BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
CT990552.5	150787	150819	+	AT_rich	Low_complexity	1	33	0	156	28	ABSENT	
	150820	150982	+	L1ME5	LINE/L1	5941	6126	-68				
	151002	151034	+	(GAA)n	Simple_repeat	2	33	0				
	151138	151261	C	AluSz	SINE/Alu	-182	130	1				
	151289	151515	C	SVA_A	Other	-686	701	467				
AC187943.2	26381	26950	+	SVA_A	Other	142	701	-686	190	29	AAGGCCTTCATTTGG	CCTT/AA
	26979	27086	+	AluSz6	SINE/Alu	1	108	-204				
	27162	27229	+	T-rich	Low_complexity	3	70	0				
	27276	27406	C	L1ME5	LINE/L1	-117	6077	5941				
AC190010.2	52786	52948	+	L1ME5	LINE/L1	5941	6126	-68	171	25	AAACATTTGAACA	GTTT/AG
	53119	53225	C	AluSz6	SINE/Alu	-204	108	2				
	53250	53663	C	SVA_A	Other	-511	876	437				
CT954299.8	136672	137040	+	SVA_A	Other	451	831	-556	156	29	GAAAAAAGTGCCTTT	TTTC/AA
	137069	137188	+	AluSz6	SINE/Alu	1	130	-182				
	137344	137503	C	L1ME5	LINE/L1	-68	6126	5941				
AC199991.2	125610	125772	+	L1ME5	LINE/L1	5941	6126	-68	171	29	AAGTGGGATTAa/gCA	ACTT/AT
	125792	125824	+	(GAA)n	Simple_repeat	2	33	0				
	125943	126050	C	AluSz6	SINE/Alu	-204	108	1				
	126079	126601	C	SVA_A	Other	-515	872	436				
AC198155.2	114762	114917	+	L1ME5	LINE/L1	5941	6126	-68	169	24	AAGATATAAATGTTTC	TCTT/AA
	115086	115192	C	AluSz6	SINE/Alu	-204	108	1				
	115216	115647	C	SVA_A	Other	-511	876	435				
AC198875.2	118433	119337	+	SVA_A	Other	9	872	-515	150	29	AAAATGGATGAAAGA	TTTT/AA
	119351	119527	+	SVA_A	Other	395	584	-803				
	119556	119678	+	AluSz6	SINE/Alu	1	130	-182				
	119828	119989	C	L1ME5	LINE/L1	-68	6126	5941				
AC202760.1	170786	171917	+	SVA_A	Other	116	872	-515	156	65	AAAATGAAGTTGG	TTTT/TT
	171929	173605	+	SVA_A	Other	436	872	-515				
	173612	174033	+	SVA_A	Other	436	872	-515				
	174098	174219	+	AluSz6	SINE/Alu	1	130	-182				
	174323	174355	+	(TTC)n	Simple_repeat	2	33	0				
	174375	174531	C	L1ME5	LINE/L1	-68	6126	5945				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
AC199992.2	72024	73400	+	SVA_A	Other	436	872	-515	153	30	Ns at target site	
	73402	74110	+	SVA_A	Other	436	872	-515				
	74140	74262	+	AluSz6	SINE/Alu	1	130	-182				
	74415	74574	C	L1ME5	LINE/L1	-68	6126	5941				
AC198102.2	18364	19155	+	SVA_A	Other	436	872	-515	154	29	AGAAGGGGCAGGGT	TCTT/GA
	19184	19306	+	AluSz6	SINE/Alu	1	130	-182				
	19371	19444	+	CT-rich	Low_complexity	1	72	0				
	19460	19622	C	L1ME5	LINE/L1	-68	6126	5941				
	19632	19673	+	(A)n	Simple_repeat	1	42	0				
AC200373.2	128684	128708	+	AT_rich	Low_complexity	1	25	0	156	30	insertion into polyA-tail	
