

Repeat	RepeatModeler	Class	Sub-Class	Super-Family	Notes
rnd-1_family-66	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-224	DNA/hAT-hATw	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-91	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 153.
rnd-1_family-152	DNA/hAT-hATw	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-292	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.
rnd-1_family-85	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-240	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-154	SINE/B4	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-268	LTR/DIRS	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.
rnd-1_family-191	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-1_family-124	Retroposon	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-42	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-1_family-104	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.

rnd-1_family-294	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 73.
rnd-1_family-178	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-49	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-1_family-201	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.
rnd-1_family-5	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 241.
rnd-1_family-58	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is ATT.
rnd-1_family-56	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-1_family-26	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-1_family-295	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-62	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TAT.
rnd-1_family-142	DNA/hAT-Tip100	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD
rnd-1_family-40	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 87.

rnd-1_family-63	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-180	DNA/TcMar-Fot1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 22.
rnd-1_family-8	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	No TSD consensus. Maximum TSD length is 3.
rnd-1_family-76	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TTA.
rnd-1_family-306	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-163	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TAT.
rnd-1_family-118	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-73	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-211	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 4.
rnd-1_family-68	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TAT.

rnd-1_family-44	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 87.
rnd-1_family-30	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD
rnd-1_family-32	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 201.
rnd-1_family-194	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-1_family-80	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-1_family-55	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-1_family-151	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-1_family-205	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.
rnd-1_family-284	DNA/hAT-Ac	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia)	No TSD consensus. Maximum TSD
rnd-1_family-37	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 94.
rnd-1_family-21	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 243.
rnd-1_family-43	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 66.
rnd-1_family-239	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 68.

rnd-1_family-278	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-10	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF(H-> piggybac)	-
rnd-1_family-184	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-1_family-266	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 63.
rnd-1_family-97	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Poly A trail length is 8.
rnd-1_family-88	DNA/MULE-MuDR	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 36.
rnd-1_family-297	DNA/hAT-Charlie	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 105.
rnd-1_family-300	DNA/hAT-Blackjack	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 6.
rnd-1_family-117	SINE/ID	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-170	SINE/tRNA-Deu-CR1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is CAT.
rnd-1_family-65	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-130	LINE/R1	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.

rnd-1_family-27	DNA/CMC-Transib	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 70.
rnd-1_family-15	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-69	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-22	DNA	C()	SC(H-> non-ltr retrotransposon dna transposon)	SF()	-
rnd-1_family-114	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-1_family-260	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-1_family-74	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine)	Short sequence repeated is TAT.
rnd-1_family-181	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr)	SF()	Short sequence repeated is CC.
rnd-1_family-75	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-1_family-47	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-1_family-179	DNA/hAT-hATx	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-61	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine)	Short sequence repeated is TAT.

rnd-1_family-138	DNA/Harbinger	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-46	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 80.
rnd-1_family-51	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 283.
rnd-1_family-102	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 46.
rnd-1_family-36	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.
rnd-1_family-187	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-144	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-158	SINE/Alu	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is AC.
rnd-1_family-162	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-71	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-57	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-60	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.
rnd-1_family-83	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-1_family-173	SINE/MIR	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD

rnd-1_family-38	DNA/TcMar	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 364.
rnd-1_family-223	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 197.
rnd-1_family-25	DNA/TcMar-Sagan	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.
rnd-1_family-108	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-23	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 81.
rnd-1_family-79	LINE/Tad1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-1_family-164	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-1_family-19	LINE/RTE-BovB	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-1_family-214	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 117.
rnd-1_family-90	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-1_family-132	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 85.
rnd-1_family-53	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TAT.
rnd-1_family-146	SINE/tRNA	C(S_LTR-> i S_SSR-> i)	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr	SF()	Terminal Repeat consensus length is



rnd-1_family-248	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/f b)	No TSD consensus. Maximum TSD length is 9. TIR consensus
rnd-1_family-309	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 14.
rnd-1_family-127	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TAT.
rnd-1_family-220	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 105.
rnd-1_family-149	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Poly A trail length is 9.
rnd-1_family-112	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-120	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-82	RC/Helitron	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-145	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-67	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-6	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 251.
rnd-1_family-185	DNA/CMC-EnSpm	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus

rnd-1_family-287	DNA/Crypton	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 6.
rnd-1_family-279	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.
rnd-1_family-177	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 20.
rnd-1_family-98	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-322	DNA/Sola	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-334	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-330	SINE/5S-Deu-L2	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-340	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-335	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-	RC/Helitron	C()	SC(H-> helitron)	SF()	-
rnd-1_family-344	DNA/hAT	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-354	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-1_family-360	DNA/TcMar-Fot1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 118.
rnd-1_family-366	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-401	DNA	C()	SC(H-> dna transposon)	SF()	-

rnd-1_family-419	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-	RC/Helitron	C()	SC(H-> helitron)	SF()	-
rnd-1_family-434	DNA/hAT-Blackjack	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-445	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-1_family-446	LINE/RTE-BovB	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-1_family-447	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-453	DNA/hAT	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-460	DNA	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 6.
rnd-1_family-464	LINE/I	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is 40.
rnd-1_family-469	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-475	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-485	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-489	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-1_family-490	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is 46
rnd-1_family-462	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-500	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-503	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-1_family-506	LTR/Gypsy	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	No TSD consensus. Maximum TSD length is 2.Terminal Repeat
rnd-1_family-510	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-518	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	No TSD consensus. Maximum TSD
rnd-1_family-524	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-1_family-528	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-532	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-1_family-537	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-541	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-1_family-542	DNA/CMC-Transib	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-544	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-545	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.
rnd-1_family-559	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TAA.
rnd-1_family-566	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-1_family-578	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-1_family-583	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-1_family-584	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Poly A trail length is 7.
rnd-1_family-594	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	No TSD consensus. Maximum TSD length is 3.
rnd-1_family-596	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-1_family-598	LTR/Copia	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is 46

rnd-1_family-613	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-1_family-619	RC/Helitron	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 43.
rnd-1_family-625	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-630	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD
rnd-1_family-633	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-646	LTR	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 2.
rnd-1_family-661	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-662	Unknown	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-1_family-669	LINE/CR1	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.
rnd-1_family-676	DNA/CMC-Transib	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Poly A trail length is 8.
rnd-1_family-668	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.

rnd-1_family-677	LTR/ERV1	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	Palindrome length is 16.
rnd-1_family-679	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-681	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 113.
rnd-1_family-683	Unknown	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-1_family-686	LTR	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-689	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-1_family-708	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Poly A trail length is 8.
rnd-1_family-732	DNA/hAT-Blackjack	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-734	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-1_family-737	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.
rnd-1_family-739	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD
rnd-1_family-763	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-1_family-765	DNA/hAT-Ac	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-776	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-783	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia)	No TSD consensus. Maximum TSD
rnd-1_family-792	DNA/PIF-Harbinger	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-795	Unknown	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 24. Terminal Repeat consensus
rnd-1_family-805	DNA/hAT-Blackjack	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-813	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-832	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 84.
rnd-1_family-835	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-838	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr)	SF()	Poly A trail length is 7.
rnd-1_family-854	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-855	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-857	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-



rnd-1_family-867	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-874	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-1_family-879	LINE/L1	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-1_family-888	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-894	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-2_family-164	DNA/PiggyBac	C(S_TIR-> ii T-> ii)	SC(H-> dna transposon S_TIR-> dna transposon T-> dna transposon)	SF(T-> is5/pif/harbinge r is630/tc1/marin er)	TSD consensus length is 3.TIR consensus length is 244.
rnd-2_family-49	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF(H-> piggybac)	TIR consensus length is 144.
rnd-2_family-353	Satellite	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD
rnd-2_family-89	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-2_family-117	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TAT.

rnd-2_family-173	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 249.
rnd-2_family-106	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-2_family-242	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.
rnd-3_family-77	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-3_family-97	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF(H-> piggybac)	-
rnd-3_family-98	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TCA.
rnd-3_family-303	DNA	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-3_family-153	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 153.
rnd-3_family-48	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 60.
rnd-3_family-132	DNA/hAT-Blackjack	C(S_TIR-> ii T-> i)	SC(S_TIR-> dna transposon T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 4.TIR consensus
rnd-3_family-100	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-

rnd-4_family-51	DNA/CMC-EnSpm	C(S_LTR-> i S_SSR-> i)	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr	SF()	Terminal Repeat consensus length is 8.Short
rnd-4_family-694	DNA/hAT-Tip100	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-4_family-825	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-4_family-785	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 151.
rnd-4_family-672	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-4_family-330	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 108.
rnd-4_family-258	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non- ltr	SF()	Short sequence repeated is
rnd-4_family-771	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-4_family-155	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-4_family-692	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is ATT.
rnd-4_family-332	DNA/Crypton	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-624	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-4_family-604	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 70.

