Map of Hits

SVG viewer **is required to view graphical representation of the map as Scalable Vector Graphics (SVG plot).**

TE_00000002#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000002#MITE@unknown	1	131	SINE2-1_PMaj	6	135	NonLTR/SINE/SINE2	d	0.8931	1.6250	958

TE_00000010#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000010#MITE@unknown	1	299	GymnSINE	3	300	NonLTR/SINE/SINE3	d	0.8528	1.6000	1706

TE_00000012#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000012#MITE@unknown	48	157	TguERVL2b5_LTR	375	486	ERV/ERV3	c	0.7264	1.6000	332
TE_00000012#MITE@unknown	361	603	ERV3-28_PMaj-LTR	317	626	ERV/ERV3	c	0.7551	1.7241	750

TE_00000022#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000022#MITE@unknown	218	450	fAlbLTR2	22	241	ERV/ERV1	c	0.6205	2.1111	349

TE_00000023#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000023#MITE@unknown	138	257	LTR11_MEu	128	251	ERV/ERV1	c	0.6613	1.6818	241

TE_00000028#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000028#MITE@unknown	1	574	TguLTR5c	1	586	ERV/ERV3	d	0.7936	1.6897	2678

TE_00000032#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000032#MITE@unknown	282	382	ERV1-6_MM-I	2968	3061	ERV/ERV1	d	0.6804	2.0000	227

TE_00000033#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000033#MITE@unknown	180	225	RTE-1B_DAn	801	848	NonLTR/RTE	d	0.7872	1.8000	218

TE_00000034#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000034#MITE@unknown	71	308	fAlbLTRL2	74	301	ERV/ERV3	d	0.6903	2.1111	341

TE_00000036#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000036#MITE@unknown	167	237	L1-35_ALy	1515	1586	NonLTR/L1	d	0.7260	1.4545	247

TE_00000040#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score

| TE_00000040#MITE@unknown | 84 | 145 | Hitchcock_LTR | 172 | 238 | LTR | d | 0.7969 | 1.2500 | 302 |

TE_00000068#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000068#MITE@unknown	98	1007	CR1-X1_Pass	3465	4421	NonLTR/CR1	d	0.8777	3.7308	6080

TE_00000071#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000071#MITE@unknown	3	236	CR1-E_Pass	2835	3076	NonLTR/CR1	d	0.8201	2.7143	1311

TE_00000073#MITE@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00000073#MITE@unknown	49	115	TguERVL2b1_LTR-La_fAlb	464	539	ERV/ERV3	c	0.7941	2.4000	263
TE_00000073#MITE@unknown	366	421	ERV3-28_PMaj-LTR	566	619	ERV/ERV3	c	0.8182	1.3333	311

TE_00001107_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00001107_LTR#LTR@unknown	246	359	L1-4B_LA-5end	1649	1762	NonLTR/L1	d	0.7281	1.9167	281

TE_00001324_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00001324_LTR#LTR@unknown	349	387	Mariner-2_NV	2023	2057	DNA/Mariner	d	0.8889	1.5000	233

TE_00002464_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002464_LTR#LTR@unknown	60	236	Gypsy-65_PIT-I	2911	3071	LTR/Gypsy	c	0.7239	1.7647	237
TE_00002464_LTR#LTR@unknown	254	472	CR1-J1_Pass	3723	3961	NonLTR/CR1	c	0.7668	3.4286	827

TE_00002563_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002563_LTR#LTR@unknown	56	107	ERV3-N2_MUn-LTR	191	241	ERV/ERV3	d	0.7885	1.2857	257
TE_00002563_LTR#LTR@unknown	353	426	HARB-9_ALy	311	388	DNA/Harbinger	c	0.7568	1.6667	214

TE_00002676_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002676_LTR#LTR@unknown	21	317	CR1-X1_Pass	4111	4419	NonLTR/CR1	d	0.8717	3.2000	1716

TE_00002809_LTR#LTR@Gypsy (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002809_LTR#LTR@Gypsy	311	358	Mariner-1_Crp	303	347	DNA/Mariner	c	0.8478	5.0000	225

TE_00002832_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002832_LTR#LTR@unknown	1	433	CR1-J3_Pass	3826	4255	NonLTR/CR1	d	0.8051	1.7234	2428

TE_00002986_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00002986_LTR#LTR@unknown	15	391	CR1-J1_Pass	3552	3960	NonLTR/CR1	d	0.7714	3.7143	1552

TE_00003054_INT#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003054_INT#LTR@unknown	385	571	ERV3-23_PMaj-I	1533	1715	ERV/ERV3	d	0.6703	1.5946	598
TE_00003054_INT#LTR@unknown	632	674	ERV3-1_MUn-I	2023	2065	ERV/ERV3	d	0.7209	1.2000	206
TE_00003054_INT#LTR@unknown	675	1051	ERV3-18_PMaj-I	3982	4437	ERV/ERV3	d	0.7604	1.3333	1612
TE_00003054_INT#LTR@unknown	1122	1347	ERV3-23_PMaj-I	3301	3577	ERV/ERV3	d	0.7665	1.6538	706

TE_00003386_LTR#LTR@Gypsy (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003386_LTR#LTR@Gypsy	124	171	Gypsy103-I_Dr	1007	1055	LTR/Gypsy	c	0.7755	1.4286	230

TE_00003595_INT#LTR@Gypsy (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	702	885	hAT-1_SIt	3774	3938	DNA/hAT	c	0.6959	1.9000	349
TE_00003595_INT#LTR@Gypsy	960	1271	RTAg4	1985	2277	NonLTR/R1	c	0.6622	1.9792	606
TE_00003595_INT#LTR@Gypsy	1406	1438	BARBARA_TM_I	4384	4416	LTR/Copia	d	0.8788	2.0000	228
TE_00003595_INT#LTR@Gypsy	2024	2067	Copia-32_BD-I	4071	4112	LTR/Copia	d	0.8140	1.7500	204
TE_00003595_INT#LTR@Gypsy	2081	2122	I-73_AAe	2571	2613	NonLTR/I	d	0.8140	2.3333	208
TE_00003595_INT#LTR@Gypsy	2499	2550	Copia-51_CCri-I	775	826	LTR/Copia	d	0.7692	1.5000	271
TE_00003595_INT#LTR@Gypsy	2955	3381	ERV2-9_UCy-I	2069	2495	ERV/ERV2	d	0.6444	1.8028	464
TE_00003595_INT#LTR@Gypsy	3530	4378	ERV2-17_UCy-I	3412	4258	ERV/ERV2	d	0.6518	2.1508	1539
TE_00003595_INT#LTR@Gypsy	4600	4631	LINE1-32_SBi	1578	1609	NonLTR/L1	c	0.8750	1.3333	224
TE_00003595_INT#LTR@Gypsy	4927	4995	ERV2-17_UCy-I	4785	4853	ERV/ERV2	d	0.7500	1.7500	227
TE_00003595_INT#LTR@Gypsy	5043	5885	ERV2-11_GG-I	4332	5169	ERV/ERV2	d	0.6711	1.9826	1319
TE_00003595_INT#LTR@Gypsy	6040	6073	RNERVK23	5595	5628	ERV/ERV2	d	0.8529	1.2500	226
TE_00003595_INT#LTR@Gypsy	6428	6500	Gypsy-38B_NS-LTR	875	948	LTR/Gypsy	c	0.7432	1.6667	214

TE_00003627_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003627_LTR#LTR@unknown	113	194	CATS	1771	1855	NonLTR/R1	d	0.7500	2.2500	283

TE_00003665_LTR#LTR@Gypsy (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003665_LTR#LTR@Gypsy	184	269	Nimb-1_PH	2137	2226	NonLTR/Nimb	d	0.7683	2.5000	240

TE_00003992_INT#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	127	352	ERV3-23_PMaj-I	3301	3577	ERV/ERV3	c	0.7621	1.6296	694
TE_00003992_INT#LTR@unknown	392	504	LTR3B_Ami	650	788	LTR/Gypsy	c	0.6638	1.8000	268
TE_00003992_INT#LTR@unknown	506	875	ERV3-18_PMaj-I	3982	4430	ERV/ERV3	c	0.7745	1.2623	1629
TE_00003992_INT#LTR@unknown	889	937	GGERVL-A2-I	2416	2464	ERV/ERV3	c	0.7959	1.6000	215
TE_00003992_INT#LTR@unknown	975	1161	ERV3-23_PMaj-I	1533	1715	ERV/ERV3	c	0.6885	1.6364	603

TE_00004237_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004237_LTR#LTR@unknown	67	141	ERV3-5_NuM-LTR	190	265	ERV/ERV3	d	0.7273	1.8000	281
TE_00004237_LTR#LTR@unknown	364	415	R_Av	23352	23403	NonLTR/Penelope	d	0.7925	1.3333	202

TE_00004276_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004276_LTR#LTR@unknown	36	95	ERV2-12C_PMaj-LTR	209	270	ERV	c	0.7581	1.7143	214

TE_00004455_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004455_LTR#LTR@unknown	3	186	CR1-E_Pass	2865	3056	NonLTR/CR1	c	0.8342	2.5455	1026

TE_00004571_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004571_LTR#LTR@unknown	1	68	CR1-1_ACC	4264	4330	NonLTR/CR1	c	0.7941	1.8571	332
TE_00004571_LTR#LTR@unknown	161	461	CR1-J3_Pass	3959	4258	NonLTR/CR1	c	0.7800	1.5897	1534

TE_00004824_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004824_LTR#LTR@unknown	76	148	Hitchcock_LTR	165	238	LTR	d	0.7746	2.1667	258
TE_00004824_LTR#LTR@unknown	424	475	R_Av	23352	23403	NonLTR/Penelope	d	0.7925	1.3333	202

TE_00004863_INT#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00004863_INT#LTR@unknown	593	883	EnSpm-1_TC	266	556	DNA/EnSpm/CACTA	d	0.7203	2.1154	241
TE_00004863_INT#LTR@unknown	990	1060	BEL-4_DAn-LTR	165	241	LTR/BEL	c	0.7600	2.3333	219
TE_00004863_INT#LTR@unknown	1217	1277	ERV17_MD_I	4872	4929	ERV/ERV2	c	0.7797	2.0000	271

TE_00005070_LTR#LTR@unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
TE_00005070_LTR#LTR@unknown	1	168	CR1-C4	4321	4491	NonLTR/CR1	d	0.8353	1.6250	962

rnd-1_family-100#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-100#Unknown	193	359	Gypsy-71_PTr-LTR	1185	1330	LTR/Gypsy	c	0.7200	1.7222	294

rnd-1_family-102#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-102#Unknown	139	315	Rex1-1_HRo	3651	3797	NonLTR/Rex1	d	0.7237	1.7222	256
rnd-1_family-102#Unknown	608	678	CR1-3_HM	157	225	NonLTR/CR1	d	0.7286	1.7000	217

rnd-1_family-103#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	234	337	ERV2-12_GG-I	1098	1199	ERV/ERV2	d	0.6931	1.6471	301
rnd-1_family-103#LTR@ERVK	462	615	TguLTRK2e_I	1963	2116	ERV/ERV2	d	0.6667	1.6154	275
rnd-1_family-103#LTR@ERVK	1004	1702	ERV2-11D_GG-I	1897	2601	ERV/ERV2	d	0.6246	1.8729	439
rnd-1_family-103#LTR@ERVK	1964	2772	ERV2-12_UCy-I	2612	3420	ERV/ERV2	d	0.6836	1.8254	1845
rnd-1_family-103#LTR@ERVK	3298	4494	ERV2-12_UCy-I	3931	5124	ERV/ERV2	d	0.6715	1.9080	1890

rnd-1_family-105#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-105#Unknown	434	495	Gypsy-31_MAc-I	7369	7435	LTR/Gypsy	d	0.7656	2.1667	220

rnd-1_family-107#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-107#LTR@ERVL	67	4318	ERV3-18_PMaj-I	871	5181	ERV/ERV3	d	0.7645	2.0331	22804

rnd-1_family-113#LINE@CR1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-113#LINE@CR1	120	3167	CR1-J3_Pass	76	3113	NonLTR/CR1	d	0.7718	1.6000	15733

rnd-1_family-114#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-114#Unknown	264	309	Copia-11_RC-I	3351	3397	LTR/Copia	c	0.7660	1.2500	228

rnd-1_family-117#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	117	174	Tgu_rep3-L_Ucy	706	763	ERV/ERV3	d	0.7931	1.5000	319
rnd-1_family-117#Unknown	590	661	Gypsy-22_CT-I	3937	4002	LTR/Gypsy	c	0.7500	1.3000	222
rnd-1_family-117#Unknown	1049	1084	Gypsy-4_DWil-I	3041	3079	LTR/Gypsy	c	0.8378	1.0000	216
rnd-1_family-117#Unknown	1140	1197	Gypsy-51_MLP-LTR	1494	1552	LTR/Gypsy	c	0.8246	1.2000	256
rnd-1_family-117#Unknown	1712	1767	Gypsy-21_SM-I	12951	13007	LTR/Gypsy	c	0.7679	1.3750	200
rnd-1_family-117#Unknown	1906	1935	Mariner-2_NV	2023	2052	DNA/Mariner	d	0.9000	1.5000	226

rnd-1_family-119#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-119#Unknown	134	197	SMAR18	2420	2489	DNA/Mariner	c	0.8235	3.5000	244
rnd-1_family-119#Unknown	422	546	ERV3-3_ACD-LTR	152	283	ERV/ERV3	c	0.6953	1.6000	323

rnd-1_family-122#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	26	94	Gypsy20-VV_I	2234	2300	LTR/Gypsy	c	0.6957	1.4615	212
rnd-1_family-122#LTR@ERVL	465	646	MuDR-1_GAr	8001	8156	DNA/MuDR	c	0.7546	1.9412	526
rnd-1_family-122#LTR@ERVL	890	924	Harbinger-1_PGr	5150	5184	DNA/Harbinger	d	0.8571	1.6667	224
rnd-1_family-122#LTR@ERVL	1207	1310	Gypsy-12_ATr-LTR	3135	3237	LTR/Gypsy	c	0.6765	1.9375	259
rnd-1_family-122#LTR@ERVL	1311	1767	ERV3-23_PMaj-I	937	1396	ERV/ERV3	d	0.6798	1.5632	1327
rnd-1_family-122#LTR@ERVL	2152	2199	Gypsy-129_GM-I	174	220	LTR/Gypsy	d	0.7292	1.0000	209
rnd-1_family-122#LTR@ERVL	2202	3245	ERV3-23_PMaj-I	1545	2570	ERV/ERV3	d	0.7109	1.6176	3520

rnd-1_family-126#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-126#Unknown	1	182	Tgu_rep3-L_Ucy	2	212	ERV/ERV3	d	0.7611	2.1250	588
rnd-1_family-126#Unknown	205	913	ERV3-28_PMaj-LTR	221	1038	ERV/ERV3	d	0.7983	1.9483	3215

rnd-1_family-128#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-128#Unknown	1982	2039	Copia-9_HAE-I	663	720	LTR/Copia	d	0.7586	2.0000	280

rnd-1_family-129#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-129#Unknown	592	649	Copia-9_HAE-I	663	720	LTR/Copia	c	0.7586	2.0000	280

rnd-1_family-130#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-130#Unknown	257	384	Gypsy-18_MN-I	7680	7813	LTR/Gypsy	c	0.7164	1.5000	284

rnd-1_family-134#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-134#Unknown	83	400	TguLTRK2d_I	4899	5189	ERV/ERV2	c	0.6815	1.9762	574
rnd-1_family-134#Unknown	703	875	Gypsy-12_SLy-LTR	1186	1349	LTR/Gypsy	c	0.7195	1.8421	259
rnd-1_family-134#Unknown	996	1073	EnSpm-3_ALy	3974	4057	DNA/EnSpm/CACTA	d	0.7284	2.0000	203
rnd-1_family-134#Unknown	1753	1896	MERMITEJ	1004	1148	DNA/MuDR	c	0.7305	2.1538	259

rnd-1_family-138#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-138#Unknown	475	611	Penelope-73N1_LMi	197	323	NonLTR/Penelope	d	0.7200	2.1667	236
rnd-1_family-138#Unknown	744	801	Copia-9_HAE-I	663	720	LTR/Copia	c	0.7586	2.0000	280

rnd-1_family-143#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-143#Unknown	613	670	Copia-9_HAE-I	663	720	LTR/Copia	c	0.7586	2.0000	280

rnd-1_family-145#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-145#Unknown	542	625	Gypsy-6_IS-I	3937	4014	LTR/Gypsy	d	0.7711	3.2500	216

rnd-1_family-150#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-150#Unknown	1929	1986	Copia-9_HAE-I	663	720	LTR/Copia	d	0.7586	2.3333	286

rnd-1_family-152#Unknown ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-152#Unknown	422	488	Copia-80_Mad-I	2574	2642	LTR/Copia	d	0.7391	1.6250	210
rnd-1_family-152#Unknown	575	667	Gypsy-96_GM-I	708	798	LTR/Gypsy	c	0.6774	1.7333	227
rnd-1_family-152#Unknown	1133	1394	TE-X-12_DR	576	833	Multicopy_gene	c	0.6589	2.2647	518

rnd-1_family-16#LINE@CR1 ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-16#LINE@CR1	1	420	CR1-J1_Pass	3516	3960	NonLTR/CR1	d	0.7972	3.9000	1999

rnd-1_family-18#LINE@CR1 ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-18#LINE@CR1	29	397	CR1-J1_Pass	3586	3961	NonLTR/CR1	d	0.7941	3.2727	1666

rnd-1_family-21#LINE@CR1 ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-21#LINE@CR1	1	559	CR1-YB2_Pass	3297	3857	NonLTR/CR1	d	0.9571	11.0000	4451

rnd-1_family-26#LINE@CR1 ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-26#LINE@CR1	7	477	CR1-C4	4015	4495	NonLTR/CR1	d	0.8484	2.0606	2878

rnd-1_family-27#LINE@RTE-BovB ([SVG Plot]; [Alignments]; [Masked])

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-27#LINE@RTE-BovB	23	3997	AviRTE_GRu	3	3976	NonLTR/RTE	d	0.9701	1.5733	33974

rnd-1_family-29#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-29#Unknown	199	304	Coprina_Cc1	21	127	NonLTR/Penelope	c	0.8037	4.0000	521
rnd-1_family-29#Unknown	558	664	Coprina_Cc1	21	127	NonLTR/Penelope	c	0.8131	4.0000	558
rnd-1_family-29#Unknown	919	1022	TREP_CE	123	226	Interspersed_Repeat	d	0.7500	6.5000	365

rnd-1_family-30#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-30#Unknown	90	254	ERV3-7_PMaj-LTR	131	303	ERV/ERV3	d	0.6970	1.7391	339

rnd-1_family-31#LINE@CR1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-31#LINE@CR1	1	1123	CR1-2_ACC	2708	3852	NonLTR/CR1	d	0.8291	2.7612	7467

rnd-1_family-44#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-44#Unknown	1	593	TguLTR5d	1	595	ERV/ERV3	d	0.9143	2.7222	4734

rnd-1_family-45#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-45#Unknown	1	594	TguLTR5d	1	595	ERV/ERV3	d	0.9007	4.8333	4704

rnd-1_family-47#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-47#LTR@ERVL	1	595	TguLTR5b	1	596	ERV/ERV3	d	0.9379	3.2727	4945

rnd-1_family-51#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-51#Unknown	1	589	TguLTR5d	1	590	ERV/ERV3	d	0.9066	4.9091	4701

rnd-1_family-52#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-52#LTR@ERVL	1	1113	ERV3-4_PMaj-LTR	1	1134	ERV/ERV3	d	0.8286	8.8000	7112

rnd-1_family-53#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-53#Unknown	180	214	Gypsy-62_MLP-I	3006	3040	LTR/Gypsy	d	0.8286	2.0000	226
rnd-1_family-53#Unknown	596	645	BEL-732_AA-I	2188	2234	LTR/BEL	c	0.8163	1.4000	247
rnd-1_family-53#Unknown	710	751	Penelope-11_HM	2692	2732	NonLTR/Penelope	c	0.8095	1.4000	211

rnd-1_family-54#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-54#LTR@ERVL	70	114	EnSpm-N5_HM	3855	3898	DNA/EnSpm/CACTA	c	0.8444	3.0000	229
rnd-1_family-54#LTR@ERVL	489	680	ERV3-3_UCy-I	254	430	ERV/ERV3	d	0.6704	1.4324	476
rnd-1_family-54#LTR@ERVL	796	914	hAT-N9_LCh	981	1106	DNA/hAT	c	0.7119	1.2500	309
rnd-1_family-54#LTR@ERVL	948	1535	TguERVL2_I-b_fAlb	781	1372	ERV/ERV3	d	0.6808	1.7019	1895

rnd-1_family-57#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	293	474	ERV3-23_PMaj-I	1533	1710	ERV/ERV3	d	0.6910	1.6250	592
rnd-1_family-57#LTR@ERVL	541	579	ERV3-23_PMaj-I	1875	1916	ERV/ERV3	d	0.8250	1.0000	231
rnd-1_family-57#LTR@ERVL	580	949	ERV3-18_PMaj-I	3982	4430	ERV/ERV3	d	0.7666	1.3115	1599
rnd-1_family-57#LTR@ERVL	950	1062	LTR3B_Ami	649	787	LTR/Gypsy	d	0.6810	1.4783	258
rnd-1_family-57#LTR@ERVL	1083	1308	ERV3-23_PMaj-I	3301	3577	ERV/ERV3	d	0.7621	1.6296	694

rnd-1_family-64#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-64#Unknown	577	663	Chapaev-8_HM	7241	7329	DNA/EnSpm/CACTA	d	0.7619	1.6000	210

rnd-1_family-68#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-68#Unknown	395	471	Mariner-1_Crp	303	374	DNA/Mariner	d	0.7600	2.8000	247
rnd-1_family-68#Unknown	586	636	Tx1-5_FR	2375	2426	NonLTR/Tx1	c	0.7885	1.8000	221

rnd-1_family-79#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-79#LTR@ERVL	1	1047	TguLTRL4b	1	1064	ERV/ERV3	d	0.8458	5.4074	6720

rnd-1_family-81#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-81#Unknown	339	370	hAT-N126_CPB	298	329	DNA/hAT	d	0.8750	1.3333	206

rnd-1_family-84#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	402	472	ATHILA7A_I	282	354	LTR/Gypsy	c	0.7606	1.2000	220
rnd-1_family-84#Unknown	868	934	Tx1-1_CPB	546	606	NonLTR/Tx1	d	0.7846	1.5000	210
rnd-1_family-84#Unknown	1335	1373	Gypsy-82_MLP-I	2598	2635	LTR/Gypsy	c	0.8205	1.5000	237
rnd-1_family-84#Unknown	1418	1509	ATHILA7A_I	282	373	LTR/Gypsy	c	0.7391	1.3077	238
rnd-1_family-84#Unknown	1547	1732	Gypsy-29_CT-I	5942	6129	LTR/Gypsy	d	0.6910	1.6154	267

rnd-1_family-88#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	106	160	ATHILA7A_I	293	353	LTR/Gypsy	d	0.7759	1.1250	209
rnd-1_family-88#Unknown	1068	1251	Gypsy-29_CT-I	5942	6127	LTR/Gypsy	c	0.6995	1.9524	288
rnd-1_family-88#Unknown	1411	1451	Gypsy-82_MLP-I	2596	2635	LTR/Gypsy	d	0.8049	1.4000	238
rnd-1_family-88#Unknown	1852	1918	Tx1-1_CPB	546	606	NonLTR/Tx1	c	0.7846	1.5000	210
rnd-1_family-88#Unknown	2296	2379	CR1-1_PMo	1905	1981	NonLTR/CR1	c	0.7470	1.7500	243
rnd-1_family-88#Unknown	2396	2451	ATHILA7A_I	293	354	LTR/Gypsy	d	0.7797	1.2857	212

rnd-1_family-97#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-97#Unknown	24	72	Gypsy139-I_DR	3341	3390	LTR/Gypsy	d	0.7400	1.2000	205
rnd-1_family-97#Unknown	385	464	CR1-9_NVi	673	765	NonLTR/CR1	c	0.7805	2.3333	237

rnd-1_family-98#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-98#Unknown	482	541	L1-30_ACar	1726	1784	NonLTR/L1	c	0.7500	3.5000	202
rnd-1_family-98#Unknown	614	671	Copia-9_HAE-I	663	720	LTR/Copia	c	0.7586	1.7500	274
rnd-1_family-98#Unknown	2127	2172	StubV_scSl1	5389	5433	IntegratedVirus/Caulimovirus	d	0.8261	3.0000	213

rnd-1_family-99#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-99#Unknown	382	493	BEL-2_HMM-I	5525	5629	LTR/BEL	c	0.7431	1.9091	243

rnd-3_family-53#LINE@CR1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-3_family-53#LINE@CR1	67	4027	CR1-J3_Pass	299	4263	NonLTR/CR1	d	0.7980	1.5241	23044

rnd-4_family-336#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-4_family-336#Unknown	566	903	ERV3-3_PMaj-LTR	833	1175	ERV/ERV3	d	0.6687	1.7222	588

rnd-5_family-10335#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-10335#Unknown	206	252	I-66_AAe	4938	4984	NonLTR/I	c	0.8125	2.3333	228

rnd-5_family-10372#Satellite (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-10372#Satellite	332	460	Copia-13B_DR-I	2013	2152	LTR/Copia	c	0.7068	1.6111	217
rnd-5_family-10372#Satellite	1018	1101	Gypsy-6_IS-I	3937	4014	LTR/Gypsy	c	0.7711	3.2500	216

rnd-5_family-1147#LTR@ERV1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	307	436	LTR-12B_Crp	140	270	LTR	d	0.7419	1.6429	253
rnd-5_family-1147#LTR@ERV1	537	835	TguERV2_I	352	659	ERV/ERV1	d	0.6881	1.8780	533
rnd-5_family-1147#LTR@ERV1	1105	1134	tRNA-Ala-GCY_	46	75	Multicopy_gene/tRNA	d	0.9000	1.5000	202
rnd-5_family-1147#LTR@ERV1	1243	1431	TguERV2_I	1136	1324	ERV/ERV1	d	0.7407	1.9600	771
rnd-5_family-1147#LTR@ERV1	1575	1701	ERV1-1_GG-I	1701	1828	ERV/ERV1	d	0.6772	1.6818	315
rnd-5_family-1147#LTR@ERV1	1734	1897	ERV1-7_MM-I	1900	2062	ERV/ERV1	d	0.7375	1.3913	472
rnd-5_family-1147#LTR@ERV1	1926	1985	Copia-130_SB-I	778	836	LTR/Copia	d	0.7705	2.2000	231
rnd-5_family-1147#LTR@ERV1	2042	2091	TguERV1_I	3922	3971	ERV/ERV1	d	0.8400	1.6000	321
rnd-5_family-1147#LTR@ERV1	2285	5696	TguERV2_I	1712	5120	ERV/ERV1	d	0.6870	1.9172	8020
rnd-5_family-1147#LTR@ERV1	6176	6292	TguERV2_I	5345	5461	ERV/ERV1	d	0.7265	1.8667	379
rnd-5_family-1147#LTR@ERV1	6908	7498	TguERV2_I	6052	6646	ERV/ERV1	d	0.7069	1.9221	1464

rnd-5_family-12159#LINE@CR1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-12159#LINE@CR1	1	1142	CR1-X1_Pass	3259	4419	NonLTR/CR1	d	0.9328	2.0000	8613

rnd-5_family-1373#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score

rnd-5_family-1373#LTR@ERVK	786	844	hAT-N56B_CPB	306	359	DNA/hAT	d	0.8679	2.0000	213
rnd-5_family-1373#LTR@ERVK	1040	1363	Ag-Jock-1	1181	1471	NonLTR/Jockey	c	0.7021	1.8182	751
rnd-5_family-1373#LTR@ERVK	1500	1532	BARBARA_TM_I	4384	4416	LTR/Copia	d	0.8788	2.0000	228
rnd-5_family-1373#LTR@ERVK	2118	2161	Copia-32_BD-I	4071	4112	LTR/Copia	d	0.8140	1.7500	204
rnd-5_family-1373#LTR@ERVK	2175	2216	I-73_AAe	2571	2613	NonLTR/I	d	0.8140	2.3333	208
rnd-5_family-1373#LTR@ERVK	2593	2644	Copia-51_CCri-I	775	826	LTR/Copia	d	0.7692	1.7143	263
rnd-5_family-1373#LTR@ERVK	2928	4144	ERV2-9_UCy-I	1948	3158	ERV/ERV2	d	0.6548	1.9661	1431
rnd-5_family-1373#LTR@ERVK	4243	4426	ERV2-15_PMaj-I	3989	4162	ERV/ERV2	d	0.6554	2.0000	303

rnd-5_family-14611#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-14611#Unknown	1	267	Tgu_rep3-L_Ucy	1	318	ERV/ERV3	d	0.8154	1.8421	979
rnd-5_family-14611#Unknown	322	845	Tgu_rep3-L_Ucy	469	996	ERV/ERV3	d	0.8400	1.7692	3066

rnd-5_family-1533#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1533#Unknown	1	51	MuDRx-4_PI	32	82	DNA/MuDR	c	0.7885	1.5000	232
rnd-5_family-1533#Unknown	206	440	ERV3-7_PMaj-LTR	166	395	ERV/ERV3	d	0.6844	1.6111	480
rnd-5_family-1533#Unknown	560	670	TguERVL2b1_LTR-La_fAlb	427	539	ERV/ERV3	d	0.7453	1.5000	304

rnd-5_family-15382#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-15382#Unknown	212	281	Gypsy-232_OS-LTR	1419	1495	LTR/Gypsy	d	0.7042	1.1875	258
rnd-5_family-15382#Unknown	533	581	hAT-N20_TrPr	261	308	DNA/hAT	d	0.8125	1.2000	230

rnd-5_family-1599#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1599#Unknown	449	494	ERV1-2_ACC-LTR	479	525	ERV/ERV1	d	0.8298	1.1667	283

rnd-5_family-16196#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-16196#Unknown	6	79	hAT-N17_NS	225	302	DNA/hAT	d	0.7733	1.7143	211
rnd-5_family-16196#Unknown	246	293	ERV44_MD_I	4921	4967	ERV/ERV1	d	0.7917	2.2500	217

rnd-5_family-1704#LTR@ERVL (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	733	979	ERV3-23_PMaj-I	449	695	ERV/ERV3	d	0.6367	1.5849	544
rnd-5_family-1704#LTR@ERVL	1405	1468	Gypsy20-VV_I	2234	2301	LTR/Gypsy	c	0.7077	1.4167	210
rnd-5_family-1704#LTR@ERVL	1514	1582	Gypsy20-VV_I	2234	2300	LTR/Gypsy	c	0.6957	1.4615	212
rnd-5_family-1704#LTR@ERVL	1891	2047	EnSpm-2_NS	2148	2318	DNA/EnSpm/CACTA	c	0.7562	1.7059	487
rnd-5_family-1704#LTR@ERVL	2086	2193	ATCOPIA26I	2612	2710	LTR/Copia	c	0.6990	1.9286	264
rnd-5_family-1704#LTR@ERVL	2695	2798	Gypsy-12_ATr-LTR	3135	3237	LTR/Gypsy	c	0.6765	1.9375	259
rnd-5_family-1704#LTR@ERVL	2799	3255	ERV3-23_PMaj-I	937	1396	ERV/ERV3	d	0.6776	1.5747	1317

rnd-5_family-1706#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1706#Unknown	1	1894	ERV3-22_PMaj-I	3440	5335	ERV/ERV3	d	0.7780	1.4754	10184
rnd-5_family-1706#Unknown	1936	2014	Gypsy-12_DRh-I	2448	2523	LTR/Gypsy	d	0.7500	1.7778	262

rnd-5_family-17134#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-17134#Unknown	1	109	ERV3-28_PMaj-LTR	935	1038	ERV/ERV3	c	0.8037	1.4167	541
rnd-5_family-17134#Unknown	149	245	EnSpm1_HV	5077	5166	DNA/EnSpm/CACTA	d	0.6882	1.4444	272

