Repeat	RepeatModeler Classification	Class	Sub-Class	Super-Family	Notes
rnd-1_family-146	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-198	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-43	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 81.
rnd-1_family-93	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-1_family-20	DNA/hAT-Blackjack	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 121.
rnd-1_family-83	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-234	Simple_repeat	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-302	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-231	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 255.
rnd-1_family-78	DNA/Academ	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 163.
rnd-1_family-88	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-1_family-216	LTR/Copia	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.Terminal Repeat consensus length is 17.
rnd-1_family-489	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 132.
rnd-1_family-282	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-412	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-229	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 99.
rnd-1_family-244	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-305	DNA/TcMar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.

rnd-1_family-75	SINE/MIR	C()	SC(H-> non-ltr retrotransposon non-ltr retrotransposon)	SF(H-> sine)	-
rnd-1_family-492	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGGT.
rnd-1_family-391	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-1_family-480	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.
rnd-1_family-63	LINE/Rex-Babar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-68	SINE/MIR	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-1_family-392	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACC.
rnd-1_family-28	SINE/ID	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-1_family-323	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-425	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-1_family-365	DNA	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.TIR consensus length is 312.
rnd-1_family-309	DNA/Sola	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-61	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.TIR consensus length is 213.
rnd-1_family-4	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCGAG.
rnd-1_family-197	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-1_family-11	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 252.
rnd-1_family-84	LINE/Jockey	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.

rnd-1_family-133	LINE/L1	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> ltr retrotransposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.Terminal Repeat consensus length is 113.
rnd-1_family-409	LINE/L1	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-488	Unknown	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 18.Terminal Repeat consensus length is 21.
rnd-1_family-410	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-336	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 221.
rnd-1_family-97	LTR/Pao	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.TIR consensus length is 35.
rnd-1_family-58	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-1_family-165	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-1_family-401	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 61.
rnd-1_family-236	DNA/Ginger	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GT.
rnd-1_family-0	LTR/Ngaro	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-1_family-362	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.
rnd-1_family-53	SINE/MIR	C()	SC(H-> non-ltr retrotransposon non-ltr retrotransposon)	SF(H-> sine)	-
rnd-1_family-432	LINE/L1	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 35.
rnd-1_family-135	LTR/Ngaro	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAA.
rnd-1_family-264	DNA/Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 164.
rnd-1_family-257	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.

rnd-1_family-54	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 212.
rnd-1_family-87	LTR/Copia	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 24.Short sequence repeated is AAAAA.
rnd-1_family-426	DNA/MULE-MuDR	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 64.
rnd-1_family-16	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-1_family-44	SINE/MIR	C(S_SSR-> i)	SC(H-> ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-1_family-71	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-474	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-493	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-1_family-183	DNA/PiggyBac	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-1_family-127	LTR/Gypsy	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 50.
rnd-1_family-320	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 79.
rnd-1_family-366	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.
rnd-1_family-29	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 96.
rnd-1_family-321	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-1_family-169	DNA/hAT-Ac	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	No TSD consensus. Maximum TSD length is 8.TIR consensus length is 28.
rnd-1_family-172	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-141	LTR	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-5	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.

rnd-1_family-164	DNA/Zator	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-326	DNA/TcMar-ISRm11	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-1_family-371	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.
rnd-1_family-277	Satellite	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 24.
rnd-1_family-3	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-102	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-73	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-1_family-255	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-1_family-217	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-35	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-1_family-227	LTR/Gypsy	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 28.
rnd-1_family-233	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 31.
rnd-1_family-181	LTR/Gypsy	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 65.
rnd-1_family-230	LINE	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-64	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 27.
rnd-1_family-240	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 123.
rnd-1_family-57	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-364	LTR/Copia	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> unknown)	TSD consensus length is 6.TIR consensus length is 23.
rnd-1_family-262	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.

rnd-1_family-482	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 338.
rnd-1_family-247	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 14.
rnd-1_family-33	LTR/Gypsy	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 29.
rnd-1_family-145	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-47	SINE/MIR	C()	SC(H-> non-ltr retrotransposon non-ltr retrotransposon)	SF(H-> sine)	-
rnd-1_family-111	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-1_family-464	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-491	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-32	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 12.
rnd-1_family-268	LTR/ERV1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGGGG.
rnd-1_family-322	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 225.
rnd-1_family-280	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 57.
rnd-1_family-434	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-354	LTR/Copia	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> transib)	TSD consensus length is 5.TIR consensus length is 35.
rnd-1_family-279	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-182	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 94.
rnd-1_family-107	DNA/TcMar-Tc4	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 231.
rnd-1_family-21	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-1_family-27	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 61.
rnd-1_family-207	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 91.