rnd-4_family-435	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-2695	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.
rnd-4_family-300	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-653	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-4_family-	RC/Helitron	C()	SC(H-> helitron)	SF()	-
rnd-4_family-1502	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-914	DNA/TcMar-Tc2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-4_family-1305	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-551	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-1499	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-4_family-126	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-50	DNA/hAT-hATw	C(S_SSR-> i)	SC(S_SSR-> non-ltr)	SF()	Short sequence repeated is TT.
rnd-4_family-1104	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-257	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-4_family-453	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-4_family-850	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 204.
rnd-4_family-1022	DNA/TcMar-ISRm11	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-410	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 223.
rnd-4_family-182	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-4_family-485	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 51.
rnd-4_family-2964	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 104.
rnd-4_family-439	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-4_family-706	DNA/hAT-Blackjack	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-4_family-1492	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-4_family-1100	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-503	DNA/CMC-EnSpm	C(T-> i S_LTR-> i)	SC(T-> ltr retrotransposon S_LTR-> Short Terminal Repeat)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 6.Terminal Repeat
rnd-4_family-159	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-4_family-3141	DNA/TcMar-Pogo	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-870	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-4_family-226	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TT.
rnd-4_family-1449	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 17.
rnd-4_family-123	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-5_family-168	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is ATC.
rnd-5_family-134	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-5_family-667	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> helitron)	SF()	Palindrome length is 10.
rnd-5_family-489	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-5_family-760	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.
rnd-5_family-1188	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 73.
rnd-5_family-1476	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-5_family-2362	LINE	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-390	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 110.

rnd-5_family-221	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-580	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-5_family-1758	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-54	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-1871	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2687	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-5_family-308	LINE/L1-Tx1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Poly A trail length is 7.
rnd-5_family-626	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 87.
rnd-5_family-2144	DNA/hAT-Blackjack	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-2929	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-2153	DNA/TcMar-Tc1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-5_family-745	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.TIR consensus length is 83.
rnd-5_family-2157	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-5_family-378	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TCA.
rnd-5_family-251	Unknown	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 6.
rnd-5_family-1868	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1509	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-5_family-1037	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1016	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-5_family-6	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3667	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-5473	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3239	DNA/Academ	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is 30.
rnd-5_family-1266	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-5_family-93	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1177	LTR/Gypsy	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD



rnd-5_family-1396	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-5_family-1968	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 464.
rnd-5_family-4443	DNA/P	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-5_family-933	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-2777	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 68.
rnd-5_family-1370	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-985	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-18	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr)	SF()	Short sequence repeated is
rnd-5_family-4482	Unknown	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia)	No TSD consensus. Maximum TSD
rnd-5_family-1590	DNA/TcMar-Sagan	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 59.
rnd-5_family-1028	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-7	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2076	LINE/CR1	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 61. Poly A trail length is 7.

rnd-5_family-501	LTR	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	No TSD consensus. Maximum TSD
rnd-5_family-816	DNA/P	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-5_family-3141	Satellite	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	No TSD consensus. Maximum TSD length is 3.
rnd-5_family-137	DNA/hAT-Charlie	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-544	DNA/TcMar	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 347.
rnd-5_family-803	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1201	LINE/RTE-BovB	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 76.
rnd-5_family-2004	LINE/I	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1494	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-5_family-807	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-4063	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-419	Unknown	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1066	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.

rnd-5_family-5040	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-867	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-5_family-411	DNA/hAT	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 24.
rnd-5_family-1591	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 83.
rnd-5_family-3568	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 190.
rnd-5_family-1497	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-801	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-886	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-5_family-944	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-499	LINE/R2-NeSL	C(T-> ii S_SSR-> i)	SC(T-> helitron S_SSR-> non-ltr retrotransposon )	SF()	TSD consensus length is 2.Short sequence repeated is
rnd-5_family-2176	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2184	DNA/PIF-Harbinger	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF(H-> harbinger)	TSD consensus length is 2.
rnd-5_family-409	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-315	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is

rnd-5_family-6828	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2116	LTR/Pao	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 76.
rnd-5_family-1031	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2661	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-789	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-697	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-5_family-3231	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-5_family-774	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-5157	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TC.
rnd-5_family-512	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-829	LINE/RTE-BovB	C(S_TIR-> ii)	SC(H-> non-ltr retrotransposon S_TIR-> dna transposon)	SF()	TIR consensus length is 75.
rnd-5_family-1237	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3485	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-5_family-5010	LTR	C(S_LTR-> i)	SC(H-> dna transposon S_LTR-> Short Terminal	SF(H-> mudr)	Terminal Repeat consensus length is 8.
rnd-5_family-1011	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 152.
rnd-5_family-1096	DNA/hAT-Charlie	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-750	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-1613	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1200	Satellite	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.TIR consensus length is 41
rnd-5_family-5647	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-3193	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-327	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-6885	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-4009	LINE/Dong-R4	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1737	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3362	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.

