Repeat	RepeatModeler Classification	Class	Sub-Class	Super-Family	Notes
rnd-1_family-25	DNA/Harbinger	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 109.
rnd-1_family-323	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 57.
rnd-1_family-333	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-1_family-229	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 171.
rnd-1_family-138	LTR/Ngaro	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine H-> sine)	-
rnd-1_family-463	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-223	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-1_family-75	LINE/Tad1	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 28.
rnd-1_family-33	LINE/Tad1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-139	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-243	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.
rnd-1_family-487	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.
rnd-1_family-261	LINE/Proto1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.

rnd-1_family-148	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 121.
rnd-1_family-26	LTR	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 95.
rnd-1_family-91	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-452	DNA/Zator	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.
rnd-1_family-270	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-464	DNA/hAT-Charlie	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 27.Short sequence repeated is TT.
rnd-1_family-160	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 71.
rnd-1_family-51	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-1_family-224	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-185	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.
rnd-1_family-34	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 51.
rnd-1_family-179	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 196.
rnd-1_family-447	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-36	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 51.
rnd-1_family-236	DNA/CMC-Chapaev	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 230.

rnd-1_family-331	LTR/Pao	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 36.Short sequence repeated is AAAAA.
rnd-1_family-432	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-1_family-310	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-42	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 75.
rnd-1_family-479	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-382	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 78.
rnd-1_family-444	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAG.
rnd-1_family-180	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-1_family-163	DNA/CMC-Transib	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-82	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 46.
rnd-1_family-370	DNA/Academ	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-134	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.
rnd-1_family-151	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-86	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.

rnd-1_family-72	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-1_family-132	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-467	DNA/Maverick	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-19	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 358.
rnd-1_family-170	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-79	DNA/CMC-Transib	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-338	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 58.
rnd-1_family-347	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-1_family-83	LINE/L1-Tx1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 85.
rnd-1_family-121	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-130	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 66.
rnd-1_family-433	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-90	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 71.
rnd-1_family-32	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 427.
rnd-1_family-173	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-1_family-339	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-336	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.

rnd-1_family-161	DNA/Zator	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 AAAAA.
rnd-1_family-11	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-1_family-260	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 77.
rnd-1_family-5	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.
rnd-1_family-468	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-49	LINE	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 94.
rnd-1_family-0	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.
rnd-1_family-282	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.
rnd-1_family-303	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-18	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-1_family-455	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-94	LTR	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 59.
rnd-1_family-215	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 153.
rnd-1_family-101	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.

rnd-1_family-56	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 237.
rnd-1_family-359	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-200	LINE/L1	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-46	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 147.
rnd-1_family-348	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-44	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-1_family-297	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-365	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-21	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-67	LTR/Ngaro	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-1_family-80	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-357	DNA/Zator	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 length is 24.
rnd-1_family-441	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-16	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 210.
rnd-1_family-366	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 10.

rnd-1_family-361	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-1_family-201	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 94.
rnd-1_family-53	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-1_family-465	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-13	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 450.
rnd-1_family-244	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-219	LINE/L2	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 58.
rnd-1_family-156	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-168	SINE/tRNA-V	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine H-> sine)	Short sequence repeated is TTA.
rnd-1_family-100	LINE/RTE-BovB	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-1_family-344	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-1_family-250	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-1_family-377	DNA/hAT-Charlie	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-17	DNA/TcMar-Tigger	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 consensus length is 46.

rnd-1_family-329	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.
rnd-1_family-209	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 136.
rnd-1_family-389	DNA/Sola	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-418	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 47.
rnd-1_family-186	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-1_family-210	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-106	DNA/Academ	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-1_family-182	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-1_family-24	DNA	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 43.
rnd-1_family-269	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGATA.
rnd-1_family-309	DNA/hAT-Tip100	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TSD consensus length is 2.Terminal Repeat consensus length is 33.
rnd-1_family-470	DNA/P	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-1_family-77	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.