rnd-1_family-204	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-143	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 92.
rnd-1_family-329	Unknown	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 23.Terminal Repeat consensus length is 8.
rnd-1_family-341	DNA/TcMar-ISRm11	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 256.
rnd-1_family-110	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-131	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 232.
rnd-1_family-213	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-1_family-269	SINE/tRNA-V	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-289	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-370	LTR/Copia	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-1_family-36	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CAGTA.
rnd-1_family-34	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 59.
rnd-1_family-422	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 44.
rnd-1_family-104	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-45	DNA/hAT-Charlie	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-49	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-1_family-239	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 70.
rnd-1_family-122	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-1_family-315	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-1_family-112	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.

rnd-1_family-394	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 63.
rnd-1_family-342	LTR/ERV1	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-52	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-1_family-459	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 24.
rnd-1_family-232	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 28.
rnd-1_family-8	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-142	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.
rnd-1_family-226	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-138	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-1_family-31	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCGAG.
rnd-1_family-77	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-1_family-350	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.
rnd-1_family-513	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-517	LINE/Penelope	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 121.
rnd-1_family-520	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-299	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-521	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-523	DNA/hAT-Tag1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-1_family-525	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 143.
rnd-1_family-526	SINE/tRNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 9.

rnd-1_family-476	Unknown	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 consensus length is 33.
rnd-1_family-201	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-540	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 221.
rnd-1_family-541	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-546	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-170	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCGAG.
rnd-1_family-548	DNA/TcMar-Sagan	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> transib)	TSD consensus length is 5.TIR consensus length is 17.
rnd-1_family-560	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 61.
rnd-1_family-564	DNA/hAT-Charlie	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 223.
rnd-1_family-575	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 71.
rnd-1_family-576	DNA/hAT-hATm	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-586	DNA/TcMar-Mariner	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-578	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-603	DNA/hAT-Ac	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-605	LTR/Gypsy	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-1_family-612	DNA/Academ	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-615	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 242.
rnd-1_family-618	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 76.
rnd-1_family-626	DNA/TcMar-ISRm11	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-627	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-1_family-630	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.

rnd-1_family-636	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCGAC.
rnd-1_family-642	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-646	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-652	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 54.
rnd-1_family-662	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-657	DNA/CMC-EnSpm	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 27.Terminal Repeat consensus length is 24.
rnd-1_family-665	LINE/I	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 12.
rnd-1_family-673	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-1_family-675	DNA/PIF-Harbinger	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-682	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-1_family-687	DNA/hAT-Blackjack	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 88.
rnd-1_family-696	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 153.
rnd-1_family-709	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-725	DNA/Zator	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-739	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 18.
rnd-1_family-743	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 10.
rnd-1_family-744	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 22.
rnd-1_family-752	DNA/Crypton	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-775	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.

rnd-1_family-777	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-1_family-805	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 106.
rnd-1_family-808	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-813	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-804	LTR/Pao	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-819	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 78.
rnd-1_family-824	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-827	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-838	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-840	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-1_family-854	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-1_family-835	Simple_repeat	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 31.
rnd-1_family-867	DNA/CMC-EnSpm	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 34.
rnd-1_family-872	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GC.
rnd-1_family-879	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-893	Unknown	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 consensus length is 14.
rnd-1_family-896	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGGGG.
rnd-1_family-910	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-913	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-914	LINE/Penelope	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.

rnd-1_family-925	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-1_family-926	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-1_family-930	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.
rnd-1_family-935	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 108.
rnd-1_family-940	LTR/ERV1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-1_family-951	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-953	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-956	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 206.
rnd-1_family-975	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-989	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-991	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1005	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1026	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-1_family-1045	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-1_family-1046	DNA/Kolobok-Hydra	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-1_family-1051	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-1039	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-1058	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1061	DNA	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-1075	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAT.
rnd-1_family-1081	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1095	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-1_family-1108	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 25.
rnd-1_family-1126	LTR/Ngaro	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-1_family-1130	LTR/DIRS	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-1134	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-1145	LTR/Pao	C(T-> i)	SC(H-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 5.
rnd-1_family-1149	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-1150	DNA/Maverick	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.
rnd-1_family-1162	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1168	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-1173	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1188	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-1210	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-1_family-1213	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-1214	LTR/ERV4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-1_family-1221	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 21.
rnd-2_family-26	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.
rnd-3_family-101	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-3_family-62	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.
rnd-3_family-613	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 102.

