

Repeat	RepeatModeler	Class	Sub-Class	Super-Family	Notes
[rnd-1_family-196]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.]
[rnd-1_family-250]	DNA/TcMar-Pogo	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.]
[rnd-1_family-170]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8. TIR consensus length is
[rnd-1_family-12]	LINE/CR1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-79]	DNA/TcMar-Tc1	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-351]	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is
[rnd-1_family-301]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.]
[rnd-1_family-162]	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.]
[rnd-1_family-134]	RC/Helitron	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 86.]
[rnd-1_family-128]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.]
[rnd-1_family-317]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-298]	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-293]	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 14.]
[rnd-1_family-182]	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-1_family-21]	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-98]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-323]	RC/Helitron	C(S_LTR-> i)	SC(S_LTR-> ltr retrotransposon)	SF()	Terminal Repeat consensus length is 101.]
[rnd-1_family-66]	DNA	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-1_family-169]	DNA/TcMar-Pogo	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.]

[rnd-1_family-402	Unknown	C(T-> i S_LTR	SC(T-> ltr retrotransposon S_LTR-> Short Terminal Repeat)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 5.Terminal Repeat consensus length is 8.]
[rnd-1_family-369	LINE/R2-NeSL	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-404	LTR/ERV1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-161	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-294	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 73.]
[rnd-1_family-25	DNA/hAT-Blackjack	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-302	DNA/hAT-hAT5	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-1_family-6	RC/Helitron	C(T-> ii)	SC(H-> dna transposon helitron T-> helitron)	SF()	Palindrome length is 10.]
[rnd-1_family-22	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-409	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.]
[rnd-1_family-361	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.]
[rnd-1_family-265	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-253	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.]
[rnd-1_family-261	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-247	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 64.]
[rnd-1_family-175	DNA/TcMar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 52.]
[rnd-1_family-289	DNA/hAT-Tip100	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.]
[rnd-1_family-228	DNA/PIF-Harbinger	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.]
[rnd-1_family-242	LTR/Copia	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> unknown)	TSD consensus length is 6.TIR consensus length is
[rnd-1_family-300	DNA	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.]

[rnd-1_family-249]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-327]	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.]
[rnd-1_family-54]	LTR/ERV4	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.]
[rnd-1_family-58]	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon dna transposon)	SF(H-> sine)	-]
[rnd-1_family-171]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-24]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 10.TIR consensus length is
[rnd-1_family-381]	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-312]	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 15.]
[rnd-1_family-295]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-1_family-19]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.]
[rnd-1_family-218]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 87.]
[rnd-1_family-139]	DNA/hAT-Pegasus	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-303]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.]
[rnd-1_family-210]	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 13.]
[rnd-1_family-357]	LTR/DIRS	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-229]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-168]	DNA/TcMar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]

[rnd-1_family-213]	SINE/MIR	C(S_SSR-> ii)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAA]
[rnd-1_family-410]	DNA/hAT-Ac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.]
[rnd-1_family-88]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]
[rnd-1_family-226]	DNA/PIF-Harbinger	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.]
[rnd-1_family-325]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.TIR consensus length is
[rnd-1_family-4]	LINE/Jockey	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-1]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-343]	DNA	C(T-> ii)	SC(H-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-9]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-189]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.TIR consensus length is
[rnd-1_family-155]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.]
[rnd-1_family-82]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-1_family-274]	DNA/TcMar-Pogo	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-198]	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-74]	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-231]	DNA	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 44.]
[rnd-1_family-258]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.]
[rnd-1_family-158]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-306]	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-275]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-164]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-316]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 18.]
[rnd-1_family-97]	DNA	C()	SC(H-> dna transposon)	SF()	-]

[rnd-1_family-104	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-125	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]
[rnd-1_family-190	DNA/PiggyBac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-1_family-329	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-1_family-16	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-136	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.TIR consensus length is 93.]
[rnd-1_family-72	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-159	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-138	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-1_family-50	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-121	DNA/PiggyBac	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 61.]
[rnd-1_family-193	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-208	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.]
[rnd-1_family-20	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-67	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-362	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-1_family-206	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAT.]
[rnd-1_family-233	DNA	C()	SC(H-> dna transposon)	SF()	-]