rnd-1_family-43	DNA/MULE-NOF	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-15	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.
rnd-1_family-2	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 346.
rnd-1_family-257	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-315	LTR/DIRS	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 11.
rnd-1_family-95	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-1_family-150	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 342.
rnd-1_family-196	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-286	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-1_family-294	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 198.
rnd-1_family-35	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-1_family-424	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.
rnd-1_family-267	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 91.
rnd-1_family-225	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-1_family-162	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.

rnd-1_family-112	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-1_family-69	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 73.
rnd-1_family-233	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.
rnd-1_family-248	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 90.
rnd-1_family-384	LTR/DIRS	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 59.
rnd-1_family-278	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 17.
rnd-1_family-409	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAATT.
rnd-1_family-276	LINE/L1-Tx1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-1_family-68	DNA	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-167	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATTG.
rnd-1_family-29	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 50.
rnd-1_family-381	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-1_family-368	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 75.
rnd-1_family-22	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-1_family-288	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.

rnd-1_family-442	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 57.
rnd-1_family-129	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-1_family-218	LINE/L2	C(T-> i)	SC(H-> non-ltr retrotransposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-66	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-1_family-298	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 118.
rnd-1_family-40	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.
rnd-1_family-120	LTR/Ngaro	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine H-> sine)	-
rnd-1_family-10	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 455.
rnd-1_family-277	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 274.
rnd-1_family-109	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-354	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-478	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-451	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-1_family-387	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-376	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.

rnd-1_family-410	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-52	DNA/Kolobok-Hydra	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-1_family-272	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-205	SINE/MIR	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-392	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.
rnd-1_family-502	DNA/hAT-Tip100	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 91.
rnd-1_family-397	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-346	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-491	DNA/P	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.
rnd-1_family-506	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAC.
rnd-1_family-511	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-1_family-512	DNA/Kolobok-T2	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 306.
rnd-1_family-516	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-1_family-524	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 141.
rnd-1_family-519	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-530	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 62.
rnd-1_family-535	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 133.
rnd-1_family-537	RC/Helitron	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-539	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-1_family-540	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.
rnd-1_family-542	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-556	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-557	DNA/TcMar-Tc1	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-558	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-1_family-560	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-561	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-1_family-531	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-564	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-568	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-569	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-1_family-575	DNA/hAT-Tag1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-576	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-

rnd-1_family-577	LTR	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-580	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-578	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 66.
rnd-1_family-583	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-584	DNA/hAT-Tag1	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 95.
rnd-1_family-585	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-587	DNA/Sola	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-592	DNA/TcMar-Fot1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	Palindrome length is 16.
rnd-1_family-595	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 177.
rnd-1_family-597	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 58.
rnd-1_family-601	LTR/Pao	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-602	DNA/hAT-hAT5	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-1_family-603	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.
rnd-1_family-604	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 13.
rnd-1_family-605	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.

rnd-1_family-611	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 31.
rnd-1_family-612	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-614	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-615	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-1_family-617	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-622	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-627	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-1_family-628	LTR/Copia	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-629	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 25.
rnd-1_family-634	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-1_family-638	DNA/hAT-Tip100	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-654	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-657	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-658	DNA/hAT-Charlie	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-668	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-669	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-671	DNA/hAT-Charlie	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-677	LINE/L1-Tx1	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-680	LTR	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 20.Terminal Repeat consensus length is 21.
rnd-1_family-691	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 14.
rnd-1_family-616	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-694	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-698	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-1_family-701	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-702	Unknown	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-704	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-714	LTR/ERV4	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-719	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-721	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-730	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 9.

rnd-1_family-738	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-739	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.TIR consensus length is 19.
rnd-1_family-741	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTT.
rnd-1_family-746	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-1_family-737	SINE/ID	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-
rnd-1_family-753	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-734	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-1_family-762	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 69.
rnd-1_family-770	DNA/hAT-Tip100	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-783	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-791	DNA/TcMar-Sagan	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is 177.
rnd-1_family-799	Unknown	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-800	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.

