	44223234	44223635
chr2	44394712	44395113	chr2	44394516	44394760 L2a	LINE	L2
chr2	46925671	46926072
chr2	53994565	53994966
chr2	54013850	54014251
chr2	54557852	54558253
chr2	54784627	54785028
chr2	54950396	54950797
chr2	55459285	55459686
chr2	55496205	55496606	chr2	55496584	55496725 T-rich	Low_complexity	Low_complexity
chr2	55845818	55846219	chr2	55845772	55845956 AluSc8	SINE	Alu
chr2	55920752	55921153
chr2	58274232	58274633
chr2	60983241	60983642
chr2	63815801	63816202
chr2	64246338	64246739	chr2	64246359	64246472 (CCG)n	Simple_repeat	Simple_repeat
chr2	64246338	64246739	chr2	64246563	64246623 GC_rich	Low_complexity	Low_complexity
chr2	64371497	64371898
chr2	64751252	64751653
chr2	65357172	65357573
chr2	68384532	68384933
chr2	68694334	68694735
chr2	69240317	69240718
chr2	69870914	69871315
chr2	70314333	70314734	chr2	70314644	70314716 C-rich	Low_complexity	Low_complexity
chr2	70417691	70418092
chr2	71295547	71295948
chr2	73053021	73053422
chr2	73298735	73299136
chr2	73441157	73441558
chr2	73461236	73461637
chr2	73964365	73964766	chr2	73964703	73964823 MIR3	SINE	MIR
chr2	74681920	74682321	chr2	74681806	74681963 L2c	LINE	L2
chr2	74699623	74700024
chr2	74710050	74710451
chr2	74756759	74757160
chr2	75873688	75874089	chr2	75873485	75873781 L2b	LINE	L2
chr2	84686435	84686836
chr2	85581634	85582035
chr2	85829740	85830141
chr2	86332531	86332932
chr2	86421885	86422286
chr2	88990878	88991279	chr2	88991260	88991302 GC_rich	Low_complexity	Low_complexity

chr21	43299338	43299739	chr21	43299497	43299608	G-rich	Low_complexity	Low_complexity
chr21	45079146	45079547	chr21	45078896	45079205	AluJr	SINE	Alu
chr21	45079146	45079547	chr21	45079415	45079438	GC_rich	Low_complexity	Low_complexity
chr21	46221552	46221953
chr21	46359691	46360092	chr21	46360034	46360098	GC_rich	Low_complexity	Low_complexity
chr21	46962217	46962618	chr21	46962362	46962399	GC_rich	Low_complexity	Low_complexity
chr21	47878412	47878813	chr21	47878459	47878494	GC_rich	Low_complexity	Low_complexity
chr22	17640048	17640449	chr22	17640042	17640089	GC_rich	Low_complexity	Low_complexity
chr22	18560462	18560863
chr22	19132083	19132484
chr22	19466887	19467288
chr22	19842403	19842804
chr22	20067264	20067665
chr22	20104703	20105104
chr22	20748170	20748571
chr22	20861629	20862030
chr22	21271471	21271872	chr22	21271654	21271685	GC_rich	Low_complexity	Low_complexity
chr22	21336262	21336663
chr22	21921786	21922187	chr22	21921814	21921918	L2b	LINE	L2
chr22	21921786	21922187	chr22	21921757	21921804	L2a	LINE	L2
chr22	22020065	22020466
chr22	22337008	22337409
chr22	24059351	24059752
chr22	24951714	24952115
chr22	29137702	29138103
chr22	29168455	29168856	chr22	29168411	29168508	MIR	SINE	MIR
chr22	30162815	30163216
chr22	30752442	30752843	chr22	30752393	30752541	MER5A1	DNA	hAT-Charlie
chr22	30819845	30820246
chr22	30987989	30988390
chr22	31743327	31743728	chr22	31743717	31743855	MIRc	SINE	MIR
chr22	31795235	31795636
chr22	36903006	36903407
chr22	36925335	36925736	chr22	36925645	36925755	MIRb	SINE	MIR
chr22	37447552	37447953	chr22	37447628	37447681	(CGGGG)n	Simple_repeat	Simple_repeat
chr22	37447552	37447953	chr22	37447824	37447856	GC_rich	Low_complexity	Low_complexity
chr22	38245166	38245567	chr22	38244999	38245287	AluSp	SINE	Alu
chr22	38349479	38349880
chr22	39898172	39898573
chr22	40766360	40766761	chr22	40766061	40766379	AluSx1	SINE	Alu
chr22	41215017	41215418
chr22	41600972	41601373	chr22	41600983	41601045	L2a	LINE	L2
chr22	41682155	41682556
chr22	41844513	41844914	chr22	41844472	41844523	C-rich	Low_complexity	Low_complexity
chr22	41844513	41844914	chr22	41844759	41844899	MIRb	SINE	MIR
chr22	41864483	41864884
chr22	42342158	42342559
chr22	42915576	42915977
chr22	42977832	42978233
chr22	43010819	43011220
chr22	43485275	43485676	chr22	43485407	43485428	GC_rich	Low_complexity	Low_complexity
chr22	43583503	43583904	chr22	43583855	43584015	BLACKJACK	DNA	hAT-Blackjack
chr22	44208145	44208546
chr22	44351034	44351435
chr22	46692505	46692906
chr22	47158578	47158979
chr22	50624057	50624458	chr22	50623959	50624156	MIRc	SINE	MIR
chr22	50624057	50624458	chr22	50624167	50624205	GC_rich	Low_complexity	Low_complexity
chr22	50624057	50624458	chr22	50624311	50624350	(CCCCG)n	Simple_repeat	Simple_repeat
chr22	50624057	50624458	chr22	50624455	50624551	G-rich	Low_complexity	Low_complexity
chr22	50638205	50638606
chr22	50963509	50963910
chr22	51020766	51021167	chr22	51020832	51020891	GC_rich	Low_complexity	Low_complexity
chr3	3221187	3221588
chr3	4344785	4345186	chr3	4345170	4345204	GC_rich	Low_complexity	Low_complexity
chr3	4534730	4535131	chr3	4535084	4535136	(GGA)n	Simple_repeat	Simple_repeat
chr3	9004970	9005371
chr3	9404613	9405014
chr3	9438548	9438949
chr3	9958599	9959000
chr3	11313771	11314172
chr3	12598242	12598643
chr3	12882865	12883266
chr3	14166202	14166603
chr3	14219693	14220094
chr3	14692899	14693300
chr3	15106650	15107051
chr3	15373616	15374017	chr3	15373790	15373853	CT-rich	Low_complexity	Low_complexity
chr3	15643309	15643710
chr3	23958363	23958764
chr3	25469471	25469872
chr3	28390395	28390796	chr3	28390635	28390663	GC_rich	Low_complexity	Low_complexity
chr3	32147726	32148127	chr3	32148050	32148082	GC_rich	Low_complexity	Low_complexity
chr3	33481999	33482400
chr3	37217678	37218079
chr3	37284987	37285388
chr3	39196005	39196406	chr3	39195993	39196174	L2c	LINE	L2
chr3	39424658	39425059
chr3	39448247	39448648
chr3	40350920	40351321	chr3	40351234	40351276	(TCC)n	Simple_repeat	Simple_repeat
chr3	40498478	40498879	chr3	40498717	40498742	(CACG)n	Simple_repeat	Simple_repeat
chr3	41240634	41241035
chr3	43147410	43147811
chr3	44802965	44803366
chr3	45429843	45430244	chr3	45429935	45429977	GC_rich	Low_complexity	Low_complexity
chr3	46037136	46037537
chr3	47018035	47018436	chr3	47018369	47018406	(CCCCG)n	Simple_repeat	Simple_repeat
chr3	47422221	47422622
chr3	47517259	47517660	chr3	47517313	47517356	(CGG)n	Simple_repeat	Simple_repeat
chr3	47517259	47517660	chr3	47517573	47517596	(CCGGG)n	Simple_repeat	Simple_repeat
chr3	47554707	47555108	chr3	47554481	47554781	AluSx	SINE	Alu
chr3	47844390	47844791
chr3	48229998	48230399
chr3	48282319	48282720
chr3	48481356	48481757	chr3	48481231	48481413	L2	LINE	L2

chr3	48936167	48936568	chr3	48936537	48937014	L2a	LINE	L2
chr3	48956099	48956500
chr3	49203644	49204045
chr3	49449386	49449787
chr3	49466525	49466926	chr3	49466847	49467152	AluSx1	SINE	Alu
chr3	49967115	49967516
chr3	49977246	49977647
chr3	50126135	50126536
chr3	50329750	50330151
chr3	50365571	50365972
chr3	50388333	50388734
chr3	50396915	50397316
chr3	50606644	50607045
chr3	51534108	51534509	chr3	51534132	51534168	(A)n	Simple_repeat	Simple_repeat
chr3	52007812	52008213
chr3	52029725	52030126
chr3	52188538	52188939	chr3	52188810	52188844	AluSp	SINE	Alu
chr3	52312401	52312802	chr3	52312377	52312472	(CGGGG)n	Simple_repeat	Simple_repeat
chr3	52312401	52312802	chr3	52312701	52312787	(CGGGG)n	Simple_repeat	Simple_repeat
chr3	52739888	52740289
chr3	53381480	53381881
chr3	57541589	57541990
chr3	57583209	57583610
chr3	57741759	57742160
chr3	58419652	58420053	chr3	58419926	58420018	L3	LINE	CR1
chr3	58419652	58420053	chr3	58420042	58420179	MIR	SINE	MIR
chr3	61235645	61236046	chr3	61235607	61235664	(CA)n	Simple_repeat	Simple_repeat
chr3	67048350	67048751
chr3	69135458	69135859
chr3	69788302	69788703
chr3	75834624	75835025
chr3	88198802	88199203
chr3	97483157	97483558
chr3	98241705	98242106	chr3	98241803	98241853	GC-rich	Low_complexity	Low_complexity
chr3	98241705	98242106	chr3	98242010	98242145	MIR3	SINE	MIR
chr3	98312309	98312710
chr3	99979414	99979815	chr3	99979587	99979610	GC-rich	Low_complexity	Low_complexity
chr3	100119774	100120175
chr3	101405321	101405722
chr3	101443563	101443964
chr3	101497850	101498251
chr3	112709552	112709953
chr3	112738070	112738471
chr3	113464890	113465291	chr3	113465097	113465129	GC-rich	Low_complexity	Low_complexity
chr3	113775245	113775646
chr3	119217107	119217508	chr3	119216948	119217116	AluSq	SINE	Alu
chr3	119395788	119396189	chr3	119395850	119395879	(CGGGG)n	Simple_repeat	Simple_repeat
chr3	119395788	119396189	chr3	119395884	119395972	G-rich	Low_complexity	Low_complexity
chr3	120461013	120461414	chr3	120461002	120461028	AT-rich	Low_complexity	Low_complexity
chr3	121468630	121469031
chr3	122233656	122234057
chr3	122785619	122786020	chr3	122785538	122785705	MIRb	SINE	MIR
chr3	122920599	122921000
chr3	123304110	123304511
chr3	124449099	124449500
chr3	125094018	125094419	chr3	125094091	125094146	(TCC)n	Simple_repeat	Simple_repeat
chr3	126422816	126423217	chr3	126423202	126423323	(CGGGG)n	Simple_repeat	Simple_repeat
chr3	127770910	127771311	chr3	127771156	127771182	(CGCGG)n	Simple_repeat	Simple_repeat
chr3	127770910	127771311	chr3	127771236	127771260	(CCGGG)n	Simple_repeat	Simple_repeat
chr3	127842597	127842998
chr3	128879906	128880307
chr3	128902733	128903134
chr3	129118083	129118484	chr3	129117915	129118219	AluSx1	SINE	Alu
chr3	129409184	129409585	chr3	129409328	129409481	MLT11	LTR	ERV1-MaLR
chr3	130745492	130745893
chr3	139062623	139063024
chr3	149470176	149470577	chr3	149470412	149470519	L2a	LINE	L2
chr3	149470176	149470577	chr3	149470528	149470707	MIR	SINE	MIR
chr3	150264346	150264747
chr3	151986606	151987007
chr3	155572130	155572531	chr3	155572394	155572417	GC-rich	Low_complexity	Low_complexity
chr3	156272891	156273292
chr3	156877793	156878194	chr3	156877772	156877800	(TCG)n	Simple_repeat	Simple_repeat
chr3	158288737	158289138
chr3	158362101	158362502
chr3	160117200	160117601
chr3	160472728	160473129
chr3	167452563	167452964
chr3	169939683	169940084
chr3	178865704	178866105
chr3	180319693	180320094
chr3	180630320	180630721	chr3	180630373	180630423	C-rich	Low_complexity	Low_complexity
chr3	183353121	183353522
chr3	183602506	183602907
chr3	183735612	183736013
chr3	183851823	183852224	chr3	183851726	183851863	L3b	LINE	CR1
chr3	183892379	183892780	chr3	183892288	183892406	L1M4b	LINE	L1
chr3	183892379	183892780	chr3	183892599	183892642	GC-rich	Low_complexity	Low_complexity
chr3	183903545	183903946
chr3	184016604	184017005
chr3	184054650	184055051
chr3	186524027	186524428
chr3	196466399	196466800
chr3	196669196	196669597
chr3	197676855	197677256
chr4	667888	668289	chr4	667798	667960	G-rich	Low_complexity	Low_complexity
chr4	699025	699426	chr4	698745	699213	(CCCTAA)n	Simple_repeat	Simple_repeat
chr4	699025	699426	chr4	699382	699537	(CCCCG)n	Simple_repeat	Simple_repeat
chr4	1283429	1283830	chr4	1283827	1283900	GC-rich	Low_complexity	Low_complexity
chr4	1722731	1723132	chr4	1722740	1722765	GC-rich	Low_complexity	Low_complexity
chr4	1722731	1723132	chr4	1722782	1722807	GC-rich	Low_complexity	Low_complexity
chr4	1857830	1858231	chr4	1857873	1857902	GC-rich	Low_complexity	Low_complexity
chr4	2243665	2244066	chr4	2244022	2244164	(CGGGG)n	Simple_repeat	Simple_repeat
chr4	2420415	2420816	chr4	2420399	2420533	GC-rich	Low_complexity	Low_complexity
chr4	2470340	2470741	chr4	2470617	2470640	GC-rich	Low_complexity	Low_complexity