rnd-5_family-18364#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	1288	1352	HERVK9I	1353	1417	ERV/ERV2	c	0.8000	1.8333	312
rnd-5_family-18364#LTR@ERVK	1360	1419	ERV2-11_UCy-I	2289	2349	ERV/ERV2	c	0.7541	2.0000	249
rnd-5_family-18364#LTR@ERVK	1654	1711	Juno3_Av_I	2495	2557	LTR	d	0.7833	1.6667	223
rnd-5_family-18364#LTR@ERVK	2157	2202	Tx1-15_BF	1192	1236	NonLTR/Tx1	c	0.8043	1.1667	226
rnd-5_family-18364#LTR@ERVK	2423	2473	Tx1-8_AMi	2312	2363	NonLTR/Tx1	c	0.7692	1.8333	204
rnd-5_family-18364#LTR@ERVK	2669	2714	TguLTRL2b5	371	417	ERV/ERV3	d	0.7872	1.6000	200
rnd-5_family-18364#LTR@ERVK	3210	3245	Gypsy-13_CCO-I	1470	1504	LTR/Gypsy	c	0.8611	1.3333	220

rnd-5_family-18768#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18768#Unknown	1	976	ERV3-5_PMaj-LTR	1	982	ERV/ERV3	d	0.9266	2.9524	8080

rnd-5_family-2267#LTR@ERV1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-2267#LTR@ERV1	1	758	ERV1-5_PMaj-LTR	4	765	ERV/ERV1	d	0.9619	3.0000	6206

rnd-5_family-25903#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-25903#LTR@ERVK	22	73	Copia-11_TC-I	1626	1677	LTR/Copia	c	0.7925	2.2500	218

rnd-5_family-25903#LTR@ERVK	247	291	Gypsy-18_AG-I	2447	2496	LTR/Gypsy	d	0.8478	3.0000	236
rnd-5_family-25903#LTR@ERVK	729	829	L2_AC_9	1029	1143	NonLTR/L2	c	0.7170	1.7143	272
rnd-5_family-25903#LTR@ERVK	2045	2624	ERV2-10_UCy-I	3725	4298	ERV/ERV2	d	0.6789	1.9186	1367

rnd-5_family-3138#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	892	946	L2-21_CTe	203	255	NonLTR/L2	d	0.7593	1.7143	222
rnd-5_family-3138#Unknown	1695	1808	hAT-2_PBa	2795	2892	DNA/hAT	c	0.7549	1.5455	244
rnd-5_family-3138#Unknown	2106	2169	Copia-53_MN-I	3445	3505	LTR/Copia	d	0.8065	4.5000	249
rnd-5_family-3138#Unknown	3486	3556	Gypsy-23_GAr-LTR	386	456	LTR/Gypsy	c	0.7222	1.6364	239
rnd-5_family-3138#Unknown	3812	3844	Gypsy-4_AC-I	2426	2462	LTR/Gypsy	d	0.9118	1.0000	248
rnd-5_family-3138#Unknown	4025	4073	Mariner-N1743_AMi	392	437	DNA/Mariner	c	0.7959	1.1667	202
rnd-5_family-3138#Unknown	4311	4383	PtConagree_I	2899	2976	LTR	d	0.7333	1.2143	299

rnd-5_family-3181#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3181#Unknown	1796	1830	DIRS-6_CPB	2876	2911	LTR/DIRS	d	0.8611	1.3333	209
rnd-5_family-3181#Unknown	1840	1885	ERV2-3b_CPo-I	3169	3212	ERV/ERV2	c	0.8043	1.7500	215
rnd-5_family-3181#Unknown	2456	2539	CR1-J3_Pass	4178	4260	NonLTR/CR1	c	0.8333	2.6000	522

rnd-5_family-3861#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3861#Unknown	55	105	HAT-18_Mad	926	977	DNA/hAT	c	0.8039	1.3333	211

rnd-5_family-4174#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-4174#Unknown	1	2066	CR1-J3_Pass	76	2107	NonLTR/CR1	c	0.7456	1.5309	9442

rnd-5_family-42824#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-42824#Unknown	76	106	hAT-7_PM	780	810	DNA/hAT	d	0.9032	3.0000	223

rnd-5_family-439#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	202	272	Gypsy8-I_Dpse	244	303	LTR/Gypsy	d	0.7742	1.7143	206
rnd-5_family-439#LTR@ERVK	545	600	BEL-677_AA-I	2820	2877	LTR/BEL	d	0.7544	2.1667	220
rnd-5_family-439#LTR@ERVK	1136	1239	ERV2-12_GG-I	1098	1199	ERV/ERV2	d	0.7030	1.5882	311
rnd-5_family-439#LTR@ERVK	1906	2604	ERV2-11D_GG-I	1897	2601	ERV/ERV2	d	0.6255	1.8966	468
rnd-5_family-439#LTR@ERVK	2866	3671	ERV2-12_UCy-I	2612	3417	ERV/ERV2	d	0.6775	1.9024	1821

rnd-5_family-4633#LINE@CR1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-4633#LINE@CR1	16	498	CR1-X3_Pass	3935	4421	NonLTR/CR1	c	0.7851	20.4000	3243

rnd-5_family-5294#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	612	645	ERV1-7_Crp-I	1802	1836	ERV/ERV1	d	0.8571	1.0000	204
rnd-5_family-5294#LTR@ERVK	2133	2226	ERV2-11C_GG-I	1251	1344	ERV/ERV2	d	0.8000	2.4286	446
rnd-5_family-5294#LTR@ERVK	2388	2433	Helitron-1_HM	11321	11362	DNA/Helitron	d	0.8605	5.0000	220
rnd-5_family-5294#LTR@ERVK	2462	2551	ERV2-12_UCy-I	6711	6800	ERV/ERV2	d	0.7111	1.6250	339
rnd-5_family-5294#LTR@ERVK	2809	2882	EnSpm-N16_SBi	802	869	DNA/EnSpm/CACTA	c	0.7887	2.0000	207

rnd-5_family-6012#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6012#Unknown	172	558	TguLTR5c	114	551	ERV/ERV3	d	0.7035	2.8649	1524
rnd-5_family-6012#Unknown	1441	1507	BEL-1_CGi-I	574	647	LTR/BEL	c	0.7286	1.3333	249
rnd-5_family-6012#Unknown	1871	1936	HAT-18_Mad	3406	3469	DNA/hAT	d	0.8182	1.1667	243
rnd-5_family-6012#Unknown	3062	3215	CR1-J2_Pass	3385	3540	NonLTR/CR1	d	0.9161	2.4000	1058

rnd-5_family-6256#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6256#Unknown	1233	1290	Tgu_rep3-L_Ucy	706	763	ERV/ERV3	d	0.7931	1.5000	319
rnd-5_family-6256#Unknown	2166	2201	Gypsy-4_DWil-I	3041	3079	LTR/Gypsy	c	0.8378	1.0000	216

rnd-5_family-6290#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6290#Unknown	1	389	CR1-X1_Pass	3911	4331	NonLTR/CR1	c	0.8150	4.5000	1840
rnd-5_family-6290#Unknown	872	1207	ERV3-1_MUn-I	4055	4393	ERV/ERV3	d	0.7882	1.9143	1769

rnd-5_family-6381#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6381#Unknown	1	183	Tgu_rep3-L_Ucy	1	212	ERV/ERV3	d	0.7747	1.8235	602
rnd-5_family-6381#Unknown	206	956	ERV3-28_PMaj-LTR	221	1038	ERV/ERV3	d	0.8016	1.6618	3198

rnd-5_family-6742#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6742#Unknown	294	370	Harbinger-38_CCri	2527	2600	DNA/Harbinger	c	0.7105	1.4615	228

rnd-5_family-6995#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6995#Unknown	378	414	NonLTR-2_LVa	4112	4149	NonLTR	c	0.8947	1.0000	264

rnd-5_family-7082#LTR@ERVK (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	826	890	Helitron-2_CRe	10933	10994	DNA/Helitron	d	0.7302	1.3636	215
rnd-5_family-7082#LTR@ERVK	1001	1053	ATCOPIA9I	1928	1981	LTR/Copia	d	0.7593	2.0000	228
rnd-5_family-7082#LTR@ERVK	1116	1145	EnSpm-N2_OES	834	863	DNA/EnSpm/CACTA	c	0.9333	1.0000	231
rnd-5_family-7082#LTR@ERVK	1261	1305	Copia-36_ALY-I	2239	2288	LTR/Copia	d	0.8478	1.5000	236
rnd-5_family-7082#LTR@ERVK	2182	2283	MacERV4_int	1879	1979	ERV/ERV2	d	0.6863	1.7222	329
rnd-5_family-7082#LTR@ERVK	2284	2403	hAT-N6_OD	920	1032	DNA/hAT	d	0.6810	1.4500	220
rnd-5_family-7082#LTR@ERVK	2801	3037	TguERVK3a_I	3111	3347	ERV/ERV2	d	0.6842	1.9355	354
rnd-5_family-7082#LTR@ERVK	3089	3955	ERV2-15_PMaj-I	3396	4261	ERV/ERV2	d	0.6790	1.9741	1355
rnd-5_family-7082#LTR@ERVK	4325	4386	L1MCA_5	843	906	NonLTR/L1	d	0.7619	1.8571	239
rnd-5_family-7082#LTR@ERVK	4407	4970	TguERVK5_I	5181	5735	ERV/ERV2	d	0.6624	2.0513	736
rnd-5_family-7082#LTR@ERVK	4993	5591	ERV2-3_STr-I	5044	5644	ERV/ERV2	d	0.6683	1.8804	886
rnd-5_family-7082#LTR@ERVK	5651	5724	Jockey-6_DK	425	489	NonLTR/Jockey	d	0.8030	4.0000	266
rnd-5_family-7082#LTR@ERVK	5850	5926	Keno-5_XT	2618	2688	NonLTR/Tx1	d	0.7361	1.4545	230
rnd-5_family-7082#LTR@ERVK	6294	6376	ERV2-9_UCy-I	6362	6444	ERV/ERV2	d	0.6747	1.6875	260
rnd-5_family-7082#LTR@ERVK	6739	6988	ERV2-9_UCy-I	6579	6828	ERV/ERV2	d	0.6440	1.7200	550
rnd-5_family-7082#LTR@ERVK	7215	7272	RETROFIT2_I	2833	2887	LTR/Copia	d	0.8070	4.5000	243

rnd-5_family-7126#Unknown (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7126#Unknown	169	321	ERV2-12_PMaj-I	191	332	ERV	d	0.6875	1.7619	261
rnd-5_family-7126#Unknown	644	804	hAT-1_MAc	231	400	DNA/hAT	d	0.6890	1.6400	430

| rnd-5_family-7126#Unknown | 1609 | 1656 | ERV17_MD_I | 4882 | 4929 | ERV/ERV2 | d | 0.8125 | 1.7500 | 247 |

rnd-5_family-9233#tRNA (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-9233#tRNA	6	64	ERI1	12	70	NonLTR/SINE/SINE2	d	0.7288	1.7778	264
rnd-5_family-9233#tRNA	80	351	GymnSINE	1	300	NonLTR/SINE/SINE3	d	0.8188	1.6923	1269

rnd-5_family-963#LTR@ERV1 (SVG Plot; Alignments; Masked)

Name	From	To	Name	From	To	Class	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-963#LTR@ERV1	498	639	ERV1-2_ACD-LTR	508	653	ERV/ERV1	d	0.6986	1.5417	452

Masked Sequence

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Local Alignments*

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000002#MITE@unknown	1	131	SINE2-1_PMaj	6	135	d	0.8931	1.6250	958

```
1 TTAGCTCAGTTGGTTAAAACTTGGTTGTAATAATGCCAAGGTCATGGGTTCAATCCCCTGTGTGGGCCAT 70
  ||||||||||||||||:|:| |||| |||||||:|||||||::||||||:|||||-||:||||||||
6 TTAGCTCAGTTGGTTAGAGCATGGTGCTAATAACGCCAAGGTTGTGGGTTCGATCCCC-GTATGGGCCAT 74

71 TGACTTAAGAGTTGGACTCGATGATCCTTGTGGGTCCCTTCCAACTCAGAATAGTCTGTGA 131
   | |||||||||||||||||:||||||||||||||||||||||||||||||| |||||||
75 TCACTTAAGAGTTGGACTCAATGATCCTTGTGGGTCCCTTCCAACTCAGAATATTCTGTGA 135
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000010#MITE@unknown	1	299	GymnSINE	3	300	d	0.8528	1.6000	1706

```
1 CAGTTAAATGCCTCCCTGACATCCGATCCCGTCAGATCTCGGAAGCTAAGCAGGGTCAGCCCCGGTTAGT 70
  |||| |||||||| |||||||||:| :||||:||| ||:||:||||| ||||||||-:|||||||:||||||
3 CAGTGAAATGCCACCCTGACACCAAATCCTGTCCGACCTTGGAAGATAAGCAGG-CCAGCCCCAGTTAGT 71

71 ACTTGGATGGGAGACCTCCTGGGAAATGCCGGG---CTGTAGGTTCTAGTCCTGAGGACTTCACTGTCAC 137
   |||||||||||:||||||||||||||||--  |||:|---|||||||:||||: |||||||||||||||||
72 ACTTGGATGGAAGACCTCCTGGGAA--TCCGAGGTGCTGTAGATTCTGTTCCTGAGGACTTCACTGTCAC 139

138 TGTCCAAGCTCGCTCGGCCGTGGCAGATGAACCTCAGGACTTAAACGGTGGGGCCAGTTCTGCGCACGCT 207
    ::||||||| ||:|||||||:||||||||||||:|||| ||||| ||||||||||||:||:|||| ||
140 CATCCAAGATCACTCGGCCATGGCAGATGAACCTTAGGAGTTAAAGGGTGGGGCCAGTTTTGTGCACTCT 209

208 GAGCCTCACCTAAAAAATCCACTGCGCAGGCTGGAAGGGCACACCCACGTGGGGAGAGCCCTTCCCAAAT 277
    | ||||||||||||||-||||||||:|||||| |||||:::||||||||||| |||||||| ||||||||
210 GTGCCTCACCTAAAAA-TCCACTGCACAGGCTTGAAGGATGCACCCACGTGGGTAGAGCCCTTCCCAAAT 278

278 CTTCGTTCGCGAAGCCGAGCCA 299
    |||:|||:||:||||| |||||
279 CTTTGTTTGCAAAGCCTAGCCA 300
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-9233#tRNA	80	351	GymnSINE	1	300	d	0.8188	1.6923	1269

```
80 GGCAGTTCAATGCCTCCCTGCCATCCCATCCCGTCAGATCTCGGATGCTCAGCAGGGTCAGCCCCGGTTA 149
   ||||||  |||||| |||| ||||| ||:|  |||:||| ||:||:||| | | ||||||-:|||||||:||||
 1 GGCAGTGAAATGCCACCCTGACACCAAATCCTGTCCGACCTTGGAAGATAAGCAGG-CCAGCCCCAGTTA 69

150 GTAC------------------------CG-GGTGCTGT-GAC---AGTCCCGAGGACTTCACTGTCAC 189
    ||||------------------------||-|||||||-|||:---: |||:|||||||||||||||||
 70 GTACTTGGATGGAAGACCTCCTGGGAATCCGAGGTGCTGTAGATTCTGTTCCTGAGGACTTCACTGTCAC 139

190 TGTCCAAGCTCGCTCGGCCGTGGCAGATGGACCTCAGGACTTAAACGGTGGGGCCAGTTCTGCGCACGCT 259
    ::||||||| ||:|||||||:||||||||:||||:|||| ||||| ||||||||||||:||:|||| ||
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260 GTGCCTCACCTAAAAAATCCACTGCGCAGGCTGGAAGGGCACACCCACGTGGGGAGAGCCCTGCCCAAAT 329
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210 GTGCCTCACCTAAAAA-TCCACTGCACAGGCTTGAAGGATGCACCCACGTGGGTAGAGCCCTTCCCAAAT 278

330 CTTCGTTCGCGAAGTCTGGCCA 351
    |||:|||:||:|||:||:||||
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279 CTTTGTTTGCAAAGCCTAGCCA 300

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000012#MITE@unknown	48	157	TguERVL2b5_LTR	375	486	c	0.7264	1.6000	332

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 48 GAGAGATTACAAGTCAGAGTTACAATTTACT----------AAAAAGATTACAATAAATACAATGATACA 107
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486 GAGAGACTCCAAGTCAGAAATACAATTTATTGGGAAAAGGGAAAAAGACAAAAATACATGCAATGATACA 417

108 GA-GAAAAANTGGTTTTAACCCACAAAANNCAGATGTATAACCCAGCACCC 157
    :|-|:||:| :-------||: |||||- ||||-:||:||||:::|||||
416 AAAGGAAGACC-------ACTGACAAA-GTCAGA-ATACAACCTGACACCC 375
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-14611#Unknown	322	845	Tgu_rep3-L_Ucy	469	996	d	0.8400	1.7692	3066

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322 AANCCCCNCCCNCCGGGAAGACCACNTACACACAGGACATTCACNTGAGAGGCAGCTGAAAGGG-GTCAT 390
    || ||||| | |||||||||:|||| | |||:--||||||||||| |||||||||||||::|||-|||||
469 AAACCCCCAACCCCGGGAAGGCCACATCCACG--GGACATTCACGTGAGAGGCAGCTGAGGGGGTGTCAT 536

391 AAACCATCAAAGACCCCCAAAGTGCCCCCCG-ACTCATTCCTGAGGCCTTCNACCACCAGAGGACTGCAC 459
    || ||||||||||||||||||:||:|||||-|||||||||||||| ---|||||||| |||||||
537 AATCCATCAAAGACCCCCAAAGCGCTCCCCGGACTCATTCCTGAGGCCTTG---CACCAGAGCACTGCAC 603

460 NTGAT-CCAAGTGAGGCAACAAATCCAGAGCCTGTCACAAGAGACTG---CAAAGCTTCCCCNCCCCAGG 525
    |||:-| |||||| |||-||:|||||||:||||::||||||||||---|||| :| |||| |||||||
604 GTGACGCAAAGTGATGCA-CAGATCCAGAGTCTGTTGCAAGAGACTGTGTCAAACTTGCCCCCCCCCAGG 672

526 GGAGGTGCCTGG-------CATCT--CCTGAANGTATATTAATCCATTGGACTCTATGTTTTGTGGGACC 586
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673 GGAGGTACCTGGGCATTCCCACCTGGCCCGAACGTATATTAATCCATCGAACTCTGTGTTTTGGGGGACC 742

587 CTCACCACCAAGAAGACCAGAAGAACNGGACCNACGGGACGCCACCAGGTTCCACGGAGTGGTGATACAT 656
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    |||||--|:|:---||||||||||||| |||||||-|:||||||| ||::|||:|||||||||||||- |||
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726 CTCTNTGCCTCACATTTACCATTAAATAAAACCCATACTATTGACTTTGGCATATGGTCTCATTTGCACC 795
    |||| :|||||||||||:|||||||||||||:||||||||||||||||||||||||||:|||||:||
875 CTCTCTCTCTCACATTTACTATTAAATAAAATCCATACTATTGACTTTGGCATATGGTCTCGTTTGCGCC 944

796 TTAATTCNGGCAGAGGCATTTCT--AATAATTTTAATAACCAGATCATAACA 845
    |||||||| |||||||||||:|||--|||||||||||||||||:|||||||||
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-14611#Unknown	1	267	Tgu_rep3-L_Ucy	1	318	d	0.8154	1.8421	979

```
1 TGTGATGGACTGAA-TGTTAT---TAATGTCTTAAACATTGTCAAAATCATAGAAAGACTTTTT------- 59
  ||||| :||||||||-||||||---||||| ||||||||||||:| -------|||:|||||||-------
1 TGTGAGAGACTGAAATGTTATGGTTAATGGCTTAAACATTGTTAT-------GAAGGACTTTTTGCCCAT 63

60 ----GTCAAACTGCA--AGGAAGCAACTGCCTGTCTGNGACCACCGAAGCACCCCCCTCCCN----ATGC 119
   ----|: |||||||:|--|:|||||-----------|| ||||||||||| | ||||||||| ----||||
64 TATGGCAAAACTGTATAAAGAAGC-----------TGCGACCACCGAAGCCCACCCCTCCCTGAATATGC 122

120 CTCCTGACTGGAA-TTTGGACTGTGACT------------GGGAACTTGAGATAAGA-----------CT 165
   |||||||||||||-|||||||||||||| |------------||||||||||||||||-----------||
123 CTCCTGACTGGAACTTTGGACTGTGAGTTAAGCCGCCTAAGGGAACTTGAGATAAGATAAAGGTGACACT 192

166 ATTGTCTAATCATCTCAGGTCTGAGGAGANGTAAACAAGGCTCAGGGA--AGAATGTCTC---------- 223
   +||||+:|||:||||||||||||||||::||||| |||||||||||||--|||||||| ||----------
193 RTTGTYCAATTATCTCAGGTCTAGGGAGAAGTAAACAAGGCTGAGGGAGAAGAATGTATCCACAAGAAAG 262
```

```
224 --------------TGTGTTAAGAATCAGCCCTAGCTGAGCTCAGTGGGTGGCGGGGG 267
    --------------|||  :|:|:||||||||:||:||||:|:||:|--|||||  ||:||
263 CCAAACCCAGCAGCTGTCCTGAAAATCAGCTCTGGCTGGGTTCGG--GGTGGGGGAGG 318
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6381#Unknown	1	183	Tgu_rep3-L_Ucy	1	212	d	0.7747	1.8235	602

```
1 TGTCAGAGACTGAAATA-----GTTAATGGCTTAAACATTNTAAGATCACCAAAAGACTTTT-GTCCACT 64
  ||| ||||||||||||:-----|||||||||||||||||| | |------::||:|||||||-|:|||:|
1 TGTGAGAGACTGAAATGTTATGGTTAATGGCTTAAACATTGTTA------TGAAGGACTTTTTGCCCATT 64

65 GTAGCANA-CTGAAAAGAAACAGCTGCTCACCCAGCAAAGCCTACCCCTCCCTGAATATGCCT------- 126
   :|:|||  |-|||  |  |:|:|-||||||--: |||  |:|||||:||||||||||||||||-------
65 ATGGCAAAACTGTATAAAGA-AGCTGC--GACCACCGAAGCCCACCCCTCCCTGAATATGCCTCCTGACT 131

127 ----------ACTGNGA-------------AAGGACCTTCAGATCAGATAAGTGGGTGCCA---TTGTCC 170
    ----------||||  ||-------------|:|||  |||  ||||  ||||||:--|||| ||---||||+|
132 GGAACTTTGGACTGTGAGTTAAGCCGCCTAAGGGAACTTGAGATAAGATAAA--GGTGACACTRTTGTYC 199

171 AACTATCCCAGGT 183
    ||:|||||:|||||
200 AATTATCTCAGGT 212
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-126#Unknown	1	182	Tgu_rep3-L_Ucy	2	212	d	0.7611	2.1250	588

```
1 GTCAGAGACTGAAATA-----GTTAATGGCTTAAACATTNTAAGATCACCAAAAGACTTTT-GTCCACTG 64
  || |||||||||||||:-----|||||||||||||||||| | |------::||:|||||||-|:|||:|:
2 GTGAGAGACTGAAATGTTATGGTTAATGGCTTAAACATTGTTA------TGAAGGACTTTTTGCCCATTA 65

65 TAGCANA-CTGAAAAGAAACAGCTGCTCANCCAGCAAAGCCNACCCCTCCCTGAATATGCCTACTGNN-- 131
   |:|||  |-|||  |  |:|:|-||||||--: |||  |:|||||  ||||||||||||||||||||| |||   --
66 TGGCAAAACTGTATAAAGA-AGCTGC--GACCACCGAAGCCCACCCCTCCCTGAATATGCCTCCTGACTG 132

132 -------------------------AAAGGACCTTCAGATCAGATAAGTGGGTGCCA---TTGTCCA 170
    -------------------------||:|||  |||  ||||  ||||||:--|||| ||---||||+||
133 GAACTTTGGACTGTGAGTTAAGCCGCCTAAGGGAACTTGAGATAAGATAAA--GGTGACACTRTTGTYCA 200

171 NCTATCCCAGGT 182
    :|||||:|||||
201 ATTATCTCAGGT 212
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	117	174	Tgu_rep3-L_Ucy	706	763	d	0.7931	1.5000	319

```
117 GTGTATTAATCCATTGGACTCTACGTTTTGCTGGATCCTCACCCCTGAGCAGACCAGA 174
    ||:|||||||||||:|:|||||::||||||  |||:|||||||  |:::||  |||||||||
706 GTATATTAATCCATCGAACTCTGTGTTTTGGGGGACCCTCACCACCAAGAAGACCAGA 763
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6256#Unknown	1233	1290	Tgu_rep3-L_Ucy	706	763	d	0.7931	1.5000	319

```
1233 GTGTATTAATCCATTGGACTCTACGTTTTGCTGGATCCTCACCCCTGAGCAGACCAGA 1290
     ||:|||||||||||:|:|||||::||||||  |||:|||||||  |:::||  |||||||||
 706 GTATATTAATCCATCGAACTCTGTGTTTTGGGGGACCCTCACCACCAAGAAGACCAGA 763
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-126#Unknown	205	913	ERV3-28_PMaj-LTR	221	1038	d	0.7983	1.9483	3215

```
205 AGCTACAAACTGGATTT----CCAGATAAGGGAAGAGGCTNATAAGAGGCAAATCCTGTGAGGTGGGATA 270
    |||  |||||:|||||:|||----|||||||||||||::|||||  ||||||:|||:|||||||: ||||||||||
221 AGCAACAAGCTGGGTTTTGAGCCAGATAAGGGAGAAGGCTGATAAGAAGCAGATCCTGCTAGGTGGGATA 290
```

```
271 ATCCTTCTTATCATGCCAATGTCCTCCCTTACATGA-TGACTCTGCTGTAAAAAT-------CCCTCNNG 332
    || |||:||||||||||||||||||||||||||||::|-||:||| | ||||||| |-------||||| |
291 ATGCTTTTTATCATGCCAATGTCCTCCCTTACACAACTGGCTCAGGTGTAAAACTTCCCCTCCCCTCCGG 360

333 GGANCCTCNAAGACATT-AC---T-GGCCTG--GGCTNTTCATC---TCAAATG--------TTGGACCA 384
    |||  : | |:||||||-||---|-||||||--||-| |||||---|| :|||--------:||| :||
361 GGAGGTACCAGGACATTCACATGTAGGCCTGAAGG-TATTCATCCCTTCTGATGGGGCATAACTGGCTCA 429

385 ATNNATGCTGA-------------------GTCTTAGGAGNTGTCA----------GAGACTNNTNACAT 425
    |- |:||||:-------------------|||||||:|| |||||----------:||||: : | :|
430 A-CTACGCTGGCGTGAGAGGCAGCTGTCATGTCTTAGAAGGTGTCATAAACCATCAAAGACCCCCAAAGT 498

426 GTCCCN-------------------------------TG-ACACNATCCAT----------------- 444
    |:||| -------------------------------||-|||: |||||:-----------------
499 GCCCCCAGACTCAATTTCTGGGGCCTTCCACCAGAGGACTGCACATGATCCACAGTGTTGCATCAGACAG 568

445 TGTAAAACTCCCNACCCCAGGGGAGGTACA-AGGNNTTCCCACCTGAGCTTGAAGTGTATAATAACTCA- 512
    |||||||||||||---||||||||||||||| -:||  |||||||||||:|:|||-|:||||| ||||:||-
569 TGTAAAACTCCC---CCCAGGGGAGGTACCTGGGCGTTCCCACCTGAACCTGA-GCGTATATTAACCCAC 634

513 TGAANTCTTTGAGTTTTNGGGGGGCTTCCCCCANCCCCAANGGATCAAGAC------CATCACTTCAACC 576
    |||| ||| ||--|||: |||--|||||||||-||||| ||||||||||------|||||||||||||
635 TGAACTCTGTG--TTTCATGGG--CTTCCCCCA-CCCCAATGGATCAAGACTGTGACCATCACTTCAACC 699

577 AACAGACATNGAAGCTGCAACTACCAAGTTTCATNNCTGGATCCAGTGGGTGGTGACTATATATATCTTN 646
    |||||||||| |||::||||||| |:|||||:||:| |||||||||-::||||||||||-------||||||
700 AACAGACATCGAAATTGCAACAATCAAGTCTCGTTTCTGGATCCA-CAGGTGGTGA-------TATCTTT 761

647 NNACC-------CTTATCCTTTCTTTCTCTTTCTNT-CCTTATACATTTCCTTAAGTGTTATTTTTATGC 708
     ||:-------|||||||||||||||:|||||||| |-||||||||:||||:|||||||| |||:||||:|
762 CCACTATCTACTCTTATCCTTTCTTTTTCTTTCTTTTCCTTATATATTTTCTTAAGTGATATCTTTATAC 831

709 TTTAATATTGCTGTATTACTATAGATGATAACANCCAAAATGGCAACATACCTGTTTACCTTTGAAACAA 778
    ||| |||||||:|||| |||||||||:|||||---|||||||||| ||||||||| :|| || ||| ||| |
832 TTTTATATTGCTATATTTCTATAGATAATAAC---CAAAATGGCTACATACCTCCTTTCCATTGCAACCA 898

779 AATTGTTCTAAAATAAACCCTACATATATATGT---T-TACAAACACCGATTATTCAGTGTCNTTTCACT 844
    ||||||||||||||||||||||||||||||||||:|---|-||:|||||||:|:|:||||||||||: |||||||
899 AATTGTTCTAAAATAAACCCTACATATATATATATATATAAACACTGGTCATTCAGTGTTGTTTCACT 968

845 CTAATCCACCCCAAGGGA-TTTATTAACAAGAACCTGGGTTACCCTCCCCTTCTGGGGCGGGTCGTAACA 913
    ||||||::||||||||||-|:||||||||||||||| :||||||||||| |||||||||||||||||||||
969 CTAATCTGCCCCAAGGGAATCTATTAACAAGAACCTCAGTTACCCTCGCCTTCAGGGGCGGGTCGTAACA 1038
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6381#Unknown	206	956	ERV3-28_PMaj-LTR	221	1038	d	0.8016	1.6618	3198

```
206 AGCTACAAACTGGATTT----CCAGATAAGGGAAGAGGCTAATAAGAGGCAAATCCTGTGAGGTGGGATA 271
    ||| |||||:|||||:|||----|||||||||||||::|||||:||||||:|||:|||||| ||||||||||
221 AGCAACAAGCTGGGTTTTGAGCCAGATAAGGGAGAAGGCTGATAAGAAGCAGATCCTGCTAGGTGGGATA 290

272 ATCCTTCTTATCATGCCAATGTCCTCCCTTACATGA-TGACTCTGCTGTAAAAAT-------CCCTCNNG 333
    || |||:|||||||||||||||||||||||||||::|-||:||| | ||||||| |-------||||| |
291 ATGCTTTTTATCATGCCAATGTCCTCCCTTACACAACTGGCTCAGGTGTAAAACTTCCCCTCCCCTCCGG 360

334 GGA---ACCTCAAAGACATTTCACATCT-GGCCTG--GGCTATTCATCTCAAATGTTGGACCATGA-TGG 396
    |||---|||---|:||||||-|||||-|||||--||-|||||||:| || |||: |||:|-|||
361 GGAGGTACC---AGGACATT-CACATGTAGGCCTGAAGG-TATTCATCCCTTCTGATGGGGCATAACTGG 425

397 ----ACCATGAT----TGAT-----GCTG--A-GTCTTAGGAGGTGTCA----------GAGACTCGTGA 440
    ----||:|:|| |----||| -----||||--|-|||||||:|||||||||-----------:||||:| ::|
426 CTCAACTACGCTGGCGTGAGAGGCAGCTGTCATGTCTTAGAAGGTGTCATAAACCATCAAAGACCCCCAA 495

441 CATGTCCCGTGAC-------------------------ACT-------ATCCAT-------------- 462
    :||:|||  |||-------------------------|||-------|||||:--------------
496 AGTGCCCCCAGACTCAATTTCTGGGGCCTTCCACCAGAGGACTGCACATGATCCACAGTGTTGCATCAGA 565