rnd-1_family-813	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 69.
rnd-1_family-818	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-821	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-825	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGAA.
rnd-1_family-829	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-843	DNA/hAT-Ac	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-846	DNA/CMC-EnSpm	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-1_family-853	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-861	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 11.
rnd-1_family-859	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 15.
rnd-1_family-883	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 81.
rnd-1_family-893	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-900	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-1_family-920	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GATA.

rnd-1_family-924	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 12.
rnd-1_family-936	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-938	LTR/Copia	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-947	LTR/DIRS	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-952	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-954	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-956	LTR/Ngaro	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-959	Unknown	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-961	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.
rnd-1_family-963	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.
rnd-1_family-966	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.
rnd-1_family-972	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-976	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-979	LTR/Gypsy	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.TIR consensus length is 77.
rnd-1_family-981	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-989	LINE/R2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.

rnd-1_family-991	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAG.
rnd-1_family-982	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-998	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-1_family-1002	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1004	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.
rnd-1_family-1007	LINE/CR1	C(T-> ii S_SSR-> i)	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TSD consensus length is 2.Poly A trail length is 8.
rnd-1_family-1008	DNA/CMC-Mirage	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-1016	Unknown	C(T-> i S_LTR-> i)	SC(T-> ltr retrotransposon S_LTR-> Short Terminal Repeat)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.Terminal Repeat consensus length is 8.
rnd-1_family-996	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF(H-> line)	-
rnd-1_family-960	DNA/Ginger	C(T-> i S_LTR-> i)	SC(T-> ltr retrotransposon S_LTR-> Short Terminal Repeat)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.Terminal Repeat consensus length is 8.
rnd-1_family-1022	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1025	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1032	DNA/PIF-Harbinger	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-1035	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.

rnd-1_family-1041	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-1043	LTR/Copia	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 51.
rnd-1_family-1046	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1047	LINE	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-1048	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 40.
rnd-1_family-1049	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1057	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1066	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAC.
rnd-1_family-1069	LTR/Pao	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 10.
rnd-1_family-1072	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-1_family-1054	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1075	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1080	DNA	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 2.
rnd-1_family-1094	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-1107	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.
rnd-1_family-1113	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-1116	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-1118	LINE/CR1	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-1074	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-1_family-1121	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-1127	DNA/hAT-Tip100	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 14.
rnd-1_family-1136	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1150	DNA/Academ	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1152	DNA/TcMar-Tc2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GATT.
rnd-1_family-1159	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.
rnd-1_family-1164	Unknown	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 consensus length is 13.
rnd-1_family-1165	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.
rnd-1_family-1166	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1177	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1178	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.
rnd-1_family-1183	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1191	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-1_family-1192	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-1_family-1193	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1196	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 110.
rnd-1_family-1202	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1232	LINE/RTE-BovB	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.
rnd-1_family-1233	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1239	DNA/MULE-F	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-1241	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1244	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-1_family-1245	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1247	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 20.
rnd-1_family-1251	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-1_family-1255	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-1278	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1280	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-1281	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGAT.
rnd-1_family-1288	DNA/Academ	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1295	LINE/CR1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.

rnd-1_family-1298	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-1_family-1302	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.
rnd-1_family-1304	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1310	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1317	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 12.
rnd-1_family-1322	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-1_family-1323	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-1_family-1327	LTR/ERV4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 90.
rnd-1_family-1341	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1342	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1348	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1351	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1355	LTR/Pao	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1366	DNA/hAT-Ac	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1368	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-1370	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.