chr4	2965048	2965449	chr4	2965357	2965397	GC_rich	Low_complexity	Low_complexity
chr4	3076215	3076616	chr4	3076330	3076379	GC_rich	Low_complexity	Low_complexity
chr4	3076215	3076616	chr4	3076603	3076667	(CAG)n	Simple_repeat	Simple_repeat
chr4	3534019	3534420
chr4	4543606	4544007
chr4	8160531	8160932	chr4	8160482	8160644	C-rich	Low_complexity	Low_complexity
chr4	8160531	8160932	chr4	8160921	8161105	MIR3	SINE	MIR
chr4	13629162	13629563	chr4	13629121	13629194	(CGG)n	Simple_repeat	Simple_repeat
chr4	18023619	18024020
chr4	25161856	25162257	chr4	25162105	25162140	(CAAAA)n	Simple_repeat	Simple_repeat
chr4	25314163	25314564
chr4	25915664	25916065	chr4	25915702	25915814	C-rich	Low_complexity	Low_complexity
chr4	26585448	26585849
chr4	41936905	41937306
chr4	47916623	47917024
chr4	48832882	48833283
chr4	52710758	52711159	chr4	52710955	52710976	GC_rich	Low_complexity	Low_complexity
chr4	56252190	56252591	chr4	56251940	56252287	MLT2C1	LTR	ERV_L
chr4	56252190	56252591	chr4	56252292	56252750	MLT1J	LTR	ERV_L-MaLR
chr4	57333566	57333967
chr4	57843622	57844023
chr4	57844832	57845233
chr4	69215588	69215989
chr4	71553959	71554360
chr4	88141601	88142002	chr4	88141700	88141729	GC_rich	Low_complexity	Low_complexity
chr4	88343542	88343943
chr4	89444687	89445088
chr4	99850165	99850566	chr4	99850450	99850470	(T)n	Simple_repeat	Simple_repeat
chr4	100484950	100485351
chr4	100815380	100815781	chr4	100815685	100815751	(CCCCG)n	Simple_repeat	Simple_repeat
chr4	104020845	104021246
chr4	106395051	106395452
chr4	106629690	106630091
chr4	108641354	108641755
chr4	109541516	109541917
chr4	119604721	119605122	chr4	119604494	119605003	LTR33A	LTR	ERV_L
chr4	119604721	119605122	chr4	119605050	119605167	L2a	LINE	L2
chr4	123844011	123844412
chr4	128886250	128886651
chr4	140004881	140005282
chr4	140222384	140222785
chr4	141445194	141445595
chr4	144105946	144106347	chr4	144105927	144105983	G-rich	Low_complexity	Low_complexity
chr4	144257050	144257451	chr4	144257279	144257321	(TCCC)n	Simple_repeat	Simple_repeat
chr4	144257050	144257451	chr4	144257404	144257471	G-rich	Low_complexity	Low_complexity
chr4	146101548	146101949
chr4	152020491	152020892
chr4	152681967	152682368
chr4	159593041	159593442
chr4	169931355	169931756	chr4	169931681	169931767	MER81	DNA	hAT-Blackjack
chr4	170678867	170679268
chr4	174255892	174256293
chr4	174291784	174292185	chr4	174291850	174291872	(A)n	Simple_repeat	Simple_repeat
chr4	184365488	184365889
chr4	184425262	184425663
chr4	186316960	186317361
chr4	186346957	186347358
chr4	190861721	190862122
chr5	218935	219336
chr5	271420	271821	chr5	271129	271426	AluIb	SINE	Alu
chr5	892785	893186	chr5	892772	892804	GC_rich	Low_complexity	Low_complexity
chr5	1345045	1345446	chr5	1344956	1345049	GC_rich	Low_complexity	Low_complexity
chr5	1345045	1345446	chr5	1345168	1345204	GC_rich	Low_complexity	Low_complexity
chr5	1633868	1634269	chr5	1633710	1633897	G-rich	Low_complexity	Low_complexity
chr5	1708002	1708403	chr5	1708131	1708164	(TG)n	Simple_repeat	Simple_repeat
chr5	1708002	1708403	chr5	1708190	1708349	(TG)n	Simple_repeat	Simple_repeat
chr5	5422160	5422561
chr5	6378310	6378711
chr5	6448276	6448677	chr5	6448090	6448732	(CA)n	Simple_repeat	Simple_repeat
chr5	6585022	6585423	chr5	6585124	6585528	MLT1C	LTR	ERV_L-MaLR
chr5	7869337	7869738
chr5	8458027	8458428
chr5	10250256	10250657
chr5	10352012	10352413
chr5	10353181	10353582
chr5	14664611	14665012	chr5	14664992	14665064	GC_rich	Low_complexity	Low_complexity
chr5	16465781	16466182
chr5	16616285	16616686
chr5	16935964	16936365
chr5	17216334	17216735
chr5	17386834	17387235	chr5	17386705	17386837	FLAM_C	SINE	Alu
chr5	17386834	17387235	chr5	17386839	17386893	(GGAA)n	Simple_repeat	Simple_repeat
chr5	31532131	31532532
chr5	32173505	32173906	chr5	32173864	32173913	GC_rich	Low_complexity	Low_complexity
chr5	32444693	32445094	chr5	32444926	32444968	GC_rich	Low_complexity	Low_complexity
chr5	32444693	32445094	chr5	32445015	32445044	GC_rich	Low_complexity	Low_complexity
chr5	32710462	32710863
chr5	32712241	32712642
chr5	33441020	33441421	chr5	33441413	33441577	MIR3	SINE	MIR
chr5	33984319	33984720
chr5	34007791	34008192
chr5	34657555	34657956
chr5	34839113	34839514
chr5	34914886	34915287	chr5	34915136	34915266	MIRb	SINE	MIR
chr5	34930104	34930505
chr5	35618036	35618437
chr5	36151935	36152336
chr5	36242295	36242696
chr5	37249105	37249506
chr5	37370725	37371126
chr5	37379115	37379516	chr5	37379044	37379208	AluSx	SINE	Alu
chr5	38557324	38557725
chr5	38846273	38846674
chr5	39073483	39073884
chr5	39424365	39424766	chr5	39424572	39424630	(CA)n	Simple_repeat	Simple_repeat

chr5	40679503	40679904	chr5	40679837	40679909	(CCCCG)n	Simple_repeat	Simple_repeat
chr5	40755891	40756292
chr5	40835201	40835602	chr5	40835582	40835614	(CTG)n	Simple_repeat	Simple_repeat
chr5	41509557	41509958
chr5	41870045	41870446
chr5	41904055	41904456
chr5	41925646	41926047
chr5	42757502	42757903
chr5	43017997	43018398
chr5	43042599	43043000
chr5	43066936	43067337
chr5	43121294	43121695
chr5	43192624	43193025	chr5	43192763	43192889	(CGTG)n	Simple_repeat	Simple_repeat
chr5	43312876	43313277
chr5	43483817	43484218
chr5	43603472	43603873
chr5	44808994	44809395
chr5	54528401	54528802	chr5	54528560	54528691	MIRb	SINE	MIR
chr5	54528401	54528802	chr5	54528695	54528813	MIRc	SINE	MIR
chr5	54603614	54604015	chr5	54603661	54603700	A-rich	Low_complexity	Low_complexity
chr5	55008027	55008428
chr5	56205699	56206100
chr5	56468410	56468811
chr5	57878617	57879018
chr5	61699638	61700039
chr5	64919957	64920358
chr5	68389644	68390045
chr5	68485208	68485609
chr5	70751246	70751647
chr5	74062798	74063199
chr5	74807503	74807904	chr5	74807455	74807532	C-rich	Low_complexity	Low_complexity
chr5	78280266	78280667	chr5	78280524	78280557	GC-rich	Low_complexity	Low_complexity
chr5	78908120	78908521	chr5	78908161	78908219	G-rich	Low_complexity	Low_complexity
chr5	81267789	81268190
chr5	81574065	81574466
chr5	85913485	85913886
chr5	87564535	87564936
chr5	89705682	89706083	chr5	89706033	89706201	MER5A	DNA	hAT-Charlie
chr5	93954151	93954552
chr5	94890606	94891007
chr5	98264981	98265382
chr5	102455664	102456065
chr5	102898439	102898840	chr5	102898509	102898547	GC-rich	Low_complexity	Low_complexity
chr5	107007741	107008142
chr5	110427859	110428260
chr5	111496320	111496721
chr5	112042827	112043228	chr5	112042844	112042977	L2c	LINE	L2
chr5	114598409	114598810
chr5	114961606	114962007	chr5	114961983	114962084	AluSz6	SINE	Alu
chr5	118406182	118406583
chr5	118787917	118788318
chr5	121297304	121297705	chr5	121297393	121297442	(CA)n	Simple_repeat	Simple_repeat
chr5	125936436	125936837
chr5	131892445	131892846
chr5	132112918	132113319	chr5	132112985	132113042	GC-rich	Low_complexity	Low_complexity
chr5	132361980	132362381	chr5	132362362	132362480	G-rich	Low_complexity	Low_complexity
chr5	133702700	133703101	chr5	133703059	133703364	AluSx	SINE	Alu
chr5	133747446	133747847
chr5	133968293	133968694
chr5	134181480	134181881
chr5	134734740	134735141	chr5	134734863	134734906	GC-rich	Low_complexity	Low_complexity
chr5	134734740	134735141	chr5	134734979	134735030	GC-rich	Low_complexity	Low_complexity
chr5	137514197	137514598
chr5	137673314	137673715
chr5	137800179	137800580
chr5	138533754	138534155	chr5	138534121	138534144	GC-rich	Low_complexity	Low_complexity
chr5	138609685	138610086
chr5	138629234	138629635	chr5	138629464	138629491	(TCTCCC)n	Simple_repeat	Simple_repeat
chr5	138677762	138678163
chr5	138775031	138775432	chr5	138775286	138775493	MIRc	SINE	MIR
chr5	139944101	139944502
chr5	140027232	140027633	chr5	140027592	140027645	(TG)n	Simple_repeat	Simple_repeat
chr5	143550021	143550422
chr5	145562116	145562517
chr5	145826471	145826872
chr5	148520733	148521134
chr5	148930805	148931206
chr5	149380037	149380438
chr5	149736976	149737377	chr5	149737041	149737063	GC-rich	Low_complexity	Low_complexity
chr5	149736976	149737377	chr5	149737177	149737198	GC-rich	Low_complexity	Low_complexity
chr5	149829208	149829609
chr5	150080400	150080801
chr5	153418297	153418698
chr5	157170574	157170975	chr5	157170791	157170828	GC-rich	Low_complexity	Low_complexity
chr5	157170574	157170975	chr5	157170958	157171007	GC-rich	Low_complexity	Low_complexity
chr5	157286009	157286410	chr5	157286323	157286441	MER5A	DNA	hAT-Charlie
chr5	159435896	159436297	chr5	159435566	159435911	AluIb	SINE	Alu
chr5	159546755	159547156	chr5	159547037	159547095	L2a	LINE	L2
chr5	167913238	167913639
chr5	168006553	168006954	chr5	168006579	168006605	(CCG)n	Simple_repeat	Simple_repeat
chr5	170288466	170288867	chr5	170288798	170288874	(CCCCG)n	Simple_repeat	Simple_repeat
chr5	171433558	171433959	chr5	171433540	171433600	(CGG)n	Simple_repeat	Simple_repeat
chr5	171615282	171615683
chr5	173043576	173043977	chr5	173043548	173043606	(CGG)n	Simple_repeat	Simple_repeat
chr5	173043576	173043977	chr5	173043955	173044064	MER5A	DNA	hAT-Charlie
chr5	175395107	175395508
chr5	175788652	175789053
chr5	175792231	175792632
chr5	175815434	175815835
chr5	176778778	176779179
chr5	176829343	176829744
chr5	176943944	176944345
chr5	176981507	176981908	chr5	176981490	176981538	(CCG)n	Simple_repeat	Simple_repeat
chr5	176981507	176981908	chr5	176981843	176981957	MIRc	SINE	MIR
chr5	177018954	177019355	chr5	177018883	177019024	MIR3	SINE	MIR