463 ---TGTAAAATTCCCCACCCCAGGGGAGGTACA-AGGTGTTCCCACCTGAGCTTGAAGTGTATAATAACT 528
    ---||||||||:|||||---||||||||||||||| -:||:|||||||||||||:|:|||-|:||||| ||||:
566 CAGTGTAAAACTCCCC---CCAGGGGAGGTACCTGGGCGTTCCCACCTGAACCTGA-GCGTATATTAACC 631
```

```
529 CA-TGAAGTCTTTGAGTTTTGTGGGGGGCTTCCCCCAGCCCCAANGGATCAAGACCATCACTTTNACAGG 597
    ||-||||--||:|| ||||::||||---|||||||-||||| |||||||||||---------------
632 CACTGAA--CTCTGTGTTTCATGGG---CTTCCCCCA-CCCCAATGGATCAAGAC--------------- 680

598 ACTGNGACCACCACTTCAACCAACAGACATGGAAGCTGCAACTACCAAGTTTCATCACTGGATCCAGTGG 667
    --|| |||||:|||||||||||||||||||| |||::|||||| |:|||||:||:| ||||||||||-::|
681 --TGTGACCATCACTTCAACCAACAGACATCGAAATTGCAACAATCAAGTCTCGTTTCTGGATCCA-CAG 747

668 GTGGTGA---CTATATA-TATCTTAGGACCCTTATCCTTTCTTTCTCTTTCTCTCCCTTATACATTTCCT 733
    |||||||---|| | :|-|||||----||:||||||||||||||:|||||||:|:|||||||:||||:||
748 GTGGTGATATCTTTCCACTATCT----ACTCTTATCCTTTCTTTTTCTTTCTTTTCCTTATATATTTTCT 813

734 TAAGTGTTATTTTTATGCTTTAATATTGCTGTATTACTATAGATGATAACACCCAAAATGGCAACATACC 803
    |||||| |||:|||||:|||| |||||||||:|||| ||||||||:|||||---|||||||| |||||||
814 TAAGTGATATCTTTATACTTTTATATTGCTATATTTCTATAGATAATAAC---CAAAATGGCTACATACC 880

804 TGTTTACCTTTGAAACAAAATTGTTCTAAAATAAACCCTACATATATATGT-T---TACAAACACNGATT 869
    | :|| || ||| ||| |||||||||||||||||||||||||||||||||:|-|---||:|||||| |:|:
881 TCCTTTCCATTGCAACCAAATTGTTCTAAAATAAACCCTACATATATATATATATAAACACTGGTC 950

870 ATTCAGTGTCNTTTCACTCTAATCCACCCCAAGGGA-TTTATTAACAAGAACCTGGGTTACCCTCCCCTT 938
    ||||||||:  ||||||||||||||||::|||||||||-|:||||||||||||||||| :||||||||| ||||
951 ATTCAGTGTTGTTTCACTCTAATCTGCCCCAAGGGAATCTATTAACAAGAACCTCAGTTACCCTCGCCTT 1020

939 CTGGGGTGGGTTNTAACA 956
    | ||||:||||: |||||
1021 CAGGGGCGGGTCGTAACA 1038
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000012#MITE@unknown	361	603	ERV3-28_PMaj-LTR	317	626	c	0.7551	1.7241	750

```
361 ATATATGCTCAGGTTCAGGTGGGAATGCCCAG-TACCTCCCCCAGGGCGGGGAGTTTCACAATGGGTGAT 429
    |||||:|||||||||||||||||||||||||:||||||-|||||||||::|||---|||||||:||| || ||||
626 ATATACGCTCAGGTTCAGGTGGGAACGCCCAGGTACCTCCCCTGGGG---GGAGTTTTACACTGTCTGAT 560

430 TTAACTCTGTGAGTCATG---------------------------------------GGATATTTTTGGA 460
    :||| |||||::|||||----------------------------------------||::|:||| ||:
559 GCAACACTGTGGATCATGTGCAGTCCTCTGGTGGAAGGCCCCAGAAATTGAGTCTGGGGGCACTTTGGGG 490

461 ATCTTTGATGGT-----------CTAGGTCATTGCANCTGCCT--------------ATTGTGCCAGTC 504
    :|||||||||||-----------|||:| ||| :|| ||||||--------------:||| ||||||:
489 GTCTTTGATGGTTTATGACACCTTCTAAGACATGACAGCTGCCTCTCACGCCAGCGTAGTTGAGCCAGTT 420

505 CCTAATGGCCCATTAGCAGACATGAC--CCCTCAGGC-TGGGTGTGAAGGTGCTAATGCCTCCCCNGAGG 571
    ----|||| ||||||:|||| ||:| ||| --||:|||||||-|: :|||||||| || ||::|:||||||| ||||
419 ----ATGCCCCATCAGAAGGGATGAATACCTTCAGGCCTACATGTGAATGTCCTGGTACCTCCCCGGAGG 354

572 GGAG------TTATCACAGCTGAGTCANTGGTGTGAAG 603
    ||||------||-|:||| |||||:|| | |||||:|:|
353 GGAGGGGAAGTT-TTACACCTGAGCCAGTTGTGTAAGG 317
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-17134#Unknown	1	109	ERV3-28_PMaj-LTR	935	1038	c	0.8037	1.4167	541

```
  1 TGTTACGACCCGCTCCTGGGAAGGGGACGGGGGTAACCTAGGTTGTTATTAATC-ATTCCCTTTGGGGTG 69
    |||||||||||||:||||--||||---||:||||||||: ||||| ||:||||| -|||||||||-||||::
1038 TGTTACGACCCGCCCCTG--AAGG---CGAGGGTAACTGAGGTTCTTGTTAATAGATTCCCTT-GGGGCA 975

70 GATTAAAGTGAAACGACACTATATAATCGGTGTTTATTTA 109
   |||||:|||||||||:|||||: ||:|:|:|||||||| ||
974 GATTAGAGTGAAACAACACTGAATGACCAGTGTTTATATA 935
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000073#MITE@unknown	366	421	ERV3-28_PMaj-LTR	566	619	c	0.8182	1.3333	311

```
366 CTCAGGTNCAGGTGGGAGCCCCCAG-TGCCTCCCCCAGGGCAGGGAGTTCCACACTG 421
    ||||||| |||||||||:| |||||-|:|||||||::|||---|||||::||||||
```

```
619 CTCAGGTTCAGGTGGGAACGCCCAGGTACCTCCCCTGGGG---GGAGTTTTACACTG 566
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000022#MITE@unknown	218	450	fAlbLTR2	22	241	c	0.6205	2.1111	349

```
218 AGCCCTTGGAGGGGCTCCAAGGGGCAGTTCTGAGGAGTTCTGAGGGTGGGC-ACCAGGGGAAAATGGTAC 286
    ||||| ||||   :||||||||||||||-----|||-----:|::||  ||:|:-|||-|||| ||  ||:|  :
241 AGCCCNTGGACCAGCTCCAAGGGGC-----TGA-----CCCAGGGNTGAGTTACC-GGGGCAACTGATCT 183

287 CANGGGTTGGNTATAGATATCANATATGTTAATTACTGAAAGTTATAAAAACTGTAACATTTGGCTGANG 356
    |  :--||||  |:||   |:::|  ||||::||||||  | ||  ||||||||||:||||:  | |:   |:   :
182 CCTA--TTGGATGTACCTGCTAGATATACTAATTAATTAACCTTATAAAAATTGTAGAAATCCNNTACCA 115

357 NGNGTGCNCATA-CTTTTNGTGTGCACCTAGAAGCTTCTAATAAAGGNNCTACTTTATCTATCTATCTCC 425
    | |||| ||   -|: |     |||||||||::|||||||::|||  ||:|   :|:|||| | |-|:||---||
114 CGTGTGCGCANNGCCGTACCNGTGCACCTGAAAGCTTTCAATTAAAGANTTGCTTTTTAT-TTTA---CC 49

426 ACT--AATGTTGTTTTGAAAGTCTTTT 450
    |||--||:::|||| :|:|||:||||
 48 ACTTTAACACTGTTNNAAGAGTTTTTT 22
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000023#MITE@unknown	138	257	LTR11_MEu	128	251	c	0.6613	1.6818	241

```
138 ACAGAACTTTTTATACCCT-TTCCCGGCCGAAAGGTCCCTGCCCCCTCTTCCTATTGGCTGGGAATTG-G 205
    ||| |:|||||||| ||||-||||||:::  :  |   ||||| |||:  |:|:||:|||||||||||  |::|-:
251 ACACAGCTTTTTATTCCCTATTCCCGATTCGTATTTCCCTCCCCTGTTTCCCCATTGGCTGGGTACCGCA 182

206 GGACTCACAGTCTGGCCCGGTTCGCCTGC-CTGCCCA--AGACCCCCCACCCCCT 257
    ||::|:||||:||:-:||||  |||||: -|| ||||--  ||  :|:||:||||||
181 GGGTTTACAGCCTA-TCCGGAACGCCTAAACTCCCCACGTGAGTCTCCGCCCCCT 128
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000028#MITE@unknown	1	574	TguLTR5c	1	586	d	0.7936	1.6897	2678

```
1 TGTAGTGGGTCTGGCTGAGCCGGAATTTATTTTCCC-ATAGTAGCCCTTACAGTGCTGTGCTCTGCATTG 69
  |||| |||||||||||||||| :|||:|| |||||||||-|:||:||||||:||||||||||||:|||||||
1 TGTATTGGGTCTGGCTGAGATGGAGTTNATTTTCCCCACAGCAGCCCTCACAGTGCTGTGCTTTGCATTG 70

70 GTAGCTAGAGGAGTGTTGATAACANGCCCATGTTTTGGCTACTGCTGAGCA---------CAGCA----- 125
   |||||||||:::||||||||||||| :|| :|||||||||||||||||||-----------|||||-----
71 GTAGCTAGAAAGGTGTTGATAACACACCAGTGTTTTGGCTACTGCTGAGCAGCGCTGGCACAGCATCAGG 140

126 -CTGT------AACATTCCTTCTTCAGTCAGGGG-------------CGAGATCCTGGGAGGGGACACAGG 176
   -||||------|||||||||::|::||-:|||||-------------|:|||||:||||||||||||||||
141 GCTGTCTCTCCAACATTCCCCCCCCA-CCAGGGGGCTGGGGGTGGGCAAGATCTTGGGAGGGGACACAGC 209

177 TAGGCCAGCTGACCCACACTGACCAAGGGGATATTCCATACCATATGANGTCAACCCAG--ATATAAAGC 244
    :||| ||||||||||| |||||||:||||||||||||||||||||||| ||||:|:|||--|||-|||||
210 CAGGACAGCTGACCCAAACTGACCAAAGGGATATTCCATACCATATGACGTCAGCTCAGCAATA-AAAGC 278

245 TGAGGCAAGGAGCNGGAAGGAGG---CATTCATTGTCTNTAATGGCTGCCTGCTGA--CAACNNTTACGN 309
    |:||| ||||||  ||||||||||---|||||:||:|-| :::|| :|||||| |||:--|||| :|||||
279 TAAGGGAAGGAGGAGGAAGGAGGGGGCATTCGTTAT-TACGGTGTTTGCCTTCTGGAGCAACCGCTACGC 347

310 GTGCTGGAGCTCTGCTTNTCAGAGAAGTGGCCGACCATCGC-TGCTTATGGGAAGTAGAGATTAACTGCT 378
    ||:||||:|||:|||||| :|:|-|||||||||:|: ||||||-|||| |||||||||||||||||| ||| | :|
348 GTACTGAAGCCCTGCTTCCCGG-GAAGTGGCTGGACATCGCCTGCTGATGGGAAGTAGAGAATAAATTTT 416

379 AGCTTCTGCTTTGTGTGTGTGCACNCTGCTTTNGNTTTTTTTTNCTTTTTGCATAAATATAAACTGCCTTA 448
    ||:| |||||:  |:|:||:|  --||:||---||:||||  ||||  ---------:|||||||||||
417 TTGTTTTCCTTTGCTTCCGCGCGCG--GCCTT---TTCTTTTGCTTTA---------GTAAACTGCCTTA 472

449 TCGCAACCCACGGTTTGTGTTATTTCTTTTTCCTCCCACCTTNCTCTCTCCCCTGTCCNGCTGGGAAGGG 518
    ||  |:||||||: ||||---------|||:| ||::|---| :|||||||:|||||| ||||||:||||
473 TCTCGACCCACGAGTTGT---------TTTCCATCTTA---TTTTCTCTCCTCTGTCCCGCTGGGGAGGG 530
```

```
519 GAGTGATAGAGCAGCTGGGTGGGCACCTGGCGTTCAGCCAAGGTGAACCCACCACA 574
    ||||||||||||:|||| |||||||||||||||::|:||||||| |||||||||||
531 GAGTGATAGAGCGGCTTGGTGGGCACCTGGCGTCCGGCCAAGGTCAACCCACCACA 586
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6012#Unknown	172	558	TguLTR5c	114	551	d	0.7035	2.8649	1524

```
172 GCTGAGCAGGGCTGGCACAGC----------------CCACNTTCCTTNCCCA-----------GNNGAG 214
    |||||||||| |||||||||||||---------------|  || ||||::  ||||-----------|   |  |
114 GCTGAGCAGCGCTGGCACAGCATCAGGGCTGTCTCTCCAACATTCCCCCCCCACCAGGGGGCTGGGGGTG 183

215 GNCAAGGTNCTGGGAAGGNACACNGCCAGGCCAGCTGAGCCAGAGTGACCAGAGGGATNTTCCANATCAT 284
    |  ||||:| :|||||:|| |||| |||||| ||||||| |||:| ||||||:||||||| |||||  |:|||
184 GGCAAGATCTTGGGAGGGGACACAGCCAGGACAGCTGACCCAAACTGACCAAAGGGATATTCCATACCAT 253

285 GGNATGTCAGCTCNG--ATANAAA--GAGGANANGANGNGNAAGG-GGTGACATTNATTGTT----TGTT 345
    :  |:||||||||| |--||| ||:--:|||: | || | | ||||-|| |:|||| :||:||----|||| 
254 ATGACGTCAGCTCAGCAATAAAAGCTAAGGGAAGGAGGAGGAAGGAGGGGGGCATTCGTTATTACGGTGTT 323

346 TGCCTGCTN-AGNAGCTGCTCCGNGTGCTGAAGCCTGGCTTGCTGGGNCATGGCCAGACATCAC-TGCTG 413
    ||||| || -|| |:|:||| || ||:|||||||||: |||| |:||| :|||||::||||||:|-||||| 
324 TGCCTTCTGGAGCAACCGCTACGCGTACTGAAGCCCTGCTTCCCGGGAAGTGGCTGGACATCGCCTGCTG 393

414 ATGNGAAGNAGAGAANAANNTNGN-ATTTTCNTCTTTNTNTGTGTNCAAANTTNGGCTTTTGATTNAGTA 482
    ||| |||| |||||| || |   -:||||| |:| : | :|:|: |:: || -|||||| || |||| 
394 ATGGGAAGTAGAGAATAAATTTTTTGTTTTCCTTTGCTTCCGCGCGCGGCCTTTT-CTTTTGCTTTAGTA 462

483 AAGT------------CCCANNAGTCATTTNCCANNTTATTCTCTCNCC-CTGTCCATNTGGGNAGGGCA 539
    || |-------------|||| |||:::||| ||| ||||||:||||| ||-||||||| |||| |||| | 
463 AACTGCCTTATCTCGACCCACGAGTTGTTTTCCATCTTATTTTCTCTCCTCTGTCCCGCTGGGGAGGGGA 532

540 GTGATANAGNGGCTTGATG 558
    |||||| || ||||||:|| 
533 GTGATAGAGCGGCTTGGTG 551
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000032#MITE@unknown	282	382	ERV1-6_MM-I	2968	3061	d	0.6804	2.0000	227

```
 282 AAGCCAGCTACCACGACCTGGCCACGCGCTGGGCAGCCCAACCTCTGGCGACAGGCTGTCGCTGTCTGGG 351
     |||||  |:|||| |||:|||||||::  |||||||||| |  ||:| ||::||-- || |:|| || ||  :
2968 AAGCCCTCCACCAAGACTTGGCCACATTCTGGGCAGCCAACCCCCAGGTAAC--TCTCTTGCAGTATGTA 3035

 352 GTTGTTTACTTCTCCTTCTGGCTGCCCCAAG 382
     | ||---||--||:|||:|:|||||::| ||
3036 GATG---AC--CTTCTTTTAGCTGCTTCCAG 3061
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000033#MITE@unknown	180	225	RTE-1B_DAn	801	848	d	0.7872	1.8000	218

```
180 CAGCTGACTG--ACCAATTATGGGATGACACGGTGTGGGAGAAAGTAG 225
    ||:| ||:||--|||||||:||||| :||||||||||||||: | |||| 
801 CAACGGATTGGAACCAATCATGGGCCGACACGGTGTGGGAACACGTAG 848
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000034#MITE@unknown	71	308	fAlbLTRL2	74	301	d	0.6903	2.1111	341

```
71 ATTNGAAGCTTCCAAGGTGCACACCAAAAGC-ATGCACACACNTGATCAGGGATGT-TACAGTTTTTATA 138
   ||| :||||||:||-||||||||     | :||-||||:||||| ||:| |:|||| |-||||:|||||||| 
74 ATTGAAAGCTTTCA-GGTGCACMGRTACGGCGATGCGCACACGTGGTAAAGGATTTCTACAATTTTTATA 142

139 ACCTCCAGCCATTAGCATATATGATATCTATAGCCAACCTGGGGTACCAATTTCCCTTGGTG-CCCACCC 207
    |  |: | : |||||:||||  |:::|  ||:| ||||--:|:| :|:|:| |||:-|||:-|:||||| 
143 AGGTTAATTAATTAGTATATCTAGCAGGTACATCCAA--TAGGAGATCAGTTGCCCC-GGTAACTCACCC 209

208 ATAGAGTNCTCAGAACTGCCCCTTGGAG---------AGGCT-CTGGGCCCTCTCTATTGTTTTGTCTTC 267
```

```
      |:|:----||||-----|||||||||||---------:||||-||   ||||: |:| ||||| ||||||||
 210 CTGGG----TCAG-----CCCCTTGGAGCTGGTCCAAGGGCTTCTTTGCCCCATTTCTTGTTATGTCTTC 270


 268 --AAGCTATCTTGCAGGTGTTTCTTCAAAACACCATGTCCTTG 308
      --|||:| |------|||| ------|||||| |||||||||
 271 TTAAGTTCT-----GGTGG------AAAACAAAATGTCCTTG 301
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000036#MITE@unknown	167	237	L1-35_ALy	1515	1586	d	0.7260	1.4545	247

```
 167 AGAAGACAAAACATAAGAAGAAGGCCTAG--AGGTC-CTGGAAGATCTCCANGGGGCAGTTCTGAAGACC 233
      ||||||| |||||-:||||:|||||||||--|::||-||:|||:|-||  |  |:|||||:|:::|||| |
1515 AGAAGACCAAACA-GAGAAAAAGGCCTAGTAAAATCACTAGAAAA-CTAAAGGAGGCAGCTTCAAAGAAC 1582


 234 CCTA 237
      ||||
1583 CCTA 1586
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000040#MITE@unknown	84	145	Hitchcock_LTR	172	238	d	0.7969	1.2500	302

```
  84 GAGGGGACAGGTAT-----CATCTGACTTAAGC-AGCCAAAGAGGTATTTCATATCATCTGACATCAT 145
      |||||:|||||:-||-----||  |||||||||:|-:|||||||:|:||||:|||||:||| ||||||||||
 172 GAGGGAACAGA-ATTAGGACAGCTGACTTAAACTGGCCAAAGGGATATTCCATACCATATGACATCAT 238
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004824_LTR#LTR@unknown	76	148	Hitchcock_LTR	165	238	d	0.7746	2.1667	258

```
  76 GAGCTGGG------CTGAGCTAGCTAACAGCTGACTTCTTCTAGCCAATAATATTGTATTCCATACCATA 139
      ||||||||------| ||::|||--:||||||||||   ||:||||| :: ||---||||||||||||||
 165 GAGCTGGGAGGGAACAGAATTAG--GACAGCTGACTTAAACTGGCCAAAGGGAT---ATTCCATACCATA 229


 140 TTACATCAT 148
      | |||||||
 230 TGACATCAT 238
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-12159#LINE@CR1	1	1142	CR1-X1_Pass	3259	4419	d	0.9328	2.0000	8613

```
   1 TGTAATNTTTTTGGATTTCA----AGCTTTNNATACTGTCT-----ANNATNNTTCTGGANAAAATGTCC 61
     |||||| ||||||||||||||----|||||| |||||||||||-----|  ||  ||||||| ||||||||||
3259 TGTAATCTTTTTGGATTTCAGTAAAGCTTTCGATACTGTCTCTCACAGNATCCTTCTGGACAAAATGTCC 3328

  62 AGCACACAGCTGGATAAACACATCATGTNGTGGNTNAGCAATTGGCTCANG-------TNCACAGAGTAA 124
     ||||||||||||||||||||||||||||: :||| | |||||:||||||| |-------: || ||:|| |
3329 AGCACACAGCTGGATAAACACATCATGCGATGGGTGAGCAACTGGCTCACGGGTCGGGCACAAAGGGTTA 3398

 125 TAGTGAATGGGGTNACATCAGACTGGTGACCTGTCACTAG--GGGTTCCACAGGGCTCCATCTTNGGCCC 192
     :||||||||||||| ||||||||||||||:||||||||||||--|||||:|||||||||||||||:| ||||||
3399 CAGTGAATGGGGTGACATCAGACTGGCGACCTGTCACTAGTGGGGTTCCGCAGGGCTCCATCCTCGGCCC 3468

 193 TGTGCTCTTCAACATCTTCATAAATGACTTGGANNCAGGACTGGAAGGGATACTAAGCAAGTTTGCAGAT 262
     ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||:|||||: 
3469 TGTGCTCTTCAACATCTTCATAAATGACTTGGACGCAGGACTGGAAGGGATACTAAGCAAGTTCGCAGAC 3538

 263 GACACAAAACTGGGAGGAGCTGTTGACTCCCTNNAAGGCAGGGAGGCCCTGCAGAGAGACCTNGACAAAT 332
     ||:|||||||||||||||||||||||||||||| |||||||||||||||||||||||||||| |||||||
3539 GATACAAAACTGGGAGGAGCTGTTGACTCCCTCGAAGGCAGGGAGGCCCTGCAGAGAGACCTCGACAAAT 3608

 333 TAGAGGACTGGGCAATCACCAACCATATGAAGTTCAACAAGGGAAAGTGCNGGATTCTGCACCTGGGATG 402
     ||||||:|||||||||||||||||||:|||||||||||||||||| ||||| |||||||||||||||||||
3609 TAGAGGGCTGGGCAATCACCAACCGTATGAAGTTCAACAAGGGNAAGTGCCGGATTCTGCACCTGGGATG 3678

 403 GGGCAACCCTGGATGTANGTACAGACTGGGGAATGAGATGCTGGAAAGCAGTGCCATGGAAAGGGACCTG 472
     ||||||||||||||||| | |||||||||||||||||||||| |||||:|||||:|||::||||||||||
```

```
3679 GGGCAACCCTGGATGTACGGACAGACTGGGGAATGAGANGCTGGAGAGCAGCGCCGCGGAAAGGGACCTG 3748

 473 GGGGTCCTGGTCGATGGCAAGTTGAATATGAGTCAGCAGTGCCCTGGCAGCCAGGAGGGCCAACCGTGTC 542
     |||||||||||||||||||||||||||:|||||:|||||||||||||||||||||||||||||||| ||||
3749 GGGGTCCTGGTCGATGGCAAGTTGAACATGAGCCAGCAGTGCCCTGGCAGCCAGGAGGGCCAACCCTGTC 3818

 543 CTGGGGGGCATCAGGCACAGCATCACCAGCCGGTCNAGGGAGGGGATTGTCCCGCTCTGCTCTGCACTGG 612
     |||||||||||||||||||||||||||:|||||||| | ||||||||||||||||||||||||||:|||| 
3819 CTGGGGGGCATCAGGCACAGCATCGCCAGCCGGGCAAGGGAGGGGATTGTCCCGCTCTGCTCTGCGCTGG 3888

 613 GGCGGCCTCACCTTGAATATTGTGTGCAGTTTTGGGCACCACAATATAAGAAAGATATTAAGCTNTTAGA 682
     |||||||||||||:||:|::|| | ||||||||||||:|||||||||||||||||||:|||||||| |||||
3889 GGCGGCCTCACCTCGAGTGCTGGGGGCAGTTTTGGGCGCCACAATATAAGAAAGACATTAAGCTATTAGA 3958

 683 GAGTGTCCAAAGGAGGGCAANGAAGATGGTGAAGGGCCTTGAGGGGAAGCCGTATGAGGAGCGGCTGAGG 752
     |||:||||||||||||||| ||:|||||||||||||||||||||||||||||||||||||||||||||||
3959 GAGCGTCCAAAGGAGGGCAACGAGGATGGTGAAGGGCCTTGAGGGGAAGCCGTATGAGGAGCGGCTGAGG 4028

 753 TCACTTGGTCTGTTCAGCCTGGAGAAGAGGAGACTGAGGGGAGACCTCATTGCAGT-TACAACTTCCTNG 821
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||-||||||||||| |
4029 TCACTTGGTCTGTTCAGCCTGGAGAAGAGGAGACTGAGGGGAGACCTCATTGCAGTCTACAACTTCCTCG 4098

 822 TGAGGGGAAGAGGAGGGGCAGGCACTGATCTCTTCTCTGTGGTGACCAGTGACAGGACCCAAGGGAATGG 891
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
4099 TGAGGGGAAGAGGAGGGGCAGGCACTGATCTCTTCTCTGTGGTGACCAGTGACAGGACCCGAGGGAATGG 4168

 892 CCTGAAGTTGTGTCAGGGGAGGTTTAGGTTGGATATTAGAAAAAGGTTCTTCACCCAGAGGGTGGTTGGG 961
     |||||||:|||||||||||||||||||||||||||||:|||:|||||||||||||||||||||||||||
4169 CCTGAAGCTGTGTCAGGGGAGGTTTAGGTTGGATATCAGGAAAAGGTTCTTCACCCAGAGGGTGGTTGGG 4238

 962 CACTGGAACAGGCTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCATTTGGACA 1031
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||
4239 CACTGGAACAGGCTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCGTTTGGACA 4308

1032 ATACTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCNANGAGTTGGACTCGATGATC 1101
     ||:||||||||||||||||||||||||||||||||||||||||||||| | ||||||||||||||||||
4309 ATGCTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTCGATGATC 4378

1102 CTTGTGGGTCCCTTCCAACTCAGCATATTCTGTGATTCTGT 1142
     |||||||||||||||||||||||||||||||||||||||||
4379 CTTGTGGGTCCCTTCCAACTCAGCATATTCTGTGATTCTGT 4419
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000068#MITE@unknown	98	1007	CR1-X1_Pass	3465	4421	d	0.8777	3.7308	6080

```
  98 GNCCTGNNNTNNNTCAANAT-TTCATAAANNANTTGGANN----------AAGGNATACTAAGNAAGTTNN 157
     | |||| |  -|||| ||-||||||||| | ||||| ----------|||| |||||||| |||||
3465 GCCCTGTGCTCT-TCAACATCTTCATAAATGACTTGGACGCAGGACTGGAAGGGATACTAAGCAAGTTCG 3533

 158 -AGATGACANAAAANTGGGAGGAGCTGTTGACTCCNN--AAGN---AGNNGCCCTGCAGAGAGACCTNNA 221
     -|||:|||:| |||| ||||||||||||||||||||  --||| ---:| |||||||||||||||||| |
3534 CAGACGATACAAAACTGGGAGGAGCTGTTGACTCCCTCGAAGGCAGGGAGGCCCTGCAGAGAGACCTCGA 3603

 222 CAAATTAGAGNNNTGGGCAATNACC---CATATNNANC------ANNNNAAGTGCNNNNT-CTGCANCTG 281
     ||||||||||  |||||||| |||---|:|||  | :------| |||||| |-||||| |||
3604 CAAATTAGAGGGCTGGGCAATCACCAACCGTATGAAGTTCAACAAGGGNAAGTGCCGGATTCTGCACCTG 3673

 282 GG----GGNAACCCTNGANNNTNN---AGACTGGNAA----GATGCTGGAAAGCAGTGCCANNGAAAGGG 340
     ||----|| |||||| ||      ---|||||||  :|----|| ||||||:|||||:|||:  |||||||
3674 GGATGGGGCAACCCTGGATGTACGGACAGACTGGGGAATGAGANGCTGGAGAGCAGCGCCGCGGAAAGGG 3743

 341 A-------GTCCTGGTNNATGGCAAGTTGAATATGAGTCAGCAGT--CCTGGCAGCCAGGAGGGCCAACC 401
     |-------|||||||  |||||||||||||||||:|||||:|||||--|||||||||||||||||||||||
3744 ACCTGGGGGTCCTGGTCGATGGCAAGTTGAACATGAGCCAGCAGTGCCCTGGCAGCCAGGAGGGCCAACC 3813

 402 NTGTCCTGGGGG-CATCAGGCANAGCATCNCCAGCNNGTCNAGGGAGGGGATTGTCCNNCTCTGCTCTGC 470
     |||||||||||-||||||||| |||||| ||||| | | |||||||||||||||||  |||||||||||
3814 CTGTCCTGGGGGGGCATCAGGCACAGCATCGCCAGCCGGGCAAGGGAGGGGATTGTCCCGCTCTGCTCTGC 3883

 471 ACTGGGGCNGCCTCACCTTGAATATTGTGTGCAGTTTTGGGCACCACAATATAAGAAAGATATTAAGCTA 540
     :||||||| |||||||||||:||:|::|| | ||||||||||:|||||||||||||||||:|||||||||
```

```
3884 GCTGGGGCGGCCTCACCTCGAGTGCTGGGGGCAGTTTTGGGCGCCACAATATAAGAAAGACATTAAGCTA 3953


 541 TTAGAGAGTGTCCAAAGGAGGGCAANGAAGATGGTGAAGGGCCTTGAGGGGAAGCCGTATGAGGAGCAGC 610
     ||||||||:||||||||||||||||| ||:||||||||||||||||||||||||||||||||||||:||
3954 TTAGAGAGCGTCCAAAGGAGGGCAACGAGGATGGTGAAGGGCCTTGAGGGGAAGCCGTATGAGGAGCGGC 4023


 611 TGAGGTCACTTGGTCTGTTCAGCCTGGAGAAGAGGAGACTGAGGGGAGACCTCATTGCAGT-TACAACTT 679
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||-||||||||
4024 TGAGGTCACTTGGTCTGTTCAGCCTGGAGAAGAGGAGACTGAGGGGAGACCTCATTGCAGTCTACAACTT 4093


 680 CCTNGTGAGGGGAAGAGGAGGGGCAGGCACTGATCTCTTCTCTGTGGTGACCAGTGACAGGACCCNAGGG 749
     ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
4094 CCTCGTGAGGGGAAGAGGAGGGGCAGGCACTGATCTCTTCTCTGTGGTGACCAGTGACAGGACCCGAGGG 4163


 750 AATGGCCTGAAGTTGTGTCAGGGGAGGTTTAGGTTGGATATTAGAAAAAGGTTCTTCACCCAGAGGGTGG 819
     |||||||||||||:|||||||||||||||||||||||||||:||:||||||||||||||||||||||||||
4164 AATGGCCTGAAGCTGTGTCAGGGGAGGTTTAGGTTGGATATCAGGAAAAGGTTCTTCACCCAGAGGGTGG 4233


 820 TTGGGCACTGGAACAGGCTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCATTT 889
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||
4234 TTGGGCACTGGAACAGGCTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCGTTT 4303


 890 GGACAATACTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTNNA 959
     |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
4304 GGACAATGCTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTCGA 4373


 960 TGATCCTTGTGGGTCCCTTCCAACTCAGCATATTCTGTGATTCTGTGA 1007
     ||||||||||||||||||||||||||||||||||||||||||||||||
4374 TGATCCTTGTGGGTCCCTTCCAACTCAGCATATTCTGTGATTCTGTGA 4421
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6290#Unknown	1	389	CR1-X1_Pass	3911	4331	c	0.8150	4.5000	1840