[rnd-1_family-84]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-202]	DNA/TcMar-Tc1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-330]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.]
[rnd-1_family-232]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 67.]
[rnd-1_family-14]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-215]	DNA/Sola	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 18.]
[rnd-1_family-140]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-286]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	No TSD consensus. Maximum TSD length is
[rnd-1_family-137]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-399]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-352]	DNA/hAT-Tag1	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-63]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.]
[rnd-1_family-263]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-13]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-223]	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-1_family-260]	DNA/hAT	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> unknown)	TSD consensus length is 6.TIR consensus length is
[rnd-1_family-334]	LINE/I	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is
[rnd-1_family-314]	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.]
[rnd-1_family-141]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.]
[rnd-1_family-76]	DNA	C()	SC(H-> dna transposon)	SF(H-> piggybac)	-]
[rnd-1_family-18]	buffer	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-305]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 53.]

[rnd-1_family-17]	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF(H-> piggybac)	TIR consensus length is 198.]
[rnd-1_family-147]	DNA	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is
[rnd-1_family-207]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.]
[rnd-1_family-59]	DNA/TcMar	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-1_family-55]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-1_family-148]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.]
[rnd-1_family-56]	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-353]	rRNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.]
[rnd-1_family-150]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.]
[rnd-1_family-390]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-176]	DNA/hAT	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is
[rnd-1_family-38]	RC/Helitron	C(S_SSR-> i)	SC(H-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.]
[rnd-1_family-358]	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-8]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-307]	SINE/MIR	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine)	Short sequence repeated is ATT.]
[rnd-1_family-239]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-1_family-241]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-209]	LINE/L1	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-57]	DNA/hAT	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]

[rnd-1_family-129]	DNA/TcMar	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 125.]
[rnd-1_family-45]	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.]
[rnd-1_family-133]	SINE/tRNA	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine)	Short sequence repeated is TTA.]
[rnd-1_family-375]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.]
[rnd-1_family-331]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.]
[rnd-1_family-87]	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.]
[rnd-1_family-177]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-1_family-320]	LINE	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-195]	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-26]	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-109]	LTR/Pao	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-395]	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-378]	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]
[rnd-1_family-205]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-34]	Simple_repeat	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 8.Short sequence repeated is ATC.]
[rnd-1_family-120]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-423]	Satellite	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-214]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-427]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.]
[rnd-1_family-431]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 87.]



[rnd-1_family-433]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.]
[rnd-1_family-434]	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-442]	DNA/Kolobok-Hydra	C(S_TIR-> 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-1_family-130]	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-366]	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-452]	DNA/hAT-Ac	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-454]	Unknown	C(T-> i S_LTR)	SC(T-> ltr retrotransposon S_LTR-> Short Terminal Repeat)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 4.Terminal Repeat consensus length is 12.]
[rnd-1_family-456]	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.]
[rnd-1_family-461]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.]
[rnd-1_family-468]	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-480]	DNA/hAT-Blackjack	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	No TSD consensus. Maximum TSD length is 7.]
[rnd-1_family-484]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-490]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]
[rnd-1_family-498]	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-499]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.]
[rnd-1_family-494]	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTGT.]

[rnd-1_family-509]	LTR/Gypsy	C(S_TIR-> ii T	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 61.]
[rnd-1_family-511]	DNA/hAT-hATw	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.TIR consensus length is 46.]
[rnd-1_family-513]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.]
[rnd-1_family-516]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-522]	Unknown	C(S_TIR-> ii T	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 273.]
[rnd-1_family-517]	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-526]	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-530]	DNA/hAT-Blackjack	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.]
[rnd-1_family-549]	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-558]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 96.]
[rnd-1_family-565]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-566]	Unknown	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is
[rnd-1_family-560]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-567]	DNA/TcMar-Tigger	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.]
[rnd-1_family-571]	DNA/hAT-hAT5	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-573]	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 2.]