rnd-1_family-1329	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1374	Unknown	C(T-> i S_LTR-> i)	SC(T-> non-ltr retrotransposon penelope S_LTR-> Short Terminal Repeat)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 7.Terminal Repeat consensus length is 26.
rnd-1_family-1381	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1386	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1390	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-1392	LINE/CRE	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-1_family-1401	Unknown	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.Terminal Repeat consensus length is 32.
rnd-1_family-1422	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1443	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-1_family-1446	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1452	Unknown	C(T-> ii S_LTR-> i)	SC(T-> dna transposon S_LTR-> Short Terminal Repeat)	SF(T-> is256/mutator/fb)	No TSD consensus. Maximum TSD length is 10.Terminal Repeat consensus length is 8.
rnd-1_family-1454	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-1_family-1456	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-1459	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1461	DNA/hAT-Tag1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-1463	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1465	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.
rnd-1_family-1468	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1469	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1484	LTR	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 200.
rnd-1_family-1490	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGAT.
rnd-1_family-1491	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1498	DNA/hAT-Charlie	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-1415	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1501	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1503	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-1_family-1511	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1517	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1522	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-1_family-1525	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	No TSD consensus. Maximum TSD length is 3.
rnd-1_family-1526	DNA/hAT-Tip100	C()	SC(H-> dna transposon)	SF()	-
rnd-1_family-1527	LINE/CR1-Zenon	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-1_family-1529	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-1_family-1531	SINE/MIR	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1532	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1541	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1551	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-1_family-1558	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1562	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 11.
rnd-1_family-1580	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-1_family-1589	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-1_family-1590	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-1_family-1584	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-2_family-80	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-2_family-81	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-3_family-141	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.

rnd-3_family-108	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-3_family-81	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-3_family-575	LINE/L1	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 29.
rnd-3_family-75	Satellite	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-3_family-68	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 81.
rnd-3_family-700	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-3_family-408	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-3_family-130	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-3_family-351	DNA/Zator	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 31.Short sequence repeated is AA.
rnd-3_family-86	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-3_family-239	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 58.
rnd-3_family-653	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-3_family-645	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-3_family-111	LINE/I	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-3_family-507	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-4_family-426	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-4_family-180	DNA/CMC-Chapaev-3	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 46.
rnd-4_family-248	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-524	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-4_family-1094	DNA/hAT	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-4_family-126	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-4_family-758	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-4_family-707	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-4_family-301	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 78.
rnd-4_family-239	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-4_family-506	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-375	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 341.
rnd-4_family-1914	DNA/hAT	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	No TSD consensus. Maximum TSD length is 11.
rnd-4_family-1906	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.

rnd-4_family-1562	DNA/Kolobok-T2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-4_family-1911	LINE/Tad1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-4_family-2614	LINE/Tad1	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 64.
rnd-4_family-1768	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-4_family-1091	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-4_family-518	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-848	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-845	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-1766	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-4_family-1550	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.
rnd-4_family-279	DNA/TcMar-Mariner	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-4_family-454	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-4_family-1561	LINE/CR1-Zenon	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.
rnd-4_family-300	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-956	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.

rnd-4_family-396	LINE/L1-Tx1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-4_family-53	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-4_family-1204	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-4_family-2081	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAC.
rnd-4_family-756	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-649	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-814	Unknown	C(S_TIR-> ii T-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.TIR consensus length is 33.
rnd-4_family-743	DNA/hAT-Charlie	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.
rnd-4_family-419	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-4_family-1589	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-4_family-890	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 115.
rnd-4_family-1209	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-4_family-1788	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-16	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-4_family-175	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-148	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-250	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-685	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-3474	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-4_family-1151	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1370	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 115.
rnd-5_family-502	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-5_family-79	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.
rnd-5_family-1195	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-1356	DNA/Maverick	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-5_family-619	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-107	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1934	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-247	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.