rnd-5_family-2790	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.
rnd-5_family-2078	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1213	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-5_family-948	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is CTA.
rnd-5_family-5062	LINE	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TTGGA.
rnd-5_family-785	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TTA.
rnd-5_family-5753	LINE/RTE-BovB	C(S_TIR-> ii)	SC(H-> non-ltr retrotransposon S_TIR-> dna transposon)	SF()	TIR consensus length is 74.
rnd-5_family-2222	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2802	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1782	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is CC.
rnd-5_family-1950	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is

rnd-5_family-4509	LINE/CR1	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna	SF()	TSD consensus length is 2.
rnd-5_family-478	DNA/hAT-hAT5	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is AA.
rnd-5_family-5923	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-5_family-4235	DNA/TcMar-ISRm11	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-3095	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 27.
rnd-5_family-1154	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1490	LINE/L1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-353	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-229	DNA/MuLE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-3376	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1770	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2596	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-5328	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-5284	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.

rnd-5_family-3637	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-408	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-5341	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is AAAAA.
rnd-5_family-240	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 63.
rnd-5_family-266	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 50.
rnd-5_family-1921	DNA/hAT-Charlie	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-149	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1637	LTR/Gypsy	C()	SC(H-> ltr retrotransposon	SF()	-
rnd-5_family-5710	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-2320	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2490	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-5_family-879	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3104	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-3896	DNA	C()	SC(H-> dna transposon)	SF()	-



rnd-5_family-1411	Unknown	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	Palindrome length is 16.
rnd-5_family-1755	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-8668	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-2280	DNA/CMC-EnSpm	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-5_family-2887	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3142	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-6830	DNA/Sola	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-5_family-3946	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-994	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-5_family-974	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-5_family-1930	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-2729	LINE/RTE-X	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is AATTC.

rnd-5_family-2654	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 113.
rnd-5_family-716	LTR/DIRS	C()	SC(H-> ltr retrotransposon	SF()	-
rnd-5_family-4385	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-5_family-2510	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3174	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1555	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1073	DNA/P	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-92	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TT.
rnd-5_family-4580	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-5_family-2835	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1414	DNA/CMC-EnSpm	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.TIR consensus
rnd-5_family-3112	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-4870	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-3258	LINE/Rex-Babar	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is ATT.

rnd-5_family-2074	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-5_family-888	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-1702	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-5_family-7155	DNA/hAT-Charlie	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.TIR consensus length is 152.
rnd-5_family-1035	buffer	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 61.
rnd-5_family-2120	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-99	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-5164	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1615	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-6729	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is AA.
rnd-5_family-1421	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-3292	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-15	DNA/hAT-hATw	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-3041	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-5_family-4336	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1434	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-4859	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-5_family-2626	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1325	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-654	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-5_family-428	Unknown	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-12	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-5_family-4472	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-5_family-1629	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-78	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-6_family-866	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-825	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-6_family-2241	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.

rnd-6_family-600	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is ATT.
rnd-6_family-598	LINE/Tad1	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.TIR consensus
rnd-6_family-544	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 231.
rnd-6_family-1740	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 198.
rnd-6_family-1821	DNA/MULE-MuDR	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-743	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 54.
rnd-6_family-1466	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-62	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-585	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is CC.
rnd-6_family-1155	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 200.
rnd-6_family-1607	Simple_repeat	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-1964	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	No TSD consensus. Maximum TSD

rnd-6_family-892	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna	SF()	TIR consensus length is 241.
rnd-6_family-832	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-3446	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is CTA.
rnd-6_family-1873	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TAT.
rnd-6_family-4608	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-725	LINE/L1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-881	DNA/MuLE-MuDR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-6_family-8903	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 73.
rnd-6_family-446	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-791	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1662	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-761	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-6_family-1455	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 58.
rnd-6_family-488	DNA	C()	SC(H-> dna transposon)	SF()	-