[rnd-1_family-574]	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 85.]
[rnd-1_family-580]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 80.]
[rnd-1_family-581]	LINE	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-1_family-588]	SINE/MIR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAT.]
[rnd-1_family-578]	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.]
[rnd-1_family-593]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-594]	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-1_family-577]	Unknown	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is
[rnd-1_family-598]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-600]	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-602]	DNA/IS3EU	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-1_family-606]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 20.]
[rnd-1_family-607]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTCTC.]
[rnd-1_family-611]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 13.]
[rnd-1_family-613]	buffer	C(S_TIR-> ii S	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 53.Short sequence repeated is ACGGT.]
[rnd-1_family-617]	DNA/Academ	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-1_family-618]	LINE/L1	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-634	DNA	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	No TSD consensus. Maximum TSD length is 16.]
[rnd-1_family-635	LINE/RTE-RTE	C(T-> ii S_SSR	SC(H-> non-ltr retrotransposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TSD consensus length is 2.Short sequence repeated is TGA.]
[rnd-1_family-640	DNA/CMC-EnSpm	C(S_LTR-> i S	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 22.Short sequence repeated is
[rnd-1_family-648	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 19.]
[rnd-1_family-655	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.]
[rnd-1_family-662	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.]
[rnd-1_family-663	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-667	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 69.]
[rnd-1_family-668	LTR/Copia	C(S_LTR-> i S	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 8.Poly A trail length is 7.]
[rnd-1_family-688	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.]
[rnd-1_family-689	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-672	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 82.]
[rnd-1_family-702	LINE/L1	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.TIR consensus length is 69.]
[rnd-1_family-706	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-709	DNA/Novosib	C(S_LTR-> i S	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 27.Short sequence repeated is

[rnd-1_family-710]	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-718]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-721]	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 6.]
[rnd-1_family-723]	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAA.]
[rnd-1_family-733]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-734]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 31.]
[rnd-1_family-740]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.TIR consensus length is 32.]
[rnd-1_family-743]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-745]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAT.]
[rnd-1_family-696]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.]
[rnd-1_family-752]	DNA/CMC-Chapaev	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-722]	DNA/Crypton	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 91.]
[rnd-1_family-756]	DNA/PIF-Harbinger	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-758]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.]
[rnd-1_family-759]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.TIR consensus length is
[rnd-1_family-770]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.]

[rnd-1_family-776	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 45.]
[rnd-1_family-781	DNA/MULE-MuDR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 17.]
[rnd-1_family-782	LINE/L1	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-1_family-786	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-797	DNA/PIF-HarbS	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 36.]
[rnd-1_family-799	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-800	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.]
[rnd-1_family-805	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-815	Satellite	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-817	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-833	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-1_family-842	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.]
[rnd-1_family-850	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is5/pif/harbinger is630/tc1/mariner )	TSD consensus length is 3.]
[rnd-1_family-851	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-1_family-860	LTR/ERVK	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-874	LINE/Jockey	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]

[rnd-1_family-883]	DNA/CMC-EnSpm	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-1_family-887]	LINE/Penelope	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF(H-> penelope)	TSD consensus length is 2.]
[rnd-1_family-894]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 33.]
[rnd-1_family-897]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-901]	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 8.]
[rnd-1_family-907]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.]
[rnd-1_family-915]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-1_family-919]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGTG.]
[rnd-1_family-923]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-925]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-926]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-1_family-933]	DNA/Sola	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-936]	LINE/L2	C(T-> ii S_SSR)	SC(H-> non-ltr retrotransposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TSD consensus length is 2.Short sequence repeated is TAT.]
[rnd-1_family-946]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-952]	DNA	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.]
[rnd-1_family-953]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	No TSD consensus. Maximum TSD length is
[rnd-1_family-955]	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.]

[rnd-1_family-963]	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-965]	LINE/CR1	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-979]	Satellite	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.]
[rnd-1_family-992]	Satellite	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAATG.]
[rnd-1_family-994]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-998]	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-1_family-1003]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1008]	DNA/TcMar	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1011]	DNA	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-1014]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-1_family-1018]	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-1028]	LINE/I	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.]
[rnd-1_family-1044]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1052]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1054]	DNA/Harbinger	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-1062]	DNA/TcMar-Tc1	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 10.]