```
   1 TCACACCCTGTGCCCCAGAGCATCATCCAAACNCTCCTGGAGCTCTGNCAGCCTTGGGGCTGTGCCCACT 70
     ||||||| |||||: |||||||::|||||||| ||:|| ||:||||| ||| ||||| |||||| |||||
4331 TCACACCATGTGCCTGAGAGCATTGTCCAAACGCTTCTTGAACTCTGTCAGGCTTGGTGCTGTGACCACT 4262


  71 GCCCTGGGGAGCCTGGTC-AGTGCCCA-CCACCCTCTGGGGGAAGAAN--------AAGNTCCAACCTNA 130
     ||||||||||||||||| ||-||||||||-|||||||||||| |||||| --------:|  |||||||| |
4261 TCCCTGGGGAGCCTGTTCCAGTGCCCAACCACCCTCTGGGTGAAGAACCTTTTCCTGATATCCAACCTAA 4192


 131 CCCTGCCCTG-------------CCATTCCCT-GGTGCTGTCCCTGNTCCCCACAGAGCAGAGATCAGT 186
     ||| |||||-------------||||||||||-|||| ||||| ||| || ||||||||| ||||||||||
4191 ACCTCCCCTGACACAGCTTCAGGCCATTCCCTCGGGTCCTGTCACTGGTCACCACAGAGAAGAGATCAGT 4122


 187 GCCTGCCCCTCCTCTGCCCCTGCCCAGGAAGTTGTA-CCTGCANTGAGGTGTCCCCTCAGTCTCCTCTTG 255
     ||||||||||||| ||||| | |||||||||||||-||||| |||||| ||||||||||||||||||||||
4121 GCCTGCCCCTCCTCTTCCCCTCACGAGGAAGTTGTAGACTGCAATGAGGTCTCCCCTCAGTCTCCTCTTC 4052


 256 TGCAG-CTGAACACACCAAGTGCCCTCAGCT--TCCTCACACN-CTTCCCCTGCAGGCCCTTNCCCATCT 321
     | |||-|||||||| |||||||| ||||||:--|||||||:|| -|||||||| |||||||| |||||:
4051 TCCAGGCTGAACAGACCAAGTGACCTCAGCCGCTCCTCATACGGCTTCCCCTCAAGGCCCTTCACCATCC 3982


 322 TGGTTGCC-TCCNTTGGACACTCN--AATGGCTCAATCTCTTCCNTCTNTTNTGGTGCCCCAAAGTNCCC 388
     | ||||||-||| ||||||:|||| --||:|||:||| ||||:| | | || |||:|||| ||| | |||
3981 TCGTTGCCCTCCTTTGGACGCTCTCTAATAGCTTAATGTCTTTCTTATATTGTGGCGCCCAAAACTGCCC 3912


 389 C 389
     |
3911 C 3911
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002676_LTR#LTR@unknown	21	317	CR1-X1_Pass	4111	4419	d	0.8717	3.2000	1716

```
  21 GAGGGGCAGGCACTGANCTCTGCTCTGGGG----CAGGGACAGCACCC-AGGGAATGGC-TGGAGCTGTG 84
     |||||||||||||||||||| |||| ||||| ||-----||| ||||| ||||-||||||||||-||:||||||||
4111 GAGGGGCAGGCACTGATCTCTTCTCTGTGGTGACCAGTGACAGGACCCGAGGGAATGGCCTGAAGCTGTG 4180


  85 CCAGGGCAGGGTCAGGTTGGATCTCAGGAAAAGGTTCTTCCCCCAGAGGGTGGT-GGGCACTG-ACCAGG 152
```

```
          :|||||| |||| |:||||||||||| ||||||||||||||||| |||||||||||||-|||||||||-| ||||
4181  TCAGGGGAGGTTTAGGTTGGATATCAGGAAAAGGTTCTTCACCCAGAGGGTGGTTGGGCACTGGAACAGG 4250

 153  CTCCCCAGGGCAGTGGGCACAGCCCCAAGGCTGCCAGAGCTCCAGGAGGGTTTGGATGATGCTCT-GGGC 221
      ||||||||||| ||||| ||||| ||||| ||| ||||||:|| ||:|| |||||||::||||||-:|||
4251  CTCCCCAGGGAAGTGGTCACAGCACCAAGCCTGACAGAGTTCAAGAAGCGTTTGGACAATGCTCTCAGGC 4320

 222  ACAGGGTGTGACTCTTGGGGNGN---CTGTGCAGGGCCAGGGGTTGGACTGGATGATCCTTGTGGGTCCC 288
      ||| |||||||||||||||||   ---|||||||||||||||:|||||||| |||||||||||||||||||
4321  ACATGGTGTGACTCTTGGGGATGGTCCTGTGCAGGGCCAGGAGTTGGACTCGATGATCCTTGTGGGTCCC 4390

 289  TTCCAGCTCAGCATATTCTGTGATTCTGT 317
      |||||:||||||||||||||||||||||||
4391  TTCCAACTCAGCATATTCTGTGATTCTGT 4419
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000071#MITE@unknown	3	236	CR1-E_Pass	2835	3076	d	0.8201	2.7143	1311

```
   3  TGNNAGAGNGNAGGNTTA--TNNGATATTNGGAAGAAATTCTTCCCTGTGAGGGTGNN-AGGCCCTGNA- 68
      ||  ||||| | |:: |||--| |||||| |||||||||||: |||||||||| -||:| ||| |-
2835  TGAAAGAGGGGAAATTTAGGTTAGATATTAGGAAGAAATTCTTTACTGTGAGGGTGGTGAGACACTGGAA 2904

  69  CAGGT-GCCCAGAGAAGCTGTGGCTGCCCCATCCCTGGAAGTGTCCAAGGCCAGGTTGGACAGGGCTTGG 137
      |||||-|||||||:||:|:|||| ||||||| |||||| |||||:||||||||||||||:|:|||:| |
2905  CAGGTTGCCCAGGGAGGTTGTGGATGCCCCANCCCTGGCAGTGTTCAAGGCCAGGTTGGATAAGGCCTTG 2974

 138  AGCAACCTGGGCTAGTGGAAGGTGTCCCTGCCCATGGCAGGGGG---TGGAACNAGATGATCTTTAAGGT 204
      |||||||||| |||||||:|||||||||||||||||||||||||---|||:|| ||||||||||||||||
2975  AGCAACCTGGTCTAGTGGGAGGTGTCCCTGCCCATGGCAGGGGGGGTTGGGACTAGATGATCTTTAAGGT 3044

 205  CCCTTCCAACCCAAACCATTCTGTGATTCTNT 236
      || |||||||||  | ||||||:||||||| |
3045  CCNTTCCAACCCTTAACATTCTATGATTCTAT 3076
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004455_LTR#LTR@unknown	3	186	CR1-E_Pass	2865	3056	c	0.8342	2.5455	1026

```
   3  GGGTTGGAAGGGACCTTAAAGNNCATCC-GTNCCA----CCCCTGCCATGGGCAGGGACACCTCCCACCA 67
      ||||||||| ||||||||||| ||||:-|| |||----|||||||||||||||||||||||||||||:|
3056  GGGTTGGAANGGACCTTAAAGATCATCTAGTCCCAACCCCCCCTGCCATGGGCAGGGACACCTCCCACTA 2987

  68  GCCCAGGNTGCTCCAAGCCCTGTCCAACCTGGCCTNGGACACTCCCAGGGATGGGGCAGCCACAGCTTCT 137
      | |||||| |||||| |:|||:|:|||||||||||| |:||||| |||||| ||||||| |||||:|:||:
2986  GACCAGGTTGCTCAAGGCCTTATCCAACCTGGCCTTGAACACTGCCAGGGNTGGGGCATCCACAACCTCC 2917

 138  CTGGGCAACCTGTGCCAGGGCCTGCCCACCCTCCCAG---ANAATTCCTTCC 186
      |||||||||||| ||||| |:|| |||||||| |||---| ||||:|||||
2916  CTGGGCAACCTGTTCCAGTGTCTCACCACCCTCACAGTAAAGAATTTCTTCC 2865
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1533#Unknown	560	670	TguERVL2b1_LTR-La_fAlb	427	539	d	0.7453	1.5000	304

```
560  CAGGGTGCTGGGTTATACTTCTGGGTTTTGTG---GGTTAAAACCAATTTCTCTTTGTGCCATTGCATTT 626
     |:||||||:::||||:||-|||||:-:|:||| ---||||--------|||||-|||||:|:|||||||| |
427  CGGGGTGTCAGGTTGTA-TTCTGA-CTCTGTCAGTGGTT--------TTTCT-TTTGTACTATTGCATGT 485

627  ATTGTAATATTTT----------TATTAAAATTGTAACTCTGACTTATAATCTCT 670
     ||| || | ||:|----------||||||||||| :||||||| |:|||||
486  ATTTTATTTTTCTCTTTTTTTCCTATTAAAATTGTATTTCTGACTTGGAGTCTCT 539
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00000073#MITE@unknown	49	115	TguERVL2b1_LTR-La_fAlb	464	539	c	0.7941	2.4000	263

```
 49  AGAGATTATAAGTCAGAGTTACAATTTAATA-----------ACAATATTACAATAAATGCAATGGCACAA 108
     |||||:| :||||||||||: |||||||||||||----------| || | || |||| ||||||:|:||||
```

```
539 AGAGACTCCAAGTCAGAAATACAATTTAATAGGAAAAAAAGAGAAAAATAAAATACATGCAATAGTACAA 470


109 AGAGAAA 115
    |-||||||
469 A-AGAAA 464
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1533#Unknown	206	440	ERV3-7_PMaj-LTR	166	395	d	0.6844	1.6111	480

```
206 TCNTTAGCACCTCCACACCCAGCCT-------GAGGGGTCATGTCTGCTAATGGGCCATCAACGATTCCA 268
    || |||  |  |:|||||||||| |||-------|:|||:|   :  ||||:|||||||||||::|-| :||--
166 TCTTTATCTCTTCCACACCCATCCTCCCTCCAGGGGGATATCTTCTGTTAATGGGCCATTGA-GTCTC-- 232

269 AAATACCCCATGACTCACAGAGTCAGATCA-CCCATTGTGGAACTCCCTGCCCTGGGGGGAGGTACTGGGN 337
    ----||:  ||||||||  |:|:|:|:|  ||||-||||||||||||::|:  |:|::|||  ||||||||||  :|:::|
233 ----ACTGCATGACTGATAAAATTACATCATCCCATTGTGAGATGCTCCACCCAGGGGGAGGAGCCAAGC 298

338 GNTCCCACCTGNACCTGAGGGTATATAATCTTGGGGTTTGGGG-ACTTCGGG--ACCACTCGTC---GGA 401
    :  |||:||||||  |----------||||||||||-|:|:::|||||::-||:  |:||--:||  :||  :|---|||
299 ATTCCTACCTGGA----------TATAATCT-GAGACTTGGAACACCACAGGCAGCCTTTCTCCACTGGA 357

402 T--CCAGAGGAG-GACCAGAACC-TCGACAGGAGACCACCACT 440
    |--|||||||||:-||||||| ||-|| |||-----||||||||
358 TTCCCAGAGGAAAGACCAGACCCATCTACA-----CCACCACT 395
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-30#Unknown	90	254	ERV3-7_PMaj-LTR	131	303	d	0.6970	1.7391	339

```
 90 AATGGGCCA----TTAGCAGCAGCTGCCCAGGGAGT---CATTATCACCTTCACACCCAGCCTG-----A 147
    |||||||||----|||:  |  |||  ||---  ||  |||---|  ||||||  |:|:|||||||||  |||  -----|
131 AATGGGCCAGCTGTTAAAACCAGGTG---KGGCAGTGTTCTTTATCTCTTCCACACCCATCCTCCCTCCA 197

148 GGGGG----CGTGGCTGCTAATGGGCCATCAACAGTTCCAATACCCCCTGGCTCCCAGAGTTA-ATCA-C 211
    |||||----|  |--|||:||||||||||||||::|--||::||  |:|  ---||:||   :|:|:|||-||||-|
198 GGGGGATATCTT--CTGTTAATGGGCCATTGA--GTCTCACTGCA---TGACTGATAAAATTACATCATC 260

212 CCATTGTGTGAGTCCCCGCCCAGGGGGAGGGACTGGGTGCTCC 254
    |||||||||  ||   |:||:|||||||||||||||::|:::|:::|||
261 CCATTGTGAGATGCTCCACCCAGGGGGAGGAGCCAAGCATTCC 303
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00001107_LTR#LTR@unknown	246	359	L1-4B_LA-5end	1649	1762	d	0.7281	1.9167	281

```
 246 CAAAAC-CAAACCAAAACAAATGAA---ACAGACAAATACAATTAAAGACTTCAGGAAAGGAGAACAAGC 311
     ||||||-||:|||||||  |||:-|||---||||||||||-:||||  :||||  |||||||||: |:  |||||
1649 CAAAACACAGACCAAACCAAG-GAACACACAGACAAA-GCAATAGAAGAATTCAGGAAAACAATACAAGA 1716

 312 ATGAAA---CAATCTCACCACGTCCCGGGCTAGGAAAACCA-ACAGAAACAG 359
     |::|||---||:   |  |  ||  |::----|||||--||||||-|||:||||||
1717 ACAAAATGACAGAATAAACAGGCT----GCTAG--AAACCATACAAAAACAG 1762
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00001324_LTR#LTR@unknown	349	387	Mariner-2_NV	2023	2057	d	0.8889	1.5000	233

```
 349 TCCTGCAGGGTGGGTGGTGTTTCTTTGTCCTTGCACAGA 387
     |||||||||  |||||||:|||||:|||||||||----|||||
2023 TCCTGCAGTGTGGGTGATGTTTTTTTGTCC----ACAGA 2057
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	1906	1935	Mariner-2_NV	2023	2052	d	0.9000	1.5000	226

```
1906 TCCTGCAGGGTGGGTGGTGTTTCTTTGTCC 1935
     |||||||| |||||||:|||||:||||||||
```

```
2023 TCCTGCAGTGTGGGTGATGTTTTTTTGTCC 2052
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002464_LTR#LTR@unknown	60	236	Gypsy-65_PIT-I	2911	3071	c	0.7239	1.7647	237

```
  60 CCTNCCAGCCCNTGGAGCCCACCCTGTGCCCN----ATGCCCACCTTGGCAAAGCCCT-CCCAGCCCNTG 124
     |:| ||||:-- ||||||||||||-|| || ----||||:|||:|:|------|:||-|||||--- ||
3071 CTTTCCAGT--TTGGAGCCCACCC-GTTCCGTTGGGATGCTCACTTCG------CTCTGCCCAG---TTG 3014

 125 GAGCCCACCCTGTGCCC----GATGCCCACCTTGGCAAAGCCCTCCCAGCCCATGGAGCCCACCCTGTGC 190
     ||||||||||-|| || ----|||||:|:|:|:| :----| :|:||||----||||||||||||-|| |
3013 GAGCCCACCC-GTTCCGTTGGGATGCTCGCTTCGTT----CGTTTCCAG----TGGAGCCCACCC-GTTC 2954

 191 CC----GATGCCCACCTTGGCAAAGCCCTCCCAGCCCATGGAGCCCACCC 236
     | ----|||||:|||-|| ||----:|:||||||:--||||||||||||
2953 CGTTGGGATGCTCAC-TTCGC----TCTTCCCAGT--ATGGAGCCCACCC 2911
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-16#LINE@CR1	1	420	CR1-J1_Pass	3516	3960	d	0.7972	3.9000	1999

```
   1 CACTGAGGGGCTGGAGNNT--CCAGGGNAGGGAN---GAGCTGG--AAGGGGCTGGAGCA---------- 53
     ||:||||| ||||||| |--||||:| |||| ---|||||||--||||| ||||||||----------
3516 CATTGAGGTGCTGGAGCGTGTCCAGAGAAGGGCAACGGAGCTGGTGAAGGGTCTGGAGCACAAGTCCTGT 3585

  54 -AGGAGNNGCTGAGGGAGCTGGGGGGGCTCAGCCTGGAGAAAAGGAGGCTCAGGGGGGACCTTCTGGCTC 122
     -||||| ||||||||||||||||| |:|:|||||||||||||||||||||||||||:|||||| | ||||
3586 GAGGAGCGGCTGAGGGAGCTGGGGNTGTTTAGCCTGGAGAAAAGGAGGCTCAGGGGAGACCTTATCGCTC 3655

 123 T--GCAA-TCCCTGCCAGGAGGGGGGAGCCGGG-GGGGGTCGGGCTCTGCTCCAGGGCA--CAGGGACAG 186
     |--:|||-| |||| |||||| | ||||:||-||||||||| |||| ||||  :||||--|||  |||||
3656 TCTACAACTGCCTGAAAGGAGGNTGTAGCCAGGTGGGGGTCGGCCTCTTCTCCCAGGCAACCAGCGACAG 3725

 187 GAGGAGAGGGCACGGCCTCAGGCTGGGCCAGGGNAGGGGCAGGTNGGACATCAGGAGGAATTTCTTCNTG 256
     || ||||||:||:|||||||:|||| ||||||| ||| ||||| ||||||||||:||||||||||| :|
3726 GACGAGAGGACATGGCCTCAAGCTGCGCCAGGGGAGGTTCAGGTTGGACATCAGGAAGAATTTCTTCACG 3795

 257 GAAAGGGTGGTCAGGCACTGGCAGGGGCTGCCCAGGGAGGNT-TGGAGTNCCCANCCCTGGAGGTGTCCA 325
     |||||||||||:|:|||:||| | |||||||||||||||| -|||||| ||| ||||||||||||:||
3796 GAAAGGGTGGTTAAGCATTGGAACGGGCTGCCCAGGGAGGTGGTGGAGTCACCATCCCTGGAGGTGTTCA 3865

 326 AGGNANGACTGGNNGTGGCACTNAGTGCTCTGGGCTGGGGGACAAGGTGGGNATNGGGCACAGGNTGGAC 395
     ||: | |||||| |||||||| ||||| |||| ||:| |||| ||||| | || || ||| |||||
3866 AGAAACGACTGGACGTGGCACTTAGTGCTATGGTCTAGTTGACANGGTGGTGTTCGGTCAAAGGTTGGAC 3935

 396 TCNATGGNCTNGGAGGGCTTTTCCA 420
     || |||: || ||||| ||||||||
3936 TCGATGATCTCGGAGGTCTTTTCCA 3960
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-18#LINE@CR1	29	397	CR1-J1_Pass	3586	3961	d	0.7941	3.2727	1666

```
  29 GAGCAGCAGCTGAGGGAGCTGGGGGGGCTCAGCCTGGAGAAAAGGAGGCTCAGGGGGNACCTTCTGGCTC 98
     ||| |||:|||||||||||||||||| |:|: |||||||||||||||||||||||||: |||||| | ||||
3586 GAGGAGCGGCTGAGGGAGCTGGGGNTGTTTAGCCTGGAGAAAAGGAGGCTCAGGGGAGACCTTATCGCTC 3655

  99 T--GCAA-TCCCTGCCAGGAGGGGGGAGCCGGG-GGGGGTCGGGCTCTGCTCCAGGGCA--CAGGGACAG 162
     |--:|||-| |||| |||||| | ||||:||-||||||||| |||| ||||  :||||--|||  |||||
3656 TCTACAACTGCCTGAAAGGAGGNTGTAGCCAGGTGGGGGTCGGCCTCTTCTCCCAGGCAACCAGCGACAG 3725

 163 GAGGAGAGGGCACGGCCTCAGGCTGGGCCAGGGCAGGGGCAGGNNGGACAGCAGGAGGAATTTCTNCCTG 232
     || ||||||:||:|||||||:|||| ||||||| ||| |||| ||||| |||||:||||||||| :|
3726 GACGAGAGGACATGGCCTCAAGCTGCGCCAGGGGAGGTTCAGGTTGGACATCAGGAAGAATTTCTTCACG 3795

 233 GAAAGGGTGGTCAGGCACTGGAAGGGGCTGCCCAGGGAGGTT-TGGAGTGCCCAGCCCTGGAGGTGCCCA 301
     ||||||||||:|:|||:|||:||||| |||||||||||||| -|||||| ||| ||||||||||||::||
3796 GAAAGGGTGGTTAAGCATTGGAACGGGCTGCCCAGGGAGGTGGTGGAGTCACCATCCCTGGAGGTGTTCA 3865
```

```
 302 AGGCAGGACTGGCCGTGGCACTCAGTGCTCTGGGCTGGGGGACAAGGTGGGCATCGGGCACAGGGTGGGC 371
     ||: | |||||| |||||||||:|||||| ||| ||:| |||| |||| |||| || ||| |||:|
3866 AGAAACGACTGGACGTGGCACTTAGTGCTATGGTCTAGTTGACANGGTGGTGTTCGGTCAAAGGTTGGAC 3935

 372 TCCATGGGCTGGGAGGGCTTTNCCAA 397
     || |||: || ||||| |||| ||||
3936 TCGATGATCTCGGAGGTCTTTTCCAA 3961
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002986_LTR#LTR@unknown	15	391	CR1-J1_Pass	3552	3960	d	0.7714	3.7143	1552

```
  15 GGAGCTGG-GAAGGGGCTGGAGCA---------------GCAGCTGAGGGAGCTGGGGGGGCTCAGCCTG 68
     ||||||||-|||||| ||||||||---------------||:|||||||||||||||  |:|:||||||
3552 GGAGCTGGTGAAGGGTCTGGAGCACAAGTCCTGTGAGGAGCGGCTGAGGGAGCTGGGGNTGTTTAGCCTG 3621

  69 GAGAAAAGGAGGCTCAGGGGGCACCTTCTGGCTCT--GCAA-TCCCTGCCAGGAGGGGGGAGCCGGGACA 135
     |||||||||||||||||||||||:| ||||| | |||||--:|||-| ||||  ||||||  | ||||:|| --
3622 GAGAAAAGGAGGCTCAGGGGAGACCTTATCGCTCTCTACAACTGCCTGAAAGGAGGNTGTAGCCAGGT-- 3689

 136 GGGGGTCGGGCTCTGCTCCAGGGCA--CAGGGACAGGAGGAGAGGGCACGGCCTCAGGCTGGGCCAGGGC 203
     |||||||| |||| |||| :||||--||| ||||||| ||||||:||:||||||:|||| |||||||
3690 GGGGGTCGGCCTCTTCTCCCAGGCAACCAGCGACAGGACGAGAGGACATGGCCTCAAGCTGCGCCAGGGG 3759

 204 AGGGGCAGGGGGNACANCAGGAGGAATTTCTTCCTGGAAAGGGTGGTCAGGCNCTGGCAGGGGCTGCCCA 273
     ||| |||| | ||| ||||||:|||||||||| :||||||||||||:|:|| :||| | |||||||||
3760 AGGTTCAGGTTGGACATCAGGAAGAATTTCTTCACGGAAAGGGTGGTTAAGCATTGGAACGGGCTGCCCA 3829

 274 GGGAGG-GNTGGAGTNCCCANCCCTGGAGGTGTNCAAGGCAGNNCTGGNTGTGGCATTGNNTGCT----- 337
     ||||||-| |||||| ||| |||||||||||| |||:| | |||| :|||||:| ||||-----
3830 GGGAGGTGGTGGAGTCACCATCCCTGGAGGTGTTCAAGAAACGACTGGACGTGGCACTTAGTGCTATGGT 3899

 338 CTA------AGGNNGGCNTNGGGNNCNGGGT-GGACTCNATGGNCTNGGAGGGCTTTTCCA 391
     |||------| | ||: | || :|||-||||||| |||: || ||||| |||||||||
3900 CTAGTTGACANGGTGGTGTTCGGTCAAAGGTTGGACTCGATGATCTCGGAGGTCTTTTCCA 3960
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002464_LTR#LTR@unknown	254	472	CR1-J1_Pass	3723	3961	c	0.7668	3.4286	827

```
 254 TTGGCAAAGCCCTCCCAGCCCATGGAGCCCACCCTGTGCCCGATGCCCACCTTGTCCCCCAGCCCAGAGC 323
     |||| |||| ||||| || :||| |||:||| ||| || |||| ||||| |||| |:|| ||| |||
3961 TTGGAAAAGACCTCCGAGATCATCGAGTCCAACCTTTGACCGAACACCACCNTGTCAACTAGACCATAGC 3892

 324 ACTGAGTGCCACGGCCAGTCCTGCCTTGGGCACCTCCAGGGCTGGGCACTCCAA-ACCTCCCTGGGCAGC 392
     |||:||||||||| |||||| | :||||::|||||||||| ||| |||||| -||||||||||||||
3891 ACTAAGTGCCACGTCCAGTCGTTTCTTGAACACCTCCAGGGATGGTGACTCCACCACCTCCCTGGGCAGC 3822

 393 CCCTGCCAGTGCCTGNCCACCCTTTCCAGGNAGAAATTCCT-----TGTNC----------CNCCCTGGC 447
     || | |||:|||:|: |||||||||||: | ||||||||:|-----||| |----------: |||||||
3821 CCGTTCCAATGCTTAACCACCCTTTCCGTGAAGAAATTCTTCCTGATGTCCAACCTGAACCTCCCCTGGC 3752

 448 CCAGCCTGAGGCN----CCTCTNCTCCTG 472
     ||||:|||||| ----|||||  |||||
3751 GCAGCTTGAGGCCATGTCCTCTCGTCCTG 3723
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002563_LTR#LTR@unknown	56	107	ERV3-N2_MUn-LTR	191	241	d	0.7885	1.2857	257

```
  56 AGGAGAGACAGGTATCACCTGACTTAAGC-AACCAAAGAAATATTTCATACCA 107
     || |||||||||| --||||||||::||:|-|:|||||||::|||:|||||||
 191 AGCAGAGACAGGA--CACCTGACCCAAACTAGCCAAAGAGGTATTCCATACCA 241
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002563_LTR#LTR@unknown	353	426	HARB-9_ALy	311	388	c	0.7568	1.6667	214

```
 353 ATTGTTGTTATATCTAACTTGTGTAA-GTGTGTGTTATATTGTAGTTTTCTTTTAATTTTCTCTT----- 416
```

```
           ||||||||| |||| |||:||||:|||-:| |:|||| |  |||:|||||||||---::|||||-----
     388 ATTGTTGTAATATATAATTTGTATAATATTTATGTTTTCATGTAATTTTCTTTT---CCTCTCTTGTTTT 322

     417 -TTCTGTATAA 426
          -||:|||:|||
     321 ATTTTGTGTAA 311
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-68#Unknown	395	471	Mariner-1_Crp	303	374	d	0.7600	2.8000	247

```
     395 CTCTCCCGGGTCACTGCCCCAGCCGGGGC-AGGCAGGCCGTGACGGTGCAGGCGATGGTGAGACCGGAGC 463
          |||:|||||----||||||| ||||||||-||||||||| ||| ||| ||- ||| :||-| |:||| :|
     303 CTCCCCCGG----CTGCCCCGCCGGGGCGAGGCAGGCAGTGCCGGGGC-TGCGCCGG-GCGGCCGCGGG 366

     464 AGAGGCCG 471
          |||:||||
     367 AGAAGCCG 374
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002809_LTR#LTR@Gypsy	311	358	Mariner-1_Crp	303	347	c	0.8478	5.0000	225

```
     311 GCACCGTCACGGCCTGCCT-GCCCCGGCTGGGGCAGTGACCCGGGAGAG 358
          || ||| ||| ||||||||-||||||| |||||||----|||||:|||
     347 GCCCCGGCACTGCCTGCCTCGCCCCGGCGGGGGCAG----CCGGGGGAG 303
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-3_family-53#LINE@CR1	67	4027	CR1-J3_Pass	299	4263	d	0.7980	1.5241	23044

```
      67 GAACCCTCTAAAAAGGATGCAGCCACTCAGGCCTCTGGCTGCATAGACTGTTTGAGCCTGGANC--TNCT 134
         |||||||||:||||||||||||: |:::||||:||:|| |||:::::|| ||||:|||||:|--| |--| |
     299 GAACCCTCCAAAAAGGATGCGTCTGTCCAGACCCCTTCCTGTGCGGAGTGTTCGAGCTT--ATCAGTGGT 366

     135 ACCAGAGGACAGTNTGAGAAGCNCCTGCATACGATGTGAGCAGGTGAACGATTTGCTGNGTCTGGTGGCA 204
         :|||:||:|: | :|::::: ||||| |:|:|||||:||||||||||||:| || |||||||||
     367 TTCAGGGGGCGTTGCGGAGGAAACCTGCCTGCGGTGTGAACAGGTGAACGATCTCCTTTCGCTGGTGGCT 436

     205 GAGCTAAAGGAAGAGGTNGATAGGCTCAGAAACATAAGGGAGAGTGAAAGGGAAATTGACTGGTGGAGTC 274
         || || |||||:||:|| || ||:|| ||:|::|| ||:|||||||||||||||| ||||||||||||:
     437 GANCTTAAGGAGGAAGTAGAAAGACTAAGGAGTATTAGAGAAAGTGAAAGGGAAATAGACTGGTGGAGTT 506

     275 ACACCCTTTCNACTCCTAAG-GAAGCCCAGCAGGAGGTGGTGAAGCCCAGCCCCTCCTGCCATCAGGCAG 343
         ||||||||-| |::|:|:||-||||||||| |||| | ::| |:| :|| :: ||||||:||||||||||
     507 TCACCCTT-CCATCCTTGAGAGAAGCCCACCAGGNGTCAGAGGACTCCCATGCCTCCCGCCATCAGGCAG 575

     344 ANNGAACAGACCATANGGATGGGGANGAATGGAAACAGGTGCCTGGTCGTAGAGGCAAAAACAC---CCC 410
         ||: ||||| : :|||||::|: ||||||||||:||| ||| ||| :||||:|| ||:| ---::|
     576 NAGGAGGAGACCTAGTAGATGAAGGGGAATGGAAACGGGTCCCTNCTCGGGGAGGTAATAATAAAAATTC 645

     411 CTCTCGACCCCTTTCACCTGCCAGGGTGCCCTTAAAAAACAGGTATATGGCCCTGGACTCNGANAGTCTG 480
         |||:||||||||: |||||| || :||||| :| |:|:|||||: |||||||||::| || :|||| |
     646 CTCCCGACCCCCATCACCTNCCCAGGTGCCACTTCAGAATAGGTATGAGGCCCTGGATCCGGAGGGTCAG 715

     481 TTGGAGGACAGTCAGGAGGANGATCTNTCTACAAGNTCTTCTGGTTACCCCCAGTCTACCGGACGGGTTA 550
         ::|| |||| : |:||:: :|||| :|:: |:: :||:::||||: |:: :|||::|:|||||:|
     716 NCAGATGACATCGAAGAAAATAATCTGCCCGGAGAGCCTCCCAGTTATACTTCATCTGTCAGACGGATCA 785

     551 CNACTACAGGTAAGAGGAAAAAGAGAAGGGTTGTTGTAATCGGTGACTCCCTTCTGAGGGGAACTGAGGG 620
         | :|: | :|:| |::||:||:|||||| ||:|||:| |||||||||||||||||||:| |||||
     786 CTGCCTCTAGCATTAAAAAGAAAAGAAGGGTAGTCGTAGTAGGTGACTCCCTTCTGAGGGGAACAGAGGG 855

     621 CCCTNTATGTCGGCCAGACCCNTCCCACAGGGAAGTTTGCTGCCTTCCCGGGGCCAGGGTGAGGGATATT 690
         |||: ||||||||:|::|||| |||||||||||||:|:|:|||||||:|:|||||| |||||: ||||||:
     856 CCCCGTATGTCGACTGGACCCATCCCACAGGGAGGTCTGCTGCCTCCCTGGGGCCCGGGTACGGGATATC 925

     691 ACCAAAAGACTTCCTAANCTTATCCAACCCTCAGACTATTACCCACTGTTGGTTGTCCAGGTTGGAAGTG 760
         |||:|:||||||:|||:: || ||:||:||||| ||:||||||||||||:|:| |||||||:||| ||||
     926 ACCGAGAGACTCCCTGGGCTGATTCAGCCCTCTGATTATTACCCACTGCTGATNGTCCAGGCTGGCAGTG 995
```