rnd-3_family-20	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 248.
rnd-3_family-400	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-3_family-1451	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-3_family-188	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCAG.
rnd-4_family-1702	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 54.
rnd-4_family-89	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-4_family-27	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-4_family-84	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.
rnd-4_family-340	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 156.
rnd-4_family-1071	DNA/hAT-Tip100	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.
rnd-4_family-383	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-4_family-22	DNA/Maverick	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-4_family-2126	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTCGG.
rnd-4_family-15	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-4_family-2652	LTR/Copia	C(T-> ii S_SSR-> i)	SC(T-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Palindrome length is 12.Short sequence repeated is GG.
rnd-4_family-264	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CAGA.
rnd-4_family-840	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.
rnd-4_family-725	buffer	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-4_family-444	LINE/L1-Tx1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 248.
rnd-4_family-1763	DNA	C()	SC(H-> dna transposon)	SF()	-
rnd-4_family-530	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 213.
rnd-4_family-306	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.

rnd-4_family-855	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-4_family-295	LINE/Jockey	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.
rnd-4_family-738	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-4_family-1052	LTR/ERV1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-4_family-1322	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-4_family-1155	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-4_family-873	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-4_family-54	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-4_family-591	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTGAA.
rnd-4_family-2357	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-4_family-883	LINE/RTE-BovB	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-4_family-2024	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 79.
rnd-4_family-885	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-4_family-1381	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-4_family-36	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-60	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-4_family-574	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-642	DNA/Harbinger	C(T-> i S_SSR-> i)	SC(T-> ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.Short sequence repeated is GG.
rnd-5_family-1094	LINE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-179	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(H-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-5_family-3331	DNA/Crypton	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-5_family-3430	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 54.
rnd-5_family-1483	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-5_family-2603	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-936	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-676	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-2890	DNA/CMC-Chapaev	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-5_family-2553	DNA/MULE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-446	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-778	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 85.
rnd-5_family-2991	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 59.
rnd-5_family-3168	LTR/DIRS	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-5_family-473	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-5_family-2114	DNA/hAT-hAT5	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-2026	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2608	DNA/Kolobok-Hydra	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-1	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.

rnd-5_family-548	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-1666	DNA/Zator	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AA.
rnd-5_family-503	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-3417	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-2199	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3410	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-176	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 55.
rnd-5_family-1249	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 138.
rnd-5_family-1039	DNA	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 26.Terminal Repeat consensus length is 8.
rnd-5_family-2802	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 249.
rnd-5_family-311	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-5_family-2029	LTR/Gypsy	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 28.Short sequence repeated is AA.
rnd-5_family-703	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-5_family-1388	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-5_family-1251	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-828	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.
rnd-5_family-1199	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATTGA.
rnd-5_family-721	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.

rnd-5_family-192	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-285	buffer	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 27.
rnd-5_family-1381	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-398	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-6075	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-5314	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2210	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3299	DNA/hAT-Blackjack	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 70.
rnd-5_family-5013	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 249.
rnd-5_family-1404	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-1338	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-5_family-681	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-5_family-5497	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-754	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-271	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-1268	LTR/Ngaro	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-5_family-1287	LINE/CR1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAT.
rnd-5_family-3322	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-2288	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3925	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 172.
rnd-5_family-916	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-5063	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-9026	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.
rnd-5_family-2306	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.
rnd-5_family-65	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-15835	LTR/Gypsy	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.Terminal Repeat consensus length is 42.
rnd-5_family-7132	LTR/ERV1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-4869	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3051	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-5_family-335	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-866	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-5_family-1746	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-5_family-4268	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-1179	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1087	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-3293	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-8306	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3439	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 162.
rnd-5_family-597	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 130.
rnd-5_family-5487	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 139.
rnd-5_family-4654	LTR/ERVK	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-5_family-945	DNA/TcMar-ISRm11	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-6051	DNA/Sola	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-1549	Unknown	C(T-> i S_SSR-> i)	SC(T-> ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	Palindrome length is 16.Short sequence repeated is GG.
rnd-5_family-1235	SINE/MIR	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-1276	LINE/Jockey	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-5745	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-5_family-1715	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2493	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-4794	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3928	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-554	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-5_family-3262	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4153	DNA/TcMar-Tc1	C()	SC(H-> dna transposon)	SF()	-