[rnd-1_family-1063]	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1069]	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTA.]
[rnd-1_family-1056]	LINE/L2	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-1_family-1081]	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 29.]
[rnd-1_family-1083]	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-1_family-1066]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1100]	DNA/hAT-Tip100	C(T-> i)	SC(H-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-1_family-1103]	Unknown	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-1_family-1104]	DNA/hAT-hATm	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-1_family-1112]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.]
[rnd-1_family-1128]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 39.]
[rnd-1_family-1130]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1135]	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAG.]
[rnd-1_family-1136]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-1_family-1141]	DNA/hAT-hAT6	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-1142]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-1_family-1147]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1148]	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.]
[rnd-1_family-1153]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1169]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-1_family-1179]	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-1_family-1194]	DNA/CMC-Transib	C()	SC(H-> dna transposon)	SF()	-]
[rnd-1_family-1197]	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-1199]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-1_family-1202]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.]
[rnd-2_family-5]	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-]
[rnd-2_family-347]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-2_family-63]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.]
[rnd-3_family-1]	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-]
[rnd-3_family-51]	Unknown	C(T-> ii S_SSR)	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-3_family-276]	LTR/ERV4	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-3_family-302]	LTR/Gypsy	C(S_TIR-> ii T)	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 37.]
[rnd-3_family-6]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-3_family-220]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AC.]

[rnd-3_family-274	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATG.]
[rnd-3_family-360	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-3_family-399	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-3_family-48	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-3_family-80	DNA/TcMar-Tigger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 24.Terminal Repeat consensus length is 8.]
[rnd-3_family-340	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-3_family-1109	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-4_family-297	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-]
[rnd-4_family-167	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 183.]
[rnd-4_family-41	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.]
[rnd-4_family-901	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-4_family-320	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAC.]
[rnd-4_family-815	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-4_family-55	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGG.]
[rnd-4_family-1498	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> transib)	TSD consensus length is 5.TIR consensus length is
[rnd-4_family-223	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAATG.]
[rnd-4_family-647	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.]
[rnd-4_family-1422	DNA	C()	SC(H-> dna transposon)	SF()	-]

[rnd-4_family-1152]	DNA	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 30.]
[rnd-4_family-575]	LINE/L1	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 9.]
[rnd-4_family-773]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> piggybac)	TSD consensus length is 4.]
[rnd-4_family-824]	SINE/tRNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATAT.]
[rnd-4_family-917]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-4_family-258]	LTR/Copia	C(S_TIR-> 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
[rnd-4_family-1605]	DNA/Maverick	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-4_family-1168]	DNA/hAT-hAT5	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-4_family-521]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.]
[rnd-4_family-446]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-4_family-516]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CGC.]
[rnd-4_family-97]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GGT.]
[rnd-4_family-78]	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TG.]
[rnd-4_family-467]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-4_family-749]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-4_family-56]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.]
[rnd-4_family-86]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]

[rnd-4_family-381]	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CAAGT.]
[rnd-4_family-685]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AATA.]
[rnd-4_family-3103]	LINE/Jockey	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-4_family-283]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-4_family-1362]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.TIR consensus length is 69.]
[rnd-4_family-1336]	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.]
[rnd-4_family-1035]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-4_family-2110]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 45.]
[rnd-4_family-639]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-5_family-52]	DNA/PiggyBac	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-425]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAT.]
[rnd-5_family-142]	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-1924]	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-858]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-123]	Unknown	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-5_family-51]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-102]	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-5_family-264	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CTA.]
[rnd-5_family-1074	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-369	LINE	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-185	SINE/MIR	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.]
[rnd-5_family-6427	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-5_family-1019	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-898	LTR	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 9.]
[rnd-5_family-216	LTR/Gypsy	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-823	SINE/tRNA	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(H-> sine)	Short sequence repeated is TTA.]
[rnd-5_family-5193	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> hat p is1016/merlin)	TSD consensus length is 7.]
[rnd-5_family-601	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 240.]
[rnd-5_family-4080	DNA	C(S_SSR-> i)	SC(H-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ACAA.]
[rnd-5_family-600	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.]
[rnd-5_family-379	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTA.]
[rnd-5_family-8	DNA	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]