```
 761 ATGACATTAATAAAAGGAGTACCAGAGTAATTAAAAAAGATTTCAAGGCACTGACCCGATCTCTTCANGG 830
     |:||  ::|:|  ||:|||||||||||:|:||||||||::||:||||:|||  |||: :|||  :   || | ||
 996 ACGAGGCTGANAAGAGGAGTACCAGGGCAATTAAAAGGGACTTCAGGGCTCTGGGTCGAGTGGTTGATGG 1065

 831 GACAGGAGCACAGGTAGTAATTGCCTCAGTTCCTGTGCTAGCTGGGATGAATGAGGAGAGGTTTAGGAAA 900
     ||||||||||||||||:||: |:  ||||||:|||  :| |:|| ||||:||||||| ||:|||  :||||:|
1066 GACAGGAGCACAGGTGGTGTTCTGCTCAGTCCCTTCGGTGGCAGGGACGAATGATGAAAGGAACAGGAGA 1135

 901 GCCCAGCTTACCAATAGGTGGCTTAGGGGATGGTGCTATCGTCAAAATTTTGGGTT-TTTGATCATGGNG 969
     :||||  |||:||||:|:||||||||:||| ||||||:|||: |::||||||||||–||||||||||| |
1136 ACCCACGTTATCAACAAGTGGCTTAAGGGCTGGTGCCATCAGCGGAATTTTGGGTTCTTTGATCATGGGG 1205

 970 CAAACTCNGTGTTGCCCAGTCTCGTCAAAGC-AGATGGGCTTCATTTATCTAGGAAGGGCAAAAGAACTG 1038
     ||| :|: ::| ::||:::|:||–|::|:|||–|||||||||:|||:|||||:  |||||||||||:|:|
1206 CAACTTTTACGGCACCTGGCCT-GCTAGAGCCAGATGGGCTCCATCTATCTGTCAAGGGCAAAAGGATTC 1274

1039 TAGCCCATAAGTTGGCAGGGTTGGTTAGGAGGGCTTTAAACTAGGTTTGAAGGGGGAAGGGACGGCAACT 1108
     ||||||||:|:|||||||||||:| :||::|||||||||||||||||||||||||||||||:  |  |||:
1275 TAGCCCATGAATTGGCAGGGCTNATTGAGAGGGCTTTAAACTAGGTTTGAAGGGGGAAGGGGATGNAACC 1344

1109 GGGCTCTCCAGAGATAGGCCTAAGGGCATAGAGCCCGAGTTGAGAATGAAATCAATGGCCCAGCTGAAGT 1178
     :|||||||||||||::|||::|||||::  :||||  ||||:::||:|||||||:::||||||||||||||
1345 AGGCTCTCCAGAGACGAGCCCGAGGGTGGTAAGCCAGAGTCAGGGGTGAAATCAGCAGCCCAGCTGAAGT 1414

1179 GCATGTACACCAATGCACGCAGTATGGGAAACAAACAAGAGGAGCTGGAAGCCATAGTGCAGCAGGAAAA 1248
     ||||  ||||||:||||||||||:|||| |||||||||:|||||||||||||||::||  ||||||||||:
1415 GCATNTACACTAATGCACGCAGCATGGGTAACAAACAGGAGGAGCTGGAAGCCACGGTNCAGCAGGAAAG 1484

1249 CTATGACATAGTTGCTGTCACAGAAACGTGGTGGGATGAATCACATGACTGGAGTGCTGCTATGGGGGGC 1318
     |||||||:||||:||:||::||||:|||||||||||||||| ||||:||||||||||||||  ||||: |||
1485 CTATGACGTAGTCGCCATCACGGAAACGTGGTGGGATGACTCACGTGACTGGAGTGCTGCAATGGATGGC 1554

1319 TACAAGCTCTTCAGAAAAGACAGGCAGGGAAGGAGAGGTGGAGGGGTGGCTTTATATGTTAGAGAGTCTC 1388
     ||||||||||||||:|||||||||||||:||||||:|:||:|||||||||||||||:|:||:|||:|||  |||
1555 TACAAGCTCTTCAGAAGAGACAGGCGAGGGAGAAGAGGTGGAGGGGTGGCTCTGTACATTAGGGAGGCTC 1624

1389 TTGACTCTGTTGAAGTTGAGGTCAGCAGTGACAAGGTTGAGTGCCTGTGGGCCAGAATCAGGGGCAAGGC 1458
     ||||| |:|: ||: |||||||||||:|:::|||:|||||||||||||||:||||: |||||||||  |||||
1625 TTGACGCCGCGGAGCTTGAGGTTAATGATGATAAGGTTGAGTGCCTATGGGTGAGAATCAGGGGAAGGC 1694

1459 CAACAAGGCTGACACCCTTGTGGGTGTCTGTTACAGACCGCCCAACCAGGATGATGAAGGGGATGAATTG 1528
     |||||||||:||||||||||||||||||:|||||:||||||||||||||||||||  ||:| ||||||||:
1695 CAACAAGGCCGACATCCTGGTGGGAGTCTGTTATAGACCACCCAACCAGGATGAAGAGGTGGATGAATTA 1764

1529 TTCTACAAGCAGCTGGCAGATGTCTCAAAATCTCCAGCCCTTGTTCTTGTGGGTGACTTTAACCTGCCAG 1598
     |||||:|||||||||  :|||||:|||  :|||  ||||||||||||||||||||  ||||||||||||:|
1765 TTCTATAAGCAGCTGGAGGATGTTTCANGATCACCAGCCCTTGTTCTTGTGGGAGACTTTAACCTGCCGG 1834

1599 ATATCTGCTGGGAGCTTCATACTGCAGAGAAGAGGCAGTCAAGGAGGTTCCTGGAGTGTATAGAGGACAA 1668
     |:|||||||||||:||: :|||  ||:||||||||||||||||:|:|||||||:|:|||||||||||||
1835 ACATCTGCTGGGAACTCAACACAGCGGAGAAGAGGCAGTCTAGGAGGTTCTTAGAGTGTGTGGAGGACAA 1904

1669 TTTCCT-TCATCAACTGGTAAATGAGCCTACCAGGGGGAAGGCCCTGCTAGACCTACTGTTTACAAACAG 1737
     :|||:|–|||–|:|||||||:|:::||||||||||||||  ::|||: ||||||||||:|||||:|||||||
1905 CTTCTTGTCA-CAGCTGGTGAGCGAGCCTACCAGGGGNGGGGCTNTGCTAGACCTGCTGTTTGCAAACAG 1973

1738 AGAGGGGCTGGTGGATGATGTAGTGGTTGGAGGCCGCCTGGGGCATAGTGACCATGAAATAATAGAATTT 1807
     |||:|||||||||: |||||:|||||:|||||||:|:|||||||||:|:||||||||||||| |:|||:||:
1974 AGAAGGGCTGGTGGGAGATGTGGTGGTCGGAGGCTGTCTGGGGCACAGCGACCATGAAATNACAGAGTTC 2043

1808 TCAGTCCTCAGGGATGTAAGGAGAGCCACCATTAAAACCTCTACTTTGGACTTCCGGAGAGCAGATTTTG 1877
     |||:| :||:| ||  ::|||||:| ||:|| :||||||:|| :|||||:|||||||||||:||||||:||||
2044 TCAATATTCGGTGAAACAAGGAGGGGCATCAACAAAACTTCCACACTGGACTTCCGGAGGGCAGACTTTG 2113

1878 GCCTATTCAAAAAACTGATTCAGAGCATACCCTGGGAAACAACCCTTAAAGGCAAGGGGGTCCAGGAGGG 1947
     ||||||||:::||  |||||||||:|||  :| ||:|||||:||:||||||||::|||:|||||:||||||||
2114 GCCTATTCAGGANACTGATTCGGAGAGTCCCTTGGGAAGCAGCCCTTAAAAACAAAGGGGCCCAGGAAGG 2183

1948 ATGGACATGTTTTAAGAGGGAGATTTTGAATGCACAGCAACAGGCTGTCCCAGTGTGCCGAAAGGCCAGC 2017
     ||||||||:::||:|||||::||:||:||:|||| |||||| |:||||:|||||||||||||||||||::|||
2184 NTGGACATACTTCAAGAAAGAAATCTTGAAGGCACAGGAGCAGGCCGTCCCTGTGTGCCGAAAGATGAGC 2253
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2018 CGGAGGGGAAGACGGCCAGCTTGGTTAAATAGGGAGATTCTGCAAGAAATCAGGGATAAAAAGAAAGTTT 2087
     |||| ||||||||||:||:||:||| |:|::||||||| ||::|||:||| | ||||| ||||||||::|| |
2254 CGGCGGGGAAGACGACCGGCCTGGNTGAGCAGGGAGCTTTCGCAGGAACTNAGGGAAAAAAAGAGGGTGT 2323

2088 ACAGACTATGGAAAAAAGGGCTGGCTACTTATGAAGAATTTACAGATAGAGCTAGGTCATGCAGGAAAAA 2157
     |: : || |||||||:|:|||| ||| |||:||:| |||| :|||| :|||: |:|||||||||||||:||:||
2324 ATCACCTTTGGAAAGAGGGGCAGGCAACTCAGGAAGTGTTTAAGGATGTCGTTAGGTCATGCAGAAAGAA 2393

2158 AATTAGGGAAAGAAAAGTGGAATTTGAAGTTAATTTGGCTATTTCAGTTAGGGATAACAAAAAGTCCTTT 2227
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2228 TATAAATACATTAATAACAAAAGGAGGGGCAAGGAAAACCTCCATTCTCTGTTGGACTTGGAGGGAAATA 2297
     |||||||||||||||||:||||||||||||||||||||||||||||||||||:|:|||||| :||:|||:|||
2464 TATAAATACATTAATAGCAAAAGGAGGGGCAAGGAAAACCTCCATTCTTTATTGGACGCGGGGGGGAATN 2533

2298 TAGTTAAGGAAGATGAGGAGAAGGCTGAGGTACTTAACACCTACTTTGCCTCAGTTTTCACCAGTAAGAC 2367
     |||| | :||||||||||:||||| ||||||||||||||||| |||||||||||||||||||| |||||||||
2534 TAGTNACCAAAGATGAGGAAAAGGCNGAGGTACTTAACACCTTCTTTGCCTCAGTTTTCAACAGTAAGAC 2603

2368 AGGTGGCCCTCAAGACAACTGGCCTCTGGAGCTGGTGGACAGGGAGAGGGAGCTGAATACCCCTCCTGTA 2437
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2604 AGGTCGTCCTCAGGACAACTGGCCTCCTGAGCTGGTAGACGGGGACGGGGAGCAGAATAGNCCCCCTGTA 2673

2438 TTCCAGGAGGAAATAGTGACCGACTTACTGAGCCAGCTGGATCCTAACAAGTCTATGGGACCAGATGGGA 2507
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2674 ATCCAGGAGGAAGCAGTTAGTGACCTGCTGAGCCACTTAGATGCTCACAAGTCTATGGGACCAGATGGGA 2743

2508 TCCATCCCAGGGTGATGAAGGAGCTGGCAGAAGAGCTTGCCAAACCGCTCTCCATCATCTTCCAACAGTC 2577
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2578 CTGGCTCTCTGGGGAGGTCCCAGATGATTGGAGGTTGGCGAATGTCACCCCAATCCACAAAAAGGGCTGC 2647
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2814 CTGGCTCACCGGGGAGGTCCCAGATGACTGGAAGCTGGCCAGTGTGACGCCCATCCACAAGAAGGGCCGG 2883

2648 AAGCAGGACCCTGGCAACTACAGGCCTGTCAGCCTGACCTCCGTGCCTGGCAGGGTTATGGAGCAGTTCA 2717
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2884 AAGGAGGATCCGGGAAACTACAGGCCTGTCAGCCTGACCTCGGTGCCCGGCAAGGTTATGGAACAGATCA 2953

2718 TCCTGAGTGCAATCACACAGCACCTTCAGGGTGGACAAGGGATTAGACCCAGCCAGCATGGGTTTAGGAG 2787
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2788 GGGCAGGTCCTGTCTGACCAACCTGATCTCTTTTTTACGATCAGGTGACCCACCTGGTGGATGAGGGGAAG 2857
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3024 GGGCAGGTCCTGCCTGACCAACCTGATCTCCTTTTATGACCAGGTGACCCGCCTGGTGGATGNGGGAAAG 3093

2858 GCTGTGGATGTGGTCTATCTGGACTTCAGCAAGGCCTTTGACACTGTCTCCCATAATATACTCCTGGAAA 2927
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3094 GCTGTGGATGTTGTCTACCTGGACTTCAGCAAAGCCTTTGACACCGTCTCCCACAGCACACTCCTGGAAA 3163

2928 AGCTGGTAGCCCATGGCCTGGACAAGTGTACCCTCTCCTGGATTAAGAGCTGGCTGGAGGGTCGGGCCCA 2997
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2998 GAGAGTGCTGGTGAACGGAGCTGCATCCAGCTGGCGGCCGGTCACTAGTGGTGTTCCCCAGGGGTCTGTA 3067
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3068 TTGGGTCCAGTCCTGTTTAACATCTTTATTGATGATTAGATGAGGGGATTGAGTCCATCATCAGCAAAT 3137
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3304 TTGGGCCCAGTCCTGTTTAATATCTTTATTGATGATCTGGATGAGGGGATTGAGTCTACCATTAGCAAAT 3373

3138 TTGCTGATGACACCAAGTTGGGAGGGAGTGTCGACCTGCTGGAAGGCAGGAGGGCTCTGCAGAGGGATCT 3207
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3374 TTGCAGATGACACCAAGCTGGGNGCGAGTGTCGATCTGCTGGAGGGTAGGAGGGCTCTGCAGAGGGACCT 3443

3208 GGATAGACTTGAGAGATGGGCTGATTCCAATGGGATGAAGTTCAATAAGGCCAAGTGCCGGGTCCTGCAC 3277
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3444 GGACAGGCTGGATNGATGGGCCGAGTCCAACGATATGAGGTTTAACAAGACCAAGTGCCGGGTCCTGCAC 3513

3278 TTTGGCCACAACAACCCCCTGCAGCGCTACAGGCTGGGCACAGAGTGGCTGGAGAGCAGCCAGGCAGAAA 3347
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      ||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||| |||:||||||||||||
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3348 GGGACCTTGGAGTACTAATTGACAGGAAGCTCAACATGAGCCAACAGTGTGCCCAGGTGGCCAAGAAGGC 3417
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3584 GGGACCTGGGGGTGCTGGTCGACAGCNGGCTGAACATGAGCCAGCAGTGTGCCCAGGTGGCCAAGAAGGC 3653

3418 CAATGGGATCCTGGCCTGTATCAAAAATAGCGTGGCCAGCAGGACCAGGGAAGTGATCCTTCCCCTGTAC 3487
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3488 TCTGCATTGGTGAGGCCACACCTTGAGTACTGTGTTCAGTTCTGGGCCCCTCAGTTCAGAAAGGATATTG 3557
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3558 AGGTGCTGGAGCGGGTCCAGAGAAGAGCAACAAGGCTGGTGAAGGGACTGGAGCACAAGTCCTATGGGGA 3627
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3628 GAGGCTGAGGGAGCTGGGGTTGTTTAGCCTGGAGAAGAGGAGGCTCAGAGGTGACCTCATCACTGTCTAG 3697
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3864 GCGGCTGAGGGAGCTGGGGTTGTTTAGCCTGGAGAAAAGGAGGCTCAGGGGAGACCTTATCACTCTCTAC 3933

3698 AACTACCTGAAGGGAAGTTCTAGCCAGGTGGGGGTTGGTCTCTTCTCCCAGGCACTCAGCAATAGGACAA 3767
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3768 GGGGGCACGGGCTTAAGCTCTGCCAGGGGAAATTTAAGTTGGATATCAGAAAAAAATTCTTTNCAGAGAG 3837
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4004 GAGGACACAGTCTTAAGCTGCGCCAGGGGAGGTTTAGGTTGGACATTAGGAAGAANTTCTTCACAGAAAG 4073

3838 AGTAATCAGGCATTGGAATGGGCTGCCCAGAGAGGTGGTGGATTCACCATCCCTAGAGATTTTTAAACNC 3907
      :||:||::||||||||||||||||||||||||||||:|||||||||| |||||:|||||:|||:| |||||:
4074 GGTGATTGGGCATTGGAATGGGCTGCCCAGGGAGGTGGTGGAGTCACCGTCCCTGGAGGTGTTTAAGGAA 4143

3908 AGATTGGACGTGGCGCTGAGTGCCATGATCTAGTAAATGGACTGGAGTTGGACCAAGGGTTGGACTCGAT 3977
      |||:|||||||||:|| |||||||||:||||| :|::::| ||| ||| |::|| :|||||||||||||||
4144 AGACTGGACGTGGCACTCAGTGCCATGGTCTAGTTGACAAGGTGGTGTTNGGTCATAGGTTGGACTCGAT 4213

3978 GATCTTGGAGGTCTTTTCCAACCCAATCGATTCTATGATTCTATGATTCT 4027
      |||||::||||||||||||||:|:|:|||||||:||||||:||||||||
4214 GATCTCAGAGGTCTTTTCCAACCTAGTTGATTCTGTGATTCTGTGATTCT 4263
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-113#LINE@CR1	120	3167	CR1-J3_Pass	76	3113	d	0.7718	1.6000	15733

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120 GGAGCGCGGCGAACAGGAGCG--CAAACAGGGGCGTGGCACGTCAGTGAGGGCGTGGCACGGCAGTTTCG 187
     ||||||||||||||||||||||--|||||:||||||:||||   ||-------------||:||||||||-||
 76 GGAGCGCGGCGAACAGGAGCGGGCAAACGGGGGCGCGGCAGCTC-------------GCGCGGCAGTT-CG 132

188 CACAGGCAGGGCNAACAGGCAGGGCANAAG-------CCTA-------GGTATTTN---TGNNG--CNTT 238
     |:||||||||||  |:|||||||||:     ||-------|||:-------||| ||| ---|| |--| :
133 CGCAGGCAGGGCAAGCAGGCAGGGTTGCAGGNTTCCTCCTGCTAGTAGGGTTTTTAGTTTGTTGTTCGCG 202

239 NTNTNTNTGTTTGTTTGTTTNTCTTTTCTACCTTTCCCCACAGCTCAAGGCAGTCATGCCTCCCAAAAAA 308
     | | | |||| ||| ||| |--||| :::|||||:-----------||:||| ||| :|:::|| | :|
203 GTGTTTCTGTTGGTTGGTTGGT--TTTGGGTTTTTCT-----------GGTAGTAATGGTTTTTACACGA 259

309 ATGAAAGCTGTTGCTCCTGTTACCAGTAGAGGGGTGTCAATACAGACAGAACCCTCTAAAAAGGATGCAG 378
     :|||||:|||------| ||||---||| |:| ||:|   | ||||::||||||||:|||||||||||||:
260 TCGAAAACTG------CAGTTA---GTACAAGTGTATGTAACCAGATGGAACCCTCCAAAAAGGATGCGT 320

379 CCACTCAGGCCTCTGGCTGCATAGACTGTTTGAGCCTGGACC--TGCTACCAGAGGACAGTGTGAGAAGC 446
     |:::::|||:||:|:|   ||||:::|| ||||:|||||:|--:|:--|| | :|||:|||:|: ||:|:::::
321 CTGTCCAGACCCCTTCCTGTGCGGAGTGTTCGAGCTT--ATCAGTGGTTTCAGGGGGCGTTGCGGAGGAA 388

447 ACCTGCATACGATGTGAGCAGGTGAACGATTTGCTGTGTCTGGTGGCAGAGCTAAAGGAAGAGGTGGAAA 516
     ||||||  |:||:|||||||:||||||||||||||||||||:| || |  |||||||| || || |||||:||:|||||
389 ACCTGCCTGCGGTGTGAACAGGTGAACGATCTCCTTTCGCTGGTGGCTGANCTTAAGGAGGAAGTAGAAA 458

517 GGCTCAGAAACATAAGGGAGAGTGAAAGGGAAATTGACTGGTGGAGTCACACCCTTTCNACTCCTAAG-G 585
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        |:|| ||:|::|| ||:||:|||||||||||||||| |||||||||||::  ||||||||-|  |::|:|:||-|
 459 GACTAAGGAGTATTAGAGAAAGTGAAAGGGAAATAGACTGGTGGAGTTTCACCCTT-CCATCCTTGAGAG 527

 586 AAGCCCAGCAGGAGGTGGTGAAGCCCAGCCCCTCCTGCCATCAGGCAGANAGAACAGACCATATGGATGG 655
     |||||||  ||||  |  ::|  |:| :|| ::  ||||:||||||||||  :||:  |||||  :|:||||:
 528 AAGCCCACCAGGNGTCAGAGGACTCCCATGCCTCCCGCCATCAGGCAGNAGGAGGAGACCTAGTAGATGA 597

 656 GGANGAATGGAAACAGGTGCCTGGTCGTAGAGGCAAAAACAC---CCCCTCTCGACCCCTTTCACCTGCC 722
     :|:  ||||||||||||:||| |||  ||| :|||||:|| ||:| ---::||||:|||||||: ||||||  ||
 598 AGGGGAATGGAAACGGGTCCCTNCTCGGGGAGGTAATAATAAAAATTCCTCCCGACCCCCATCACCTNCC 667

 723 AGGGTGCCCTTAAAAAACAGGTATATGGCCCTGGACTCAGACAGTCTGTTGGAGGACAGTCAGGAGGAAG 792
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 793 ATCTGTCTACAAGGTCTTCTGGTTACCCCCAGTCTACCGGACGGGTTACAACTACAGGTAAGAGGAAAAA 862
     |||||:|:: |::|:||:|:||||: |:: :||||::|:|||||:|:|| :|: | :|:|  |::||:||
 738 ATCTGCCCGGAGAGCCTCCCAGTTATACTTCATCTGTCAGACGGATCACTGCCTCTAGCATTAAAAAGAA 807

 863 GAGAAGGGTTGTTGTAATCGGTGACTCCCTTCTGAGGGGAACTGAGGGCCCTATATGTCGGCCAGACCCA 932
     :|||||||| ||:|||:| ||||||||||||||||||||||||||||||:: ||||||:||:|||||||
 808 AAGAAGGGTAGTCGTAGTAGGTGACTCCCTTCTGAGGGGAACAGAGGGCCCCGTATGTCGACTGGACCCA 877

 933 TCCCACAGGGAAGTTTGCTGCCTTCCCGGGGCCAGGGTGAGGGATATTACCAAAAGACTTCCTAAGCTTA 1002
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1003 TCCAACCCTCAGACTATTACCCACTGTTGGTTGTCCAGGTTGGAAGTGATGACATTAATAAAAGGAGTAC 1072
     |:||:||||| ||:|||||||||||||:||:| |||||||:||| ||||||:|| ::|:| ||:||||||||
 948 TTCAGCCCTCTGATTATTACCCACTGCTGATNGTCCAGGCTGGCAGTGACGAGGCTGANAAGAGGAGTAC 1017

1073 CAGGGTAATTAAAAAAGATTTNAAGGCACTGACCCGATCACTTCATGGGACAGGAGCACAGGTAGTAATT 1142
     |||||:||||||||::||:|| |:||| |||: :||| :: || |||||||||||||||||||||:||: |:
1018 CAGGGCAATTAAAAGGGACTTCAGGGCTCTGGGTCGAGTGGTTGATGGGACAGGAGCACAGGTGGTGTTC 1087

1143 GCCTCAGTTCCTGTGCTAGCTGGGATGAATGAGGAGAGGTTTAGGAAAGCCCAGCTTACCAATAGGTGGC 1212
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1088 TGCTCAGTCCCTTCGGTGGCAGGGACGAATGATGAAAGGAACAGGAGAACCCACGTTATCAACAAGTGGC 1157

1213 TTAGGGGATGGTGCTATCGTCAAAATTTTGGGTT-TTTGATCATGGGGCAAACTCCGTGTTGCCCAGTCT 1281
     |||:|||  |||||||:|||: ::|||||||||- |||||||||||||  :|::::| ::||::|:||
1158 TTAAGGGCTGGTGCCATCAGCGGAATTTTGGGTTCTTTGATCATGGGGCAACTTTTACGGCACCTGGCCT 1227

1282 CGTCAAACCAGATGGGCTTCATTTATCTAGGAAGGGCAAAAGAACTGTAGCCCATAAGTTGGCAGGGTTG 1351
      |  :|:||||||||||||| :||||||||||::  |||||||||||:|:|  |||||||:|:|||||||||:|
1228 GCTAGAGCCAGATGGGCTCCATCTATCTGTCAAGGGCAAAAGGATTCTAGCCCATGAATTGGCAGGGCTN 1297

1352 GTTAGGAGGGCTTTAAACTAGGTTTGAAGGGGGAAGGGACGGCAACTGGGCTCTCCAGAGATAAGCCTAA 1421
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1422 GGGCGTAGAGCCCGAGTTGAGAATGAAATCAATGGCCCAGCTGAAGTGCATGTACACCAATGCACGCAGT 1491
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1492 ATGGGAAACAAACAAGAGGAGCTGGAAGCCATAGTGCAGCAGGAAAACTATGACATAGTTGCTGTCACAG 1561
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1438 ATGGGTAACAAACAGGAGGAGCTGGAAGCCACGGTNCAGCAGGAAAGCTATGACGTAGTCGCCATCACGG 1507

1562 AAACGTGGTGGGATGACTCACATGACTGGAGTGCTGCTATGGGGGGCTACAAGCTCTTCAGAAAGGACAG 1631
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1632 GCAGGGAAGGAGAGGTGGAGGGGTGGCTTTATATGTTAGAGAGTCTCTTGACTCTGTTGAAGTTGAGGTC 1701
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1578 GCGAGGGAGAAGAGGTGGAGGGGTGGCTCTGTACATTAGGGAGGCTCTTGACGCCGCGGAGCTTGAGGTT 1647

1702 AGCAGTGACAAGGTTGAGTGCCTGTGGGCCAGAATCAGGGGGNAAGGCCAACAAGGCTGACACCCTTGTGG 1771
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1648 AATGATGATAAGGTTGAGTGCCTATGGGTGAGAATCAGGGGGAAGGCCAACAAGGCCGACATCCTGGTGG 1717

1772 GTGTCTGTTACAGACCGCCCAACCAGGATGATGAAGGNGATGAATTNTTCTACAAGCAGCTGGCAGATGT 1841
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1718 GAGTCTGTTATAGACCACCCAACCAGGATGAAGAGGTGGATGAATTATTCTATAAGCAGCTGGAGGATGT 1787

1842 CTCAAAATCTCCAGCCCTTGTTCTTGTGGGTGACTTTAACCTGCCAGATATCTGCTGGGAGCTTCATACT 1911
     :|||  :|||  ||||||||||||||||||||||||| ||||||||||||:||:||||||||||:||: |:||
1788 TTCANGATCACCAGCCCTTGTTCTTGTGGGAGACTTTAACCTGCCGGACATCTGCTGGGAACTCAACACA 1857

1912 GCAGAGAAGAGGCAGTCAAGGAGGTTCCTGGAGTGTATAGAGGACAATTTCCT-TCATCAACTGGTAAAT 1980
     ||:|||||||||||| ||||||||||:|:|||||:|:||||||||:|||:|-|||-||:|||||:|::
1858 GCGGAGAAGAGGCAGTCTAGGAGGTTCTTAGAGTGTGTGGAGGACAACTTCTTGTCA-CAGCTGGTGAGC 1926

1981 GAGCCTACCAGGGGTAAGGCCCTGCTAGACCTACTGTTTACAAACAGAGAGGGGCTGGTGGATGATGTAG 2050
     |||||||||||||| ::||: |||||||||:|||||:|||||||||||:||||||||| ||||:|
1927 GAGCCTACCAGGGGNGGGGCTNTGCTAGACCTGCTGTTTGCAAACAGAGAAGGGCTGGTGGGAGATGTGG 1996

2051 TGGTTGGAGGCCGCCTGGGGCATAGTGACCATGAAATAATAGAATTTTCAGTCCTCAGGGATGTAAGGAG 2120
     ||||:|||||||:|:|||||||||:||:||||||||||| |:|||:|:|||:| :||:| || ::|||||
1997 TGGTCGGAGGCTGTCTGGGGCACAGCGACCATGAAATNACAGAGTTCTCAATATTCGGTGAAACAAGGAG 2066

2121 AGCCACCATTAAAACCTCTACTCTGGACTTCCGGAGGGCAGATTTTGGCCTATTCAAAAAACTGATTCAG 2190
     :|  ||:|| :|||||:||:|| ||||||||||||||||||:||||||||||||::| ||||||||:|
2067 GGGCATCAACAAAACTTCCACACTGGACTTCCGGAGGGCAGACTTTGGCCTATTCAGGANACTGATTCGG 2136

2191 AGCATACCCTGGGAAACAACCCTTAAAGGCAAGGGGGTCCAGGAGGGATGGACATGTTTTAAGAAGGAAA 2260
     || :| ||:|||:||:||||::||:||||||||||:|| ||||||:|| ||||||::||:|||||:||||
2137 AGAGTCCCTTGGGAAGCAGCCCTTAAAAACAAAGGGGCCCAGGAAGGNTGGACATACTTCAAGAAAGAAA 2206

2261 TTTTGANTGCACAGCAACAGGCTGTCCCAGTGTGCCGAAAGGCCAGCCGGAGGGGAAGACGGCCAGCTTG 2330
     |:||||  |||||| |:|||||:||||| ||||||||||||:: |||||| |||||||||:|:||:||:||
2207 TCTTGAAGGCACAGGAGCAGGCCGTCCCTGTGTGCCGAAAGATGAGCCGGCGGGGAAGACGACCGGCCTG 2276

2331 GTTAAATAGGGAGATTCTGNAAGAAATCAGGGATAAAAAGAAAGTTTACAGACTATGGAAAAAAGGGCTG 2400
     |  |:|::|||||| ||:: |:||| | ||||| ||||||::|| ||: : || |||||||:|:|||| |
2277 GNTGAGCAGGGAGCTTTCGCAGGAACTNAGGGAAAAAAAGAGGGTGTATCACCTTTGGAAAGAGGGGCAG 2346

2401 GCTACTTATGAAGAATTTACAGATAGAGCTAGGTCATGCAGGAAAAAAATTAGGGAAAGAAAAGTGGAAT 2470
     ||  |||:|| ||||  :||||  :|||| :|||: |:||||||||||||||||||:|:||||||||:||::  |:|
2347 GCAACTCAGGAAGTGTTTAAGGATGTCGTTAGGTCATGCAGAAAGAAAATTAGAGAGGCGAAAGCTCAGT 2416

2471 TTGAAGTTAATTTGGCTANTTCAGTTAGGGATAACAAAAAGTCCTTTTATAAATACATTAATAACAAAAG 2540
     | |||| |||||:||||:| ||| || |:||||||:||||||| :|||||||||||||||||||:||||||
2417 TAGAACTTAATCTGGCCACTTCTGTAAAGGATAATAAAAAGTGTTTTTATAAATACATTAATAGCAAAAG 2486

2541 GAGGGGCAAGGAAAACCTCCATTCTCTGTTGGACTTGGAGGGAAATATAGTTAAGGAAGATGAGGAGAAG 2610
     ||||||||||||||||||||||||||:|:|||||| :||:|||:||| |||| |  :|||||||||||:|||
2487 GAGGGGCAAGGAAAACCTCCATTCTTTATTGGACGCGGGGGGGAATNTAGTNACCAAAGATGAGGAAAAG 2556

2611 GCTGAGGTACTTAACACCTACTTTGCCTCAGTTTTCACCAGTAAGACAGGTGGCCCTCAAGACAACTGGC 2680
     ||  |||||||||||||| ||||||||||||||||||| ||||||||||||||:||||||:|||||||||||
2557 GCNGAGGTACTTAACACCTTCTTTGCCTCAGTTTTCAACAGTAAGACAGGTCGTCCTCAGGACAACTGGC 2626

2681 CTCTGGAGCTGGTNGACAGGGAGAGGGAGCTGAATANCCCTCCTGTATTCCAGGAGGAAATAGTGACNGA 2750
     ||||:  |||||||| |||:|||| :||||| ||||||   ||:||||| |||||||||||||::||| |  ||
2627 CTCCTGAGCTGGTAGACGGGGACGGGGAGCAGAATAGNCCCCCTGTAATCCAGGAGGAAGCAGTTAGTGA 2696