rnd-6_family-526	Unknown	C()	SC(H-> non-ltr retrotransposon	SF(H-> i)	-
rnd-6_family-5209	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-6_family-152	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-654	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF(H-> sine)	Short sequence repeated is TAT.
rnd-6_family-2556	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-6_family-4392	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is CC.
rnd-6_family-3212	DNA/TcMar-Pogo	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-370	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-4255	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-6_family-2325	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-1777	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1310	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1859	LTR/Gypsy	C()	SC(H-> ltr retrotransposon	SF()	-
rnd-6_family-611	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is

rnd-6_family-327	LTR/Copia	C(S_LTR-> i S_SSR-> i)	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr	SF()	Terminal Repeat consensus length is
rnd-6_family-3267	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 199.
rnd-6_family-1773	LINE/CR1	C(S_SSR-> i)	SC(S_SSR-> non- ltr	SF()	Short sequence repeated is ATT.
rnd-6_family-3035	DNA/Kolobok-T2	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-805	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 67.
rnd-6_family-265	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-2240	Unknown	C(S_SSR-> i)	SC(S_SSR-> non- ltr	SF()	Short sequence repeated is
rnd-6_family-653	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-6_family-2612	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-4384	LTR/ERV1-MaLR	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 4.
rnd-6_family-630	LINE/L1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-3088	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TTA.



rnd-6_family-3240	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-2983	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TAT.
rnd-6_family-937	DNA/MULE-NOF	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-626	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-2922	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-6_family-18	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-5110	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-636	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is NN.
rnd-6_family-211	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-6_family-349	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-2820	LINE/L1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-6338	LTR/Pao	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-999	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-2886	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-8648	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.

rnd-6_family-1373	Simple_repeat	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-6_family-3109	LTR/Gypsy	C()	SC(H-> ltr retrotransposon	SF()	-
rnd-6_family-4340	SINE/MIR	C()	SC(H-> non-ltr retrotransposon	SF(H-> sine)	-
rnd-6_family-920	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-170	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-3310	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-1981	LINE/L1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-2289	DNA/CMC-Transib	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-6_family-1052	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 2.
rnd-6_family-435	DNA	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 6.
rnd-6_family-3821	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-3574	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-7892	DNA/CMC-Chapaev	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-6_family-3775	LTR/Copia	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna	SF()	TSD consensus length is 2.

rnd-6_family-4590	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1904	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-2415	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is AATA.
rnd-6_family-2644	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-3265	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1297	Unknown	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-4261	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1686	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-2225	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon )	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-6_family-1217	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is TTTTT.
rnd-6_family-2831	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1937	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1935	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 57.

rnd-6_family-2531	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-6_family-13860	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-93	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-3183	LINE/Tad1	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna	SF()	TSD consensus length is 2.
rnd-6_family-2235	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-373	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-6_family-7945	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-7283	LINE	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-2400	LINE/L1	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna	SF()	TSD consensus length is 2.
rnd-6_family-4553	LINE/L1	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-2354	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 333.
rnd-6_family-1811	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-6_family-2700	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.

rnd-6_family-1257	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-6_family-2940	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-6_family-479	LINE/L1	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is TT.
rnd-6_family-1096	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-8339	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-6_family-3899	DNA/P	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-6_family-2939	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon	SF()	Short sequence repeated is NNNNN.
rnd-6_family-1965	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-3500	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1102	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1990	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-4154	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-3019	LINE/CR1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1853	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-6_family-5711	LINE/Penelope	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TATA.
rnd-6_family-7885	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr	SF()	Short sequence repeated is
rnd-6_family-17	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-6_family-7327	DNA	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinge r)	TSD consensus length is 3.TIR consensus length is 18.
rnd-6_family-6771	Unknown	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-484	DNA/hAT-Tip100	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 66.
rnd-6_family-1623	LINE/RTE-BovB	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus
rnd-6_family-2302	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-4770	LINE/L2	C(T-> i)	SC(H-> non-ltr retrotransposon T-> ltr	SF(T-> ty3/gypsy ty1/copia	TSD consensus length is 5.
rnd-6_family-2178	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-4383	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon	SF()	-
rnd-6_family-1425	LINE/L2	C()	SC(H-> non-ltr retrotransposon	SF()	-

rnd-6_family-2388	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-2048	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-4175	DNA/TcMar-Tc4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.