[rnd-5_family-43]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-165]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-1922]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-274]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-906]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-5_family-1049]	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-310]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.]
[rnd-5_family-1189]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-9698]	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 86.]
[rnd-5_family-1560]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-5350]	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 46.]
[rnd-5_family-4342]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-4145]	LINE/Rex-Babar	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.]
[rnd-5_family-3427]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-6344]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.]
[rnd-5_family-4699]	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 46.]
[rnd-5_family-1450]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1261]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.]
[rnd-5_family-1067]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1404]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-5_family-5534	DNA/PIF-Harbinger	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 28.]
[rnd-5_family-547	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 74.]
[rnd-5_family-1483	LTR/DIRS	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 35.]
[rnd-5_family-610	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-5_family-6092	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.]
[rnd-5_family-591	DNA/Sola	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACTG.]
[rnd-5_family-1302	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-5_family-3135	DNA/hAT-Tag1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 80.]
[rnd-5_family-5257	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-5998	RC/Helitron	C(T-> i S_SSR	SC(T-> ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.Short sequence repeated is CGTC.]
[rnd-5_family-955	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.]
[rnd-5_family-1001	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-5_family-1398	DNA/hAT-Ac	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.TIR consensus length is 17.]
[rnd-5_family-1207	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-298	DNA/TcMar-Pogo	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-5_family-4190	LTR/Gypsy	C(S_LTR-> i S	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 28.Short sequence repeated is



[rnd-5_family-984	LTR/Gypsy	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is
[rnd-5_family-3208	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1080	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-4528	Unknown	C(S_TIR-> ii S	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 46.Short sequence repeated is NN.]
[rnd-5_family-410	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-87	Unknown	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.]
[rnd-5_family-3147	LINE/I	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GT.]
[rnd-5_family-2420	LTR/Gypsy	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 11.TIR consensus length is 109.]
[rnd-5_family-399	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-1077	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ACAA.]
[rnd-5_family-389	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-3921	LTR/ERVL-MaLR	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is
[rnd-5_family-398	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-5_family-178	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.]
[rnd-5_family-2606	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1042	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-166	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 76.]
[rnd-5_family-255	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1696	LTR/Pao	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.]
[rnd-5_family-184	DNA/Crypton	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-365	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-6458	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-972	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1677	LINE/L2	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-103	Unknown	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is
[rnd-5_family-944	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NN.]
[rnd-5_family-3195	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1312	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-453	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.]
[rnd-5_family-2489	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is

[rnd-5_family-2308]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-213]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-5_family-2301]	DNA/CMC-Transib	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-5362]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.]
[rnd-5_family-319]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1400]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-5_family-609]	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-646]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-1415]	LINE/Penelope	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-5_family-1336]	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is 2.]
[rnd-5_family-2734]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 42.]
[rnd-5_family-7325]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-4482]	LINE/L2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 41.]
[rnd-5_family-688]	DNA/TcMar-Tigger	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-593]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-179]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-437]	buffer	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-1642]	DNA/Sola	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 34.]
[rnd-5_family-2952]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	No TSD consensus. Maximum TSD length is 2.TIR consensus length is
[rnd-5_family-239]	DNA/PiggyBac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]

[rnd-5_family-1205]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAC.]
[rnd-5_family-3150]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAA.]
[rnd-5_family-3035]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-1039]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1733]	LTR	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-873]	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.]
[rnd-5_family-526]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.]
[rnd-5_family-3416]	LTR	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-1076]	DNA	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is
[rnd-5_family-2831]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-5_family-5645]	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 36.]
[rnd-5_family-3714]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 40.]
[rnd-5_family-3438]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-451]	DNA/Sola	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-1021]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-2605]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-391]	LINE	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AATA.]
[rnd-5_family-1305]	LINE/RTE-BovB	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]

[rnd-5_family-341]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-435]	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-325]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-132]	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1860]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1362]	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-4067]	DNA/MULE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GG.]
[rnd-5_family-516]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-6296]	DNA/hAT-hATw	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-3780]	DNA	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-5_family-443]	DNA/hAT-Ac	C(T-> i)	SC(H-> dna transposon T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-5_family-6312]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 49.]
[rnd-5_family-1090]	LINE/Jockey	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-5_family-6780]	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-1654]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 25.]