chr5	177026870	177027271	chr5	177026865	177026952	MIR3	SINE	MIR
chr5	177026870	177027271	chr5	177027060	177027172	GC_rich	Low_complexity	Low_complexity
chr5	177580683	177581084
chr5	178157548	178157949
chr5	178286719	178287120
chr5	178322675	178323076	chr5	178322422	178322707	AluSq2	SINE	Alu
chr5	178450520	178450921
chr5	178487142	178487543
chr5	179245871	179246272
chr5	180237756	180238157
chr6	2765419	2765820	chr6	2765416	2765446	GC_rich	Low_complexity	Low_complexity
chr6	2765419	2765820	chr6	2765819	2765856	GC_rich	Low_complexity	Low_complexity
chr6	5003717	5004118	chr6	5003983	5004034	GC_rich	Low_complexity	Low_complexity
chr6	7590245	7590646
chr6	11093754	11094155
chr6	13407013	13407414	chr6	13407121	13407284	MLT1J	LTR	ERV1-MaLR
chr6	13615337	13615738
chr6	15245474	15245875	chr6	15245423	15245515	G-rich	Low_complexity	Low_complexity
chr6	17707060	17707461	chr6	17706983	17707146	(CCG)n	Simple_repeat	Simple_repeat
chr6	27342839	27343240
chr6	27440801	27441202	chr6	27440922	27440953	GC_rich	Low_complexity	Low_complexity
chr6	27440801	27441202	chr6	27441148	27441453	AluSx4	SINE	Alu
chr6	28048487	28048888
chr6	30312676	30313077
chr6	30524867	30525268
chr6	30594619	30595020
chr6	30687737	30688138
chr6	30854087	30854488
chr6	30875656	30876057	chr6	30875957	30876011	CT-rich	Low_complexity	Low_complexity
chr6	30881870	30882271	chr6	30881997	30882020	GC_rich	Low_complexity	Low_complexity
chr6	31165639	31166040
chr6	31633524	31633925
chr6	31802137	31802538	chr6	31802039	31802177	AluJb	SINE	Alu
chr6	31802137	31802538	chr6	31802331	31802354	GC_rich	Low_complexity	Low_complexity
chr6	31866128	31866529
chr6	31926877	31927278
chr6	32096043	32096444
chr6	32097640	32098041
chr6	33168078	33168479	chr6	33168086	33168118	(CCG)n	Simple_repeat	Simple_repeat
chr6	33239526	33239927
chr6	33257142	33257543
chr6	33290624	33291025
chr6	35227030	35227431
chr6	36410507	36410908	chr6	36410751	36410785	GC_rich	Low_complexity	Low_complexity
chr6	36853469	36853870
chr6	36953725	36954126	chr6	36953829	36953893	(CCCCAG)n	Simple_repeat	Simple_repeat
chr6	38670800	38671201
chr6	41703227	41703628	chr6	41703223	41703306	(CCG)n	Simple_repeat	Simple_repeat
chr6	41703227	41703628	chr6	41703307	41703329	GC_rich	Low_complexity	Low_complexity
chr6	41747492	41747893	chr6	41747478	41747508	(CGCG)n	Simple_repeat	Simple_repeat
chr6	41747492	41747893	chr6	41747518	41747590	(CCCCG)n	Simple_repeat	Simple_repeat
chr6	41747492	41747893	chr6	41747634	41747655	(CCCCG)n	Simple_repeat	Simple_repeat
chr6	42018099	42018500	chr6	42017841	42018135	AluSz	SINE	Alu
chr6	42018099	42018500	chr6	42018204	42018228	(CCCCG)n	Simple_repeat	Simple_repeat
chr6	42185416	42185817
chr6	42531441	42531842	chr6	42531396	42531466	L2a	LINE	L2
chr6	42847176	42847577
chr6	42981676	42982077
chr6	43445134	43445535
chr6	43596946	43597347	chr6	43596939	43596962	(CCG)n	Simple_repeat	Simple_repeat
chr6	43603346	43603747
chr6	43655322	43655723
chr6	46620502	46620903
chr6	52149630	52150031
chr6	52860015	52860416	chr6	52859938	52860041	G-rich	Low_complexity	Low_complexity
chr6	52929498	52929899
chr6	56911144	56911545
chr6	56954611	56955012
chr6	57036728	57037129
chr6	71276504	71276905
chr6	74230641	74231042
chr6	74363600	74364001
chr6	79576997	79577398
chr6	80340750	80341151
chr6	83777193	83777594	chr6	83777055	83777201	MIR3	SINE	MIR
chr6	84937383	84937784
chr6	86303722	86304123
chr6	88182299	88182700
chr6	88299618	88300019
chr6	88411902	88412303
chr6	89673125	89673526	chr6	89673460	89673501	(CCCCG)n	Simple_repeat	Simple_repeat
chr6	90348056	90348457
chr6	96025466	96025867
chr6	99873024	99873425
chr6	105307587	105307988
chr6	108582270	108582671
chr6	108615890	108616291
chr6	109416460	109416861
chr6	110501113	110501514
chr6	111136519	111136920	chr6	111136526	111136555	(TCC)n	Simple_repeat	Simple_repeat
chr6	116989737	116990138	chr6	116990022	116990256	AluY	SINE	Alu
chr6	117002192	117002593	chr6	117002274	117002308	(CCG)n	Simple_repeat	Simple_repeat
chr6	135375790	135376191
chr6	136610884	136611285
chr6	139094409	139094810
chr6	143771677	143772078
chr6	144416674	144417075	chr6	144417027	144417317	AluSx3	SINE	Alu
chr6	146135830	146136231	chr6	146135926	146135967	GC_rich	Low_complexity	Low_complexity
chr6	146135830	146136231	chr6	146136189	146136306	MIR3	SINE	MIR
chr6	146285229	146285630
chr6	147523455	147523856
chr6	150039081	150039482
chr6	150070669	150071070	chr6	150070876	150070960	(CGG)n	Simple_repeat	Simple_repeat
chr6	151773120	151773521
chr6	157800914	157801315	chr6	157800850	157801008	MIR	SINE	MIR

chr7	128502550	128502951	chr7	128502513	128502607	L2c	LINE	L2
chr7	128502550	128502951	chr7	128502671	128502713	(TGAA)n	Simple_repeat	Simple_repeat
chr7	128864390	128864791	chr7	128864737	128864915	G-rich	Low_complexity	Low_complexity
chr7	129592699	129593100
chr7	129691002	129691403
chr7	129845099	129845500
chr7	129932690	129933091
chr7	132766858	132767259	chr7	132767190	132767236	L2c	LINE	L2
chr7	132937504	132937905
chr7	133811853	133812254	chr7	133811893	133811995	A-rich	Low_complexity	Low_complexity
chr7	134001627	134002028
chr7	134670959	134671360
chr7	134855314	134855715
chr7	135194812	135195213
chr7	135242260	135242661
chr7	135347040	135347441
chr7	135661875	135662276
chr7	139025127	139025528	chr7	139025445	139025517	tRNA-Arg-AG	tRNA	tRNA
chr7	140098158	140098559	chr7	140098536	140098563	(T)n	Simple_repeat	Simple_repeat
chr7	140396548	140396949
chr7	141437929	141438330
chr7	148787690	148788091
chr7	148823229	148823630
chr7	148892497	148892898	chr7	148892855	148892926	GC-rich	Low_complexity	Low_complexity
chr7	148936477	148936878
chr7	149157506	149157907	chr7	149157408	149157606	GC-rich	Low_complexity	Low_complexity
chr7	149194674	149195075	chr7	149194667	149194709	GC-rich	Low_complexity	Low_complexity
chr7	149194674	149195075	chr7	149194955	149194984	(CCCCG)n	Simple_repeat	Simple_repeat
chr7	149321672	149322073
chr7	149411654	149412055	chr7	149411763	149411798	(CGGGGG)n	Simple_repeat	Simple_repeat
chr7	149411654	149412055	chr7	149411884	149411906	GC-rich	Low_complexity	Low_complexity
chr7	149411654	149412055	chr7	149411996	149412055	C-rich	Low_complexity	Low_complexity
chr7	149535236	149535637
chr7	150066173	150066574
chr7	150689789	150690190
chr7	150725571	150725972
chr7	150754944	150755345	chr7	150755232	150755255	GC-rich	Low_complexity	Low_complexity
chr7	150777702	150778103
chr7	150780432	150780833	chr7	150780608	150780630	GC-rich	Low_complexity	Low_complexity
chr7	150924204	150924605
chr7	155437131	155437532	chr7	155437289	155437328	GC-rich	Low_complexity	Low_complexity
chr7	155437131	155437532	chr7	155437347	155437372	GC-rich	Low_complexity	Low_complexity
chr7	158649050	158649451
chr8	182252	182653	chr8	182274	182336	C-rich	Low_complexity	Low_complexity
chr8	17779998	17780399
chr8	18067327	18067728
chr8	19674612	19675013	chr8	19674619	19674648	(CCCCCG)n	Simple_repeat	Simple_repeat
chr8	19674612	19675013	chr8	19674949	19674987	(CGG)n	Simple_repeat	Simple_repeat
chr8	21775794	21776195	chr8	21775670	21776110	LTR67B	LTR	ERVL
chr8	21999781	22000182
chr8	27631687	27632088	chr8	27631683	27631745	AluSc	SINE	Alu
chr8	28747612	28748013	chr8	28748012	28748068	C-rich	Low_complexity	Low_complexity
chr8	29120557	29120958	chr8	29120621	29120679	G-rich	Low_complexity	Low_complexity
chr8	30515622	30516023	chr8	30515654	30515700	(CGG)n	Simple_repeat	Simple_repeat
chr8	30601716	30602117
chr8	30890884	30891285	chr8	30890845	30890891	G-rich	Low_complexity	Low_complexity
chr8	30890884	30891285	chr8	30891178	30891306	G-rich	Low_complexity	Low_complexity
chr8	37707282	37707683
chr8	37887757	37888158	chr8	37888004	37888039	(CGGGG)n	Simple_repeat	Simple_repeat
chr8	38240328	38240729
chr8	38326039	38326440
chr8	42698324	42698725
chr8	42911058	42911459	chr8	42910804	42911077	AluJb	SINE	Alu
chr8	48872594	48872995
chr8	48873160	48873561
chr8	53626826	53627227
chr8	56986934	56987335
chr8	63951249	63951650
chr8	67340933	67341334
chr8	67525588	67525989	chr8	67525584	67525717	G-rich	Low_complexity	Low_complexity
chr8	67579411	67579812
chr8	67782802	67783203
chr8	74206046	74206447
chr8	74884496	74884897
chr8	75262432	75262833
chr8	80942264	80942665
chr8	81398296	81398697	chr8	81398222	81398415	(CCCCAG)n	Simple_repeat	Simple_repeat
chr8	82633352	82633753
chr8	82754849	82755250
chr8	92082358	92082759
chr8	94766908	94767309	chr8	94766846	94766922	Tigger5	DNA	TcMar-Tigger
chr8	95565579	95565980
chr8	95908710	95909111
chr8	96037041	96037442
chr8	97247576	97247977
chr8	99057573	99057974	chr8	99057920	99058242	AluJb	SINE	Alu
chr8	99129252	99129653
chr8	101734724	101735125
chr8	103875446	103875847	chr8	103875494	103875517	GC-rich	Low_complexity	Low_complexity
chr8	103875446	103875847	chr8	103875841	103875875	(CCG)n	Simple_repeat	Simple_repeat
chr8	104427372	104427773
chr8	109799685	109800086	chr8	109799849	109799874	(CGGGG)n	Simple_repeat	Simple_repeat
chr8	110346185	110346586
chr8	110552123	110552524
chr8	117778520	117778921
chr8	119634026	119634427	chr8	119634401	119634429	GC-rich	Low_complexity	Low_complexity
chr8	120844783	120845184
chr8	124053963	124054364
chr8	124084761	124085162
chr8	124253464	124253865
chr8	124286332	124286733
chr8	125551210	125551611
chr8	130951841	130952242
chr8	141521282	141521683
chr8	143484458	143484859	chr8	143484282	143484462	C-rich	Low_complexity	Low_complexity

chr8	143808507	143808908	chr8	143808501	143808522	GC_rich	Low_complexity	Low_complexity
chr8	143808507	143808908	chr8	143808742	143808763	GC_rich	Low_complexity	Low_complexity
chr8	144636430	144636831	chr8	144636508	144636682	(CA)n	Simple_repeat	Simple_repeat
chr8	144636430	144636831	chr8	144636697	144636782	(CA)n	Simple_repeat	Simple_repeat
chr8	144636430	144636831	chr8	144636808	144636972	(CA)n	Simple_repeat	Simple_repeat
chr8	144699634	144700035	chr8	144699847	144699869	GC_rich	Low_complexity	Low_complexity
chr8	144816078	144816479	chr8	144815978	144816156	C-rich	Low_complexity	Low_complexity
chr8	144897836	144898237	chr8	144898044	144898067	GC_rich	Low_complexity	Low_complexity
chr8	144911402	144911803
chr8	145023686	145024087
chr8	145133349	145133750
chr8	145149859	145150260	chr8	145149871	145149927	C-rich	Low_complexity	Low_complexity
chr8	145149859	145150260	chr8	145150040	145150082	GC_rich	Low_complexity	Low_complexity
chr8	145149859	145150260	chr8	145150140	145150171	GC_rich	Low_complexity	Low_complexity
chr8	145159616	145160017	chr8	145159669	145159759	C-rich	Low_complexity	Low_complexity
chr8	145550441	145550842
chr8	145597520	145597921	chr8	145597897	145598179	Alu/b	SINE	Alu
chr8	145669863	145670264	chr8	145669825	145669938	(CCGG)n	Simple_repeat	Simple_repeat
chr8	145669863	145670264	chr8	145669947	145669983	GC_rich	Low_complexity	Low_complexity
chr8	145703258	145703659	chr8	145703266	145703340	C-rich	Low_complexity	Low_complexity
chr8	145703258	145703659	chr8	145703618	145703739	G-rich	Low_complexity	Low_complexity
chr8	145734232	145734633
chr8	145980800	145981201
chr8	146017664	146018065
chr8	146176009	146176410	chr8	146176001	146176090	C-rich	Low_complexity	Low_complexity
chr9	4679458	4679859
chr9	4984321	4984722	chr9	4983831	4984345	L2a	LINE	L2
chr9	7799622	7800023	chr9	7799886	7800008	GC_rich	Low_complexity	Low_complexity
chr9	14314842	14315243
chr9	14693551	14693952	chr9	14693756	14693908	MER5A1	DNA	hAT-Charlie
chr9	15422550	15422951	chr9	15422765	15422802	GC_rich	Low_complexity	Low_complexity
chr9	19102826	19103227	chr9	19103185	19103298	MIRc	SINE	MIR
chr9	19102826	19103227	chr9	19103220	19103377	L2	LINE	L2
chr9	19379880	19380281
chr9	21335091	21335492
chr9	25677436	25677837
chr9	26947280	26947681
chr9	32572972	32573373
chr9	33024909	33025310
chr9	33290689	33291090
chr9	34376998	34377399
chr9	34637820	34638221	chr9	34637988	34638401	L2c	LINE	L2
chr9	34988990	34989391
chr9	35079835	35080236
chr9	35096153	35096554
chr9	35102924	35103325
chr9	35116398	35116799
chr9	35161948	35162349
chr9	35488925	35489326	chr9	35488380	35488987	MER5A1	LTR	ERV1
chr9	35488925	35489326	chr9	35488987	35489065	MER50B	LTR	ERV1
chr9	35488925	35489326	chr9	35489065	35489412	THE1D	LTR	ERV1-MaLR
chr9	35732344	35732745
chr9	35748950	35749351	chr9	35749308	35749332	(CCG)n	Simple_repeat	Simple_repeat
chr9	37079430	37079831
chr9	37120015	37120416
chr9	37485570	37485971	chr9	37485572	37485712	MER115	DNA	hAT-Tip100
chr9	37576211	37576612	chr9	37576483	37576715	L3	LINE	CR1
chr9	37753556	37753957
chr9	37800496	37800897
chr9	37903815	37904216
chr9	40791993	40792394	chr9	40792302	40792584	L1MC5	LINE	L1
chr9	72374814	72375215	chr9	72374929	72374950	GC_rich	Low_complexity	Low_complexity
chr9	72374814	72375215	chr9	72374961	72374992	GC_rich	Low_complexity	Low_complexity
chr9	72435384	72435785	chr9	72435348	72435389	(CA)n	Simple_repeat	Simple_repeat
chr9	74526312	74526713
chr9	82186536	82186937
chr9	86322725	86323126
chr9	86571555	86571956
chr9	88555637	88556038
chr9	88896856	88897257
chr9	95432390	95432791	chr9	95432674	95432794	MIRc	SINE	MIR
chr9	95527120	95527521	chr9	95527122	95527181	GC_rich	Low_complexity	Low_complexity
chr9	95527120	95527521	chr9	95527226	95527251	GC_rich	Low_complexity	Low_complexity
chr9	97021349	97021750	chr9	97021330	97021352	AT_rich	Low_complexity	Low_complexity
chr9	98079778	98080179
chr9	99540202	99540603
chr9	99616656	99617057
chr9	100000457	100000858
chr9	100395493	100395894
chr9	102861187	102861588	chr9	102861159	102861205	(GGCTG)n	Simple_repeat	Simple_repeat
chr9	104160841	104161242
chr9	111882109	111882510	chr9	111882106	111882145	GC_rich	Low_complexity	Low_complexity
chr9	114244925	114245326	chr9	114245096	114245119	GC_rich	Low_complexity	Low_complexity
chr9	114361539	114361940
chr9	115480222	115480623	chr9	115480562	115480634	(CGGG)n	Simple_repeat	Simple_repeat
chr9	115774314	115774715
chr9	115818883	115819284
chr9	115912987	115913388	chr9	115913262	115913284	(CGG)n	Simple_repeat	Simple_repeat
chr9	115983378	115983779
chr9	116037616	116038017
chr9	116172726	116173127
chr9	123342353	123342754
chr9	123555230	123555631
chr9	123964210	123964611	chr9	123964512	123964580	MIRb	SINE	MIR
chr9	124855498	124855899	chr9	124855455	124855526	(CCG)n	Simple_repeat	Simple_repeat
chr9	125667636	125668037
chr9	125675398	125675799	chr9	125675462	125675488	(TCC)n	Simple_repeat	Simple_repeat
chr9	125675398	125675799	chr9	125675791	125676085	AluSq2	SINE	Alu
chr9	125693655	125694056
chr9	126692285	126692686	chr9	126692383	126692474	(CCG)n	Simple_repeat	Simple_repeat
chr9	126692285	126692686	chr9	126692504	126692542	GC_rich	Low_complexity	Low_complexity
chr9	127177503	127177904
chr9	127624055	127624456
chr9	127703206	127703607
chr9	127952065	127952466	chr9	127952014	127952067	(CGG)n	Simple_repeat	Simple_repeat