2751 CTTACTGAGCCAGCTGGATCCTAACAAGTCTATGGGACCAGATGGGATCCATCCCAGGGTGATGANGGAG 2820
     |:|:|||||||| :|:||| || ||||||||||||||||||||||||||||||:|||||||||| |||||
2697 CCTGCTGAGCCACTTAGATGCTCACAAGTCTATGGGACCAGATGGGATCCATCCTAGGGTGATGAGGGAG 2766

2821 CTGGCAGAAGAGCTTGCCAAACCGCTCTCCATCATCTTCCAACAGTCCTGGCTCTCTGGGGAGGTCCCAG 2890
     |||||:|||||||| ||||||||||||||||||||:| :|| |||||||||||||||:|||||||||||||
2767 CTGGCGGAAGAGCTCGCCAAGCCGCTCTCCATCATTTATCATCAGTCCTGGCTCACCGGGGAGGTCCCAG 2836

2891 ATGATTGGAGGTTGGCGAATGTCACCCCAATCCACAAAAAGGGCTGCAAGCAGGACCCTGGCAACTACAG 2960
     ||||:|||||:|:||||  |:||| || || |||||||||:||||||:| ||| ||||:||| || ||||||||
2837 ATGACTGGAAGCTGGCCAGTGTGACGCCCATCCACAAGAAGGGCCGGAAGGAGGATCCGGGAAACTACAG 2906

2961 GCCTGTCAGCCTGACCTCCGTGCCTGGCAGGGTTATGGAGCAGTTCATCCTGAGTGCAATCACACAGCAC 3030
     ||||||||||||||||||| |||||:|||||:||||||||||||||:||| |||||:||||||||:|||||||
2907 GCCTGTCAGCCTGACCTCGGTGCCCGGCAAGGTTATGGAACAGATCATCTTGAGTGCGATCACACGGCAC 2976

3031 CTTCAGGNTGGACAAGGGATTAGACCCAGCCAGCATGGGTTTAGGAGGGGCAGGTCCTGTCTGACCAACC 3100
     ||  ||||| :||  |::|||||:|||||||||||||||||||||||||||||||||||||:|||||||||||
2977 CTACAGGACGGCCGGGGGATCAGACCCAGCCAGCATGGGTTTAGGAGGGGCAGGTCCTGCCTGACCAACC 3046
```

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3101 TGATCTCTTTTTACGATCAGGTGACCCACCTGGTGGATGAGGGGAAGGCTGTGGATGTGGTCTATCT 3167
     ||||||||:|||||:||:||||||||||:|||||||||| |||:|||||||||||| |||||:||
3047 TGATCTCCTTTTATGACCAGGTGACCCGCCTGGTGGATGNGGGAAAGGCTGTGGATGTTGTCTACCT 3113
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-4174#Unknown	1	2066	CR1-J3_Pass	76	2107	c	0.7456	1.5309	9442

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   1 CTGCNCTCCGGAAGTCCANAGTAGAGGTTTTAATGGTGGCTCTCCTTACATCCCTGAGGACTGAAAATTC 70
     |||| ||||||||||||||  ||:||:|||||: ||:|| |:|||||||:: || |:||: |:|||:||:||
2107 CTGCCCTCCGGAAGTCCAGTGTGGAAGTTTTGTTGATGCCCCTCCTTGTTTCACCGAATATTGAGAACTC 2038

  71 TATTATTTCATGGTCACTATGCCCCAGGCGGCCTCCAACCACTACATCATCCACCAGCCCCTCTCTGTTT 140
     |:| |||||||||||||:||:|||||||||:|:|||||:|||||:||||| :|||||||||||:|||||||||
2037 TGTNATTTCATGGTCGCTGTGCCCCAGACAGCCTCCGACCACCACATCTCCCACCAGCCCTTCTCTGTTT 1968

 141 GTAAACAGTAGGTCTAGCAGGGCCTTNCCCCTGGTAGGCTCATTTACCAGTTGATGA-AGGAAATTGTCC 209
     |:|||||||:|||||||||||| :|||:: |||||||||||||||||::|:|||||:||-|||-|:|||:||||||
1967 GCAAACAGCAGGTCTAGCANAGCCCCNCCCCTGGTAGGCTCGCTCACCAGCTG-TGACAAGAAGTTGTCC 1899

 210 TCTATACACTCCAGGAACCTCCTTGACTGCCTCTTCTCTGCAGTATGAAGCTCCCAGCAGATATCTGGCA 279
     ||:|:||||||:|:|||||||| |||||||||||||||:|| ||:| :||:||||||||||||||:||:||||
1898 TCCACACACTCTAAGAACCTCCTAGACTGCCTCTTCTCCGCTGTGTTGAGTTCCCAGCAGATGTCCGGCA 1829

 280 GGTTAAAGTCACCCACAAGAACAAGGGCTGGAGATTTTGAGACATCTGCCAGCTGCTTGTAGAACAATTC 349
     ||||||||| ||||||||||||||||||||||| |||: ||:||||: ||||||||||:|||||:|||||
1828 GGTTAAAGTCTCCCACAAGAACAAGGGCTGGTGATCNTGAAACATCCTCCAGCTGCTTATAGAATAATTC 1759

 350 ATCCCCTTCATCATCCTGGTTGGGCGGTCTGTAACAGACACCCACAAGGGTGTCAGCCTTGTTGGCCTTG 419
     |||| |:||| |||||||||||||||||||:|||||:|||||||| ||||| |||:||||:||||||||||||
1758 ATCCACCTCTTCATCCTGGTTGGGTGGTCTATAACAGACTCCCACCAGGATGTCGGCCTTGTTGGCCTTC 1689

 420 CCCCTGATTCTGGCCCACAGGCACTCAACCTTGTCACTGCTGACCTCAACTTCAACAGAGTCAAGAGACT 489
     |||||||||||| :|||||:|||||||||||||||:|||::::|:|||||||| :|| :|:| |||||||| ||
1688 CCCCTGATTCTCACCCATAGGCACTCAACCTTATCATCATTAACCTCAAGCTCCGCGGCGTCAAGAGCCT 1619

 490 CTCTAACATATAAAGCCACCCCTCCACCTCTCCTTCCCTGCCTGTCTTTTCTGAAGAGCTTGTAGCCCCC 559
     |:||||::||:|:|||||||||||||||||||||:||:||::||||||||:|||||||||||||||||| :|
1618 CCCTAATGTACAGAGCCACCCCTCCACCTCTTCTCCCTCGCCTGTCTCTTCTGAAGAGCTTGTAGCCATC 1549

 560 CATAGCAGCACTCCAGTCATGTGATTCATCCCACCACGTTTCTGTGACAGCAACTATGTCATAGTTTTCC 629
     ||| |||||||||||||:||||  |||||||||||||||||:||||::||:|||||:||||||||:||||
1548 CATTGCAGCACTCCAGTCACGTGAGTCATCCCACCACGTTTCCGTGATGGCGACTACGTCATAGCTTTCC 1479

 630 TGCTGCACTATGGCTTCCAGCTCCTCTTGTTTGTTTCCCATACTGCGTGCATTGGTGTACATGCACTTCA 699
     |||||| ||:::||||||||||||||:||||||| |||||:|||||||||||||:||||| ||||||||||
1478 TGCTGNACCGTGGCTTCCAGCTCCTCCTGTTTGTTACCCATGCTGCGTGCATTAGTGTANATGCACTTCA 1409

 700 GCTGGGCCATTGATTTCATTCTCAACTCGGGCTCTATGCCCTTAGGCCTATCTCTGGAGAGCCCAGTTGC 769
     |||||||:::||||||||::|::::|||| ||||: ::|||::||::|::|||||||||||||:::||| |
1408 GCTGGGCTGCTGATTTCACCCCTGACTCTGGCTTACCACCCTCGGGCTCGTCTCTGGAGAGCCTGGTTNC 1339

 770 CGTCCCTTCCCCCTTCAAACCTAGTTTAAAGCCCTCCTAACCAACCCTGCCAACTTATGGGCTACAGTTC 839
     :||||||||||||||||||||||||||||||||||||::||: |:|||||||||:|:||||||||| |:|:|
1338 ATCCCCTTCCCCCTTCAAACCTAGTTTAAAGCCCTCTCAATNAGCCCTGCCAATTCATGGGCTAGAATCC 1269

 840 TTTTGCCCTTCCTAGATAAATGAAGCCCATCTGNTTTGACGAGACTGGGCAACACGGAGTTTGCNCCATG 909
     |||||||||| :|||||:||:|:||||||||||| :|: | ||:|::||:: |:::::|: |||| |||||
1268 TTTTGCCCTTGACAGATAGATGGAGCCCATCTGGCTCTAGCAGGCCAGGTGCCGTAAAAGTTGCCCCATG 1199

 910 ATCAAAAAACCCAAAATTTTGACGATAGCACCATCCCCTAAGCCACCTATTGGTAAGCTGGGCTTTCCTA 979
     ||||||:|||||||||||::| :|||:|||||| |||:|||||||||:|:||||:||| ||||:|:||||:
1198 ATCAAAGAACCCAAAATTCCGCTGATGGCACCAGCCCTTAAGCCACTTGTTGATAACGTGGGTTCTCCTG 1129

 980 AACCTCTCCTCATTCATCCCAGCTAGCACAGGAACTGAGGCAATTACTACCTGTGCTCCTGTCCCCTGAA 1049
      |||:|| ||||||:||||  ||:| |: |||:||||||  :| :|||:||||||||||||||||| | ||
1128 TTCCTTTCATCATTCGTCCCTGCCACCGAAGGGACTGAGCAGAACACCACCTGTGCTCCTGTCCCATCAA 1059

1050 GAGATCGGGTCAGTGCCTTGAAATCTTTTTTAATTACTCTGGTACTCCTTTTATTAATGTCATCACTTCC 1119
       : |||: :|||| |||:|||||:||::||||||||:|:||||||||||||||:|| |:|:: ||:|||||| ||
1058 CCACTCGACCCAGAGCCCTGAAGTCCCTTTTAATTGCCCTGGTACTCCTCTTNTCAGCCTCGTCACTGCC 989
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1120 AACCTGGACAACCAACAGTGGGTAATAGTCTGAGGGTTGGATAAGTTTAGGAAGTCTTTTGGTAATATCC 1189
     |:|||||||| |:||:||||||||||||||:|| |||||:||:|| ||:::|||:|||||:|:|||:||||||
 988 AGCCTGGACNATCAGCAGTGGGTAATAATCAGAGGGCTGAATCAGCCCAGGGAGTCTCTCGGTGATATCC 919

1190 CTCACCCTGGCCCCGGGAAGGCAGCAAACTTCCCTGTGGGANGGGTCTGGCCGACATATAGGGCCCTCAG 1259
     | :||||| |||||:||:|||||||||:||:|||||||||| |||||::|:|||||||::|||||||| |
 918 CGTACCCGGGCCCCAGGGAGGCAGCAGACCTCCCTGTGGGATGGGTCCAGTCGACATACGGGGCCCTCTG 849

1260 TTCCCCTCAGAAGGGAGTCACCGATTACAACAACCCTTCTCTTTTTCCTCTTACCTGTAGTCGTAACCCG 1329
     |||||||||||||||||||||| |:|||:|| |||||||||:||:||:| |:|: | :|: ||:|:|||
 848 TTCCCCTCAGAAGGGAGTCACCTACTACGACTACCCTTCTTTTCTTTTTAATGCTAGAGGCAGTGATCCG 779

1330 TCCGGTAGACTGGGGGTAACCAGAAGATCTTGTAGATAGATCCTCCTCCTGACTGTCCTCCAACAGACTG 1399
     ||:|::|||: ::| :|||||::|:||:::| ::|:||||| |::||:| : |||| ||:: | |||:
 778 TCTGACAGATGAAGTATAACTGGGAGGCTCTCCGGGCAGATTATTTTCTTCGATGTCATCTGNCTGACCC 709

1400 TCCGAGTCCAGGGCCATATACCTGTTTTTTAAGGGCACCCTGGCAGGTGAAAGGGGTCGAGAGGGGGT-- 1467
     ||||:::|||||||||| :|||||||:||:| |: |||||||: || ||||||| :|||||||:||||:: |--
 708 TCCGGATCCAGGGCCTCATACCTATTCTGAAGTGGCACCTGGGNAGGTGATGGGGGTCGGGAGGAATTTT 639

1468 -GTTTTTGCCTCTACGACCAGGCACCTGTTTCCATTCNTCCCCATCC-CTATGGTCTGTTCTGTCTGCCT 1535
     -:|| ||:|||||: ||| ||| |||:|||||||||| :|::|||:-|||-|||||| :||: |||||
 638 TATTATTACCTCCCCGAGNAGGGACCCGTTTCCATTCCCCTTCATCTACTA-GGTCTCCTCCTNCTGCCT 570

1536 GATGGCAGGAGGGGCTGGGCTTCACCACCTCCTGCTGGGCTTC-CTTAGGAGTGGAAAGGGTGTGACTCC 1604
     ||||||:||||| :: ||: |:| |:: | |||| |||||||||-||:|:|::||||||-||||| :|||||
 569 GATGGCGGGAGGCATGGGAGTCCTCTGACNCCTGGTGGGCTTCTCTCAAGGATGGAA-GGGTGAAACTCC 501

1605 ACCAGTCAATTTCCCTTTCACTCTCCCTTATGTTTCTGAGCCTATCNACCTCTTCCTTTAGCTCTGCCAC 1674
     ||||||| |||||||||||||||||:||:|| ||::|:|| ||:|| || ||:|:||||| || || |||||
 500 ACCAGTCTATTTCCCTTTCACTTTCTCTAATACTCCTTAGTCTTTCTACTTCCTCCTTAAGNTCAGCCAC 431

1675 CAGACCCAGCAAATCGTTCACCTGCTCACATCGTATGCAGGCGCTTCTCATACTGTCCTCTGGTAGTA-- 1742
     ||| || |:|||||||||||||:|||||:||:| |||||: :::::|::| :|:||:|||: | :|--
 430 CAGCGAAAGGAGATCGTTCACCTGTTCACACCGCAGGCAGGTTTCCTCCGCAACGCCCCCTGAAACCACT 361

1743 GGTCCAGGCTCANACAGTCTATGCAGCCAGAGGCCTGAGTGGCTGCATCCTTTTTAGAGGGTTCTGTCTG 1812
     |:|--|:|||: ||| ||:::::||| ||:||:|||:::| :||||||||||||||:||||||||::|||||
 360 GAT--AAGCTCGAACACTCCGCACAGGAAGGGGTCTGGACAGACGCATCCTTTTTGGAGGGTTCCATCTG 293

1813 --TACTGACACCCCTCTACTGGTAACAGGAGCAACAGCTTTCATTTTTTTGGGAGGCATGACTGCCTTGA 1880
     --|||--:|:|| |:| ||||---||| |-------||:||||: |: | |:::|: ||| |||:||----
 292 GTTAC--ATACACTTGTACT---AACTG------CAGTTTTCGATCGTGTAAAAACCATTACTACC---- 238

1881 GCTGTGGGGAAAGGTAGAAAGAGANAAACAAACAAACAAANA-------AAAAAAAAAANAAAAGGCT-- 1941
     -------:|||||::: |||---| ||| ||| |||||:| |-------|| || ||| ||||: |:--
 237 -------AGAAAAACCCAAA---ACCAACCAACCAACAGAAACACCGCGAACAACAAACTAAAAACCCTA 178

1942 ---GCAGAAATACCTAGGCTTCTGCCCTGCCTGTTNGCCCTGC-TGTGCGAACTGCCGTGCAAACTGCCG 2007
     ---|||||:|: |---| || | :||||||||||:| |||||||-||:||||||||||||:||:|:||||||
 177 CTAGCAGGAGGA---ANCCTGCAACCCTGCCTGCTTGCCCTGCCTGCGCGAACTGCCGCGCGAGCTGCCG 111

2008 TGCCACGCCCTCACTGACGTGCCACGCCCCTGTTTGCCCGCTCCTGTTCGCCGCGCTCC 2066
     ----------------------|||||||:||||||||||||||||||||||||||||||||
 110 ----------------------CGCCCCGTTTGCCCGCTCCTGTTCGCCGCGCTCC 76
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00002832_LTR#LTR@unknown	1	433	CR1-J3_Pass	3826	4255	d	0.8051	1.7234	2428

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   1 AGGCTGGAGAAGGGACTGGAGCACAAGTGCTGTGGGGAGAGGCTGAGGGAGCTGGGGGTGTTTAGCCTGG 70
     ||||||| |||||| |||||||||||||| |||||:|||| |||||||||||||||||| ||||||||||||
3826 AGGCTGGTGAAGGGTCTGGAGCACAAGTCCTGTGAGGAGCGGCTGAGGGAGCTGGGGTTGTTTAGCCTGG 3895

  71 AGAAGAGGAGGCTCAGAGGTGACCTCAGCACTGTCTGGAACTGCCTGAAGGGAAGTTCTGGCCAGGTGGG 140
     ||||:|||||||||||||:|| |||||:| |||| |||: |||| ||||||:|||:| | |:||||||||||
3896 AGAAAAGGAGGCTCAGGGGAGACCTTATCACTCTCTACAACTNCCTGAAAGGAGGNTGTAGCCAGGTGGG 3965

 141 GGTTGGTCTCTTCTCCCAGGCACTCAGCAATAGGACAAGGGGGCACGATGGGCTCAAGCTCTGCCAGGGG 210
     |||:||||||||||||||||||||| |||||:||:|:||||||:|:|:||:||:|:|---||:||||| :||||||||
3966 GGTCGGTCTCTTCTCCCAGGCAACCAGCGACAGGACGAGAGGACACAGT---CTTAAGCTGCGCCAGGGG 4032
```

```
 211 AAATTGAAGTTGGAGATCAGAAAAAAATTCTTTGCAGAGAGAGTGCTCAGGCATTGGAATGGGCTGCCCA 280
     |::||  |:|||||| ||:||:||:||  |||||::||||:||:|||  |::||||||||||||||||||
4033 AGGTTTAGGTTGGACATTAGGAAGAANTTCTTCACAGAAAGGGTGATTGGGCATTGGAATGGGCTGCCCA 4102

 281 GAGAGGGGGTGGATTCCCCATCCCTGGAGGTTTTTCANCTGAGCTTGGCCGTGGCACTGAGTGCCATGAT 350
     |:|||| ||||||| || ||:|||||||||||| ||| |   :|| :||| ||||||||| ||||||||:|
4103 GGGAGGTGGTGGAGTCACCGTCCCTGGAGGTGTTTAAGGAAAGACTGGACGTGGCACTCAGTGCCATGGT 4172

 351 CTGGT--AAAGGGACTGGAGTTGGACCAAGGGGTTGGACTTGATGATCTCGGAGGTCTTTTCCAACCCAAT 418
     ||:||--| |:||--||| ||| |::|| :|||||||||:|||||||||:|||||||||||||||||:|:|
4173 CTAGTTGACAAGG--TGGTGTTNGGTCATAGGTTGGACTCGATGATCTCAGAGGTCTTTTCCAACCTAGT 4240

 419 CNATTCTATGATTCT 433
     : |||||:||||||||
4241 TGATTCTGTGATTCT 4255
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004571_LTR#LTR@unknown	161	461	CR1-J3_Pass	3959	4258	c	0.7800	1.5897	1534

```
 161 CATAGAATCACAGAATGGATTGGGTTGGAAAAGACCTCCGAGATCATCAAGTCCAACCCTTGGTCCAACT 230
     ||:||||||||||||||| :|:|:||||||||||||||||:||||||||:|||||||||: ||::| |||
4258 CACAGAATCACAGAATCAACTAGGTTGGAAAAGACCTCTGAGATCATCGAGTCCAACCTATGACCNAACA 4189

 231 CCAGTCCCTTT--ACCAGATCATGGCACTCAGTGCCACGGCCAAGCTCAGNTGAAAAACCTCCAGGGATG 298
     |||--||:| |--||:|||:|||||||| ||||||||||| |||: ||:    | ||| ||||||||||:|
4188 CCA--CCTTGTCAACTAGACCATGGCACTGAGTGCCACGTCCAGTCTTTCCTTAAACACCTCCAGGGACG 4121

 299 GGGAATCCACCCCCTCTCTGGGCAGCCCATTCCAATCCCTGAGCACTCTCTCTGCAAAGAATTTTTTTCT 368
     | | || ||||||| ||||:|||||||||||||||||||| ||::| |||:||:||||::||||| ||:||:||
4120 GTGACTCCACCACCTCCCTGGGCAGCCCATTCCAATGCCCAATCACCCTTTCTGTGAAGAANTTCTTCCT 4051

 369 GATCTCCAACTTCAATTTCCCCTGGCAGAGCTTGAGCCCATCGTGCCCCCTTGTCCTATTGCTGAGTGCC 438
     :||  |||||||:| ||::||||||||: |||||:|||---|::|||:|||:||:|||||:|:|||| : ||||
4050 AATGTCCAACCTAAACCTCCCCTGGCGCAGCTTAAG---ACTGTGTCCTCTCGTCCTGTCGCTGGTTGCC 3984

 439 TGGGAGAAGA--CCAACCCCCACCT 461
     ||||||||||--||:|||||||||||
3983 TGGGAGAAGAGACCGACCCCCACCT 3959
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3181#Unknown	2456	2539	CR1-J3_Pass	4178	4260	c	0.8333	2.6000	522

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2456 ATCACAGTANCCCAGAACCAATTAGTCTGNAAAAAGNCCTCTGAGATTATTGAGTCCAACCTTTGACCCA 2525
     |||||||| | | |||||:|||:||| :|| ||||-| |||||||||:|:||||||||||| ||||| |
4260 ATCACAGAATCACAGAATCAACTAGGTTGGAAAA-GACCTCTGAGATCATCGAGTCCAACCTATGACCNA 4192

2526 ACACCACCTTGTCA 2539
     ||||||||||||||
4191 ACACCACCTTGTCA 4178
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	2202	3245	ERV3-23_PMaj-I	1545	2570	d	0.7109	1.6176	3520

```
2202 TCGGTCATCTCATGC---AGCACGAGGGAAAACTGNAAGCCCCGGGAGTAAGACACAGAGTGAGCGTAGT 2268
     ||:||| |||| | |---||| |||||||||---| ||-|||::| ::| | |||:::|||||||-----
1545 TCAGTCCTCTCCTTCCCCAGCCAGAGGGAAA---GGAA-CCCCAAGTACACGCCACGAGGTGAGC----- 1605

2269 GTCATATGGACTGTTCTGCGCGAACTAGGGGAAAACATGAAAAAATGGCACGGTGAACCCACCTCTAAAC 2338
     ----| ||| :: |||||||:||| |   |||||||:||||||||:::||:|||  |:|| ||||||||||:|  |
1606 ----TCTGGTTCTTTCTGCGTGACCATGGGGAAGACATGAGGAAGTGGGATGGAGAACCCACCTCCACCC 1671

2339 TTAAAGCCCGACTGCAAGAATTAAAACAGAAANTAGCTGGCAA-------------GAAAGCTGTCCACAT 2396
     | : |||||||| |:|: |||:|:|:| :|||: |||||| |||-------------|||:||||:| :::: 
1672 TGGCAGCCCGAGTACGTGAACTGAGAGGGAAGAAAGCTGTCAAAGGGTCACCCAAGAAGGCTGCCAGTGC 1741

2397 AGTTGAAACAAAGACCCCGGAAAAGAAACATC----GATCTCAGAGACGCAAAAGAA--GCAANTCCCCC 2460
```

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      ||:|----------|||| ||--------||----|||||  ||||::|||||||--| || | | :|
1742 AGCT----------CCCGCAA--------TCTCGTGATCTCCCAGACATAAAAGAACTGAAAATGCATC 1792

2461 CATG----CCGATGAAGGAGCCTCTGACAGAGCGTCGCACACGTCAGATGGAGAA-----TGCTCCGACC 2521
     ::| ----:|:|||:||::|:|||||::  :||:|---:|:|||:|||||::||||:-----|||----|||
1793 TGTTGACCCTGGTGAGGGGACTTCTGGTCTGGCAT---ATACGCCAGACAGAGAGCAACGTGC----ACC 1855

2522 AGGAACAACAATAGAGGGGCCCTGCCTCCTGCCAGGAGGAGGAGAGGGACAAGGATGATAATCGGGTTTA 2591
     | || ||: | ||||||| |||||||||: ||||||:|||||||||||||||---------:|||||:||
1856 ATGACCAGGATTAGAGGGTCCCTGCCTCTAGCCAGGAAGAGGAGAGGGACAA---------CCGGGTCTA 1916

2592 CTGGGCTGTGTGGGTTCGATGGCCTGGCACATCGGATCCTCAGAAATACCGAGCTTTGGTAGATACTGGT 2661
     :|||:| |||||||:|:|||||||||||||||||||||||:|:|| ||:|||||: :||||||:|| ||||||:||:
1917 TTGGACAGTGTGGATCCGATGGCCTGGCACATCAGACCCACAAAAATATAMGGCTTTAGTTGATACCGGC 1986

2662 GCCCAATGTACATTAATGCCATCGGAACATGAGAGTACAGAGACTGTGTCTATTTCTGGAGTTACCGGAG 2731
     || ||:||:|| :|||||||||||:::|||| |:| :|||||: |::| |||||||||||:|| || ||:|
1987 GCWCAGTGCACTCTAATGCCATCAAGGCATGTGGGAGCAGAACCCATTTCTATTTCTGGGGTGACAGGGG 2056

2732 GGTCTCAGGACCTGTCAGTGGTAGAGGCCGACATGAGCCTAACAGGAGACCAATGGCAAAGCATTCCAT 2801
     |:||:||||| || | ||: |:||:||:||  :|||||::|||| ||::|: |:||||||:||:||::||||
2057 GATCCCAGGAGCTCACTGTACTGGAAGCTGAGGTGAGTTTAACTGGGAATGAGTGGCAGAAACACCCAT 2126

2802 TGTGACAGGACCAGAAGCCCCTAGCATCCTTGGTATGGACTATTTAAAAAGAGGNCACTTCAAGGACCCG 2871
     :||||| || ||||||:|||||    ||||||||:|||:|||||||::| |::|: || :||||||||:|||||:
2127 CGTGACTGGCCCAGAGGCCCCATGCATCCTCGGCATAGACTACCTCAGGAACGGGTACTTCAAAGACCCA 2196

2872 AAGGGGTACCGGTGGGCTTTTGGTGTAGCCAC---AGTGATTGAAGGAGAGTCNAAACAGTTGTCTACTC 2938
     ||:|| ||:|| |||||||||||||| :|||||::|---|| ||: ||--||: :||-:|||::|| |||::
2197 AAAGGTTATCGCTGGGCTTTTGGAATAGCTGCTCTAGAGACAGA--GAACATC-AGACAACTGAGTACCT 2263

2939 TCCCTGGTCTCTCAGAAGACCCTTCTGTTGTGGGATTACTCCGAGTCAAAGATCAAGAAGTACCGATGGC 3008
     | ||||||||||||||| :|||||||||:|||||||:|||| ||||::|||| ||: |||||||:|| ||
2264 TGCCTGGTCTCTCAGACAACCCTTCTGCTGTGGGACTACTGAGAGTTGAAGAACAGCAAGTACCAATTGC 2333

3009 TACTGCAACTGTACATAGGCGACAGTATCGCACAAACCGAGATGCTGTGATTCCCATCCATAAAATGATC 3078
     :| ||:|| ||:|||: | ||:|:||:||||| :|| ||||||:|:|||||||||| :||||||:
2334 CASAGCGACAGTGCACCGTCGGCAATACCGCACCGACAGAGACTCTGTGGTCCCCATCCATAMGATGATT 2403

3079 AGGAAGCTGGAAAGTCAAGGGGTGGTCAGCAGAACACACTCACCCTTCAACAGCCCTATCTGGCCTGTAC 3148
     | :||||||:||:|||||||||||||||||::| |:|||||||||||||:| ||||| ||:|
2404 CGTGAGCTGGAGAGCCAAGGAGTGGTCAGCAAGGCTCGCTCACCCTTTAACAGCCCCATATGGCCAGTGC 2473

3149 GTAAATCAGATGGAGAATGGAGACTGACTGTGGACTATCGTGGCTTGAATGAAGTTACGCCACCGCTGAG 3218
     ||||:|| ::|:||||||:|||||||||||||||:|||| :|||||||||:|||||||||||:|||||
2474 GTAAGTCCAGTAGAGAATAGAGACTGACGGTGGACTACCGTGGACTGAATGAAGTCACGCCACCACTGAG 2543

3219 TGCTGCTGTGCCAGATATGTTGGAGCT 3245
     ||| ||:|:||:|||||:|||:|||||||
2544 TGCAGCCGTACCAGACATGCTGGAGCT 2570
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	1311	1767	ERV3-23_PMaj-I	937	1396	d	0.6798	1.5632	1327

```
1311 GGAAAGTGAAATTATACGATCATTGACCCCAAAGGAGATTCGAGATATACGAAGGGATTACAGTCGGTGG 1380
     ||||||  :|||:|||: ||:|| :||||||:||  :||: |||||||: |:||||::|||||||||:|| ::|
 937 GGAAACCGAAGTTACCCGGTCCCTGACCTCATCAGAACTTCGAGACTTGCGAAAAGATTACAGCCGCCAG 1006

1381 CCCGATGAACGCATCCTCACCTGGCTGGTGCGATGTTGGGACCAGGGGGCCAGTAGTCATGTGC---TAG 1447
     || |:|||:|| ||:::::||||||| | ||||||:::|||||||---||---|:|
1007 CCAGGTGAGCGGATTTCTGCCTGGCTGCTTCGATGCTGGGATAATGGGGCTGACAGTCA---GCAATTGG 1073

1448 AAGGTCATGAAGCACAACAATTGGGATCTCTTGCCCGAGACCATGAAATAGAGCAAGAAAT-GGGACAGG 1516
     |||||||||||| |||||::||||||||||||||| :|||:|: ||||| ||: :||:|||-|:| ||:
1074 AAGGTCATGAAGCCCAACAGCTGGGATCCCTTGCTAAAGATCGGGAAATTGAAAGAGGAATTGGAAAAGA 1143

1517 GGGAGATGGCA---TCCAGTCTCTGGACCCGAATCCTCC---GTGCCGTGAGGGCAAGATACCCATTTAA 1580
     :|||||----||---| |||||||||||| ||: |||||:---|||---|||||||||||||||:|||||||
1144 AGGAG----CAATTTGCAGTCTCTGGAGACGGCTCCTCTCAAGTG---TGAGGGCAAGATATCCATTTAA 1206

1581 AGAGTATTTGCTGAGTGCTCCGAGAGAGTGGAATACCGCAGAAGAAGGCATCCAGTATCTGCGGGAACTG 1650
```

```
        :||:  ||:|   |||::  |:||::|:|:||||| :||:||||| |||||:||||||||:||| |:|||:|:
1207 GGAAGATCTTGTGAACTCCCCAGGAAAGTGGACCACTGCAGATGAAGGTATCCAGTACCTGAGAGAATTA 1276

1651 GCTATGCTGGAGATTATATACTCTGATCCAAATTACTATGACATCTT---GGTCCCAGAGAAGATGCCAT 1717
        ||  :|||||||||::|:|| ||:  |||:|:||| :: ||:|::||::---:| :||||||||:| :| || |
1277 GCAGTGCTGGAAGTCATCTATAGTGACCTAAAAAGTGATAATGTCCCTAAAGATCCAGAGGATGTCCCTT 1346

1718 GCACA-CAGCCGATGTGGGATAAGGTGATGGATGGGGCCCCTAAGTCTTAT 1767
        |||||-::|||-|||||||:: |||||||:|  | :| |||||||: :|| |||
1347 GCACAATGGCC-ATGTGGAGGAAGGTGGTTCAAAGTGCCCCTGCATCATAT 1396
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	2799	3255	ERV3-23_PMaj-I	937	1396	d	0.6776	1.5747	1317

```
2799 GGAAAGTGAAATTATACGATCATTGACCCCAAAGGAGATTCGAGATATACGNAGGGATTACAGTCGGTGG 2868
        |||||  :|||:|||: ||:|| :|||||:|| :||: |||||||: |:|| |::|||||||||:||  ::|
 937 GGAAACCGAAGTTACCCGGTCCCTGACCTCATCAGAACTTCGAGACTTGCGAAAAGATTACAGCCGCCAG 1006