rnd-5_family-1501	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-5_family-2256	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ACAAA.
rnd-5_family-299	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-1840	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-5_family-773	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 201.
rnd-5_family-10859	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4046	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-6774	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-3053	Unknown	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 59.
rnd-5_family-2963	LTR/Copia	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 205.Short sequence repeated is TTTTT.
rnd-5_family-3731	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2562	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-5_family-1667	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-386	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-195	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-8296	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2009	LTR/Gypsy-Cigr	C()	SC(H-> ltr retrotransposon)	SF()	-

rnd-5_family-2795	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-1166	LTR	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-4491	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 5.
rnd-5_family-12864	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-5_family-3156	LTR/DIRS	C(S_SSR-> i)	SC(H-> ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-5227	LTR/Copia	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 13.
rnd-5_family-1221	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-2163	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-169	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-5_family-1055	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-5_family-2011	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 6.
rnd-5_family-5543	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2698	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-5453	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.
rnd-5_family-3136	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 120.
rnd-5_family-1131	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-5822	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-5_family-2647	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1747	DNA/TcMar-Fot1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.

rnd-5_family-1037	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-850	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-784	DNA/MULE-MuDR	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> unknown)	No TSD consensus. Maximum TSD length is 6.TIR consensus length is 43.
rnd-5_family-5682	RC/Helitron	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 22.
rnd-5_family-4992	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 199.
rnd-5_family-1534	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3768	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-6322	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-6811	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-4974	LTR/Pao	C(T-> ii S_SSR-> i)	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TSD consensus length is 2.Short sequence repeated is AAATC.
rnd-5_family-4667	LINE/L1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAGT.
rnd-5_family-4080	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2066	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3335	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3856	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-676	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.

rnd-6_family-12	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-6_family-2572	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-6_family-701	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-6_family-2309	DNA/Crypton	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-908	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-2969	Unknown	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 18.
rnd-6_family-9258	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-94	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-6_family-8462	DNA/PIF-Harbinger	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-6_family-4684	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-6_family-449	LINE/Jockey	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 45.Short sequence repeated is TT.
rnd-6_family-1188	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTGT.
rnd-6_family-1239	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-6_family-2950	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-6664	LTR/DIRS	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-6_family-4850	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3989	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.

rnd-6_family-6419	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTGAA.
rnd-6_family-1443	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 132.
rnd-6_family-1975	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-3893	LINE/I	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 34.
rnd-6_family-567	LTR/Gypsy	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 28.Short sequence repeated is AA.
rnd-6_family-699	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-6_family-8845	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-254	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-6_family-906	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-6_family-1588	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 92.
rnd-6_family-2458	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.TIR consensus length is 18.
rnd-6_family-3176	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-410	LTR/Gypsy-Cigr	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-800	LTR/DIRS	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-6_family-3627	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-6_family-1988	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-6_family-842	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 406.
rnd-6_family-2641	LTR/Gypsy	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAA.
rnd-6_family-3237	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-6_family-6253	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.

rnd-6_family-7357	LINE/RTE-X	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACAT.
rnd-6_family-2034	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-6_family-3625	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-6_family-164	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 54.
rnd-6_family-3880	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AGTC.
rnd-6_family-3948	LINE/I	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 204.
rnd-6_family-76	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-6_family-6385	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-480	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-6_family-2603	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3892	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-6_family-3178	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-6_family-55	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3931	Unknown	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 17.
rnd-6_family-12058	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-6_family-10754	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-6_family-2925	LTR/Gypsy	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-6_family-754	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-111	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2796	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-8268	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACCG.
rnd-6_family-1504	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-317	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-6_family-1264	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-1902	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-982	LTR/ERV1	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-6_family-4410	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-1184	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-837	SINE/MIR	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-582	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-5856	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-6_family-16	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-12012	LTR/Gypsy	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 171.
rnd-6_family-2509	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 152.
rnd-6_family-5465	DNA/MuLE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-6_family-3702	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.

rnd-6_family-7659	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-6_family-12923	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-6_family-6236	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-3411	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-6_family-779	LINE/L1-Tx1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-6_family-466	RC/Helitron	C()	SC(H-> helitron)	SF()	-
rnd-6_family-1926	LTR/Gypsy-Cigr	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-4193	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-6_family-8183	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAG.
rnd-6_family-573	DNA/Zator	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AA.
rnd-6_family-2035	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-190	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-6_family-2166	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-1971	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-6750	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-