chr9	128003688	128004089
chr9	128023844	128024245	chr9	128024119	128024178	(CGG)n	Simple_repeat	Simple_repeat	.
chr9	128469298	128469699
chr9	128508316	128508717
chr9	129089572	129089973
chr9	129567106	129567507
chr9	129622510	129622911	chr9	129622879	129623092	G-rich	Low_complexity	Low_complexity	.
chr9	130186198	130186599
chr9	130213603	130214004
chr9	130341109	130341510	chr9	130341026	130341157	FRAM	SINE	Alu	.
chr9	130497400	130497801
chr9	130548033	130548434	chr9	130548157	130548200	(CGG)n	Simple_repeat	Simple_repeat	.
chr9	130548033	130548434	chr9	130548256	130548432	(CGG)n	Simple_repeat	Simple_repeat	.
chr9	130565170	130565571
chr9	130639854	130640255	chr9	130640024	130640054	(GGGA)n	Simple_repeat	Simple_repeat	.
chr9	130639854	130640255	chr9	130640163	130640346	MIRc	SINE	MIR	.
chr9	130699988	130700389
chr9	130828596	130828997	chr9	130828494	130828752	L2b	LINE	L2	.
chr9	130890055	130890456
chr9	130965341	130965742	chr9	130965318	130965411	L2	LINE	L2	.
chr9	130965341	130965742	chr9	130965632	130965653	GC_rich	Low_complexity	Low_complexity	.
chr9	131038059	131038460
chr9	131084635	131085036
chr9	131102530	131102931	chr9	131102742	131102763	GC_rich	Low_complexity	Low_complexity	.
chr9	131102530	131102931	chr9	131102900	131102988	(CGGGG)n	Simple_repeat	Simple_repeat	.
chr9	131266909	131267310
chr9	131418891	131419292	chr9	131418893	131418923	GC_rich	Low_complexity	Low_complexity	.
chr9	131446789	131447190	chr9	131446958	131447189	L2b	LINE	L2	.
chr9	131466373	131466774	chr9	131466773	131466919	MIR	SINE	MIR	.
chr9	131534235	131534636
chr9	131789448	131789849	chr9	131789389	131789479	MIRb	SINE	MIR	.
chr9	131789448	131789849	chr9	131789493	131789700	MIRb	SINE	MIR	.
chr9	132586260	132586661	chr9	132586596	132586874	Alu5x1	SINE	Alu	.
chr9	132815936	132816337
chr9	133587900	133588301
chr9	134000788	134001189
chr9	134153446	134153847	chr9	134153429	134153449	(CGG)n	Simple_repeat	Simple_repeat	.
chr9	134164851	134165252
chr9	134406478	134406879	chr9	134406701	134406722	GC_rich	Low_complexity	Low_complexity	.
chr9	134955118	134955519
chr9	135282051	135282452
chr9	135545267	135545668
chr9	136214909	136215310
chr9	136283039	136283440
chr9	136324936	136325337
chr9	136932989	136933390	chr9	136932965	136933043	GC_rich	Low_complexity	Low_complexity	.
chr9	136932989	136933390	chr9	136933080	136933115	GC_rich	Low_complexity	Low_complexity	.
chr9	136932989	136933390	chr9	136933210	136933386	GC_rich	Low_complexity	Low_complexity	.
chr9	137029840	137030241
chr9	138853120	138853521	chr9	138853116	138853230	(CCG)n	Simple_repeat	Simple_repeat	.
chr9	138853120	138853521	chr9	138853448	138853682	MER33	DNA	hAT-Charlie	.
chr9	138985988	138986389
chr9	139258055	139258456	chr9	139258191	139258213	GC_rich	Low_complexity	Low_complexity	.
chr9	139294525	139294926	chr9	139294823	139294943	MIRb	SINE	MIR	.
chr9	140117857	140118258
chr9	140149536	140149937	chr9	140149744	140149881	(CGGGG)n	Simple_repeat	Simple_repeat	.
chr9	140473151	140473552	chr9	140473294	140473324	GC_rich	Low_complexity	Low_complexity	.
chr9	140512909	140513310
chrX	7895560	7895961	chrX	7895917	7896054	MIRc	SINE	MIR	.
chrX	11128111	11128512	chrX	11128416	11128718	LTR16A	LTR	ERVL	.
chrX	11777402	11777803
chrX	14890954	14891355
chrX	16804128	16804529
chrX	39957606	39958007	chrX	39957675	39957741	(CGG)n	Simple_repeat	Simple_repeat	.
chrX	46404702	46405103
chrX	47049891	47050292	chrX	47049887	47049919	MIRc	SINE	MIR	.
chrX	47078406	47078807	chrX	47078435	47078477	GC_rich	Low_complexity	Low_complexity	.
chrX	48334260	48334661
chrX	48432462	48432863
chrX	48554738	48555139	chrX	48554929	48554965	(CCG)n	Simple_repeat	Simple_repeat	.
chrX	48814638	48815039	chrX	48814663	48814750	(CCG)n	Simple_repeat	Simple_repeat	.
chrX	48814638	48815039	chrX	48814738	48814809	(CGG)n	Simple_repeat	Simple_repeat	.
chrX	48814638	48815039	chrX	48814977	48815021	(CGG)n	Simple_repeat	Simple_repeat	.
chrX	48931522	48931923
chrX	48979974	48980375	chrX	48980282	48980591	Alu5c8	SINE	Alu	.
chrX	49091707	49092108
chrX	53024507	53024908
chrX	53077580	53077981	chrX	53077548	53077582	(CCCCG)n	Simple_repeat	Simple_repeat	.
chrX	53077580	53077981	chrX	53077626	53077665	(TCCC)n	Simple_repeat	Simple_repeat	.
chrX	53449412	53449813
chrX	54208725	54209126	chrX	54208783	54208874	(TAGG)n	Simple_repeat	Simple_repeat	.
chrX	54209918	54210319	chrX	54210023	54210052	(CGGGG)n	Simple_repeat	Simple_repeat	.
chrX	57312977	57313378	chrX	57312798	57312994	MIRb	SINE	MIR	.
chrX	64196193	64196594
chrX	64754585	64754986
chrX	67653510	67653911
chrX	67718622	67719023
chrX	70315422	70315823
chrX	71792697	71793098	chrX	71793074	71793094	(A)n	Simple_repeat	Simple_repeat	.
chrX	74375890	74376291
chrX	77154668	77155069
chrX	85302423	85302824
chrX	100645733	100646134
chrX	102884404	102884805
chrX	102942850	102943251
chrX	106045619	106046020
chrX	106361839	106362240
chrX	107334744	107335145
chrX	118987004	118987405
chrX	119005608	119006009	chrX	119005768	119005796	GC_rich	Low_complexity	Low_complexity	.
chrX	119763493	119763894
chrX	122866768	122867169
chrX	129402676	129403077	chrX	129402773	129402808	(GGA)n	Simple_repeat	Simple_repeat	.
chrX	130037126	130037527
chrX	134478472	134478873	chrX	134478868	134478889	GC_rich	Low_complexity	Low_complexity	.

chrX	135055818	135056219	chrX	135056164	135056353	G-rich	Low_complexity	Low_complexity
chrX	148622341	148622742
chrX	149106474	149106875	chrX	149106697	149106847	(CACG)n	Simple_repeat	Simple_repeat
chrX	149736632	149737033
chrX	152110026	152110427
chrX	153775558	153775959

chr1 205414449 205414450

chr1 207097649 207097650 chr1 207097184 207097924 (TG)n Simple_repe:Simple_repeat

chr1 210536672 210536673

chr1 210547813 210547814

chr1 210827361 210827362

chr1 212376159 212376160

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chr1 234812137 234812138 chr1 234811720 234812316 L1ME3A LINE L1

chr1 235099141 235099142

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chr10 38774500 38774501 chr10 38774489 38774537 (GAATG)n Satellite Satellite

chr10 38776497 38776498 chr10 38776268 38776627 (GAATG)n Satellite Satellite

chr10 38817716 38817717 chr10 38817677 38818632 (GAATG)n Satellite Satellite

chr10 38872161 38872162 chr10 38871825 38872621 (GAATG)n Satellite Satellite

chr10 38881800 38881801 chr10 38881691 38882189 HSATII Satellite Satellite

chr10 39094333 39094334 chr10 39094326 39094504 (CATTG)n Satellite Satellite

chr10 39111272 39111273 chr10 39111231 39111404 (CATTG)n Satellite Satellite

chr10 39138171 39138172 chr10 39138046 39138469 (GAATG)n Satellite Satellite

chr10 42531937 42531938 chr10 42527021 42546685 ALR/Alpha Satellite centr

chr10 42532571 42532572 chr10 42527021 42546685 ALR/Alpha Satellite centr

chr10 42542185 42542186 chr10 42527021 42546685 ALR/Alpha Satellite centr

chr10 42599982 42599983 chr10 42598546 42601361 HSATII Satellite Satellite

chr10 42797315 42797316 chr10 42797274 42797445 (CATTG)n Satellite Satellite

chr10 42800158 42800159 chr10 42799444 42800323 (CATTG)n Satellite Satellite

chr10 42817731 42817732 chr10 42817135 42818362 ALR/Alpha Satellite centr

chr10 43950921 43950922

chr10 47058659 47058660 chr10 47058582 47058924 (CA)n Simple_repe:Simple_repeat

chr10 52852335 52852336

chr10 69609230 69609231

chr10 71754252 71754253 chr10 71754203 71754300 MLTIJ LTR ERVL-MaLR

chr10 72288765 72288766 chr10 72288492 72288873 MLTIJ LTR ERVL-MaLR

chr10 73083386 73083387 chr10 73083027 73083494 MLTIJ LTR ERVL-MaLR

chr10 73137256 73137257

chr10 73620304 73620305

chr10 73736070 73736071

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chr10 75608937 75608938

chr10 77716624 77716625 chr10 77716380 77716661 MLTIJ LTR ERVL-MaLR

chr10 79706050 79706051 chr10 79705708 79706156 MLTIJ LTR ERVL-MaLR

chr10 90145422 90145423

chr10 94561952 94561953 chr10 94561857 94562339 MLTIJ LTR ERVL-MaLR

chr10 95226250 95226251

chr10 95511780 95511781

chr10 98561469 98561470 chr10 98561361 98561539 GA-rich Low_comple:Low_complexity

chr10 99486598 99486599 chr10 99486255 99486610 MLTIJ LTR ERVL-MaLR

chr10 105344802 105344803

chr10 114602987 114602988 chr10 114602587 114603055 LTR33B LTR ERVL

chr10 116571840 116571841 chr10 116571334 116571976 MLT2F LTR ERVL

chr10 118947040 118947041 chr10 118946916 118947196 MLTIJ LTR ERVL-MaLR

chr10 123185965 123185966 chr10 123185882 123186488 LTR67B LTR ERVL

chr10 125705220 125705221 chr10 125705164 125705285 MLTIJ LTR ERVL-MaLR

chr10 126973705 126973706 chr10 126973365 126973794 MLTIJ LTR ERVL-MaLR

chr10 127888063 127888064

chr10 132505897 132505898

chr10 134177915 134177916 chr10 134177891 134178071 C-rich Low_comple:Low_complexity

chr10 135500715 135500716 chr10 135500000 135502705 BSR/Beta Satellite Satellite

chr11 919256 919257 chr11 919227 919368 MLTIJ LTR ERVL-MaLR

chr11 3611613 3611614 chr11 3611582 3611963 MLTIJ LTR ERVL-MaLR

chr11 8051851 8051852

chr11 8710555 8710556

chr11 11005975 11005976 chr11 11005957 11006276 MLTIJ LTR ERVL-MaLR

chr11 17725776 17725777 chr11 17725601 17725807 MLTIJ LTR ERVL-MaLR

chr11 27256142 27256143

chr11 28131829 28131830

chr11 33423702 33423703 chr11 33423586 33424074 L2 LINE L2

chr11 33529738 33529739 chr11 33529672 33529834 LTR67B LTR ERVL

chr11 36355730 36355731 chr11 36355474 36355842 MLTIJ LTR ERVL-MaLR

chr11 43665752 43665753

chr11 44394763 44394764 chr11 44394547 44394885 MLTIJ LTR ERVL-MaLR

chr11 45668303 45668304 chr11 45668254 45668606 MLTIJ LTR ERVL-MaLR

chr11 45823442 45823443 chr11 45823376 45823535 MLTIJ LTR ERVL-MaLR

chr11 46134725 46134726

chr11 47879597 47879598

chr11 47976976 47976977 chr11 47976677 47977067 MLTIJ LTR ERVL-MaLR

chr11 48172367 48172368

chr11 48893066 48893067 chr11 48886840 48900993 ALR/Alpha Satellite centr

chr11 51567315 51567316 chr11 51567242 51594205 ALR/Alpha Satellite centr

chr11 51573371 51573372 chr11 51567242 51594205 ALR/Alpha Satellite centr

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chr11 54890851 54890852 chr11 54889181 54893528 ALR/Alpha Satellite centr