[rnd-5_family-2798]	LINE/RTE-X	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATCTT.]
[rnd-5_family-2520]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon S_SSR-> non-ltr retrotransposon)	SF()	TIR consensus length is 19.Short sequence repeated is NNNNN.]
[rnd-5_family-673]	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 82.]
[rnd-5_family-4277]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-5490]	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 55.]
[rnd-5_family-23]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-2687]	DNA/Academ	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-2915]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GAC.]
[rnd-5_family-1805]	DNA	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 5.]
[rnd-5_family-4672]	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1354]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-263]	LINE/CR1-Zenon	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 8.]
[rnd-5_family-3514]	DNA/MuLE-MuDR	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-2804]	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-7176]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 47.]
[rnd-5_family-1287]	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]

[rnd-5_family-1399]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-3384]	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-2157]	LINE/Penelope	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-2471]	LTR/Pao	C(S_TIR-> ii)	SC(S_TIR-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	TIR consensus length is 109.Terminal Repeat consensus length is 10.]
[rnd-5_family-2]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-2173]	LTR/Gypsy	C(T-> ii)	SC(H-> ltr retrotransposon T-> helitron)	SF()	Palindrome length is 12.]
[rnd-5_family-3358]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AACTG.]
[rnd-5_family-2306]	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-5_family-865]	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.]
[rnd-5_family-4784]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-3750]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-5453]	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 66.]
[rnd-5_family-427]	LINE/L1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.]
[rnd-5_family-2060]	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-730]	DNA/Maverick	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 20.]
[rnd-5_family-4380]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]

[rnd-5_family-404	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-206	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-5_family-2637	LINE/Proto1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-1229	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-11981	DNA/MuLE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAAA.]
[rnd-5_family-1098	LTR/Pao	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TATTG.]
[rnd-5_family-4075	DNA/Kolobok-T2	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 37.]
[rnd-5_family-253	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-4732	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1851	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-7913	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-2677	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATGT.]
[rnd-5_family-3029	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-8006	LTR/Gypsy	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF()	TSD consensus length is 2.TIR consensus length is



[rnd-5_family-1239]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-69]	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 196.]
[rnd-5_family-5865]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-2013]	LTR/Gypsy	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-5_family-2102]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CTA.]
[rnd-5_family-242]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-2287]	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is GTGT.]
[rnd-5_family-5086]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1233]	LTR/ERVK	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-3074]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1474]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATACC.]
[rnd-5_family-1875]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-116]	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-436]	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-5_family-560]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AC.]

[rnd-5_family-4166	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-]
[rnd-5_family-3859	Satellite	C(T-> ii S_SSR-> non-ltr retrotransposon)	SC(T-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Palindrome length is 12.Short sequence
[rnd-5_family-2578	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 32.]
[rnd-5_family-6157	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-6856	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CTA.]
[rnd-5_family-2366	DNA/Merlin	C()	SC(H-> dna transposon)	SF()	-]
[rnd-5_family-2705	DNA/CMC-EnSpm	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 21.]
[rnd-5_family-856	RC/Helitron	C(S_SSR-> i)	SC(H-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-5_family-4490	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-5_family-4201	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 48.]
[rnd-5_family-2494	DNA/Crypton	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	TSD consensus length is 2.]
[rnd-5_family-643	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-5_family-1940	LINE/R1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-5_family-692	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-6452	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-1339	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 24.]
[rnd-5_family-2795	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-5_family-4409]	LTR/Gypsy	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-1744]	LINE/RTE-BovB	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AG.]
[rnd-5_family-6174]	LTR/Copia	C(T-> ii)	SC(H-> helitron T-> helitron)	SF()	Palindrome length is 12.]
[rnd-5_family-2152]	DNA/TcMar-Tc2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.]
[rnd-5_family-3375]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-5_family-7249]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-2181]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-5_family-434]	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-772]	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGA.]
[rnd-6_family-916]	DNA/Maverick	C()	SC(H-> dna transposon)	SF()	-]
[rnd-6_family-1192]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CTA.]
[rnd-6_family-770]	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-1025]	LTR/Gypsy	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-6_family-1740]	DNA	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-773]	DNA/CMC-EnSpm	C(S_LTR-> i)	SC(H-> dna transposon S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]

[rnd-6_family-1482]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-172]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-6_family-106]	LINE/CR1	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 24.]
[rnd-6_family-792]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TAC.]
[rnd-6_family-1574]	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 23.]
[rnd-6_family-222]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-129]	DNA/hAT-Tip100	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CC.]
[rnd-6_family-1722]	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-6_family-2194]	Simple_repeat	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 30.]
[rnd-6_family-242]	LINE/RTE-X	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 26.]
[rnd-6_family-700]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3668]	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-2084]	DNA/Academ	C()	SC(H-> dna transposon)	SF()	-]
[rnd-6_family-1092]	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1112]	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.]
[rnd-6_family-597]	DNA/Novosib	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.]
[rnd-6_family-135]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TATTG.]