2869 CCCGATGAACGCATCCTCACCTGGCTGGTGCGATGTTGGGACCAGGGGGCCAGTAGTCATGTGC---TAG 2935
        || |:|||:|| ||:::::|||||||| | |||||:||:  |||||:::|||||---||---|:|
1007 CCAGGTGAGCGGATTTCTGCCTGGCTGCTTCGATGCTGGGATAATGGGGCTGACAGTCA---GCAATTGG 1073

2936 AAGGTCATGAAGCACAACAATTGGGATCTCTTGCCCGAGACCATGAAATAGAGCAAGAAAT-GGGACAGG 3004
        ||||||||||||||| |||||::||||||||||||: :|||:|: ||||| ||: :||:|||-||:| ||:
1074 AAGGTCATGAAGCCCAACAGCTGGGATCCCTTGCTAAAGATCGGGAAATTGAAAGAGGAATTGGAAAGA 1143

3005 GGGAGATGGCA---TCCAGTCTCTGGACCCGAATCCTCC---GTGCCGTGAGGGCAAGATACCCATTTAA 3068
        :|||||----||---| |||||||||||  ||: |||||:---|||---|||||||||||||||:|||||||
1144 AGGAG----CAATTTGCAGTCTCTGGAGACGGCTCCTCTCAAGTG---TGAGGGCAAGATATCCATTTAA 1206

3069 AGAGTATTTGCTGAGTGCTCCGAGAGAGTGGAATACCGCAGAAGAAGGCATCCAGTATCTGCGGGAACTG 3138
        :||: ||:|   |||:: |:||::||:||||||| :|:||||| |||||:|||||||||:||| |:|||:|:
1207 GGAAGATCTTGTGAACTCCCCAGGAAAGTGGACCACTGCAGATGAAGGTATCCAGTACCTGAGAGAATTA 1276

3139 GCTATGCTGGAGATTATATACTCTGATCCAAATTACTATGACATCTT---GGTCCCAGAGAAGATGCCAT 3205
        || :|||||||||::|:|| ||:  |||:|:||| :: ||:|::||::---:| :||||||:| :| || |
1277 GCAGTGCTGGAAGTCATCTATAGTGACCTAAAAAGTGATAATGTCCCTAAAGATCCAGAGGATGTCCCTT 1346

3206 GCACA-CAGCCGATGTGGGATAAGGTGATGGATGGGGCCCCTAAGTCTTAT 3255
        |||||-::|||-|||||||:: |||||||:|  | :| |||||||: :|| |||
1347 GCACAATGGCC-ATGTGGAGGAAGGTGGTTCAAAGTGCCCCTGCATCATAT 1396
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003054_INT#LTR@unknown	1122	1347	ERV3-23_PMaj-I	3301	3577	d	0.7665	1.6538	706

```
1122 GGATGGGATGATCCCAATGTGTGCCTCAAGGACATTTAACCTTGAGAAAAAAAGGTAACTTGCATTTTGA 1191
        |||||||: ||-|||::|||||||||||||||||| ||||||||||:|::|||||--||::||:: | |||
3301 GGATGGGAGA-CCCGGTGTGTGCCTCAAGGAGATTTAACCTTGGGGGAAAA--TAATCTGTGGTGTGA 3367

1192 GTTCTGTGTTGCAGGACATGAACCATCAG---------------ATGAAGAA------------------ 1228
        ||| |:|||||||||| :|:|| || |||---------------|||||||||------------------
3368 GTTGTATGTTGCAGGAAGTAAAGCAGCAGGAGTGACATGAACTGATGAAGAATGAATTTTGCGAGGAGCA 3437

1229 ----------------GACCTGAGCTGAACTGGTGTTGGTGTCCAATGATGAACTGT----TTTTTCCTG 1278
        ----------------:|||||||||||:: |||||||:|||| :|||||||||||| || |||----:||:|||||
3438 AGGAGAATGCGACGACAACCTGAGCTGGGCTGGTGTCGGTGCCCAATGATCAAGTGTGCTGCTTCTCCTG 3507

1279 -CCTGAAGTACCTACCCCATCCTAATGGACTATTGCCTA---CA---ATATGGAGGGGTGGAAGACGGCC 1341
        -|||||-----|:||||-|||||:||||| |: |||:|---||---|| ||||||||||||||:|| |||
3508 TCCTGA-----CCACCC-ATCCTGATGGAATGGAGCCCAAGTCATGGATCTGGAGGGGTGGAGGAAGCCC 3571

1342 CTGGAA 1347
        ||:||
3572 ATGAAA 3577
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	127	352	ERV3-23_PMaj-I	3301	3577	c	0.7621	1.6296	694

```
 127 TTCCAGGGCCGTCTTCCACCCCTCCATAT---TG---TAGGCAATAGTCCATTAGGATGGGGTAGGTACT 190
     ||:|| || | ||:|||||||||||| ||---||---|:|||  :| |||||:|||||||-|:|-----
3577 TTTCATGGGCTTCCTCCACCCCTCCAGATCCATGACTTGGGCTCCATTCCATCAGGATGGG-TGG----- 3514

 191 TCAGG-CAGGAAAAA----ACAGTTCATCATTGGACACCAACACCAGTTCAGCTCAGGTC---------- 245
     |||||-|||||:||:---|||| || |||||||||:|||||:|||||||::|||||||||:----------
3513 TCAGGACAGGAGAAGCAGCACACTTGATCATTGGGCACCGACACCAGCCCAGCTCAGGTTGTCGTCGCAT 3444

 246 -----------------------TTCTTCATC---------------TGATGGTTCATGTCCTGCAACA 276
     -----------------------|||||||||---------------|| || ||:|: ||||||||||
3443 TCTCCTTGCTCCTCGCAAAATTCATTCTTCATCAGTTCATGTCACTCCTGCTGCTTTACTTCCTGCAACA 3374

 277 CAGAACTCAAAATGCAAGTTACCTTTTTTTCTCAAGGTTAAATGTCCTTGAGGCACACATTGGGATTATC 346
     :| ||||||| | ::||::|||--|||||::|:||||||||||| |||||||||||||||::||| :|-:|
3373 TACAACTCACACCACAGATTA--TTTTTCCCCAAGGTTAAATCTCCTTGAGGCACACACCGGGTCT-CC 3307

 347 CCATCC 352
     ||||||
3306 CCATCC 3301
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	1083	1308	ERV3-23_PMaj-I	3301	3577	d	0.7621	1.6296	694

```
1083 GGATGGGATAATCCCAATGTGTGCCTCAAGGACATTTAACCTTGAGAAAAAAAGGTAACTTGCATTTTGA 1152
     |||||||: :|-|||::|||||||||||||||| |||||||||||:|::|||||--||:::||:: | |||
3301 GGATGGGGAGA-CCCGGTGTGTGCCTCAAGGAGATTTAACCTTGGGGGAAAAA--TAATCTGTGGTGTGA 3367

1153 GTTCTGTGTTGCAGGACATGAACCATCAG---------------ATGAAGAA------------------ 1189
     ||| |:|||||||||| :|:|| || |||---------------||||||||------------------
3368 GTTGTATGTTGCAGGAAGTAAAGCAGCAGGAGTGACATGAACTGATGAAGAATGAATTTTGCGAGGAGCA 3437

1190 ----------------GACCTGAGCTGAACTGGTGTTGGTGTCCAATGATGAACTGT----TTTTTCCTG 1239
     ----------------:||||||||||::||||||:|||:||||||||| || |||----:||:|||||
3438 AGGAGAATGCGACGACAACCTGAGCTGGGCTGGTGTCGGTGCCCAATGATCAAGTGTGCTGCTTCTCCTG 3507

1240 -CCTGAAGTACCTACCCCATCCTAATGGACTATTGCCTA---CA---ATATGGAGGGGTGGAAGACGGCC 1302
     -|||||-----|:|||||-|||||:|||||| |:  |||:|---||---|| |||||||||||||:|| | ||
3508 TCCTGA-----CCACCC-ATCCTGATGGAATGGAGCCCAAGTCATGGATCTGGAGGGGTGGAGGAAGCCC 3571

1303 CTGGAA 1308
     ||:||
3572 ATGAAA 3577
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	975	1161	ERV3-23_PMaj-I	1533	1715	c	0.6885	1.6364	603

```
 975 TTTACCAGCTTTCTTACGTTTTGATTTCCATACCTGGACTTCAAGCACAGAAGTAGATGCACTGTCCCAC 1044
     |||: ||||||||||| | |:|::::|:  |:|||::||:|| | || :::||:||:|:| | |::||||||
1715 TTTGACAGCTTTCTTCCCTCTCAGTTCACGTACTCGGGCTGCCAGGGTGGAGGTGGGTTCTCCATCCCAC 1646

1045 CTCCTCATGTCTTTCCCCTGGTCACACAGGAAGGACNACAGTTCACCATGTGACTCACGCTTGGGGTT-- 1112
     :|||||||||||||:||| |||||||||:|||:|||:|| | ||:|||| :|||:| ::::|||||||||--
1645 TTCCTCATGTCTTCCCCATGGTCACGCAGAAAGAACCAGAGCTCACCTCGTGGCGTGTACTTGGGGTTCC 1576

1113 -TGCTCTCTGTTGAGGTGAGGCAGGAGAGAAAGACAGCTTGCTTTGGCTG 1161
     -| |:|||||----| ||:|| |||||||---||| | |: ||| |||||
1575 TTTCCCTCTG----GCTGGGGAAGGAGAG---GACTGATCTCTTGGGCTG 1533
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003054_INT#LTR@unknown	385	571	ERV3-23_PMaj-I	1533	1715	d	0.6703	1.5946	598

```
 385 CAGCCAAAGCAAGCTGTCTTTCTCTCCTGCCTCACCTCGACAGAGAGCAAACCCCAAGCGTGAGTCACAT 454
     |||||| ||| :| | |||---|||||||| ||:|| |: || :||:||-:||||||||||:::: |:|||:
1533 CAGCCCAAGAGATCAGTC---CTCTCCTTCCCCAGCCAGAGGGAAAG-GAACCCCAAGTACACGCCACGA 1598
```

```
 455 GGTGAACTGTNGTCCTTCCTGTGTGACCAGGGGAAAGGCATGAGGAGGTGGGACAGTGCATCTACTTCTG 524
     |||||:|| |  ||:||:::||:|||||| |||:|||:||||||||:||||||::| | |:|:||:||::
1599 GGTGAGCTCTGGTTCTTTCTGCGTGACCATGGGGAAGACATGAGGAAGTGGGATGGAGAACCCACCTCCA 1668

 525 TGCTTGAAGTCCAGGTATGGAAATCAAAACGTAAGAAAGCTGGTAAA 571
     : || | ||:||::|||:| :|||::::|:| | ||||||||||| :|||
1669 CCCTGGCAGCCCGAGTACGTGAACTGAGAGGGAAGAAAGCTGTCAAA 1715
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	293	474	ERV3-23_PMaj-I	1533	1710	d	0.6910	1.6250	592

```
 293 CAGCCAAAGCAAGCTGTCTTTCTCTCCTGCCTCACCTCAACAGAGAGCAA---ACCCCAAGCGTGAGTCA 359
     ||||| ||| :| |  |||---||||||| ||:|| |----|||||:| ||---|||||||||:::: |:||
1533 CAGCCCAAGAGATCAGTC---CTCTCCTTCCCCAGC----CAGAGGGAAAGGAACCCCAAGTACACGCCA 1595

 360 CATGGTGAACTGTNGTCCTTCCTGTGTGACCAGGGGAAAGACATGAGGAGGTGGGACAGTGCATCTACTT 429
     |: |||||:|| |  ||:||:|:|||:||||||||  |||:||||||||||||||:|||||||::| |  |:|:||:|:|
1596 CGAGGTGAGCTCTGGTTCTTTCTGCGTGACCATGGGGAAGACATGAGGAAGTGGGATGGAGAACCCACCT 1665

 430 CTGTGCTTGAAGTCCAGGTATGGAAATCAAAACGTAAGAAAGCTG 474
     |:::  || |  ||:||:::|||:|  :||::::|:| | |||||||||||
1666 CCACCCTGGCAGCCCGAGTACGTGAACTGAGAGGGAAGAAAGCTG 1710
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	733	979	ERV3-23_PMaj-I	449	695	d	0.6367	1.5849	544

```
 733 CCAGTCCCTGGGTGGGAAGGGGCTTGGTTGGATCTCGGTAAAGTGCTAGGGCGTATCTCACCCCCCATTA 802
     |||||:|||||||||| |:|| |: |||  |||||:| ||:|:: | |||||||:| |  |||||:||||||:
 449 CCAGTTCCTGGGTGGCAGGGTGTGTGGAAGGATTTGGGCAGGTTCCTAGGGTGGTTATCACCTCCCATTG 518

 803 ATTGGAAGTTCACGTCAGAACAAGTATGTGATTCTGGTGAGGTGGCCCG-CTGTTTATCAGAAGAGTGTT 871
     :|||:| ||:||::| |||||:||| ::|::||||::|: ||:|||||-| |:| ||-|||||:|||::
 519 CCTGGGACTTTACACCTGAACAGGTAATCAACCCTGACAAACTGACCCGTCAGCTGAT-AGAAGGGTGCC 587

 872 TTTCCTAC------GAGGACCCGTATATGCAAGTCTCTGCTTTGTGTTGGGGCCTGGCTAGTGCTTATCG 935
     || ||:||------||::||| |:|---||---|:::|||::||||:|||||||||||||: ||||:||:||
 588 TTGCCCACCCCAGTGAAAACCAGCA---GC---TTCTTGCCCTGTGCTGGGGCCTGGCCTGTGCCTACCG 651

 936 ATCTGCCATGGACTACTGTCAATGGCTTGAGGACAGGATAGGAA 979
     |  |:::::|   |||| |||: || :|| || :::|::|||||
 652 AGCCACTGTTCAGTACTCTCAGAGGACTGTGGTTGAGGCAGGAA 695
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	541	579	ERV3-23_PMaj-I	1875	1916	d	0.8250	1.0000	231

```
 541 CCCTGCCTCCAGCCGAGAGGAGGAGA---ACAACCAAGTCTA 579
     ||||||||||:||||:::||:|||||||---||||||::|||||
1875 CCCTGCCTCTAGCCAGGAAGAGGAGAGGGACAACCGGGTCTA 1916
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	889	937	GGERVL-A2-I	2416	2464	c	0.7959	1.6000	215

```
 889 TCTCCTCCTCCTGGCTGGAGGCAGGGCGGCTTAATTGCTGTT--CTTGGCT 937
     |:||||:|||||||||||||||:|||||||||  ||:  |||--||||--|||||:|
2464 TTTCCCCCTCCTGGCTGGGGGCAGGGCCCCTCTATT--TGTTACCTTGGTT 2416
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6290#Unknown	872	1207	ERV3-1_MUn-I	4055	4393	d	0.7882	1.9143	1769

```
 872 TCTCTGNTCCCACTCNTG-ATGGTGNCAAATGCCCTGTGGG-TGGGTGCAGCANTGGCAGCAGAAGAAC 939
     |||||:  |: |||| ||-|||||| ||||||||||||||||-||| ||||||||| ||| |||||:| |||
4055 TCTCTATACTGACTCATGGATGGTGGCAAATGCCCTGTGGGGGTGGTTGCAGCAATGGAAGCAGAGCAAC 4124
```

```
 940 TGGCAGCACAGGGGCAAACCCATCTGGGCTGCTGCCTTGTGGCAAAGGNATCAGTGCCCNGGTGGAGCAC 1009
     |||||:|:|||:||:||||||||||||||||||| :||||||-|: |||: ||||| |||| || ||
4125 TGGCAACGCAGAGGTAAACCCATCTGGGCTGCTGCACTGTGGCAA-GATATCGCTGCCCGGGTGCAGAAC 4193

1010 CTGCTG-TGAAGGTGTGTCATG-GGGTGCTCCTGTACCCAAGAGTCAGGCCCCTGAAGAACAGCAGAACA 1077
     ||| ||-||||||||::|:||||-:|:|||:| :||||||||||||:|||| |||:|||||| |||||||
4194 CTGGTGGTGAAGGTACGCCATGTAGATGCCCACGTACCCAAGAGTCGGGCCACTGAGGAACACCAGAACA 4263

1078 ACCAGCAGGTGGCTCAGGCTGCTGGCATTGAAGGGGCTCAGGTGCNTTGGCATTGGCAGCACAAGGGGGA 1147
     ||||:||:||||| | |:|||||||:: |||||||| ||||||||:|| :| : |||||||||:||:||:|| ||
4264 ACCAACAAGTGGATAAAGCTGCTAAGATTGAAGTGGCTCAGATGGACTTAGATTGGCAACATAAAGGTGA 4333

1148 ATTATTTCTGGCTCCNTGGGCCCAGGACACCTCGGGCCATCAAGGCAGAGATGGAACATA 1207
     ||||||||:||||:| |||||||||| |||||:||:|||||||||:||||||||| ||||||
4334 ATTATTTTTGGCCCGGTGGGCCCATGACACTTCAGGCCATCAGGGCAGAGATGCAACATA 4393
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003054_INT#LTR@unknown	632	674	ERV3-1_MUn-I	2023	2065	d	0.7209	1.2000	206

```
 632 GCCCTGCCTCCAGCCGAGAGGAGGAGGAGAACAACCAAGTCTA 674
     |||||||||||||||||::| ||||| :|:|:||||:|:::|:||
2023 GCCCTGCCTCCAGCCAGGTGGAGGTAGGGGACAATCGGATTTA 2065
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-107#LTR@ERVL	67	4318	ERV3-18_PMaj-I	871	5181	d	0.7645	2.0331	22804

```
  67 GCNCANCCAGGGGGACAGTNNAAGCCNATGGNAGTTGCCCCTNTCCAGAAA--AGGAAATANAAGACCAA 134
     || | ||| ::||:|||| |||| ::| ||||||||||||| |--:||||--|||||:| ||||: ||
 871 GCTGAACCACAAGGGCAGTCACAGCCAGCAGCTGTTGCCCCTGT--GGAAACGAGGAAGTCTAAGATGAA 938

 135 ACCAGTCCGTNNAGNGGATGATGAGGNNGNGGCNGNACCTTCACAGCANGCAG---ANNCAGAGCCNGAN 201
     |:|| |:: | |||:| || : : :| | :|:|||||:| :|||---| ||||| : ||
 939 ATCACAGCACCCTGTTGATAAGGATAAGAAAGGAGGGCCCTCACAACCCACAGGGGAGCCAGAGGTTGAA 1008

 202 ATNATCACNNNGTCATTGTCNNTNGANNANCTNCGTGNTNTNCGGANAGANNTNNCTCGACANCCAGNNG 271
     || |||||| ||| :|| | || : || |||: | | |::| ||| | : |:|: : |
1009 ATCATCACCGAGTCCCTGACATATGAGAGTCTCCGTAATCTGCAAAAAGACATTGTGAGGCGGGGGCGTG 1078

 272 AG-CCCATCCTGACNTGGNTGNTCCGANTTTGGGACCNNANNGGTNAAANN------CTNGATGGTNNTG 334
     ||-|::||  |-:|| ||| |: |:||: |:||||||| | ||| |: ------|| |||||| ||
1079 AGGCTTATAC-AACCTGGTTACTTCGGGTCTGGGACCTTATGGGTACAGGCGTGCAGCTGGATGGTGGTG 1147

 335 AAGCNAGGNNNNTGGGNNCTNTGGCCCNNGATGTGGNNATTGANCAGGT---TGNNANGGNANNNAAGNC 401
     |:|| |||    ||||    |: ||:||| ||: ::| :| :| |||||---:| ||| : ::| |
1148 AGGCAAGGAATGTGGGACCCTTGACCCAGGACTCAGGTGTGAATCAGGTATTCGTCAGGGAGCCAGGGCC 1217

 402 NCTNNNNCTCTGGNCNCGACTNNTNNNNAGTGTNAGNGAGANNTNTNTNTATANAGAANNCCTGCAGGNN 471
     ||    ||||||    ||:|| |    ||||| || ||||   | | | :|:| |||:    || |:|
1218 CCTTTCCCTCTGGGAGCGGCTTTTGATGAGTGTAAGAGAGAGGTTTGTCCACAGAGAGAGAATGGAAGAG 1287

 472 CA---TCANANNNAG---TGGAANACNATGGAAGAAGGNATTCNANGTCTGAGGGANNTGGCNATGNTGG 535
     ||---|||  | :|---||||| || || || ||:|||||  ||:| | :|||||:|| |||| :|: :|
1288 CACTATCATAGAAGGGGCTGGAAAACCATTGAGGAAGGGATCCAACAGCTGAGAGAAGTGGCGGTATTAG 1357

 536 AANTNNTNTTTNNAANGGNTGNGCAAANCANTAANGACCCTGANAAGGTCAGATGCACACCNCANATGTG 605
     |:  |  | ||| :| || || :||: ::  |||  |||||:|| ||:|||||:||||| || ||||
1358 AGGTCCTTTTTGGGAGGGGTGGACAGCATGATAATGACCCCGACAAAGTCAGGTGCACTGGGCAGATGTT 1427

 606 GTNGAACCTTNCACACNCNGGGCCAGNTGNATACACCNANTNCCTGGCA-----TGNANNGGGAAGAGAAN 671
     || ||::||  ||  |: : ||||||  || ||||||| | | |||----|  | || :| |:
1428 GTGGAGTCTGGCAAATCTAGGGCCACGTGAATACACCACCTTCATTGCAACGATTAATGCCGATAACAGC 1497

 672 NAAGAAANNGTGGGCGCTNTAGNAANNAANCTCNGGATNTATGAAGGCATNNNCCNNANCCCANTGCANG 741
     :||||:|  ||||||: || || |   |: ||: |:|  ||||::|:|||  || : ||:: ||| |
1498 CGAGAGACGGTGGGTTCTGTCGCCACCAGGCTTAGAAATTTTGAGAGTATGGTCCATGGCCTGCAGCAGG 1567

 742 CCCGTATTTCNGCTGTNG-------------AGACAANACTGNCTGNANAGGNANAGGAGATTAAGNNNN 798
     |:|: :|:|| |||||| :------------||| :| |-|| | | |: : |:||||| |:|
1568 CTCAGGTCTCTGCTGTGATTAAGGAACTCAAAGAGGAGA-TGAGGGAAATGAGGGAAGAGATGAGGAAGA 1636
```

```
 799 GANTTNTCCANNTNGCNCCAGTNCNAATGAGANNCTCTGNANTCAGANNCAGACGCCCCCCANCCAGAGN 868
     |    | :|||  | ||  ||||| | |:|  | |   |:| :  | || :|  | :|||:|||||| |:||||
1637 GCAGTTCCCATATGGCACCAGTGCGAGTCACAAGCCCAAAACTCCAAGCCCAACGTCCCCCAGCTAGAGA 1706

 869 GANNGGACAGACNNCACGNANNGAGATGTGGTNCTTCCTGNNCAAACATGGAGAAGACATGNGANNGTGG 938
     ||   ||::| || |||| :  ||| ||||||| |||:||: ::| |||||:||||||||| ||  ||||
1707 GAGAGGGTACACCCCACGAGCTGAGCTGTGGTTCTTTCTACGTGACCATGGGGAAGACATGGGAAAGTGG 1776

 939 GATGGGAAACCCACCNNTNCCCTTGCAGCCCGAGTACAAGAACTGAANGAG---------AANGNAAGAA 999
     ||||||||||||||:  |  |||| ||||| ||||||:|:  |||| |: |||---------||   :|:||
1777 GATGGGAAACCCACTTCTGCCCTGGCAGCACGAGTGCGTCAACTCAGGGAGGGAACCATTAACCAGAAAA 1846

1000 NGTCNGTGAGANTAANTGCNGTCCCAGTNTCCCATGGGCAAGNNTC---------------------TGA 1048
     ||  :: |:| |:|   |: |:|:||:: ||||:||:  |||:    |---------------------|||
1847 GTTCCACTAAAGTGAAGGTAGCCTCAACCTCCCGTGACCAAACTGCCAGATATTACAGAAAAGAGGATGA 1916

1049 CCCACANGAGGGCACCTCC--CAGNTGTACTCATNAAGAAAANGTTCNGACTGCTACGACCAGTGTTAGG 1116
     :|| |   ||:||  |||||:--||   |:|:|:||   :|:|:|  |-----------|:||||||||||:|||:
1917 TCCCCTTGAAGGAACCTCTAGCATGTATGCCCAGGGAGGAGAGG-----------ATGACCAGTGCTAGA 1975

1117 GGGGCCCTGCCTCTAGCCAGGTAGAGGNANGGGACAANCGNGTCTATTGGACTGTGTGGATTCGATGGCC 1186
     |||||||||||||||||||||  ||||| | |||| || || |||| |||||| |||||||:||||||||
1976 GGGGCCCTGCCTCTAGCCAGGAAGAGGCACGGGAAAACCGGGTCTTTTGGACGGTGTGGATCCGATGGCC 2045

1187 TGGCACATCAGACCCACAAAANTATAAGGCTTTGGTTGATACNGGCGCNCAATGCACATTAATGCCATCA 1256
     ||||||||||||| |||||||  ||:::|:|||||:|||||| ||:|| ||:|:|| :|||||||||||||
2046 TGGCACATCAGAGCCACAAAAATACGAAGCTTTAGTTGATACTGGTGCACAGTGTACCCTAATGCCATCA 2115

1257 GGACATGTGGGCNCAGAGACTATTTCTATTTCTGGGGTGACAGGGGGATCTCAAGAGTTGACTGTGCTAG 1326
     |||||||||||| ||||: ||:||||:||| |||||||||||:|||||||| ||: ||||||||| ||:|:|
2116 GGACATGTGGGGGCAGAACCTGTTTCCATTGCTGGGGTGACGGGGGGATCGCAGCAGTTGACTCTGTTGG 2185

1327 AAGCTGAAGTGAGCTTGACAGGGAGAGATTGGCANAAACACCCCATTGTGACTGGTCCAGCNGCCCCATG 1396
     ||||:||:|||||||:|||| |||||::|| ||||| |||||:||||||||||||||||||:|||| |||||:||
2186 AAGCCGAGGTGAGCCTGACTGGGAAGGAGTGGCAGAAACATCCCATTGTGACTGGCCCAGAGGCCCCGTG 2255

1397 TATCCTGGGCATTGACTATCTCAGGAATGGATATTTTAAGGACCCAAAGGGACATAGATGGGCTTTTGGA 1466
     ||| :|||||||| ||||:||: |||||||| |||| :||:|||||||||||||| :||:||||||||||||
2256 TATTCTGGGCATAGACTTCCTTCGGAATGGCTATTACAAAGACCCAAAGGGACTCAGGTGGGCTTTTGGA 2325

1467 ATAGCCACTGTAGAGACAGAAGGGATTGAACAATTGANCTCATTGCCAGGTCTCTCAGAAAGTCCTTCTG 1536
     |||||::||||:|||:|||:||: |||:|:|||||| | | ||||| || || ||||:|::|| ||||
2326 ATAGCTGCTGTGGAGGCAGAGGACATTAAGCAATTGAACACCTTGCCTGGACTATCAGAGAACCCATCTG 2395

1537 CTGTNGGACTGTTGAAAGTTGAGGAACAGCAGGTGCCAATNGCCACCACAACAGTGCACCGTCGGCAATA 1606
     | ||  :||||| :|||||| :||||||||||||:||||||::||:||||| ||||||| |:||:||||||||:||
2396 CAGTAAGACTCCTGAAAGTGGAAGAACAGCGAGTACCAATTGCCACCTCGACGGTGCACCGCCGGCAGTA 2465

1607 CCGAACGAACCGCGATGCTGTGATTCCCATCCATAAGATGATCCGTGAACTGGAGAGCCAAGGGGTGGTC 1676
     :  |:||:||:||  ||||||||||||||||:||||||||:||||||||||| ||:|||||||||||||||||
2466 TAGGACAAATCGAGATGCTGTGATCCCCATCCACAAGATGATCCGAGAGCTGGAGAGCCAAGGGGTGGTC 2535

1677 AGCAAAACCCACTCACCCTTCAACAGCCCCATCTGGCCTGTACGTAAGTCTGATGGAGAATGGAGATTGA 1746
     |||||||||||||||||||||||||||||||||||||||||||:||:|||||||||::||||||||||||:|||
2536 AGCAAAACCCACTCACCCTTCAACAGCCCCATCTGGCCTGTGCGCAAGTCTGACAGAGAATGGAGACTGA 2605

1747 CTGTGGACTATCGTGGCTTGAATGAAGTTACCCCACCGCTGAGTGCCGCTGTGCCGGACATGCTGGAGCT 1816
     ||||||||||||||||| ||||||||||| ||:||||||||||||| |:||||||||||||||||||||||
2606 CTGTGGACTATCGTGCATTGAATGAAGTGACTCCACCGCTGAGCGCTGCCGTGCCGGACATGCTGGAGCT 2675

1817 CCAGTATGAGCTGGAGTCCAAGGCAGCAAAGTGGTATGCCACTATTGACATTGCCAATGCNTTCTTCTCC 1886
     ||||||||||||||||||||||||||||:||||||||:||||||||||||||||||||||| ||:||||||
2676 CCAGTATGAGCTGGAGTCCAAGGCAGCGAAGTGGTACGCCACTATTGACATTGCCAATGCATTTTTTCTCC 2745

1887 ATTCCTCTGGCACCAGAGTGCAGGCCACAGTTTGCTTTTACNTGGAGGGGCGTGCAGTACACCTGGAACC 1956
     |||||:||||||  |||:|||||||||| |||||:||:|| |||||||| |||||||||||||||||||||
2746 ATTCCCCTGGCAGCAGAATGCAGGCCTCAGTTTGCCTTCACGTGGAGGGGAGTGCAGTACACCTGGAACC 2815