chr11 55026423 55026424 chr11 55020818 55027630 ALR/Alpha Satellite centr

chr11 61266516 61266517 chr11 61266182 61266558 MLTIJ LTR ERVL-MaLR

chr11 61661558 61661559 chr11 61661280 61661561 Alub SINE Alu

chr11 64027110 64027111

chr11 64038438 64038439

chr11 64212443 64212444 chr11 64212396 64212756 MLTIJ LTR ERVL-MaLR

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chr11 65186219 65186220

chr11 65244996 65244997

chr11 65319270 65319271

chr11 65635718 65635719

chr11 65660950 65660951

chr11 66649636 66649637

chr11 66799380 66799381

chr11 67007548 67007549

chr11 67593726 67593727

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LTR40b	1
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MER74B	1
L1M3a	1
(CATG)n	1
MER77	1
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LTR16D	1
LTR16E1	1
MLT1H2	1
L1M3e	1
LTR86B1	1
L1MCc	1
L1P3	1
MLT1A0-int	1
MER103C	1
L1MA5	1
LTR16B1	1
MST-int	1
LTR56	1
FLAM_C	1
AluS6	1
L1P8A	1
L1P10	1
HERV-int	1
MER50	1
Harlequin-int	1
L1M2a1	1
L1MA2	1
L1MA7	1
LTR57-int	1
LOR1b	1
MLT1A1-int	1
LTR35A	1
MLT1H1	1
THE1A-int	1
L1P6	1
THE1D-int	1
MER51A	1
THE1C-int	1
MER5A1	1
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L1M3c	1
MER57D	1
LTR16C	1
AmnSINE1	1
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L1P11	1
FordPrefect_a	1
MER61D	1
MER48	1
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THE1C	1
(TTGGGG)n	1
LTR41	1
LTR86B2	1
CER	1
(CAGG)n	1
(TC)n	1
L1MD	1

chr16	86986561	86986562	chr16	86986494	86986924	LTR33A	LTR	ERVL
chr16	87009143	87009144	chr16	87009026	87009535	MLT1J	LTR	ERVL-MaLR
chr16	87691449	87691450	chr16	87691352	87691561	MLT1J	LTR	ERVL-MaLR
chr16	88367176	88367177
chr16	89572075	89572076
chr16	90025215	90025216
chr17	1371318	1371319
chr17	1572933	1572934	chr17	1572698	1573773	L2	LINE	L2
chr17	4923092	4923093
chr17	5015204	5015205
chr17	6231838	6231839	chr17	6231525	6231922	MLT1J	LTR	ERVL-MaLR
chr17	6374139	6374140
chr17	6411304	6411305	chr17	6411267	6411399	(CTGGGG)n	Simple_repe:Simple_repeat	
chr17	7095000	7095001
chr17	7118437	7118438
chr17	7358879	7358880
chr17	7738755	7738756
chr17	8076997	8076998
chr17	8750155	8750156	chr17	8750073	8750260	MLT1J1	LTR	ERVL-MaLR
chr17	12280122	12280123	chr17	12280057	12280151	MLT1J1	LTR	ERVL-MaLR
chr17	12530688	12530689
chr17	15401663	15401664	chr17	15401346	15401753	MLT1J2	LTR	ERVL-MaLR
chr17	16439126	16439127
chr17	17319611	17319612	chr17	17319253	17319718	MLT1J	LTR	ERVL-MaLR
chr17	17512633	17512634	chr17	17512580	17512960	MLT1J2	LTR	ERVL-MaLR
chr17	17598171	17598172
chr17	17653464	17653465	chr17	17653396	17653528	MLT1J2	LTR	ERVL-MaLR
chr17	17743726	17743727
chr17	17753482	17753483
chr17	17936919	17936920
chr17	18601306	18601307
chr17	19912594	19912595
chr17	21002430	21002431
chr17	21226481	21226482	chr17	21226436	21226514	MLT1J	LTR	ERVL-MaLR
chr17	22253223	22253224	chr17	22241551	22263006	ALR/Alpha	Satellite	centr
chr17	22260080	22260081	chr17	22241551	22263006	ALR/Alpha	Satellite	centr
chr17	22261583	22261584	chr17	22241551	22263006	ALR/Alpha	Satellite	centr
chr17	25265149	25265150	chr17	25265028	25265260	(GAATG)n	Satellite	Satellite
chr17	25574584	25574585
chr17	25783411	25783412
chr17	26543776	26543777	chr17	26543633	26543894	MLT1J	LTR	ERVL-MaLR
chr17	27139815	27139816
chr17	27482789	27482790
chr17	28927301	28927302
chr17	29058408	29058409
chr17	31149685	31149686	chr17	31149606	31149693	GC_rich	Low_comple:Low_complexity	
chr17	32013391	32013392
chr17	33478160	33478161	chr17	33478114	33478275	LSU-rRNA_HrRNA	rRNA	rRNA
chr17	34114329	34114330
chr17	36607700	36607701
chr17	37029122	37029123
chr17	37379455	37379456
chr17	37769379	37769380
chr17	38269661	38269662
chr17	38527749	38527750	chr17	38527662	38527794	MLT1J1	LTR	ERVL-MaLR
chr17	39808065	39808066
chr17	40559725	40559726
chr17	40776409	40776410
chr17	41116480	41116481
chr17	41381966	41381967	chr17	41381806	41382224	ERV3.6A3_H	LTR	ERVL
chr17	41400981	41400982	chr17	41400485	41401528	LTR13	LTR	ERVK
chr17	41438829	41438830
chr17	41445584	41445585
chr17	41798225	41798226
chr17	42600726	42600727
chr17	43205138	43205139	chr17	43205116	43205198	(TG)n	Simple_repe:Simple_repeat	
chr17	45214563	45214564
chr17	45221272	45221273
chr17	45234375	45234376
chr17	45235645	45235646
chr17	45249333	45249334
chr17	45258962	45258963
chr17	48105281	48105282
chr17	48201546	48201547
chr17	48255583	48255584
chr17	49450193	49450194	chr17	49449875	49450301	MLT1J1	LTR	ERVL-MaLR
chr17	55612781	55612782
chr17	55852476	55852477	chr17	55852401	55852584	MLT1J1	LTR	ERVL-MaLR
chr17	56736815	56736816
chr17	61044429	61044430
chr17	62127452	62127453	chr17	62127378	62127555	MIRc	SINE	MIR
chr17	63319346	63319347	chr17	63319041	63319399	MLT1J2	LTR	ERVL-MaLR
chr17	64927358	64927359	chr17	64926980	64927449	MLT1N2	LTR	ERVL-MaLR
chr17	65477403	65477404	chr17	65477365	65477607	MLT1J	LTR	ERVL-MaLR
chr17	66016023	66016024	chr17	66016015	66016083	tRNA-Arg-AG	tRNA	tRNA
chr17	70405990	70405991	chr17	70405847	70406322	MLT1J	LTR	ERVL-MaLR
chr17	72186504	72186505	chr17	72186445	72186545	MLT1J	LTR	ERVL-MaLR
chr17	72389166	72389167	chr17	72389081	72389524	MLT1J2	LTR	ERVL-MaLR
chr17	72564814	72564815	chr17	72564548	72564864	(TG)n	Simple_repe:Simple_repeat	
chr17	75734977	75734978
chr17	75945130	75945131	chr17	75944792	75945153	MLT1J2	LTR	ERVL-MaLR
chr17	76250653	76250654
chr17	76480447	76480448	chr17	76480344	76480453	L2a	LINE	L2
chr17	76579451	76579452	chr17	76579350	76579467	MLT1J	LTR	ERVL-MaLR
chr17	76879268	76879269
chr17	77702553	77702554	chr17	77702398	77702638	MLT1J	LTR	ERVL-MaLR
chr17	78428566	78428567
chr17	79392933	79392934
chr17	79544482	79544483
chr17	79701749	79701750
chr17	80225830	80225831
chr18	10520276	10520277
chr18	11962850	11962851
chr18	18512292	18512293	chr18	18510901	18520342	ALR/Alpha	Satellite	centr
chr18	18518132	18518133	chr18	18510901	18520342	ALR/Alpha	Satellite	centr
chr18	19494930	19494931
chr18	22264091	22264092	chr18	22263874	22264238	MLT1J2	LTR	ERVL-MaLR

chr18	23083782	23083783	chr18	23083326	23083899	MLT2F	LTR	ERVL
chr18	26728031	26728032	chr18	26728001	26728097	LTR67B	LTR	ERVL
chr18	32227484	32227485	chr18	32227229	32227546	MLT1J2	LTR	ERVL-MaLR
chr18	43904790	43904791	chr18	43904437	43904907	MLT1J	LTR	ERVL-MaLR
chr18	46333154	46333155
chr18	50319180	50319181	chr18	50319112	50319228	(CATT)n	Simple_repe:Simple_repeat	
chr18	57084258	57084259	chr18	57084008	57084364	MLT1J	LTR	ERVL-MaLR
chr18	74608907	74608908
chr18	74822594	74822595
chr18	76252428	76252429
chr18	77331352	77331353
chr19	489051	489052
chr19	524185	524186
chr19	1311902	1311903
chr19	1848544	1848545
chr19	2494509	2494510
chr19	2524469	2524470	chr19	2524327	2524485	(TG)n	Simple_repe:Simple_repeat	
chr19	2950601	2950602
chr19	3036265	3036266
chr19	3244518	3244519	chr19	3244343	3244785	(TG)n	Simple_repe:Simple_repeat	
chr19	3369639	3369640
chr19	3435315	3435316
chr19	3743737	3743738	chr19	3743648	3743890	MLT1J	LTR	ERVL-MaLR
chr19	3990342	3990343
chr19	4180299	4180300	chr19	4180281	4180351	MLT1J	LTR	ERVL-MaLR
chr19	4577572	4577573
chr19	4815759	4815760	chr19	4815667	4815837	MLT1J	LTR	ERVL-MaLR
chr19	5058101	5058102	chr19	5057947	5058147	MLT1J1	LTR	ERVL-MaLR
chr19	5308883	5308884
chr19	5352360	5352361
chr19	5407561	5407562	chr19	5407536	5407635	MLT1J1	LTR	ERVL-MaLR
chr19	5453039	5453040	chr19	5452957	5453326	MLT1J	LTR	ERVL-MaLR
chr19	6604188	6604189	chr19	6604075	6604286	MLT1J	LTR	ERVL-MaLR
chr19	6761207	6761208	chr19	6761121	6761519	MLT1J2	LTR	ERVL-MaLR
chr19	6812112	6812113	chr19	6811786	6812216	MLT1J2	LTR	ERVL-MaLR
chr19	7515791	7515792
chr19	7616409	7616410
chr19	8989208	8989209	chr19	8989109	8989305	LTR33A_	LTR	ERVL
chr19	10028101	10028102	chr19	10028053	10028462	LTR33A	LTR	ERVL
chr19	10155253	10155254	chr19	10155236	10155398	MLT1J	LTR	ERVL-MaLR
chr19	10156255	10156256	chr19	10155856	10156346	LTR33B	LTR	ERVL
chr19	10479287	10479288	chr19	10479267	10479349	MLT1J2	LTR	ERVL-MaLR
chr19	10990015	10990016	chr19	10989762	10990113	MLT1J	LTR	ERVL-MaLR
chr19	11513084	11513085
chr19	11602018	11602019	chr19	11601971	11602102	MLT1J1	LTR	ERVL-MaLR
chr19	13283418	13283419
chr19	13507632	13507633	chr19	13507572	13507728	LTR33	LTR	ERVL
chr19	13512361	13512362	chr19	13512331	13512658	MLT1J1	LTR	ERVL-MaLR
chr19	13668754	13668755	chr19	13668721	13668783	MLT1J2	LTR	ERVL-MaLR
chr19	13800129	13800130	chr19	13800087	13800390	MLT1J1	LTR	ERVL-MaLR
chr19	13817029	13817030	chr19	13817023	13817085	MLT1J2	LTR	ERVL-MaLR
chr19	13842561	13842562
chr19	13898818	13898819
chr19	13954455	13954456
chr19	14032150	14032151	chr19	14031816	14032253	MLT1J	LTR	ERVL-MaLR
chr19	14192299	14192300
chr19	14593275	14593276
chr19	14743281	14743282	chr19	14743153	14743585	MLT1J	LTR	ERVL-MaLR
chr19	17721442	17721443	chr19	17721332	17721557	MLT1J	LTR	ERVL-MaLR
chr19	17782847	17782848	chr19	17782711	17783139	MLT1J	LTR	ERVL-MaLR
chr19	18279183	18279184
chr19	19477757	19477758
chr19	24184068	24184069	chr19	24183459	24184250	LSU-rRNA_HrRNA	rRNA	centr
chr19	24526186	24526187	chr19	24515480	24529460	ALR/Alpha	Satellite	centr
chr19	27732142	27732143	chr19	27731784	27741731	ALR/Alpha	Satellite	centr
chr19	27738489	27738490	chr19	27731784	27741731	ALR/Alpha	Satellite	centr
chr19	27967140	27967141	chr19	27960649	27972538	ALR/Alpha	Satellite	centr
chr19	30023205	30023206	chr19	30023089	30023218	MLT1J1	LTR	ERVL-MaLR
chr19	30336203	30336204
chr19	34625480	34625481
chr19	36066539	36066540	chr19	36066505	36066675	LSU-rRNA_HrRNA	rRNA	
chr19	36099360	36099361	chr19	36099332	36099562	MLT1J2	LTR	ERVL-MaLR
chr19	36363264	36363265
chr19	36422612	36422613
chr19	36618831	36618832
chr19	37709060	37709061
chr19	38510142	38510143	chr19	38509783	38510229	MLT1J	LTR	ERVL-MaLR
chr19	38640427	38640428	chr19	38640351	38640540	MLT1J	LTR	ERVL-MaLR
chr19	38653536	38653537	chr19	38653246	38653614	MLT1J2	LTR	ERVL-MaLR
chr19	39174942	39174943
chr19	41571051	41571052	chr19	41570924	41571310	MLT1J	LTR	ERVL-MaLR
chr19	41755857	41755858	chr19	41755680	41755905	LTR33A	LTR	ERVL
chr19	42748974	42748975
chr19	42772935	42772936
chr19	44711624	44711625
chr19	45216573	45216574
chr19	45316983	45316984
chr19	45829608	45829609	chr19	45829466	45829645	MLT1N2	LTR	ERVL-MaLR
chr19	45894751	45894752	chr19	45894728	45895071	MLT1J	LTR	ERVL-MaLR
chr19	45982018	45982019
chr19	45988745	45988746
chr19	46027205	46027206
chr19	46220901	46220902
chr19	46431107	46431108	chr19	46431009	46431177	LTR67B	LTR	ERVL
chr19	47049963	47049964	chr19	47049903	47050044	MLT1J2	LTR	ERVL-MaLR
chr19	47402252	47402253	chr19	47402072	47402363	LTR33A	LTR	ERVL
chr19	47867490	47867491	chr19	47867322	47867608	MLT1J2	LTR	ERVL-MaLR
chr19	47942250	47942251	chr19	47942168	47942438	MLT1J2	LTR	ERVL-MaLR
chr19	48707318	48707319
chr19	48832907	48832908
chr19	48848341	48848342
chr19	48903854	48903855
chr19	48907041	48907042
chr19	48922683	48922684
chr19	49013945	49013946
chr19	49228292	49228293
chr19	49238377	49238378