[rnd-6_family-3412	LTR/ERV1	C(T-> ii S_SSR-> ii)	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> is5/pif/harbinger is630/tc1/mariner )	TSD consensus length is 3.Short sequence repeated is ATTTG.]
[rnd-6_family-497	DNA/hAT-Charlie	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.]
[rnd-6_family-622	RC/Helitron	C(S_SSR-> i)	SC(H-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.]
[rnd-6_family-618	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 82.]
[rnd-6_family-760	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Poly A trail length is 7.]
[rnd-6_family-2905	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1703	DNA	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 67.]
[rnd-6_family-495	LINE/L1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-844	LINE/I	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-6_family-3155	LINE	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CACAC.]
[rnd-6_family-3755	Unknown	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-5146	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3770	LTR/Gypsy	C()	SC(H-> ltr retrotransposon)	SF()	-]
[rnd-6_family-154	LTR/Copia	C(T-> ii)	SC(T-> dna transposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.]
[rnd-6_family-1053	Simple_repeat	C()	SC(H-> ltr retrotransposon)	SF()	-]
[rnd-6_family-833	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-6_family-500	LINE/Penelope	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-564	DNA/CMC-Transib	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 65.]
[rnd-6_family-588	LINE/L2	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-2941	LTR/Gypsy	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 10.]
[rnd-6_family-2015	LINE	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CA.]
[rnd-6_family-167	buffer	C(S_LTR-> i S	SC(S_LTR-> Short Terminal Repeat S_SSR-> non-ltr retrotransposon)	SF()	Terminal Repeat consensus length is 8.Short sequence repeated is TCA.]
[rnd-6_family-3297	RC/Helitron	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 38.]
[rnd-6_family-939	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCAAT.]
[rnd-6_family-927	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is
[rnd-6_family-837	LTR	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 22.]
[rnd-6_family-3039	DNA/PiggyBac	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCCCC.]
[rnd-6_family-8788	LTR/Copia	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TCAAA.]
[rnd-6_family-2184	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1895	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-3667	DNA/CMC-EnSpm	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3657	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-6_family-5319]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-170]	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-6_family-478]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-6_family-2163]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAATG.]
[rnd-6_family-3089]	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is ATT.]
[rnd-6_family-911]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1136]	Unknown	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-6_family-4374]	DNA/PiggyBac	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF(H-> piggybac)	TIR consensus length is 199.]
[rnd-6_family-512]	LTR/Pao	C(T-> ii)	SC(T-> helitron)	SF()	No TSD consensus. Maximum TSD length is
[rnd-6_family-3228]	LINE/RTE-X	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1670]	RC/Helitron	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is NNNNN.]
[rnd-6_family-1265]	DNA/MULE-MuDR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CCGGG.]
[rnd-6_family-350]	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-2787]	LINE/L1	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon)	SF(T-> transib)	TSD consensus length is 5.TIR consensus length is

[rnd-6_family-1190]	LTR	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-4751]	RC/Helitron	C()	SC(H-> helitron)	SF()	-]
[rnd-6_family-7161]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3206]	DNA/Kolobok-T2	C(T-> ii)	SC(T-> helitron)	SF()	Palindrome length is 12.]
[rnd-6_family-474]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-471]	Unknown	C(S_TIR-> ii T	SC(S_TIR-> dna transposon T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 9.TIR consensus length is 49.Short sequence
[rnd-6_family-2822]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1383]	DNA/hAT-Tip100	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-6_family-5699]	DNA	C(T-> ii S_SSR	SC(T-> dna transposon S_SSR-> non-ltr retrotransposon)	SF(T-> cacta/en/spm is5/pif/harbinger)	TSD consensus length is 3.Short sequence repeated is GG.]
[rnd-6_family-3470]	LTR/Gypsy	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 9.]
[rnd-6_family-4451]	LTR	C(T-> i)	SC(T-> ltr retrotransposon)	SF(T-> ty3/gypsy ty1/copia retroviral)	TSD consensus length is 4.]
[rnd-6_family-4088]	DNA	C()	SC(H-> dna transposon)	SF()	-]
[rnd-6_family-606]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3008]	LINE/RTE-BovB	C(T-> ii)	SC(H-> non-ltr retrotransposon T-> helitron)	SF()	Palindrome length is 10.]