	128709	128867	+	L1ME5	LINE/L1	5941	6126	-68				
	128887	128919	+	(GAA)n	Simple_repeat	2	33	0				
	129023	129145	C	AluSz6	SINE/Alu	-182	130	1				
	129175	130307	C	SVA_A	Other	-515	872	4				
AC200373.2	145247	145274	+	AT_rich	Low_complexity	1	28	0			AAAATGCAAATGCTC	TTTT/AA
	145278	145440	+	L1ME5	LINE/L1	5941	6126	-68				
	145464	145496	+	(GAA)n	Simple_repeat	2	33	0				
	145615	145720	C	AluSz6	SINE/Alu	-204	108	3				
	145787	146775	C	SVA_A	Other	-515	872	436				
	146820	147225	C	SVA_A	Other	-515	872	437				
	147274	147684	C	SVA_A	Other	-519	868	437				
	147696	148795	C	SVA_A	Other	-515	872	436				
AC200383.2	116780	117964	+	SVA_A	Other	3	885	-502	156	14	AAGAGATGAAG	TCTT/GA
	117978	118100	+	AluSz6	SINE/Alu	1	130	-182				
	118204	118236	+	(TTC)n	Simple_repeat	2	33	0				
	118256	118418	C	L1ME5	LINE/L1	-68	6126	5941				
AC203718.2	150972	151610	+	SVA_B	Other	213	867	-516	153	29	AT-rich sequence	
	151621	151871	+	SVA_A	Other	404	701	-686				
	151900	152022	+	AluSz6	SINE/Alu	1	130	-182				
	152175	152337	C	L1ME5	LINE/L1	-68	6126	5941				
	152338	152378	+	AT_rich	Low_complexity	1	41	0				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
AC203714.2	309	464	+	L1ME5	LINE/L1	5941	6126	-68	157	29	AAGAAGAAAATT-/tCCT	TCTT/AT
	484	557	+	GA-rich	Low_complexity	2	74	0				
	621	740	C	AluSz6	SINE/Alu	-182	130	1				
	769	998	C	SVA_A	Other	-727	660	435				
	1041	2320	C	SVA_A	Other	-515	872	436				
	2321	4157	C	SVA_B	Other	-515	872	151				
AC203721.2	110178	110903	+	SVA_A	Other	64	875	-512	156	25	AAAATGTTGGGATTACA	TTTT/TG
	110928	111047	+	AluSz6	SINE/Alu	1	130	-182				
	111203	111362	C	L1ME5	LINE/L1	-68	6126	5941				
	111363	111397	+	AT_rich	Low_complexity	1	35	0				
AC204794.2	1232	1391	+	L1ME5	LINE/L1	5941	6126	-68	156	29	AAAATTATTTCTC	TTTT/AG
	1547	1666	C	AluSz6	SINE/Alu	-182	130	1				
	1695	2037	C	SVA_A	Other	-593	794	436				
	2049	2460	C	SVA_A	Other	-517	870	437				
	2507	3214	C	SVA_A	Other	-515	872	160				
AC204185.2	166116	166138	+	AT_rich	Low_complexity	1	23	0	171	29	AAAAGAATAG	TTTT/AA
	166174	166336	+	L1ME5	LINE/L1	5941	6126	-68				
	166507	166614	C	AluSz6	SINE/Alu	-204	108	1				
	166643	166803	C	SVA_A	Other	-593	794	627				
AC206079.2	61415	61436	+	AT_rich	Low_complexity	1	22	0	169	107	AAGAATATCCTCAGGATT	TCTT/AA
	61437	61596	+	L1ME5	LINE/L1	5941	6126	-68				
	61765	61871	C	AluSz6	SINE/Alu	-204	108	1				
	61978	62516	C	SVA_A	Other	-515	872	436				
AC207854.2	168332	169008	+	SVA_A	Other	436	872	-515	152	29		
	169037	169159	+	AluSz6	SINE/Alu	1	130	-182				
