

Repeat	RepeatModeler Classification	Class	Sub-Class	Super-Family	Notes
rnd-1_family-65	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-13	DNA/hAT-hATm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-1_family-110	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 96.
rnd-1_family-131	LINE/L2	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 50.
rnd-1_family-6	RC/Helitron	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-31	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-21	LINE/CR1	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-1_family-107	DNA/Maverick	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CA.
rnd-1_family-146	LINE/CR1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ACTAA.
rnd-1_family-167	LINE/L1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-163	DNA/hAT-hAT5	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-10	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-45	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-53	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAT.
rnd-1_family-66	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-84	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-16	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-111	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-1_family-42	DNA/hAT-Tip100	C(T-> i)	SC(H-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-186	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-1_family-68	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-1_family-69	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-102	LINE/Jockey	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-105	DNA/hAT-Blackjack	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-35	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-132	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 124.
rnd-1_family-92	LINE/CR1	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> maverick)	SF()	TSD consensus length is 6.TIR consensus length is 146.
rnd-1_family-41	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 18.
rnd-1_family-56	SINE/tRNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-1_family-138	DNA	C(S_LTR-> i S_SSR-> i)	SC(H-> dna transposon S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 22.Short sequence repeated is CACA.
rnd-1_family-77	LTR/ERVK	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-1_family-61	SINE/U	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 6.
rnd-1_family-12	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CACA.
rnd-1_family-52	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.

rnd-1_family-176	LINE/Penelope	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-1_family-173	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-1_family-113	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 9.
rnd-1_family-192	Simple_repeat	C()	SC(H-> helitron)	SF()	-
rnd-1_family-190	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-1_family-198	DNA/hAT-Charlie	C(S_TIR-> ii T-> ii)	SC(H-> dna transposon S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 17.
rnd-1_family-199	DNA/Kolobok-T2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 9.
rnd-1_family-175	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 13.
rnd-1_family-207	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-218	DNA/TcMar-Tc1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 16.
rnd-1_family-223	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-225	LINE/L1-Tx1	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-234	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-236	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-243	LINE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-246	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-248	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-269	Simple_repeat	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-276	DNA	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 102.
rnd-1_family-277	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-278	SINE/MIR	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-285	DNA/hAT-Tip100	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-292	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 599.
rnd-1_family-280	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-298	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-1_family-299	DNA/P	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-1_family-300	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-317	LTR	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-321	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-329	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 104.
rnd-1_family-332	DNA/hAT-Charlie	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-326	LTR/Copia	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 26.
rnd-1_family-339	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-341	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-345	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-351	buffer	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.TIR consensus length is 33.
rnd-1_family-359	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-368	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 304.
rnd-1_family-375	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-379	DNA/hAT-hATw	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-1_family-380	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-1_family-390	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-373	Satellite	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 5.
rnd-1_family-399	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-417	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-1_family-418	LTR/DIRS	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-423	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-425	DNA/hAT-Blackjack	C(T-> i)	SC(H-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-427	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-449	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-450	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 22.
rnd-1_family-453	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-457	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-461	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-473	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-475	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-479	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-492	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-494	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.

rnd-1_family-502	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-1_family-507	LINE/Rex-Babar	C(S_LTR-> i S_SSR-> i)	SC(H-> non-ltr retrotransposon S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 8.Short sequence repeated is CTTTT.
rnd-1_family-526	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-534	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-1_family-537	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-539	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-540	DNA/TcMar-Tc2	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	No TSD consensus. Maximum TSD length is 8.
rnd-1_family-543	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-1_family-553	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-559	LTR/Copia	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-560	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-565	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 17.
rnd-1_family-574	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 33.
rnd-1_family-575	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-1_family-581	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 12.
rnd-1_family-583	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-592	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.