rnd-5_family-6219	SINE	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 43.
rnd-5_family-3529	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 22.
rnd-5_family-2099	LINE/Penelope	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 84.
rnd-5_family-416	Unknown	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 NNNNN.
rnd-5_family-1208	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 92.
rnd-5_family-1791	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 32.
rnd-5_family-809	LINE/CR1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAG.
rnd-5_family-880	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.
rnd-5_family-52	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2986	LINE/L2	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-1894	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 87.
rnd-5_family-567	DNA/TcMar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-5_family-2951	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-5_family-4072	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-5_family-4694	LTR/ERV4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-5_family-12	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-5_family-2051	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 56.
rnd-5_family-2685	DNA/hAT-Tip100	C(T-> ii S_SSR-> i)	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.Short sequence repeated is CC.
rnd-5_family-2169	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-374	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.
rnd-5_family-481	LINE/CR1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-1445	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-5_family-1237	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 116.
rnd-5_family-434	DNA/MULE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAC.
rnd-5_family-4205	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-5_family-1174	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-771	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 71.
rnd-5_family-420	LTR/ERV4	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-5_family-1272	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.

rnd-5_family-3778	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-5_family-1411	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.
rnd-5_family-114	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-3771	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1273	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TATG.
rnd-5_family-2476	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 68.
rnd-5_family-876	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.
rnd-5_family-1628	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1305	LTR	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 11.
rnd-5_family-1372	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTA.
rnd-5_family-1386	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 202.
rnd-5_family-2284	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-220	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.

rnd-5_family-2585	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-5_family-3069	LTR/ERV1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-4732	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.
rnd-5_family-4858	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 69.
rnd-5_family-1617	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-948	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-42	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1014	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-82	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-32	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 33.
rnd-5_family-2149	LINE/R2-Hero	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-66	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-5_family-791	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-5_family-2737	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-143	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.

rnd-5_family-4747	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2734	DNA/hAT	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-5_family-3135	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 59.
rnd-5_family-2171	DNA/hAT	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.
rnd-5_family-1840	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-11030	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGGGG.
rnd-5_family-3238	Satellite	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 22.
rnd-5_family-3435	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1075	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-5582	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-5_family-355	LTR/Copia	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 28.
rnd-5_family-5872	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 357.
rnd-5_family-2603	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2568	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-2735	DNA/PIF-Harbinger	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-5_family-2150	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-5_family-80	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-5_family-2793	Unknown	C(S_TIR-> ii T-> ii S_SSR-> i)	SC(S_TIR-> dna transposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is 31.Short sequence repeated is NNNNN.
rnd-5_family-306	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-261	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3623	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-5_family-2449	LINE/Rex-Babar	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-2124	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is5/pif/harbinger is630/tc1/mariner)	TSD consensus length is 3.
rnd-5_family-1364	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-347	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is5/pif/harbinger is630/tc1/mariner)	TSD consensus length is 3.
rnd-5_family-5366	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-5_family-6321	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 102.
rnd-5_family-1835	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.

rnd-5_family-344	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-4981	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1025	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-1635	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1487	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-5063	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-5_family-2871	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-5_family-1010	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 246.
rnd-5_family-1063	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4020	LTR/Pao	C(S_TIR-> ii S_LTR-> i)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 218.Terminal Repeat consensus length is 8.
rnd-5_family-5906	LINE/RTE-X	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 132.
rnd-5_family-5941	LINE/R2-Hero	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1693	DNA/Dada	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.
rnd-5_family-2595	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 172.
rnd-5_family-1643	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-4010	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.
rnd-5_family-4132	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2001	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-2195	DNA/CMC-Chapaev	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.
rnd-5_family-226	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2296	Unknown	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 33.
rnd-5_family-3369	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-5_family-5447	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-153	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3082	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-5_family-1452	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.
rnd-5_family-1002	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-4249	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1864	LINE/Jockey	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.
rnd-5_family-3646	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-3786	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.
rnd-5_family-766	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-1888	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-10881	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-5_family-3930	LTR/Ngaro	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.
rnd-5_family-1440	LINE/L1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-6097	LTR/Pao	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 11.
rnd-5_family-1486	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-5_family-1535	LTR	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-4521	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-3611	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.
rnd-5_family-621	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2192	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3791	LINE/RTE-X	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-5_family-5522	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1437	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3140	SINE/tRNA	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 35.
rnd-5_family-194	DNA/hAT-Ac	C()	SC(H-> dna transposon)	SF()	-