	169259	169291	+	(TTC)n	Simple_repeat	2	33	0				
	169311	169473	C	L1ME5	LINE/L1	-68	6126	5941				
	169477	169510	+	(TAAAAA)n	Simple_repeat	2	36	0				
AC205441.3	61612	62764	+	SVA_A	Other	436	872	-515	153	24	poly-A sequence	
	62808	64110	+	SVA_A	Other	436	876	-511				
	64134	64256	+	AluSz6	SINE/Alu	1	130	-182				
	64409	64568	C	L1ME5	LINE/L1	-68	6126	5941				
	64569	64589	+	AT_rich	Low_complexity	1	21	0				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
AC203720.2	98665	98697	+	(T)n	Simple_repeat	1	33	0	156	24	AAGGATGTGG	
	98698	98857	+	L1ME5	LINE/L1	5941	6126	-68				
	99013	99135	C	AluSz6	SINE/Alu	-182	130	1				
	99159	100592	C	SVA_A	Other	-511	876	436				
	100638	101925	C	SVA_A	Other	-515	872	142				
AC203720.2	125944	127435	+	SVA_A	Other	142	872	-515	169	29	AAGGATGTGG	
	127436	128201	+	SVA_A	Other	436	870	-517				
	128230	128337	+	AluSz6	SINE/Alu	1	108	-204				
	128506	128662	C	L1ME5	LINE/L1	-68	6126	5945				
	128664	128688	+	AT_rich	Low_complexity	1	25	0				
AC207853.2	76286	76309	+	AT_rich	Low_complexity	1	24	0			Ns in flanking at beginnin of element	
	76310	76472	+	L1ME5	LINE/L1	5941	6126	-68				
	76492	76524	+	(GAA)n	Simple_repeat	2	33	0				
	76628	76749	C	AluSz6	SINE/Alu	-182	130	2				
	76779	77344	C	SVA_A	Other	-517	870	436				
AC204186.3	96756	97260	+	SVA_B	Other	347	865	-518	169	65	Ns at target site	
	97309	97725	+	SVA_A	Other	436	872	-515				
	97790	97897	+	AluSz6	SINE/Alu	1	108	-204				
	98066	98225	C	L1ME5	LINE/L1	-68	6126	5941				
	98226	98250	+	AT_rich	Low_complexity	1	25	0				
AC216158.2	177170	178486	+	SVA_A	Other	436	872	-515	209	24	AGAAATATTTGCTGAAGTC	TTCT/AT
	178488	178912	+	SVA_A	Other	436	876	-511				
	178936	179042	+	AluSz6	SINE/Alu	1	108	-204				
	179251	179370	C	L1ME5	LINE/L1	-133	6061	5941				
	179371	179412	+	A-rich	Low_complexity	1	42	0				
AC208823.3	8006	8909	+	SVA_A	Other	436	870	-517	156	29	AAAGAATGGGCAAGG	CTTT/GT
	8938	9058	+	AluSz6	SINE/Alu	1	130	-182				
	9162	9194	+	(TTC)n	Simple_repeat	2	33	0				
	9214	9372	C	L1ME5	LINE/L1	-68	6126	5941				
	9373	9423	+	A-rich	Low_complexity	1	48	0				
AC217745.2	120834	122427	+	SVA_A	Other	61	876	-511	168	24	AAAAGTAAGAAATTG	TTTT/GT
	122451	122558	+	AluSz6	SINE/Alu	1	108	-204				
	122726	122882	C	L1ME5	LINE/L1	-68	6126	5945				
	122884	122933	+	A-rich	Low_complexity	1	50	0				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
AC215319.3	41070	42642	+	SVA_A	Other	15	872	-515	169	29	UNKNOWN	
	42671	42778	+	AluSz6	SINE/Alu	1	108	-204				
	42947	43109	C	L1ME5	LINE/L1	-68	6126	5941				