[rnd-6_family-296	Unknown	C(T-> ii S_SSR-> ii)	SC(T-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Palindrome length is 12.Short sequence
[rnd-6_family-620	LTR/ERV1	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 99.]
[rnd-6_family-491	LTR/Gypsy	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.]
[rnd-6_family-3635	LINE/Proto2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-7861	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-2736	LTR/Copia	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 27.]
[rnd-6_family-4622	DNA/hAT-Tip100	C(T-> ii)	SC(T-> dna transposon)	SF()	TSD consensus length is 2.]
[rnd-6_family-117	LINE/L2	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGTTT.]
[rnd-6_family-1850	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGTAAT.]
[rnd-6_family-1362	Simple_repeat	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is CAAGT.]
[rnd-6_family-3066	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 44.]
[rnd-6_family-5530	LTR/Gypsy	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-13	SINE/MIR	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-6_family-4284	DNA/CMC-EnSpm	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3569	DNA/CMC-EnSpm	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TT.]
[rnd-6_family-6090	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-1281	Unknown	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is

[rnd-6_family-1603]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAAAA.]
[rnd-6_family-1367]	RC/Helitron	C(S_SSR-> i)	SC(H-> helitron S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTTT.]
[rnd-6_family-484]	SINE/tRNA	C()	SC(H-> non-ltr retrotransposon)	SF(H-> sine)	-]
[rnd-6_family-1152]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1161]	buffer	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1346]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-188]	DNA	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGTG.]
[rnd-6_family-7414]	DNA/TcMar-Tc1	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 36.]
[rnd-6_family-3703]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-5904]	Unknown	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is630/tc1/mariner )	No TSD consensus. Maximum TSD length is 2.]
[rnd-6_family-5388]	LINE/CR1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-646]	Unknown	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAATG.]
[rnd-6_family-2539]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3212]	LTR/ERV1	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 44.]
[rnd-6_family-3802]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-6_family-3472]	LTR/Copia	C(T-> i)	SC(T-> non-ltr retrotransposon penelope)	SF(T-> line/sine)	No TSD consensus. Maximum TSD length is 9.]
[rnd-6_family-2921]	LTR/Gypsy	C(S_TIR-> ii)	SC(S_TIR-> dna transposon)	SF()	TIR consensus length is 43.]
[rnd-6_family-2856]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-2714]	DNA/TcMar-Mariner	C(S_TIR-> ii)	SC(H-> dna transposon S_TIR-> dna transposon)	SF()	TIR consensus length is 174.]
[rnd-6_family-3934]	LINE/Jockey	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-335]	buffer	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TTTTT.]
[rnd-6_family-1044]	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3974]	LINE/RTE-BovB	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-267]	LTR/Copia	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is AAAT.]
[rnd-6_family-6826]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1541]	DNA	C(S_LTR-> i)	SC(S_LTR-> Short Terminal Repeat)	SF()	Terminal Repeat consensus length is 8.]
[rnd-6_family-3401]	LTR/Copia	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1345]	DNA	C(T-> ii)	SC(T-> dna transposon)	SF(T-> is256/mutator/fb)	TSD consensus length is 10.]
[rnd-6_family-1804]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-4685]	LTR/ERV1	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1347]	LINE/RTE-RTE	C()	SC(H-> non-ltr retrotransposon)	SF()	-]

[rnd-6_family-5420]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-6844]	LINE/Rex-Babar	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-693]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-3284]	LINE/L1-Tx1	C(S_SSR-> i)	SC(S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGAAC.]
[rnd-6_family-2122]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-1197]	LINE/L2	C()	SC(H-> non-ltr retrotransposon)	SF()	-]
[rnd-6_family-5307]	LINE/CR1	C(S_SSR-> i)	SC(H-> non-ltr retrotransposon S_SSR-> non-ltr retrotransposon)	SF()	Short sequence repeated is TGA.]