rnd-5_family-138	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1259	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-7573	DNA/Maverick	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 28.
rnd-5_family-2332	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4258	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-973	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 65.
rnd-5_family-3334	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-7342	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-1733	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-10476	LINE/R1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-2875	Unknown	C(S_LTR-> i S_SSR-> i)	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 37.Short sequence repeated is NNNNN.
rnd-5_family-3131	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2167	DNA/hAT-Ac	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-7287	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-464	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.
rnd-5_family-2850	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4261	SINE/MIR	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-3687	LTR/Pao	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 12.
rnd-5_family-2609	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-7616	DNA/hAT-hAT19	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.
rnd-5_family-8852	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 146.
rnd-5_family-2064	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4960	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1245	DNA/Kolobok-Hydra	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-937	LTR/ERV1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4131	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-155	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-5_family-1480	LTR/ERVK	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 16.
rnd-5_family-828	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-5055	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	No TSD consensus. Maximum TSD length is 2.
rnd-5_family-5218	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2887	DNA/hAT-Tip100	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 12.
rnd-5_family-62	LTR/Copia	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 56.
rnd-5_family-1192	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-8576	DNA/CMC-Chapaev-3	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 51.
rnd-5_family-280	LTR/DIRS	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-2492	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-5_family-3713	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-5_family-2499	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 528.
rnd-5_family-2290	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-7712	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-5_family-6878	LTR/ERVK	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-5_family-544	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-4037	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3650	Unknown	C(T-> i S_SSR-> i)	SC(T-> non-ltr retrotransposon penelope S_SSR-> non-ltr retrotransposon)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 9.Short sequence repeated is TT.
rnd-5_family-4662	LTR/Copia	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 10.
rnd-5_family-3989	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4779	LINE/L1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-14448	DNA/Sola	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 125.
rnd-5_family-302	DNA/Sola	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-5_family-4124	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-11659	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-2523	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2457	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-6336	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-5_family-484	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-4066	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTGA.
rnd-5_family-8649	DNA	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-5_family-3576	DNA/hAT	C(S_TIR-> ii T-> ii S_SSR-> i)	SC(S_TIR-> dna transposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.TIR consensus length is 61.Short sequence repeated is NNNNN.
rnd-5_family-2854	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1783	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3117	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-5_family-1039	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.
rnd-5_family-643	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-2602	LINE/L2	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 26.
rnd-5_family-5519	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.
rnd-5_family-687	LTR	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-7768	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-6356	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-5_family-2605	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-11037	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.

rnd-5_family-160	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-178	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1587	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.
rnd-5_family-555	LINE/Jockey	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 16.
rnd-5_family-5021	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 63.
rnd-5_family-9410	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-1283	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.
rnd-5_family-529	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-290	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-5_family-4768	Unknown	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-5_family-2918	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 506.
rnd-5_family-3109	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-6212	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACA.
rnd-5_family-1241	LINE	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-5_family-7486	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.
rnd-5_family-4207	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-751	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-1955	SINE/MIR	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-5_family-1633	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-2370	LTR/Gypsy	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.
rnd-5_family-3394	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-3992	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGCTA.
rnd-5_family-1521	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-4862	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-5_family-6464	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-655	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 22.
rnd-6_family-614	DNA/Sola	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 242.
rnd-6_family-804	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-1221	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-6_family-1253	LTR/ERV1	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.