	43110	43132	+	AT_rich	Low_complexity	1	23	0				
AC216139.3	67922	68022	+	SVA_A	Other	777	875	-512	157	25	ACAAAATTAGCCAGGCATG	TTGT/AT
	68047	68166	+	AluSz6	SINE/Alu	1	130	-182				
	68230	68303	+	CT-rich	Low_complexity	2	72	0				
	68323	68482	C	L1ME5	LINE/L1	-68	6126	5941				
	68483	68518	+	AT_rich	Low_complexity	1	36	0				
AC214603.3	90728	91565	+	SVA_A	Other	3	872	-515	156	24	AAGAAATGTAAATGGT	TCTT/GT
	91577	91968	+	SVA_A	Other	470	876	-511				
	91992	92114	+	AluSz6	SINE/Alu	1	130	-182				
	92218	92250	+	(TTC)n	Simple_repeat	2	33	0				
	92270	92429	C	L1ME5	LINE/L1	-68	6126	5941				
	92430	92457	+	AT_rich	Low_complexity	1	28	0				
AC198100.1	103660	105105	+	SVA_A	Other	1	870	-517	156	65	AAGAAGGTAAAGC	TCTT/AA
	105117	106382	+	SVA_A	Other	436	872	-515				
	106394	107407	+	SVA_A	Other	436	872	-515				
	107453	108589	+	SVA_A	Other	436	872	-515				
	108590	109012	+	SVA_A	Other	436	872	-515				
	109058	109472	+	SVA_A	Other	436	872	-515				
	109515	109932	+	SVA_A	Other	436	872	-515				
	109997	110116	+	AluSz6	SINE/Alu	1	130	-182				
	110272	110426	C	L1ME5	LINE/L1	-68	6126	5941				
AC202765.2	108793	108833	+	(T)n	Simple_repeat	1	41	0	180	16	AGAAAGGGACAC	TCTT/AA
	108834	108993	+	L1ME5	LINE/L1	5941	6126	-68				
	109013	109045	+	(GAA)n	Simple_repeat	2	33	0				
	109173	109280	C	AluSz6	SINE/Alu	-204	108	1				
	109296	110304	C	SVA_A	Other	-507	875	428				
	110305	111127	C	SVA_A	Other	-517	870	4				
CT954291.6	37551	37713	+	L1ME5	LINE/L1	5941	6126	-68	156	65	AAGACTGTCCCTGATCAA	TCTT/CA
	37733	37765	+	(GAA)n	Simple_repeat	2	33	0				
	37869	37991	C	AluJb	SINE/Alu	-182	130	1				
	38056	38804	C	SVA_A	Other	-515	872	436				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
CT954309.16	23411	24094	+	SVA_A	Other	436	872	-515	150	29	AAAAATTAGTCGGGCA	TTTT/GT
	24123	24245	+	AluJb	SINE/Alu	1	130	-182				
	24395	24557	C	L1ME5	LINE/L1	-68	6126	5941				
AC200379.2	118910	120107	C	SVA_A	Other	-511	876	61	45	277	AAAAAGCTTATCCACCACA	TTTT/GA
	120120	120260	+	(TA)n	Simple_repeat	1	149	0				
	120384	120678	+	AluSx1	SINE/Alu	1	295	-17				
	120723	120851	C	L1ME4a	LINE/L1	-264	5860	5729				
	120852	120872	+	AT_rich	Low_complexity	1	21	0				
AC200379.2	140471	141754	+	SVA_A	Other	64	876	-511	153	24	AAAAATTAGTCGGGCA	TTTT/GT
	141778	141900	+	AluJb	SINE/Alu	1	130	-182				
	142053	142211	C	L1ME5	LINE/L1	-68	6126	5941				
	142222	142244	+	(TAAAAA)n	Simple_repeat	2	24	0				
AC206377.2	45758	45850	+	SVA_A	Other	569	660	-727	180	29	insertion into A-rich sequence	