chr19	49262561	49262562
chr19	49298786	49298787
chr19	49310056	49310057
chr19	49355695	49355696
chr19	49362071	49362072
chr19	49385180	49385181
chr19	49416567	49416568
chr19	49422160	49422161
chr19	49447990	49447991
chr19	49479652	49479653
chr19	49485753	49485754
chr19	49486905	49486906
chr19	49490394	49490395
chr19	49835072	49835073	chr19	49834909	49835121	MLT1J2	LTR	ERVL-MaLR	
chr19	49851199	49851200	chr19	49851134	49851535	MLT1J2	LTR	ERVL-MaLR	
chr19	49947116	49947117
chr19	49968817	49968818
chr19	50163200	50163201
chr19	50252787	50252788	chr19	50252717	50252872	MLT1J	LTR	ERVL-MaLR	
chr19	50339838	50339839
chr19	50501087	50501088	chr19	50500985	50501447	MLT1J	LTR	ERVL-MaLR	
chr19	50651571	50651572
chr19	50836864	50836865
chr19	51263307	51263308	chr19	51263195	51263433	MLT1J	LTR	ERVL-MaLR	
chr19	51963873	51963874	chr19	51963819	51964016	MLT2F	LTR	ERVL	
chr19	53400861	53400862
chr19	54382751	54382752
chr19	54396440	54396441
chr19	54411542	54411543
chr19	54480888	54480889
chr19	54503165	54503166
chr19	54682411	54682412
chr19	55577677	55577678
chr19	55607080	55607081
chr19	55709071	55709072
chr19	55800724	55800725
chr19	55817031	55817032
chr19	55831338	55831339
chr19	56028902	56028903
chr19	56826316	56826317
chr19	58071240	58071241
chr19	58330976	58330977
chr19	58666551	58666552
chr19	58816644	58816645
chr19	59010936	59010937
chr2	1018168	1018169
chr2	2617345	2617346	chr2	2617318	2617363	L1M6	LINE	L1	
chr2	10552734	10552735	chr2	10552532	10552786	MLT1J2	LTR	ERVL-MaLR	
chr2	20550673	20550674
chr2	23598513	23598514
chr2	24694712	24694713	chr2	24694638	24694867	MLT1J1	LTR	ERVL-MaLR	
chr2	26296434	26296435	chr2	26296350	26296544	LTR33B	LTR	ERVL	
chr2	26992075	26992076
chr2	26995744	26995745	chr2	26995708	26995868	MER117	DNA	hAT-Charlie	
chr2	27304227	27304228
chr2	27319318	27319319
chr2	28384016	28384017
chr2	28497845	28497846
chr2	28624944	28624945
chr2	36845642	36845643	chr2	36845622	36846012	MLT1J1	LTR	ERVL-MaLR	
chr2	37552153	37552154
chr2	43172092	43172093	chr2	43171997	43172164	LTR33B	LTR	ERVL	
chr2	43370347	43370348	chr2	43370002	43370437	MLT1N2	LTR	ERVL-MaLR	
chr2	46219454	46219455
chr2	70704700	70704701	chr2	70704621	70705022	MLT1J2	LTR	ERVL-MaLR	
chr2	70974631	70974632
chr2	71938857	71938858
chr2	85645703	85645704
chr2	85728579	85728580	chr2	85728173	85728663	LTR33A	LTR	ERVL	
chr2	88844874	88844875	chr2	88844752	88844960	MLT1J	LTR	ERVL-MaLR	
chr2	89867468	89867469	chr2	89867359	89867538	(CATT)n	Satellite	Satellite	
chr2	91760761	91760762	chr2	91760681	91760813	(CA)n	Simple_repeat	Simple_repeat	
chr2	91793937	91793938
chr2	92267644	92267645	chr2	92267522	92268924	HSATII	Satellite	Satellite	
chr2	92269347	92269348	chr2	92268957	92270058	HSATII	Satellite	Satellite	
chr2	92275945	92275946	chr2	92274434	92312482	ALR/Alpha	Satellite	centr	
chr2	92281336	92281337	chr2	92274434	92312482	ALR/Alpha	Satellite	centr	
chr2	92290538	92290539	chr2	92274434	92312482	ALR/Alpha	Satellite	centr	
chr2	92296854	92296855	chr2	92274434	92312482	ALR/Alpha	Satellite	centr	
chr2	92305757	92305758	chr2	92274434	92312482	ALR/Alpha	Satellite	centr	
chr2	92317747	92317748	chr2	92315719	92326171	ALR/Alpha	Satellite	centr	
chr2	92323578	92323579	chr2	92315719	92326171	ALR/Alpha	Satellite	centr	
chr2	95873244	95873245
chr2	95999571	95999572
chr2	97198153	97198154
chr2	104995367	104995368	chr2	104995282	104995711	LTR33A	LTR	ERVL	
chr2	107405909	107405910	chr2	107405701	107405923	MLT1J1	LTR	ERVL-MaLR	
chr2	110970133	110970134
chr2	118955071	118955072	chr2	118954696	118955181	MLT1J	LTR	ERVL-MaLR	
chr2	132996331	132996332	chr2	132994855	133000000	ALR/Alpha	Satellite	centr	
chr2	132997520	132997521	chr2	132994855	133000000	ALR/Alpha	Satellite	centr	
chr2	133003326	133003327	chr2	133000001	133006070	ALR/Alpha	Satellite	centr	
chr2	133023216	133023217
chr2	133090114	133090115
chr2	133105026	133105027
chr2	150600621	150600622
chr2	161098389	161098390
chr2	162138987	162138988
chr2	189494211	189494212
chr2	191885185	191885186
chr2	200324821	200324822
chr2	200524152	200524153
chr2	207288120	207288121	chr2	207287796	207288207	MLT1J2	LTR	ERVL-MaLR	
chr2	210791656	210791657
chr2	218515074	218515075	chr2	218515050	218515463	MLT1J1	LTR	ERVL-MaLR	
chr2	219260956	219260957
chr2	220151017	220151018

chr5	1653102	1653103
chr5	1662862	1662863	chr5	1662841	1663069	(TG)n	Simple_repe:Simple_repeat		
chr5	1692889	1692890	chr5	1692393	1693187	LTR1D	LTR	ERV1	
chr5	1929987	1929988	chr5	1929896	1930335	(TG)n	Simple_repe:Simple_repeat		
chr5	1960621	1960622	chr5	1960542	1960791	(CA)n	Simple_repe:Simple_repeat		
chr5	1986029	1986030
chr5	2031978	2031979
chr5	2082970	2082971
chr5	2227761	2227762
chr5	2291695	2291696
chr5	2531684	2531685	chr5	2531477	2531735	(CA)n	Simple_repe:Simple_repeat		
chr5	2541948	2541949	chr5	2541822	2542011	(TG)n	Simple_repe:Simple_repeat		
chr5	2568874	2568875	chr5	2568690	2569056	LTR33	LTR	ERVL	
chr5	2669475	2669476	chr5	2669445	2669623	(CA)n	Simple_repe:Simple_repeat		
chr5	2764763	2764764
chr5	2767425	2767426	chr5	2767266	2767611	MER74B	LTR	ERVL	
chr5	2889098	2889099	chr5	2889006	2889295	(TG)n	Simple_repe:Simple_repeat		
chr5	3042724	3042725
chr5	3238638	3238639
chr5	3324311	3324312	chr5	3324150	3324313	(TG)n	Simple_repe:Simple_repeat		
chr5	3373587	3373588	chr5	3373569	3373728	L1M3a	LINE	L1	
chr5	3481428	3481429
chr5	3727349	3727350
chr5	4080828	4080829	chr5	4080438	4080857	(CA)n	Simple_repe:Simple_repeat		
chr5	4080828	4080829	chr5	4080771	4080899	(CATG)n	Simple_repe:Simple_repeat		
chr5	4114785	4114786
chr5	4133069	4133070
chr5	4145282	4145283
chr5	4155095	4155096
chr5	4580920	4580921
chr5	4905128	4905129
chr5	4987961	4987962	chr5	4987632	4987968	MER77	LTR	ERVL	
chr5	5017296	5017297	chr5	5017268	5017664	L2a	LINE	L2	
chr5	5081236	5081237
chr5	5175914	5175915	chr5	5174945	5176223	L1M1	LINE	L1	
chr5	5183396	5183397
chr5	5340562	5340563
chr5	5470167	5470168
chr5	5491106	5491107
chr5	5514677	5514678	chr5	5514493	5514944	MLT1G	LTR	ERVL-MaLR	
chr5	5600372	5600373	chr5	5599139	5600661	ERV3.6A3_H	LTR	ERVL	
chr5	5667703	5667704
chr5	5677809	5677810
chr5	6045348	6045349
chr5	6081050	6081051	chr5	6080965	6081110	(CA)n	Simple_repe:Simple_repeat		
chr5	6409143	6409144	chr5	6409118	6409516	MLT1A1	LTR	ERVL-MaLR	
chr5	6550985	6550986
chr5	6615055	6615056
chr5	6686254	6686255	chr5	6686165	6686320	L2a	LINE	L2	
chr5	6805401	6805402
chr5	6837096	6837097
chr5	6858765	6858766	chr5	6858548	6859147	LTR16D	LTR	ERVL	
chr5	6904166	6904167
chr5	6934045	6934046	chr5	6934019	6934259	LTR16E1	LTR	ERVL	
chr5	6961418	6961419	chr5	6961217	6961652	(CA)n	Simple_repe:Simple_repeat		
chr5	7068497	7068498	chr5	7068344	7068523	MER20	DNA	hAT-Charlie	
chr5	7315228	7315229
chr5	7384591	7384592
chr5	7459344	7459345	chr5	7459275	7459368	MLT1H2	LTR	ERVL-MaLR	
chr5	7520436	7520437
chr5	7597412	7597413
chr5	7674423	7674424
chr5	7718721	7718722
chr5	7727156	7727157
chr5	7881522	7881523	chr5	7881287	7881642	ERV3.6A3_H	LTR	ERVL	
chr5	7927516	7927517
chr5	8121281	8121282	chr5	8121030	8121727	L1M3e	LINE	L1	
chr5	8143829	8143830	chr5	8143784	8143965	MLT1J2	LTR	ERVL-MaLR	
chr5	8209117	8209118	chr5	8209059	8209295	(TG)n	Simple_repe:Simple_repeat		
chr5	8543240	8543241
chr5	8615485	8615486	chr5	8615251	8615661	(CA)n	Simple_repe:Simple_repeat		
chr5	8806236	8806237	chr5	8805263	8806363	THE1B-int	LTR	ERVL-MaLR	
chr5	8844056	8844057
chr5	8935940	8935941	chr5	8935592	8937853	L1PA13	LINE	L1	
chr5	8974087	8974088	chr5	8969526	8975304	L1MA4A	LINE	L1	
chr5	8981414	8981415	chr5	8981166	8981844	MER54A	LTR	ERVL	
chr5	9271840	9271841	chr5	9271724	9278082	L1PA7	LINE	L1	
chr5	9332277	9332278
chr5	9346796	9346797	chr5	9346037	9346949	LTR1D	LTR	ERV1	
chr5	9372648	9372649
chr5	9933075	9933076	chr5	9933012	9933182	MLT1J2	LTR	ERVL-MaLR	
chr5	10126632	10126633	chr5	10126319	10126754	MLT1C	LTR	ERVL-MaLR	
chr5	10140465	10140466
chr5	10233176	10233177
chr5	10278090	10278091	chr5	10278005	10278171	LTR86B1	LTR	ERVL	
chr5	10290260	10290261
chr5	10331704	10331705
chr5	10373775	10373776
chr5	10377194	10377195
chr5	10432613	10432614
chr5	10503529	10503530
chr5	10537922	10537923
chr5	10595215	10595216
chr5	10601485	10601486	chr5	10601465	10601777	L2c	LINE	L2	
chr5	10638817	10638818
chr5	10777363	10777364	chr5	10777280	10777467	(CA)n	Simple_repe:Simple_repeat		
chr5	11174098	11174099	chr5	11173999	11174534	L2b	LINE	L2	
chr5	11181833	11181834	chr5	11181761	11182374	(TG)n	Simple_repe:Simple_repeat		
chr5	11192078	11192079	chr5	11191581	11192189	MLT2F	LTR	ERVL	
chr5	11240840	11240841	chr5	11240813	11241292	(CA)n	Simple_repe:Simple_repeat		
chr5	11258317	11258318
chr5	11373203	11373204
chr5	11467163	11467164
chr5	11484275	11484276
chr5	11561036	11561037
chr5	11642646	11642647	chr5	11642271	11642739	L2a	LINE	L2	
chr5	11721871	11721872	chr5	11721593	11722062	MLT1G1	LTR	ERVL-MaLR	