rnd-1_family-594	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-605	LINE/L1-Tx1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-1_family-607	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-612	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-619	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-624	LTR	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-632	LINE/Proto1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-639	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-652	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-1_family-680	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-1_family-681	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-683	LTR/Caulimovirus	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-1_family-689	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-691	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.
rnd-1_family-698	DNA/PIF-ISL2EU	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 100.
rnd-3_family-27	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-4_family-1102	DNA/TcMar-Pogo	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTA.
rnd-4_family-712	Unknown	C(S_TIR-> ii T-> i)	SC(S_TIR-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.TIR consensus length is 17.
rnd-4_family-1776	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-4_family-	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-4_family-209	LINE/RTE-BovB	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-913	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 98.
rnd-4_family-232	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-438	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-4_family-2898	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-4_family-684	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTT.
rnd-4_family-757	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-4_family-	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-4_family-911	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 151.
rnd-4_family-1038	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-4_family-303	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-4_family-17	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1480	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 17.
rnd-5_family-192	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTT.
rnd-5_family-	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4479	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-103	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-509	DNA/hAT	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 158.
rnd-5_family-1481	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-389	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 18.
rnd-5_family-	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-134	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1510	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 16.
rnd-5_family-575	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-296	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-	LINE/RTE-X	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-5889	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 57.
rnd-5_family-2409	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 91.
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-638	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2921	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-688	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-5_family-846	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-1575	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-883	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4863	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 75.
rnd-5_family-1936	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-5_family-3726	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-720	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3307	RC/Helitron	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-5_family-2181	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-5_family-1	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3930	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1993	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-4521	LINE/Rex-Babar	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-5263	DNA/MuLE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-5_family-654	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-303	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-792	DNA/hAT-Blackjack	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-2	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-2427	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.
rnd-5_family-5151	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.TIR consensus length is 53.
rnd-5_family-9341	DNA/hAT-Charlie	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAG.
rnd-5_family-	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-346	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-979	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-925	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-106	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	DNA/hAT-Charlie	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-691	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-43	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2403	SINE?	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-4645	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.
rnd-5_family-5650	LTR/Gypsy	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GA.
rnd-5_family-2836	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-502	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-3444	LTR/DIRS	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-865	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-5467	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-5_family-3856	LINE/Rex-Babar	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-	DNA/hAT-Tip100	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.
rnd-5_family-489	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF(H-> gypsy)	-
rnd-5_family-3110	DNA/hAT	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-7084	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-411	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-13313	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1409	LINE/Rex-Babar	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	DNA/hAT-Ac	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-367	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-10805	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-1141	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTAT.
rnd-5_family-496	DNA/IS3EU	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-1297	DNA	C(S_SSR-> i)	SC(H-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.

rnd-5_family-9652	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.
rnd-5_family-	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2861	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-5_family-	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-17	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-342	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-5_family-555	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4137	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NN.
rnd-5_family-1070	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-1055	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-5_family-317	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 14.
rnd-5_family-726	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-8249	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-132	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1817	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.

rnd-5_family-5156	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 76.
rnd-5_family-	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3942	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-6_family-4026	DNA/Ginger	C()	SC(H-> ltr retrotransposon dna transposon)	SF()	-
rnd-6_family-794	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-1690	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTT.
rnd-6_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-816	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-6_family-3762	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-6_family-222	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-6_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2421	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-6_family-453	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-688	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-6_family-568	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CACA.
rnd-6_family-690	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GATT.
rnd-6_family-1287	LINE/I	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAG.

rnd-6_family-3230	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TA.
rnd-6_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-6977	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-6_family-	LTR/Copia	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2064	LINE/L1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTT.
rnd-6_family-391	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-293	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3142	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 46.
rnd-6_family-	SINE/trRNA	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-6_family-6035	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-6_family-718	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-569	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAC.
rnd-6_family-	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-353	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-6_family-11589	RC/Helitron	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-1961	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAA.
rnd-6_family-	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-1019	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-6_family-	LTR/Pao	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-	DNA/MULE-MuDR	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-3767	LINE/L2	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-3233	DNA/CMC-EnSpm	C(S_TIR-> ii S_SSR-> i)	SC(H-> dna transposon S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 36.Short sequence repeated is ACGT.
rnd-6_family-7199	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-6_family-3228	DNA/hAT-Charlie	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-6_family-206	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TATG.
rnd-6_family-	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-878	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-486	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3584	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-6_family-	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-2371	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-6_family-	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-166	Simple_repeat	C(S_TIR-> ii T-> ii S_SSR-> i)	SC(H-> dna transposon S_TIR-> dna transposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TSD consensus length is 2.TIR consensus length is 39.Short sequence repeated is GTCGC.
rnd-6_family-8604	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.

rnd-6_family-2999	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-10018	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-1054	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-6_family-2882	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTT.
rnd-6_family-3152	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-6_family-	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF(H-> jockey)	-
rnd-6_family-	DNA/CMC-Chapaev	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-16746	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-