	45879	45987	+	AluSz6	SINE/Alu	1	108	-204				
	46081	46370	C	AluYc3	SINE/Alu	-10	290	1				
	46404	46436	+	(TTC)n	Simple_repeat	2	33	0				
	46456	46618	C	L1ME5	LINE/L1	-68	6126	5941				
	46619	46654	+	AT_rich	Low_complexity	1	36	0				
AC204446.3	160534	160561	+	AT_rich	Low_complexity	1	28	0	167	24	AAAAAAAAAGAACTAGAGGC	TTTT/GA
	160562	160724	+	L1ME5	LINE/L1	5941	6126	-68				
	160743	160814	+	GA-rich	Low_complexity	4	78	0				
	160885	161180	C	AluYc3	SINE/Alu	-9	291	2				
	161186	161308	C	AluSz6	SINE/Alu	-182	130	1				
	161332	162651	C	SVA_A	Other	-511	876	15				
AC214654.2	31664	31815	+	SVA_A	Other	142	297	-1090	156	29	insertion into middle A-rich sequence	
	31855	32933	+	SVA_A	Other	435	872	-515				
	32962	33081	+	AluSx1	SINE/Alu	1	130	-182				
	33237	33396	C	L1ME5	LINE/L1	-68	6126	5941				
	33397	33420	+	(A)n	Simple_repeat	1	24	0				
AC208823.3	144449	144489	+	T-rich	Low_complexity	1	41	0	156	24	AAAGAATGGGCAAGG	CTTT/GT
	144490	144649	+	L1ME5	LINE/L1	5941	6126	-68				
	144805	144924	C	AluSx	SINE/Alu	-182	130	1				
	144948	146201	C	SVA_A	Other	-511	876	436				

BAC Acc. Number	Position in query			Matching repeat		Position in Repeat			U2 Size	U1 Size	Target Site Duplication	Target site
	Start	Stop	Strain	Repeat	Class/Family	Start	Stop	left				
AC209355.3	165847	167150	+	SVA_B	Other	9	872	-515	171	24	unknown	CTTT/CT
	167196	167615	+	SVA_A	Other	436	876	-511				
	167639	167746	+	AluSx1	SINE/Alu	1	108	-204				
	167917	168076	C	L1ME5	LINE/L1	-68	6126	5941				
	168077	168099	+	AT_rich	Low_complexity	1	23	0				
AC214650.2	100429	100591	+	L1ME5	LINE/L1	5941	6126	-68	150	29	AAAAATTAGTCGGGCA	TTTT/GA
	100741	100863	C	AluJb	SINE/Alu	-182	130	1				
	100892	101576	C	SVA_A	Other	-515	872	436				
AC214652.3	167741	168230	+	SVA_A	Other	437	870	-517	169	29	insertion into polyA	
	168259	168365	+	AluJr	SINE/Alu	1	108	-204				
	168482	168514	+	(TTC)n	Simple_repeat	2	33	0				
	168534	168693	C	L1ME5	LINE/L1	-68	6126	5941				
	168694	168722	+	AT_rich	Low_complexity	1	29	0				
AC208960.3	117331	117448	C	SVA_A	Other	-764	623	506	169	14	AGAAAAGACAGATCCC	TTCT/AA
	117516	117944	+	SVA_A	Other	436	885	-502				
	117958	118064	+	AluSx	SINE/Alu	1	108	-204				
	118233	118392	C	L1ME5	LINE/L1	-68	6126	5941				
	118393	118417	+	(A)n	Simple_repeat	1	46	-42				
AC182776.2	79313	79432	+	L1ME5	LINE/L1	5941	6061	-133	209	29	Aa/gAAGCCTGTAGC	TTTT/AA
	79641	79747	C	AluJr	SINE/Alu	-204	108	1				
	79776	81079	C	SVA_A	Other	-515	872	436				
	81080	82389	C	SVA_A	Other	-515	872	436				