chr5	11786127	11786128
chr5	12050184	12050185	chr5	12050159	12051107	L1MCc	LINE	L1
chr5	12132951	12132952	chr5	12131916	12138444	L1PA15	LINE	L1
chr5	12299736	12299737
chr5	12320724	12320725	chr5	12320382	12321184	L1PA13	LINE	L1
chr5	12385281	12385282	chr5	12382084	12385987	L1PA13	LINE	L1
chr5	12468142	12468143	chr5	12467336	12474027	L1PREC2	LINE	L1
chr5	12488737	12488738
chr5	12532648	12532649	chr5	12531999	12533869	L1PB4	LINE	L1
chr5	12674697	12674698	chr5	12672681	12674833	L1P3	LINE	L1
chr5	12717804	12717805	chr5	12716890	12718465	MERS2A	LTR	ERV1
chr5	12805704	12805705	chr5	12804876	12805784	LTR1D	LTR	ERV1
chr5	12846126	12846127	chr5	12845574	12846452	L1M2c	LINE	L1
chr5	12877325	12877326	chr5	12876677	12877731	LTR1D	LTR	ERV1
chr5	12883805	12883806	chr5	12883622	12883944	MER1B	DNA	hAT-Charlie
chr5	12935400	12935401	chr5	12935264	12936108	HERVL18-int	LTR	ERVL
chr5	12995306	12995307
chr5	13070818	13070819	chr5	13070329	13071923	MSTA-int	LTR	ERVL-MaLR
chr5	13190019	13190020
chr5	13214541	13214542	chr5	13214376	13214611	L2c	LINE	L2
chr5	13218784	13218785	chr5	13217668	13219326	MLT1A0-int	LTR	ERVL-MaLR
chr5	13231247	13231248	chr5	13230910	13231477	MLT2B3	LTR	ERVL
chr5	13331859	13331860
chr5	13383058	13383059	chr5	13381400	13384624	L1PA16	LINE	L1
chr5	13410317	13410318	chr5	13409411	13411488	L1M2a	LINE	L1
chr5	13494322	13494323	chr5	13492445	13494628	L1PA15	LINE	L1
chr5	13538064	13538065	chr5	13537730	13538192	MLT1C	LTR	ERVL-MaLR
chr5	13554187	13554188
chr5	13663687	13663688
chr5	13888207	13888208	chr5	13887577	13888636	L2a	LINE	L2
chr5	13894186	13894187	chr5	13894120	13894321	MER103C	DNA	hAT-Charlie
chr5	13955009	13955010
chr5	13986324	13986325
chr5	14006417	14006418	chr5	14006229	14006438	MIRb	SINE	MIR
chr5	14011329	14011330
chr5	14061416	14061417	chr5	14061400	14061479	MLT1N2	LTR	ERVL-MaLR
chr5	14083426	14083427
chr5	14094858	14094859
chr5	14125574	14125575	chr5	14125549	14125647	MLT1J2	LTR	ERVL-MaLR
chr5	14157359	14157360
chr5	14262215	14262216
chr5	14268524	14268525
chr5	14394590	14394591
chr5	14452230	14452231
chr5	14491564	14491565
chr5	14542854	14542855	chr5	14542740	14543439	L1M2	LINE	L1
chr5	14751363	14751364
chr5	14802330	14802331	chr5	14802188	14802739	L2a	LINE	L2
chr5	14869097	14869098
chr5	14889004	14889005	chr5	14888927	14889353	MLT1C	LTR	ERVL-MaLR
chr5	14917675	14917676
chr5	14927127	14927128
chr5	14960856	14960857
chr5	15008827	15008828
chr5	15057293	15057294	chr5	15050505	1507959	L1MA5	LINE	L1
chr5	15077963	15077964	chr5	15076890	15078610	MSTD-int	LTR	ERVL-MaLR
chr5	15103414	15103415
chr5	15132202	15132203	chr5	15126664	15133381	L1PA15	LINE	L1
chr5	15155439	15155440
chr5	15174112	15174113	chr5	15173573	15179065	L1M1	LINE	L1
chr5	15270032	15270033	chr5	15269646	15270121	MLT1F2	LTR	ERVL-MaLR
chr5	15451627	15451628
chr5	15492841	15492842	chr5	15492815	15492915	MLT1J1	LTR	ERVL-MaLR
chr5	15793110	15793111
chr5	16204295	16204296
chr5	16403388	16403389	chr5	16403077	16403501	MSTA	LTR	ERVL-MaLR
chr5	16505878	16505879
chr5	16690660	16690661
chr5	16701317	16701318
chr5	16785301	16785302
chr5	16790426	16790427
chr5	16812486	16812487
chr5	16820402	16820403
chr5	16886042	16886043
chr5	16906496	16906497	chr5	16906424	16906609	MER20	DNA	hAT-Charlie
chr5	16965115	16965116
chr5	16983365	16983366
chr5	17181974	17181975
chr5	17232730	17232731
chr5	17241797	17241798
chr5	17252185	17252186	chr5	17251741	17252204	L2	LINE	L2
chr5	17279324	17279325
chr5	17287954	17287955
chr5	17300597	17300598
chr5	17316872	17316873
chr5	17368254	17368255
chr5	17380423	17380424	chr5	17380281	17380486	MamRep605	Unknown	Unknown
chr5	17413095	17413096	chr5	17412942	17413389	LTR16B1	LTR	ERVL
chr5	17512427	17512428
chr5	17517843	17517844
chr5	17526849	17526850
chr5	17625918	17625919
chr5	17655836	17655837
chr5	17772625	17772626	chr5	17772314	17773009	L1MDa	LINE	L1
chr5	17786272	17786273
chr5	17790280	17790281
chr5	17845232	17845233	chr5	17844338	17845549	L1PA12	LINE	L1
chr5	17886114	17886115	chr5	17885002	17886282	THE18-int	LTR	ERVL-MaLR
chr5	18198091	18198092	chr5	18197342	18198958	MST-int	LTR	ERVL-MaLR
chr5	18483828	18483829	chr5	18483701	18483873	L1M6	LINE	L1
chr5	18496288	18496289	chr5	18495898	18497045	L1MDa	LINE	L1
chr5	18564283	18564284	chr5	18564086	18564556	LTR56	LTR	ERV1
chr5	18947424	18947425	chr5	18947064	18952908	L1MA4A	LINE	L1
chr5	19045190	19045191	chr5	19044485	19046003	L1Pba	LINE	L1
chr5	19184717	19184718	chr5	19184198	19187174	L1PA15.6	LINE	L1
chr5	19200384	19200385
chr5	19209696	19209697	chr5	19208543	19210083	MERS2A	LTR	ERV1

chr5	30070338	30070339	chr5	30069262	30070533	L1PA13	LINE	L1
chr5	30106578	30106579	chr5	30106113	30106965	LTR1D	LTR	ERV1
chr5	30125995	30125996
chr5	30161288	30161289	chr5	30161048	30161639	MERS1A	LTR	ERV1
chr5	30173050	30173051	chr5	30172847	30173303	MLT1C	LTR	ERV1-MaLR
chr5	30226814	30226815
chr5	30289144	30289145	chr5	30288728	30289184	L1M2	LINE	L1
chr5	30393210	30393211	chr5	30392901	30393428	MLT1G	LTR	ERV1-MaLR
chr5	30457217	30457218
chr5	30539807	30539808	chr5	30538998	30541305	L1MA3	LINE	L1
chr5	30687861	30687862
chr5	30701243	30701244	chr5	30700354	30701948	THE1C-int	LTR	ERV1-MaLR
chr5	30857316	30857317
chr5	30942175	30942176
chr5	30992648	30992649	chr5	30992476	30992870	MLT1C	LTR	ERV1-MaLR
chr5	31087142	31087143
chr5	31273659	31273660
chr5	31294378	31294379
chr5	31317979	31317980
chr5	31496045	31496046
chr5	31503736	31503737
chr5	31513365	31513366
chr5	31559281	31559282	chr5	31559249	31559334	MIRb	SINE	MIR
chr5	31630913	31630914	chr5	31630743	31630985	L2b	LINE	L2
chr5	31672369	31672370	chr5	31672293	31672452	MERSA1	DNA	hAT-Charlie
chr5	31782105	31782106
chr5	31855631	31855632
chr5	31860764	31860765
chr5	31981773	31981774
chr5	31988179	31988180
chr5	32003113	32003114	chr5	32002673	32003186	(CA)n	Simple_repe	Simple_repeat
chr5	32037118	32037119
chr5	32089523	32089524
chr5	32101142	32101143
chr5	32168763	32168764
chr5	32204053	32204054	chr5	32203840	32204608	MERS4A	LTR	ERVL
chr5	32330001	32330002
chr5	32512318	32512319
chr5	32553216	32553217	chr5	32552435	32553429	LTR12D	LTR	ERV1
chr5	32640627	32640628
chr5	32704201	32704202	chr5	32703137	32704476	L1MA3	LINE	L1
chr5	32768138	32768139
chr5	32793817	32793818
chr5	32890029	32890030	chr5	32889799	32890309	MLT1F	LTR	ERV1-MaLR
chr5	33015109	33015110	chr5	33013764	33015674	L1M3c	LINE	L1
chr5	33042159	33042160
chr5	33050347	33050348	chr5	33049132	33051388	L1M2a	LINE	L1
chr5	33092902	33092903	chr5	33091741	33093779	L1PA16	LINE	L1
chr5	33166519	33166520	chr5	33164561	33167892	L1PBa	LINE	L1
chr5	33313466	33313467	chr5	33313143	33313575	MERS7D	LTR	ERV1
chr5	33370497	33370498
chr5	33428636	33428637	chr5	33426424	33428958	L1PA15	LINE	L1
chr5	33458045	33458046
chr5	33470780	33470781
chr5	33671932	33671933	chr5	33671921	33672284	(CA)n	Simple_repe	Simple_repeat
chr5	34035367	34035368
chr5	34497341	34497342
chr5	34504197	34504198
chr5	34532357	34532358	chr5	34532239	34532469	MER115	DNA	hAT-Tip100
chr5	34666416	34666417
chr5	35303488	35303489
chr5	35325041	35325042	chr5	35323875	35330589	L1PA13	LINE	L1
chr5	35625878	35625879
chr5	35651324	35651325	chr5	35650934	35651397	MLT1J	LTR	ERV1-MaLR
chr5	35708770	35708771	chr5	35708658	35708838	HAL1-2a_MD	LINE	L1
chr5	35753993	35753994
chr5	35810866	35810867
chr5	35822882	35822883
chr5	35901195	35901196
chr5	35919902	35919903
chr5	35946268	35946269
chr5	36444656	36444657	chr5	36444522	36444927	LTR16C	LTR	ERVL
chr5	36488319	36488320	chr5	36488197	36488397	MLT1J	LTR	ERV1-MaLR
chr5	36502856	36502857	chr5	36502770	36502903	AmnSINE1	SINE	Deu
chr5	36522170	36522171
chr5	36584131	36584132
chr5	36935172	36935173	chr5	36935075	36935399	L2b	LINE	L2
chr5	37233443	37233444	chr5	37233066	37234935	L1M2	LINE	L1
chr5	37630287	37630288	chr5	37628324	37631370	L1MA5A	LINE	L1
chr5	37666126	37666127
chr5	37685743	37685744	chr5	37680094	37686154	L1PA11	LINE	L1
chr5	37755927	37755928
chr5	37889564	37889565
chr5	38273585	38273586	chr5	38273047	38273644	L1MA8	LINE	L1
chr5	38322411	38322412	chr5	38321909	38322591	MER115	DNA	hAT-Tip100
chr5	38409597	38409598
chr5	38426995	38426996	chr5	38426647	38427077	MLT1J2	LTR	ERV1-MaLR
chr5	38493111	38493112
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chr5	38665802	38665803
chr5	38865995	38865996	chr5	38863650	38867218	L1MA4A	LINE	L1
chr5	38908545	38908546	chr5	38907241	38910830	L1PA16	LINE	L1
chr5	38933699	38933700
chr5	39092608	39092609	chr5	39092463	39092675	MLT2E	LTR	ERVL
chr5	39226309	39226310
chr5	39259466	39259467
chr5	39370891	39370892
chr5	39376713	39376714
chr5	39397084	39397085	chr5	39397005	39397621	LTR50	LTR	ERVL
chr5	39448893	39448894	chr5	39448590	39449147	MLT2B3	LTR	ERVL
chr5	39565513	39565514
chr5	39586857	39586858	chr5	39586232	39587058	LTR1	LTR	ERV1
chr5	39654809	39654810	chr5	39654692	39654878	HUERS-P3b-ii	LTR	ERV1
chr5	39656441	39656442
chr5	39868331	39868332	chr5	39867721	39868332	L2a	LINE	L2
chr5	40165548	40165549	chr5	40164850	40167715	L1PA16	LINE	L1
chr5	40509808	40509809