rnd-6_family-6610	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-6_family-767	DNA/TcMar-Mariner	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-6_family-829	Satellite	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 254.
rnd-6_family-1200	DNA/hAT-Charlie	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-6_family-5752	DNA/hAT-Ac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AGA.
rnd-6_family-667	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-2254	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-1721	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.
rnd-6_family-999	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-371	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-5737	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 62.
rnd-6_family-8168	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.
rnd-6_family-1437	DNA/TcMar-Tc1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-4109	DNA/CMC-Chapaev-3	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-4930	LTR/Pao	C(T-> ii)	SC(T-> helitron)	SF()	TSD consensus length is 2.
rnd-6_family-2492	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.

rnd-6_family-2184	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-6_family-2795	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.
rnd-6_family-1801	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.
rnd-6_family-1571	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-6_family-926	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-8015	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon dna transposon)	SF()	-
rnd-6_family-9124	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.
rnd-6_family-4169	LTR/ERV4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.
rnd-6_family-7094	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2301	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.
rnd-6_family-2357	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-906	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-6_family-327	DNA/MULE-MuDR	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.
rnd-6_family-1135	Satellite	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-2877	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.
rnd-6_family-3120	DNA/Academ	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.

rnd-6_family-1841	DNA/hAT-Ac	C(S_TIR-> ii S_SSR-> i)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 39.Short sequence repeated is AC.
rnd-6_family-574	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 85.
rnd-6_family-12430	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 60.
rnd-6_family-19	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-6_family-1202	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.
rnd-6_family-8550	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.
rnd-6_family-6130	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-6_family-525	LINE/RTE-X	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.
rnd-6_family-997	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.
rnd-6_family-2344	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-8191	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAG.
rnd-6_family-4086	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.
rnd-6_family-4809	DNA/Crypton-V	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-6_family-1312	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-6_family-7798	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 51.

rnd-6_family-1092	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.
rnd-6_family-7888	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-504	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.
rnd-6_family-3666	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-4501	SINE/MIR	C(T-> ii S_SSR-> i)	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.Short sequence repeated is TTA.
rnd-6_family-407	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-1465	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-6262	RC/Helitron	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 6.
rnd-6_family-95	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TA.
rnd-6_family-1544	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3243	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-6_family-5321	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner)	TSD consensus length is 2.
rnd-6_family-4777	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-4423	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.
rnd-6_family-1074	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.
rnd-6_family-3064	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-885	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 116.
rnd-6_family-330	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTGTA.
rnd-6_family-2126	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.
rnd-6_family-1311	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-489	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF(H-> gypsy)	-
rnd-6_family-3092	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2410	LTR/Copia	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 7.
rnd-6_family-5002	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-965	LINE/R2-Hero	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-4735	DNA/MuLE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.
rnd-6_family-6176	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-2781	DNA/MULE-NOF	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 118.
rnd-6_family-3900	LINE/R2-Hero	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-3052	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-6_family-450	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-1436	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-5186	DNA/Zator	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 72.
rnd-6_family-1780	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.
rnd-6_family-8969	DNA/TcMar-Fot1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.
rnd-6_family-6751	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.
rnd-6_family-718	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-55	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.
rnd-6_family-715	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-282	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.
rnd-6_family-506	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-11215	DNA/MuLE-MuDR	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-1435	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-8139	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-4657	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.
rnd-6_family-454	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-966	LTR	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-53	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-5090	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2065	DNA/Sola	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.
rnd-6_family-1449	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> helitron)	SF()	Palindrome length is 10.
rnd-6_family-4926	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 39.
rnd-6_family-1481	LINE/L2	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.
rnd-6_family-575	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.
rnd-6_family-1038	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-5004	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-1039	LTR/DIRS	C()	SC(H-> ltr retrotransposon)	SF()	-
rnd-6_family-2870	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-
rnd-6_family-3472	LINE/CR1-Zenon	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-256	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-859	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-

rnd-6_family-476	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF()	-
rnd-6_family-2940	DNA/PIF-HarbS	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.
rnd-6_family-527	LINE/L1-Tx1	C()	SC(H-> non-ltr retrotransposon)	SF()	-