chr5	41095117	41095118	chr5	41095013	41095410	MLT1J	LTR	ERVL-MaLR
chr5	41124660	41124661
chr5	41141080	41141081
chr5	41149005	41149006	chr5	41148948	41149108	FordPrefect	DNA	hAT-Tip100
chr5	41241202	41241203	chr5	41240282	41241389	L1M2	LINE	L1
chr5	41291271	41291272	chr5	41290066	41291451	MERS2A	LTR	ERV1
chr5	41336878	41336879	chr5	41336637	41337055	LTR16A	LTR	ERVL
chr5	41541637	41541638	chr5	41540421	41542620	L1PA15.6	LINE	L1
chr5	41650536	41650537
chr5	41696906	41696907	chr5	41694059	41697490	L1PB4	LINE	L1
chr5	41856584	41856585
chr5	42454760	42454761	chr5	42454523	42455523	L1PBa	LINE	L1
chr5	42583021	42583022	chr5	42581818	42583247	MERS2D	LTR	ERV1
chr5	42972357	42972358	chr5	42972201	42972536	MER1B	DNA	hAT-Charlie
chr5	42986118	42986119	chr5	42985951	42986366	MSTA	LTR	ERVL-MaLR
chr5	42993383	42993384
chr5	43007739	43007740	chr5	43007714	43008125	MER61D	LTR	ERV1
chr5	43075510	43075511	chr5	43075366	43075775	MER48	LTR	ERV1
chr5	43096326	43096327
chr5	43105747	43105748
chr5	43174933	43174934
chr5	43233127	43233128
chr5	43631483	43631484
chr5	43769841	43769842
chr5	44219157	44219158	chr5	44219105	44219328	LTR33B	LTR	ERVL
chr5	44553457	44553458	chr5	44553292	44554721	L1M1	LINE	L1
chr5	44638627	44638628	chr5	44638600	44638884	LTR53	LTR	ERVL
chr5	45262325	45262326
chr5	45827585	45827586
chr5	49405908	49405909	chr5	49405641	49431170	ALR/Alpha	Satellite	centr
chr5	49440087	49440088	chr5	49438846	49441620	ALR/Alpha	Satellite	centr
chr5	49450626	49450627	chr5	49447717	49451978	ALR/Alpha	Satellite	centr
chr5	58187593	58187594
chr5	61390031	61390032
chr5	65703207	65703208
chr5	66564484	66564485
chr5	71146773	71146774	chr5	71146744	71146942	LSU-rRNA_HrRNA	rRNA	.
chr5	71183674	71183675	chr5	71183425	71183840	MLT1J	LTR	ERVL-MaLR
chr5	71604364	71604365
chr5	72484949	72484950	chr5	72484576	72485051	MLT1J	LTR	ERVL-MaLR
chr5	73969409	73969410	chr5	73969337	73969520	LTR67B	LTR	ERVL
chr5	73969409	73969410	chr5	73969402	73969624	MLTIN2	LTR	ERVL-MaLR
chr5	76164089	76164090
chr5	88552105	88552106	chr5	88551834	88552211	MLT1J2	LTR	ERVL-MaLR
chr5	92641826	92641827	chr5	92641698	92642200	LTR33B	LTR	ERVL
chr5	92868285	92868286
chr5	102434899	102434900	chr5	102434840	102435024	MLT1J	LTR	ERVL-MaLR
chr5	111564491	111564492
chr5	114755754	114755755	chr5	114755382	114755856	MLT1J	LTR	ERVL-MaLR
chr5	125367840	125367841	chr5	125367804	125368013	LTR16D2	LTR	ERVL
chr5	131526050	131526051	chr5	131525954	131526120	LTR50	LTR	ERVL
chr5	131590260	131590261
chr5	134260269	134260270
chr5	137968873	137968874	chr5	137968816	137968921	MLT1J	LTR	ERVL-MaLR
chr5	138897632	138897633
chr5	141126817	141126818
chr5	142488400	142488401
chr5	147278896	147278897
chr5	148779504	148779505	chr5	148779425	148779606	LTR67B	LTR	ERVL
chr5	149643040	149643041	chr5	149642894	149643245	(CA)n	Simple_repe:Simple_repeat	.
chr5	153211706	153211707	chr5	153211660	153211836	MLT1J1	LTR	ERVL-MaLR
chr5	154136733	154136734
chr5	157476629	157476630	chr5	157476620	157476998	MLT1J2	LTR	ERVL-MaLR
chr5	157640122	157640123	chr5	157640015	157640462	MLT1J2	LTR	ERVL-MaLR
chr5	159592329	159592330
chr5	168447305	168447306	chr5	168447215	168447642	MLT1J1	LTR	ERVL-MaLR
chr5	168587795	168587796
chr5	171730835	171730836	chr5	171730713	171730842	MLT1A0	LTR	ERVL-MaLR
chr5	171864497	171864498	chr5	171864431	171864568	MIRb	SINE	MIR
chr5	171930146	171930147	chr5	171930129	171930424	MLT1J2	LTR	ERVL-MaLR
chr5	172332189	172332190
chr5	172347175	172347176
chr5	172710938	172710939
chr5	173751098	173751099
chr5	173959650	173959651	chr5	173959516	173959655	MIR	SINE	MIR
chr5	175174013	175174014	chr5	175173888	175174400	MLT1J	LTR	ERVL-MaLR
chr5	178012696	178012697
chr5	179189141	179189142
chr6	6891003	6891004	chr6	6890626	6891066	LTR33A	LTR	ERVL
chr6	10147396	10147397	chr6	10147359	10147434	L1M6	LINE	L1
chr6	10404887	10404888
chr6	14800293	14800294	chr6	14800206	14800434	MLT1J	LTR	ERVL-MaLR
chr6	20000045	20000046	chr6	20000011	20000385	MLT1J1	LTR	ERVL-MaLR
chr6	21588594	21588595
chr6	33553779	33553780
chr6	33783849	33783850	chr6	33783434	33783922	LTR33A	LTR	ERVL
chr6	34039729	34039730	chr6	34039536	34039802	(CA)n	Simple_repe:Simple_repeat	.
chr6	36270392	36270393
chr6	43215052	43215053
chr6	44020369	44020370	chr6	44020274	44020498	LTR67B	LTR	ERVL
chr6	44101557	44101558
chr6	47285286	47285287	chr6	47285229	47285358	MLT1J	LTR	ERVL-MaLR
chr6	52379503	52379504
chr6	58779083	58779084	chr6	58775920	58780161	ALR/Alpha	Satellite	centr
chr6	64308713	64308714	chr6	64308320	64308880	LTR33C	LTR	ERVL
chr6	74847954	74847955	chr6	74847521	74847987	LTR33B	LTR	ERVL
chr6	80889602	80889603	chr6	80889537	80889628	MLT1J	LTR	ERVL-MaLR
chr6	89745208	89745209
chr6	106040488	106040489
chr6	108038002	108038003	chr6	108037924	108038074	MLT1J	LTR	ERVL-MaLR
chr6	109010653	109010654
chr6	119558597	119558598
chr6	134159104	134159105
chr6	150401000	150401001	chr6	150400886	150401139	LTR67B	LTR	ERVL
chr6	159495543	159495544	chr6	159495216	159495679	MLT1J	LTR	ERVL-MaLR
chr6	163591539	163591540
chr6	167000407	167000408	chr6	167000379	167000474	MLT1J2	LTR	ERVL-MaLR

chr8	133132747	133132748	chr8	133132706	133133039	MLT1J2	LTR	ERVL-MaLR
chr8	134403360	134403361	chr8	134403166	134403666	MLT1J	LTR	ERVL-MaLR
chr8	135346413	135346414	chr8	135346371	135346727	MLT1J1	LTR	ERVL-MaLR
chr8	140688105	140688106	chr8	140688056	140688474	MLT1J2	LTR	ERVL-MaLR
chr8	145180781	145180782
chr8	145634763	145634764
chr8	145911385	145911386
chr8	146071405	146071406
chr9	326889	326890	chr9	326603	326925	MLT1J1	LTR	ERVL-MaLR
chr9	1722641	1722642	chr9	1722352	1722694	MLT1J2	LTR	ERVL-MaLR
chr9	4081361	4081362
chr9	4713988	4713989	chr9	4713888	4714195	(CA)n	Simple_repe:Simple_repeat	
chr9	7243687	7243688	chr9	7243662	7243700	LTR67B	LTR	ERVL
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chr9	7320277	7320278
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chr9	18373822	18373823
chr9	18531298	18531299	chr9	18530958	18531603	MamRep605	Unknown	Unknown
chr9	20684816	20684817
chr9	21527928	21527929	chr9	21527665	21528917	L1PA13	LINE	L1
chr9	21536368	21536369
chr9	22012337	22012338
chr9	22215567	22215568
chr9	33101387	33101388
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chr9	34074396	34074397
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chr9	35646864	35646865
chr9	36764077	36764078	chr9	36764012	36764182	(TG)n	Simple_repe:Simple_repeat	
chr9	37920567	37920568	chr9	37920471	37920623	MLT1J1	LTR	ERVL-MaLR
chr9	44877991	44877992	chr9	44877633	44878926	SST1	Satellite	centr
chr9	44993217	44993218	chr9	44993212	44994530	SST1	Satellite	centr
chr9	66457434	66457435
chr9	66833168	66833169	chr9	66832948	66836542	ALR/Alpha	Satellite	centr
chr9	66858208	66858209	chr9	66858041	66863340	CER	Satellite	Satellite
chr9	68412518	68412519
chr9	68419488	68419489	chr9	68419062	68419642	(CA)n	Simple_repe:Simple_repeat	
chr9	68424061	68424062
chr9	68425704	68425705
chr9	69982837	69982838	chr9	69948085	70000000	ALR/Alpha	Satellite	centr
chr9	72653280	72653281	chr9	72653081	72653393	(GAATG)n	Satellite	Satellite
chr9	73216271	73216272
chr9	77805938	77805939	chr9	77805767	77805967	LTR33B	LTR	ERVL
chr9	79186686	79186687	chr9	79186648	79186950	LSU-rRNA_H	rRNA	rRNA
chr9	79631159	79631160
chr9	90060733	90060734	chr9	90060621	90061102	MLT1J	LTR	ERVL-MaLR
chr9	95834045	95834046	chr9	95833974	95834101	MLT1J	LTR	ERVL-MaLR
chr9	99638243	99638244
chr9	100904682	100904683
chr9	102057318	102057319	chr9	102057209	102057495	MLT1J	LTR	ERVL-MaLR
chr9	103174075	103174076
chr9	107730622	107730623
chr9	111003835	111003836	chr9	111003690	111003922	MLT1J1	LTR	ERVL-MaLR
chr9	112505552	112505553	chr9	112505077	112505736	L1M6	LINE	L1
chr9	117731696	117731697	chr9	117731678	117732155	MLT1J	LTR	ERVL-MaLR
chr9	121094006	121094007
chr9	122914773	122914774
chr9	123295015	123295016
chr9	123322712	123322713
chr9	123484053	123484054
chr9	123837050	123837051
chr9	124089162	124089163
chr9	124308515	124308516
chr9	127533687	127533688
chr9	127581051	127581052
chr9	129066051	129066052	chr9	129065749	129066084	MLT1J1	LTR	ERVL-MaLR
chr9	129551156	129551157	chr9	129551052	129551188	LTR33C	LTR	ERVL
chr9	129933215	129933216
chr9	130007477	130007478
chr9	130597899	130597900
chr9	130652825	130652826
chr9	131397753	131397754
chr9	131938308	131938309
chr9	131965240	131965241
chr9	132031111	132031112	chr9	132031034	132031469	MLT1J2	LTR	ERVL-MaLR
chr9	132079969	132079970	chr9	132079897	132080312	MLT1J2	LTR	ERVL-MaLR
chr9	132096136	132096137	chr9	132095992	132096293	L2b	LINE	L2
chr9	132102361	132102362	chr9	132102304	132102487	(TG)n	Simple_repe:Simple_repeat	
chr9	132177092	132177093
chr9	132196739	132196740	chr9	132196382	132196777	MLT1J	LTR	ERVL-MaLR
chr9	132196739	132196740	chr9	132196707	132196836	LTR67B	LTR	ERVL
chr9	132258463	132258464
chr9	132346548	132346549	chr9	132346428	132346851	MLT1J	LTR	ERVL-MaLR
chr9	133003033	133003034	chr9	133002990	133003097	MLT1J	LTR	ERVL-MaLR
chr9	133263024	133263025	chr9	133262630	133263088	MLT1J	LTR	ERVL-MaLR
chr9	133424680	133424681	chr9	133424546	133424832	MLT1J2	LTR	ERVL-MaLR
chr9	133557857	133557858	chr9	133557778	133557881	MIR3	SINE	MIR
chr9	134278391	134278392
chr9	134917935	134917936
chr9	136591770	136591771
chr9	136996432	136996433
chr9	137739180	137739181	chr9	137739119	137739382	(TG)n	Simple_repe:Simple_repeat	
chr9	137983315	137983316	chr9	137983255	137983759	(CA)n	Simple_repe:Simple_repeat	
chr9	139525761	139525762	chr9	139525724	139525799	(CAGC)n	Simple_repe:Simple_repeat	
chr9	139668322	139668323	chr9	139668280	139668662	MLT1J	LTR	ERVL-MaLR
chr9	140188852	140188853	chr9	140188785	140189020	MLT1J	LTR	ERVL-MaLR
chr9	140250143	140250144	chr9	140249860	140250183	GA-rich	Low_comple:Low_complexity	
chr9	140843744	140843745
chrX	3214009	3214010
chrX	16790153	16790154
chrX	17265438	17265439	chrX	17265431	17265571	MLT1J1	LTR	ERVL-MaLR
chrX	24444602	24444603	chrX	24444503	24444648	LTR67B	LTR	ERVL
chrX	39433621	39433622	chrX	39433547	39433826	MLT1J2	LTR	ERVL-MaLR
chrX	39609144	39609145	chrX	39609011	39609503	MLT1J	LTR	ERVL-MaLR
chrX	39815066	39815067	chrX	39814985	39815470	LTR33A	LTR	ERVL

chrX	40856407	40856408	chrX	40856064	40856532	MLT1J	LTR	ERVL-MaLR
chrX	40869538	40869539	chrX	40869481	40870090	LTR33C	LTR	ERVL
chrX	44510868	44510869	chrX	44510489	44510957	LTR33A	LTR	ERVL
chrX	48595701	48595702
chrX	58561410	58561411	chrX	58544095	58582011	ALR/Alpha	Satellite	centr
chrX	61685642	61685643	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61691826	61691827	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61694711	61694712	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61717845	61717846	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61728612	61728613	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61734032	61734033	chrX	61682014	61736573	ALR/Alpha	Satellite	centr
chrX	61839308	61839309	chrX	61814437	61861625	ALR/Alpha	Satellite	centr
chrX	61841935	61841936	chrX	61814437	61861625	ALR/Alpha	Satellite	centr
chrX	69654348	69654349
chrX	103401532	103401533
chrX	108297735	108297736	chrX	108297348	108297830	LSU-rRNA_H:rRNA	.	rRNA
chrX	111556864	111556865	chrX	111556835	111556890	(TC)n	Simple_repe:Simple_repeat	.
chrX	117359931	117359932
chrX	129091445	129091446
chrX	129116497	129116498
chrX	135268012	135268013
chrX	136520430	136520431	chrX	136520007	136520477	L1PA7	LINE	L1
chrX	139015342	139015343
chrX	152127486	152127487
chrX	152201070	152201071
chrY	9985453	9985454	chrY	9985256	9985468	MLT1H	LTR	ERVL-MaLR
chrY	10019373	10019374	chrY	10019144	10019435	L1PREC2	LINE	L1
chrY	10025235	10025236	chrY	10025145	10025252	L1MD	LINE	L1
chrY	10029655	10029656
chrY	10031855	10031856	chrY	10031790	10031959	Alu b	SINE	Alu
chrY	10036121	10036122	chrY	10034864	10036712	SSU-rRNA_H:rRNA	.	rRNA
chrY	10037848	10037849
chrY	13137842	13137843	chrY	13137788	13137965	(CATT)n	Simple_repe:Simple_repeat	.
chrY	13466046	13466047	chrY	13464558	13469801	BSR/Beta	Satellite	Satellite
chrY	13488889	13488890
chrY	13677783	13677784	chrY	13677738	13678025	(GAATG)n	Satellite	Satellite
chrY	13680970	13680971	chrY	13680945	13681124	(GAATG)n	Satellite	Satellite
chrY	13704342	13704343	chrY	13703974	13704585	(GAATG)n	Satellite	Satellite
chrY	13706078	13706079	chrY	13705968	13706145	(GAATG)n	Satellite	Satellite
chrY	13810270	13810271	chrY	13809964	13810290	(GAATG)n	Satellite	Satellite
chrY	13852007	13852008	chrY	13851756	13852108	(GAATG)n	Satellite	Satellite
chrY	13863120	13863121	chrY	13862998	13863460	(GAATG)n	Satellite	Satellite
chrY	13869459	13869460	chrY	13869404	13869939	(GAATG)n	Satellite	Satellite
chrY	58997084	58997085	chrY	58983270	58997782	BSR/Beta	Satellite	Satellite