1957 GACTGCCCCAGGGGTGGAAACACAGTCCCACCATCTGTCATGGACTGATCCAGACTGCACTGGAGAAGGG 2026
     |||||||||||||||||||:|||||:|||||||||||:|||||||||||||||:||||| |||||:|||||
2816 GACTGCCCCAGGGGTGGAAGCACAGCCCCACCATCTGCCATGGACTGATCCAGGCTGCCCTGGAAAAGGG 2885
```

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2027 TGAGGCTCCAGAACACCTGCAATACATCGATGACATCATTGTGTGGGGGGACACAGCAGAAGAGGTTTTT 2096
     ||||||||||||||:|||||:|||||:||||||||||||||||||||||||||:||||:||||  :||:|| |||
2886 TGAGGCTCCAGAACATCTGCAGTACATTGATGACATCATTGTGTGGGGGAACACGGCAGTGGAAGTATTT 2955

2097 CAGAAAGGAGAGAAAATCATCCAGATCCTTTTGGGAGCTGGCTTTGCCATCAAACGGAGTAAGGTTAAGG 2166
     ||||||||||||:||:|||||||||||:|| :|||:||:|||:||||||||||||||: :||::||:||:||:|
2956 GAGAAAGGAGAAAAGATCATCCAGATTCTGCTGGAAGCCGGCTTTGCCATCAAGAAGAACAAAGTCAAAG 3025

2167 GACCAGCCCAAGAGATCCAGTTCCTGGGAGTGAAGTGGCAGGATGGACGCCGTCAGATTCCAACAGAGGT 2236
     ||||  ||:|:||||||||||||||||||||||:||:|||||||||:||:|||||| |||||||||| || ||:||
3026 GACCTGCTCGAGAGATCCAGTTCCTGGGGGTAAAGTGGCAAGACGGACGGCGTCAGATTCCCACTGAAGT 3095

2237 CATCAATAAGATCACAGCAATGTCTCCACCTACCAGCAAAAAGGAAACACAAGCCTTCCTGGGTGCCATA 2306
     ||||||||||||||| |||||||||||||| ||||||||||:||||||||||||||:||||||:|||||||||
3096 CATCAATAAGATCACTGCAATGTCTCCACCGACCAGCAAGAAGGAAACACAAGCTTTCCTAGGTGCCATA 3165

2307 GGGTTTTGGAGGATGCATATCCCAGCATACAGTCAGATCGTAAGCCCTCTCTACTTGGTNACCCGTAAGA 2376
     || |||||||:|||||:||||:||:|| | :|||||:||||||||:|||||||||||||:|||| ||||| ||:|
3166 GGTTTTTGGAAGATGCACATTCCTGAGTACAGCCAGATCGTGAGCCCTCTCTACCTGGTTACCCGAAAAA 3235

2377 AGAATGATTTCCACTGGGGCCCTGAACAGCAACAAGCCTTTGACCAGATCAAACANGAGATTGCTCAGGC 2446
     ||||||||||||||||||||||||||||||||||||||||||| |||||||||:|| |||||:||||| ||
3236 AGAATGATTTCCACTGGGGCCCTGAACAGCAACAAGCCTTTGCCCAGATCAAGCAGGAGATCGCTCATGC 3305

2447 TGTAGCCCTTGGACCAGTCAGGACAGGACCAGACATACAGAACATGCTCTACTCCGCTGCCGGGAATAAT 2516
     ||||||||||| ||||||||||||||||||||||::|: |||||:|||||||||:|| |||||||||:|||
3306 AGTAGCCCTTGGCCCAGTCAGGACAGGACCAGATGTGAAGAACGTGCTCTACTCTGCAGCCGGGAACAAT 3375

2517 GGCCTGTCTTGGAGCCTTTGGCAGAAGGTGCCTGGTGAGACTCGAGGCCGACCACTTGGATTCTGGAGCC 2586
     |||:|||||:|||||||||||||||||:|||||||| ||||||||||||||||||||:||||||||||||
3376 GGCTTGTCCTGGAGCCTTTGGCAGAAAGTGCCTGGGGAGACTCGAGGCCGACCACTGGGATTCTGGAGCC 3445

2587 GAGGCTACAGAGGATCCGAAGCCAACTATACCCCAACAGAGAAAGAGATCCTAGCNGCCTATGAAGGAGT 2656
     ||:|||||||||:|||||||||||||:||:|| |||||||||:|:||:|::|||| |||||||||||||||
3446 GAAGCTACAGAGGGTCCGAAGCCAACTACACTCCCACAGAGAAGGAAATTTTAGCTGCCTATGAAGGAGT 3515

2657 TCAAGCNGCCTCAGAGGTGATTGGCACNGAAGCACAGCTCTTTCTGGCACCTCGACTACCNGTGCTGAAG 2726
     ||||||| |||||||||||||||||||| |||||||||:|||:|:||||||||:|||||||| ||||||::|
3516 TCAAGCTGCCTCAGAGGTGATTGGCACAGAAGCACAACTCCTCCTGGCACCCCGACTACCAGTGCTGGGG 3585

2727 TGGATGTTGNCAGGACAGGCTGCCTCTACACATCACGCCACTGATGCTACCTGGAGCAAGTGGATTGCCC 2796
     ||||||||| |||| |||:| |: |||| ||:|||||||||:||:||||| ||||||||||||||:||||
3586 TGGATGTTTAAAGGAAAGGTTCCTGCTACCCACCACGCCACCGACGCTACATGGAGCAAGTGGATCGCCC 3655

2797 TGATTACGCAGCGCGCCCGTATGGGAAAACCAAATCGCCCTGGGATNCTGGAAATCATCACNAACTGGCC 2866
     | ||:|||||||||||||||| ||||| |||||||||||||||||| :||||:|| ||:|| ||||||||
3656 TCATCACGCAGCGCGCCCGTATTGGAAACCCAAATCGCCCTGGGATTTTGGAGATAATTACAAACTGGCC 3725

2867 TGAAGGTGAAAATTTTGGTCTAGCAGATGAAGAGGAA---GAGCAGGTGACACGTGCGGAAGAAGCTCCA 2933
     ||||||||||||:||||||||| :| ||||||||||||:---||:||:|||||||| || ||||||||||||
3726 AGAAGGTGAAAACTTTGGTCTCACTGATGAAGAGGAGCAGGAACAAGTGACACGGGCTGAAGAAGCTCCA 3795

2934 CCATACAATCAATTGCCAGAAGAAGAAATACGCTACGCCCTCTTCACTGATGGCTCCTGTCGCATTGTAG 3003
     ||:||||||:|||:|||||| ||||||||:|||||||:|||||||:|:|| ||||||||||||||||:||||
3796 CCGTACAACCAACTGCCAGCAGAAGAAACACGCTATGCTCTGTTCACTGATGGTTCCTGTCGCATCGTAG 3865

3004 GGACTAATCGCAAATGGAAAGCAGCTGTATGGAGTCCCACCCGACAAGTTGCAGAAGCTACTGAAGGAGA 3073
     ||||: ||:|| ||:||||||||||||:|||||||| ||||||:||||| |||||:||:|||||||||||||||
3866 GGATGAACCGGAAGTGGAAAGCAGCCGTATGGAGCCCCACACGACAGGTCGCAGAAGCTACTGAAGGAGA 3935

3074 AGGTGGGTCGAGTCAGTTTGCAGAGCTTAAAGCTGTGCAGTTGGCCCTGGACATTGCTGAACGAGAGAAA 3143
     :||||||:||:||:||:||:|||| ||:||:|||||||| |||::||||||||||||||||||| |||||||:
3936 GGGTGGATCAAGCCAACTTGCTGAACTCAAAGCTGTTCAACTGGCCCTGGACATTGCTGAAAGAGAGAAG 4005

3144 TGGCCAAAGCTTTACCTCTACACTGACTCATGGATGGTGGCCAATGCTCTCTGGGGATGGTTAGACCGAT 3213
     |||||||||||:|||||||||||||||:|||||||||||||:|||||||||||:||:|| |:|
4006 TGGCCAAAGCTCTACCTCTACACTGATTCATGGATGGTAGCCAATGCTCTGTGGGGATGGCTGGAAAGGT 4075

3214 GGAAGAAACCAATTGGAAACGCAGAGGGAAACCCATCTGGGCTGCNGATATATGGCAAGACATCGCCAC 3283
     |||||:|:::||||||||| |:|::||:||:|||||| ||||||||||||| |||: :|||||||||||||||:||
4076 GGAAAAGGGCCAATTGGCAGCATAGGGGAAAACCAATCTGGGCTGCTGATGAGTGGAAAGACATCGCTAC 4145

3284 CCGAGTAGAGAAGCTGATTGTGAGAGTCCGCCATGTAGATGCACACGTGCCCAAAAATCGAGCCAATGAG 3353
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          |  |:|||||||||:||| :|||||::|||||:||||||||||| ||:|| |||||:|:|||:|:|||||:
     4146 CAGGGTAGAGAAACTGTCTGTGAAGGTCCGTCATGTAGATGCCCATGTCCCCAAGAGTCGGGCTAATGAA 4215

     3354 GAACATCGCAACAACCAACAGGCAGACCGAGCTGCACAAGTGAAAGTATCACAGACAGATCTGGACTGGC 3423
          ||:||:|| ||||||: |:||||::||:|::|||||| ||:::||:|||:||| ||||||||::|:||:||||
     4216 GAGCACCGAAACAATGAGCAGGTGGATCAGGCTGCAAAGATAGAGGTGTCAAAGACAGACTTAGATTGGC 4285

     3424 AGCACAAGGGAGAGCTGTTCCTGGCTCGATGGGCCCATGATGCCTCNGGCCATCAGGGCAGAGATGCCAC 3493
          |:||||||||||||:|||||:||||||||||||||||||||||||| ||:|||||||:||||||||||||
     4286 AACACAAGGGAGAGTTGTTCCTAGCTCGATGGGCCCATGATGCCTCAGGTCATCAGGGTAGAGATGCCAC 4355

     3494 TTATAAATGGGCACGAGACCGAGGGGTGGATTTAACCATGGACATTATCTCTCAGGTTATCCATGACTGT 3563
          :|||||:|||||||||||||||||||||||:|||||||||||||| |||:||:||||||||||||||||||
     4356 CTATAAGTGGGCACGAGACCGAGGGGTGGATCTAACCATGGACAGTATTTCCCAGGTTATCCATGACTGT 4425

     3564 GAGACATGTGCTGCCATTAAGCAGGCTAAGAGAGTGAAGCCCCTGTGGTATGGTGGACGCTGGGATAAGT 3633
          |||||:|||||||::| ||:|||||||||:||| |: ||||||| ||:||||||:|||||:||:||| :||:|
     4426 GAGACGTGTGCCACGATCAAGCAGGCCAAGCGGTTGAAGCCGCTATGGTACGGTGGGCGTTGGTCCAAAT 4495

     3634 ATAAGTACGGGGAGGCCTGGCAGGTTGACTACATCACACTGCCACAGACCCGCCAAGGCAAGCGCTATGT 3703
          |||:|||:|||||||||||||||||||||||||||||||||| ||:|||||||||||||||||||||:||
     4496 ATAGGTATGGGGAGGCCTGGCAGATTGACTACATCACACTGCCCCAAACCCGCCAAGGCAAGCGCTACGT 4565

     3704 GCTCACCATGGTGGAAGCAACCACAGGGTGGCTGGAGACACACCCAGTGCCTCACGCCACTGCCCGGAAC 3773
          |||||| ||||||:||||| |||| ||:|:|||:|||| :||||| ||||||||:|||||||||||||||
     4566 GCTCACGATGGTAGAAGCCACCACTGGATGGTTGGAAACCTACCCTGTGCCTCATGCCACTGCCCGGAAC 4635

     3774 ACCATCCTAGGCCTGGAAAAACAAGTCCTGTGGCGACATGGCACCCCAGAGCGAATTGAGTCAGATAATG 3843
          ||||||||:|| || ||||||:||:||||| ||| |:|||||||||||| ||| |:||||||||||||:||||
     4636 ACCATCCTGGGACTTGAAAAGCAGGTCCTTTGGAGGCATGGCACCCCTGAGAGGATTGAGTCAGACAATG 4705

     3844 GAACNCATTTCAAGAACAGCTTAGTTGCTACCTGGGCAAGAGAGCACGGCATTGAGTGGGTGTATCATAT 3913
          |:|| ||||||||||||||||:| :| : :| ||||||| ||:|:|:|:||||||||||||||:|||||
     4706 GGACTCATTTCAAGAACAGCCTTATAAACAGCTGGGCTAGGGAACATGGCATTGAGTGGGTGTACCATAT 4775

     3914 CCCCTACCATGCACCAGCTGCNGGGAAAGTTGAACGGTGTAATGGACTGTTGAAAACCACTTTGAAGGCA 3983
          |||:||:||||||||||||||| || ||||||||||||||||:|||||| |||:| ||||||| :|||||||
     4776 CCCTTATCATGCACCAGCAGCTGGGAAAGTTGAACGGTGCAATGGCCTGCTTAAAACCAGCTTGAAGGCA 4845

     3984 TTGGGTGGAGGGACTTTCAAACACTGGGA--TCAACACTTAGCAAAGGCTACATGGNTAGTCAACACTAG 4051
          :|||||||:||:|||||||:||: ||||||:--|:||:--|||||||:||:||||| |||| |||||: |
     4846 CTGGGTGGGGGAACTTTCAAGAACTGGGAGATTAAT--TTAGCAAAAGCCACATGGTTAGTGAACACCCG 4913

     4052 AGGCTCTGTCAATCGAGCNGGTCCTGCCCAATCAGAACCCCTTCACACTGTAGATGGAGATAAAGTCCCT 4121
          |||:||:|:::::||:||||| ||:|||||||||||| ||:||||:| : || ::||||||||||||:||:||
     4914 AGGTTCCACTAACCGAGCAGGCCCTGCCCAATCTGAGCCCTTTAGAACGACAGATGGAGATAAGGTTCCA 4983

     4122 GTAATACACCTGAGAGGTATGCTAGGGAAAACAGTCTGGATTAACCCTGCNTCAGGCAAAGGCAAACCCA 4191
          ||::|||||: |||||||||||||||||||:|:|||| ||:||:|||||:||||| || :||||||:||| ||||
     4984 GTGGTACATATGAGAGGTATGCTGGGAAAAACTGTTTGGGTTAATTCTGCCTCCAGCAAAGACAATCCCA 5053

     4192 TTCGTGGGNTTGTCTTTGCTCAAGGATCTGGTTNCACCTGGTGGGTNATGCAGNAAGATGGAGAGACACG 4261
          |:|||||| |||||||||||||||:|||:| |||| |||:|||||||| |||||: |:|||||||||||| ||
     5054 TCCGTGGGGTTGTCTTTGCTCAGGGACCGGGTTGCACTTGGTGGGTGATGCAAAAGGATGGAGAGACCCG 5123

     4262 NTGTNTACCTCAAGGGAACTTANCTNT-GGGTAAANAACTCATATTGCTGTATTTGTA 4318
           ||: ||||||||||||:||:| :| |-||||:|| ||:|||: ::|||||::|||||
     5124 GTGCATACCTCAAGGGGACCTTGTTTTAGGGTGAACTACCCATGACACTGTGCTTGTA 5181
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	506	875	ERV3-18_PMaj-I	3982	4430	c	0.7745	1.2623	1629

```
      506 GTTTCACAATAGCGGATAACCTGGGAAATAATGTCCATGGTTAAATCCACCCCTCGGCCTCGT--CCACC 573
          ||:|||||:| ::||||||||||||||||||| ||||||||||||:||||||||||||:|||||--||||:
     4430 GTCTCACAGTCATGGATAACCTGGGAAATACTGTCCATGGTTAGATCCACCCCTCGGTCTCGTGCCCACT 4361

      574 TACAGGTGGC-----------------CTGAGGCATCATGGGCCCATTGAGCCAGGAACAACTCTCCCTT 626
          ||:|||||||-----------------|||||||||||||||||||||:||||:|||||||||||||||||
     4360 TATAGGTGGCATCTCTACCCTGATGACCTGAGGCATCATGGGCCCATCGAGCTAGGAACAACTCTCCCTT 4291

      627 ATG---CTAGTCCAGGTGTG------------------------------------------------A 644
```

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      :||---|:|:||:|:||  ||---------------------------------------------------:
4290  GTGTTGCCAATCTAAGTCTGTCTTTGACACCTCTATCTTTGCAGCCTGATCCACCTGCTCATTGTTTCGG 4221

 645  TGTTCCTCATTAGCTCAGCTTTTGGGCACATGAGCATCCACATGATGAATCTCCACAGAT------TCTA 708
      ||:|:|||||||||||:::||:||||| |||||:|||||:||||||:|:|:||:|||||||:------||||
4220  TGCTCTTCATTAGCCCGACTCTTGGGGACATGGGCATCTACATGACGGACCTTCACAGACAGTTTCTCTA 4151

 709  CTCAAGCAGCAGTGTCCTGCCACACACCAACAGCCCACATGGGCCT--CTCTATGCT-TCAATTAATCTT 775
      |:| :|:|||||:||||:| |||| ||:||:|||||||| || ||::|--:||||||||-:|||||:::|:|
4150  CCCTGGTAGCGATGTCTTTCCACTCATCAGCAGCCCAGATTGGTTTTCCCCTATGCTGCCAATTGGCCCT 4081

 776  CTTCCATCGGTCCAGCCACCCTCAGAGGGGCACTGGCTGTCATCTACAAGTCAGTGTAGAGGTACAGTCT 845
      :||||||:|  ||||||||||:||:|| ||:|-||:||||||::||||:|::|:||||||||||||| ||:|
4080  TTTCCACCTTTCCAGCCATCCCCACAGAG-CATTGGCTACCATCCATGAATCAGTGTAGAGGTAGAGCTT 4012

 846  TGGCTAGTTTTCTGGTTCAGCAATGTCCAG 875
      ||||:| ||:||| |||||||||||||||||
4011  TGGCCACTTCTCTCTTTCAGCAATGTCCAG 3982
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003054_INT#LTR@unknown	675	1051	ERV3-18_PMaj-I	3982	4437	d	0.7604	1.3333	1612

```
 675  CTGGACATTGCTGAACCAGANAACTAGCCAAGACTGTACCTCTACACTGACTTGTAGATGACAGCCAGTG 744
      ||||||||||||||||||||  ||| || |:||||||::|| |||||||||||||:|::|:||||::|||||:||
3982  CTGGACATTGCTGAAAGAGAGAAGTGGCCAAAGCTCTACCTCTACACTGATTCATGGATGGTAGCCAATG 4051

 745  CCCCTCTGAGGGTGGCTGGACCGATAAAAGAAGATTAATTGA-AGCATAGAG--AGGCCCATGTGGGCTG 811
      |:|-| ||:||:|||||||||  |:|::||:|:|:::|||||:|-||||||||:|--::|| || ||||||||
4052  CTC-TGTGGGGATGGCTGGAAAGGTGGAAAAGGGCCAATTGGCAGCATAGGGGAAAACCAATCTGGGCTG 4120

 812  TTGGTGTGTGGCAGGACACTGCCGCTTGAGTAGAA------TCTGTAGAGATTCNTCATGTGGATGCTCA 875
      :||:|| |||| |:|||||::||::|: |:||||||:------|||||::||:|:| ||||||:|||||:||
4121  CTGATGAGTGGAAAGACATCGCTACCAGGGTAGAGAAACTGTCTGTGAAGGTCCGTCATGTAGATGCCCA 4190

 876  TGTGCCCAAAGGCTGAGCTAATGAGGAACATC------------------------------------- 907
      |||| |||||::|::|:|||||||||:||:||:|-------------------------------------
4191  TGTCCCCAAGAGTCGGGCTAATGAAGAGCACCGAAACAATGAGCAGGTGGATCAGGCTGCAAAGATAGAG 4260

 908  -----------ACACCTGGACTAGCA---TAAGGGAGAGTTGTTCCTGGCTCGATGGGCCCATGATGCCT 963
      -----------| ||:|:||:|:|||---:|||||||||||||||||||||:||||||||||||||||||||
4261  GTGTCAAAGACAGACTTAGATTGGCAACACAAGGGAGAGTTGTTCCTAGCTCGATGGGCCCATGATGCCT 4330

 964  CAGG----------------CCACCTGTAGGTGG--ACGAGGCCGAGGGGTGGATTTAACCATGGACAT 1014
      ||||----------------|||||:||:|||||--|||||:||||||||||||||:|||||||||||||
4331  CAGGTCATCAGGGTAGAGATGCCACCTATAAGTGGGCACGAGACCGAGGGGTGGATCTAACCATGGACAG 4400

1015  TATTTCCCAGGTTATCCGCTATTGTGAAACNNNTGCC 1051
      ||||||||||||||||||::: :|||||:|||    ||||
4401  TATTTCCCAGGTTATCCATGACTGTGAGACGTGTGCC 4437
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	580	949	ERV3-18_PMaj-I	3982	4430	d	0.7666	1.3115	1599

```
 580  CTGGACATTGCTGAACCAGAAAACTAGCCAAGACTGTACCTCTACACTGACTTGTAGATGACAGCCAGTG 649
      |||||||||||||||||||  |||:|| |:||||||::|| |||||||||||||:|::|:|||||::|||||:||
3982  CTGGACATTGCTGAAAGAGAGAAGTGGCCAAAGCTCTACCTCTACACTGATTCATGGATGGTAGCCAATG 4051

 650  CCCCTCTGAGGGTGGCTGGACCGATNNAAGAAGATTAATTGA-AGCATAGAG--AGGCCCATGTGGGCTG 716
      |:|-| ||:|:|||||||||  |:| ||:|:|:::|||||:|-||||||||:|--::|| || ||||||||
4052  CTC-TGTGGGGATGGCTGGAAAGGTGGAAAAGGGCCAATTGGCAGCATAGGGGAAAACCAATCTGGGCTG 4120

 717  TTGGTGTGTGGCAGGACACTGCTGCTTGAGTAGAA------TCTGTGGAGATTCATCATGTGGATGCTCA 780
      :||:|| |||| |:|||||::|||:|: |:||||||:------|||||:|:|:|:|:||||||:|||||:||
4121  CTGATGAGTGGAAAGACATCGCTACCAGGGTAGAGAAACTGTCTGTGAAGGTCCGTCATGTAGATGCCCA 4190

 781  TGTGCCCAAANGCTGAGCTAATGAGGAACATC------------------------------------- 812
      |||| ||||||: |::|:|||||||||:||:||:|-------------------------------------
4191  TGTCCCCAAGAGTCGGGCTAATGAAGAGCACCGAAACAATGAGCAGGTGGATCAGGCTGCAAAGATAGAG 4260
```

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 813 -----------ACACCTGGACTAGCA---TAAGGGAGAGTTGTTCCTGGCTCAATGGGCCCATGATGCCT 868
     -----------| ||:|:||:|:|||---:||||||||||||||:||||:||||||||||||||||
4261 GTGTCAAAGACAGACTTAGATTGGCAACACAAGGGAGAGTTGTTCCTAGCTCGATGGGCCCATGATGCCT 4330

 869 CAGG-----------------CCACCTGTAGGTGG--ACGAGGCCGAGGGGTGGATTTAACCATGGACAT 919
     ||||-----------------||||||:||:|||||--|||||:|||||||||||||:|||||||||||
4331 CAGGTCATCAGGGTAGAGATGCCACCTATAAGTGGGCACGAGACCGAGGGGTGGATCTAACCATGGACAG 4400

 920 TATTTCCCAGGTTATCCGCTATTGTGAAAC 949
     ||||||||||||||||||||::| :||||||:||
4401 TATTTCCCAGGTTATCCATGACTGTGAGAC 4430
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003386_LTR#LTR@Gypsy	124	171	Gypsy103-I_Dr	1007	1055	c	0.7755	1.4286	230

```
 124 GCTGAACAATAATCAAAGGAACTAGTGAAGTATGCAGAA-CAAGTAGAA 171
     ||||||||| |||:|:|||||::| ||||||:|:|||||-||:| ||||
1055 GCTGAACAAGAATTAGAGGAATCACTGAAGTGTACAGAAACAGGAAGAA 1007
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	702	885	hAT-1_SIt	3774	3938	c	0.6959	1.9000	349

```
 702 CGGGCTCGAACCGG--CGCCCGGCAAACCCCGGAGNGCTC--CGGT-GCCGCGCTGCCCGCAAGTTTGCC 766
     || |||||--||||--|||||||||:::|| | | | ||:|--|||:-||||||||-|||||| :|---|||
3938 CGTGCTCG--CCGGGCCGCCCGGCGGGCCGCCGCGCGCCCGCCGGCCGCCGCGC-GCCCGCCGG---GCC 3875

 767 GGCCGGCG-CTGCGGCTGGGGGCGAGAANGCGGCGTCTACGCCACTGACTACNCA--GGCGGACAGTTCG 833
     ||||||||-|:|||||------------ ||||||: : ||||:|:| |::| |:--||| | |:|::||
3874 GGCCGGCGGCCGCGGC------------CGCGGCGCGCCCGCCGCCGCCCGCGCGCCGGCCGCCGGCCCG 3817

 834 NCGCAGGCGGCTGCCGGTGCCGGGGCCCTTGTGCCGTCCCCGTCGGCCCCCC 885
      |||-|||||-|:|||||:-||| ||||----|||| ||--|:|||| ||||
3816 CCGC-GGCG-CCGCCGGC-CCGCCGCCC----GCCGGCC--GCCGGCNCCCC 3774
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	960	1271	RTAg4	1985	2277	c	0.6622	1.9792	606

```
 960 CCNCTGTTGCCTGCTGGGGCTGGGACCGCGGCTGCTGGGGCTGTCGCCGCCGGGACTGCTGCCGGCGCGG 1029
     |: ||||||||-|||||  ||||  :||:: |||||||  |||||:| :||:|  :|||||||:| :|| |
2277 CTGCTGTTGC-TGCTGCTGCTGCCATTGCTGCTGCTGCTGCTGTTGGTGCTGCTGCTGCTGCTGCTGCTG 2209

1030 CCGCTGCCGCCGCCGTTCCCGGGTCCGTTGCNGCCCCGGGTCCGCTCCCGCNGCTNCCGCCGNTCCCGC 1099
     |:||||  |||:||:|:|  |:|:  |:|:|||  ||: |:|---:|||  |:|| |||  |||:|  | |:||
2208 CTGCTGACGCTGCTGCTGCTGACGCTGCTGCTGCTGCTG---CTGCTGCTGCTGCTGACGCTGCTGCTGC 2142

1100 TGCCGCTGCCCCTCCCGCCGCTGCTGCTGCTGCCGCCGNTCCTGCTGCTGCCGCCGATTCTGCCACCCCT 1169
     || |||||||: ||---| |||||||||||||||| |||:| | |||||||||||:|:| | ||||:: : ||
2141 TGACGCTGCTGCT---GACGCTGCTGCTGCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGATGCT 2075

1170 GCCGCTCCTGTTGCTCCTGCTGAGACTGTGTCCCGTCACGCCGGTCCCGATCCTGTCCCATCTGCTGCCG 1239
     ||:|||| ||||:|:| ||||:|:::|||| : | ||:: || ||---|:|:||------|||||||:|
2074 GCTGCTGCTGTCGTTGCTGCCGGAGCTGTGGTGGGACATAGCGCTC---ACCTTG------CTGCTGCTG 2014

1240 CTGCTGGGTTTCCTTTCGGTTCCGCTGCCGCC 1271
     ||||||---||  || ::|  |  |:||||||:|||
2013 CTGCTG---TTGCTGCTGCTGCTGCTGCTGCC 1985
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	1406	1438	BARBARA_TM_I	4384	4416	d	0.8788	2.0000	228

```
1406 TTCCGATGATGAGGACTCCGTGGCAGAGGAAGA 1438
     |||||| |||||||||||| ::|||||||||||||
4384 TTCCGAAGATGAGGACTATATGGCAGAGGAAGA 4416
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

| rnd-5_family-1373#LTR@ERVK | 1500 | 1532 | BARBARA_TM_I | 4384 | 4416 | d | 0.8788 | 2.0000 | 228 |

```
1500 TTCCGATGATGAGGACTCCGTGGCAGAGGAAGA 1532
     |||||| |||||||||||| ::|||||||||||||
4384 TTCCGAAGATGAGGACTATATGGCAGAGGAAGA 4416
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	2024	2067	Copia-32_BD-I	4071	4112	d	0.8140	1.7500	204

```
2024 TTTGTTAGGCGTTCAATCTCAGATGCTGACAGGGCAGGGTCCGT 2067
     ||||||::|||| ::--||||||||||||||| ||||||||||| ||
4071 TTTGTTGAGCGGCT--TCTCAGATGCTGACTGGGCAGGGTCGGT 4112
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	2118	2161	Copia-32_BD-I	4071	4112	d	0.8140	1.7500	204

```
2118 TTTGTTAGGCGTTCAATCTCAGATGCTGACAGGGCAGGGTCCGT 2161
     ||||||::|||| ::--||||||||||||||| ||||||||||| ||
4071 TTTGTTGAGCGGCT--TCTCAGATGCTGACTGGGCAGGGTCGGT 4112
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	2081	2122	I-73_AAe	2571	2613	d	0.8140	2.3333	208

```
2081 TATCCAGGTGGCCTTGGCCCCTGCTGTGCT-ACATCTTTCCCA 2122
     ||||| :||:|||||||||||| | |||| -||:||||||||||
2571 TATCCTAGTAGCCTTGGCCCCTTCAGTGCGGACGTCTTTCCCA 2613
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	2175	2216	I-73_AAe	2571	2613	d	0.8140	2.3333	208

```
2175 TATCCAGGTGGCCTTGGCCCCTGCTGTGCT-ACATCTTTCCCA 2216
     ||||| :||:|||||||||||| | |||| -||:||||||||||
2571 TATCCTAGTAGCCTTGGCCCCTTCAGTGCGGACGTCTTTCCCA 2613
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	5043	5885	ERV2-11_GG-I	4332	5169	d	0.6711	1.9826	1319

```
5043 AGATTCCTTACAGACACTGGAGCTTAAAGCTGTAGTGTGGACTTTT--CAAACTTGGCACCACAGACCGG 5110
     |||:|||||:|||| |||||:| :: ||| ||:|::|||:||:|:--||::--||||:----|||:|:|
4332 AGACTCCTTGCAGAATCTGGAACGCGCAGCAGTGGCATGGGCTCTCACCAGG--TGGCG----AGATCAG 4395

5111 T----AAATATTGTATCAGATTCCTTGTATGTGGTAGGAGTTGTTCTACGACTGGAACGAGCTATGCTTA 5176
     |----||||||| |||||||||| ||||:|||||||||||||| || |||||  :|||||:|||| ||||||
4396 TGTGTAAATATAGTATCAGATGCCTTATATGTGGTAGGAGTAGTGCTACGTATAGAACAAGCTTTGCTTA 4465

5177 GAGAGGTGA---AAAACACAACATTGCATGGGCTTTTGCTACATCTGTT-ACAATTGCTGAACCAGAGAA 5242
     ---|| |  ---|:||| ||| |:||-----|||:-----| |||| ||-|||---| | || |:|: ||
4466 ---AGCTCCCCAGAACCCAAGACTG-----GCTC-----AAATCTTTTTACA---GGTTAAGCGGGCAA 4519

5243 CAGA-----ACCCTA----TTTTATTACCCACTTGCGTA------GCCACTTAATGAAAGGGGGTCTTGC 5297
     :|||-----||:||:----|| || :|:||---|||:||------|:|||:||: ||  :||||||| |-
4520 TAGATGATCACTCTGAGCCTTGTAGCATCC---TGCATATCAGGAGTCACCTAGGGACCCAGGGTCTAG- 4585

5298 TATAGGG-AACGACAGAGCTGATGCTTTAGTAGCAGCCCCAGCATGGACTG----GTCCTCCCTTGGACA 5362
     | |||||-|||| : | ||||||||| :| ||--|||:||--------|||:----|| |:|| : |||:
4586 GAGAGGGCAACGCTCGTGCTGATGCGCTTGT--CAGTCC--------ACTACTACGTGCCCCGCAGGATT 4645

5363 GTTTT--GGCCAGGCAAG--GCAATCCCATTCCTTTTTCCATCAGTCTGCAAAGGTGTTA--GCACGACA 5426
     :|||--|||||--|||||--|||:--|||| | | |||||||:|| || ||||:|||:--||||--|
4646 CCTTTCAGGCC--GCAAGAAGCAG--CCATAACATGTTCCATCAATCGGCTAAGGCGTTGAGGCAC--CT 4709

5427 GTTTCACATTTCCTTACATGATGC-----TCAAGGG-ATTGTAAAAGCTTGCCCTGATTGTGGG-AGATT 5489
```

```
        |||: :|-----|| |||-|||:|-----: |||||-|||||: ::|| |||:|| | ||| :-|| :
  4710 GTTCGGC-----CTGACA-GATACAGAAGCAAAGGGCATTGTGTGGGCATGCTCTCAGTGTTCACAGCAC 4773

  5490 AGATCTAGGCCTAGGTGTGGGAGTTAATCCTAAAGGTTTACAGTCCTTAGAATTGTGGCAAATGGATGTG 5559
        :|:|||||:|-||||| |:||||||||||| ||||||||:|: ||| ||: | |||||||||||||
  4774 GGGTCTAGAC-TAGGTCTAGGAGTTAATCCAAAAGGTTTGCAAGCCTGTGAGATTTGGCAAATGGATGTC 4842

  5560 ACACACTTTCCAGAATTTGGCCGTTTGAAATACCTTCATGTGTGTATTGACACCTTTTCCA---TGGCCA 5626
        || ||: | |||||||||||| | ||:||:||: | ||||||:| : |||||||||||||:|---|||---
  4843 ACTCATATGCCAGAATTTGGGAGGTTAAAGTATGTGCATGTATCCCTTGACACCTTTTCTAGAATGG--- 4909

  5627 TATGGGCTACAGCACAAACAGGAGAAAGAACACGACATGTCATCAAACATCTTTACA-TGTGTTTTGCTG 5695
        |:|||||||||:|||||::| || ||||:::|| ||||| :| |::|||-|| |||-: ||:||||| |
  4910 TGTGGGCTACGGCACAGGCTGGTGAAAAGGCAATCCATGTGGTGAGGCAT-TTGACAGCTTGCTTTGCAG 4978

  5696 TTTTAGGGGTTCCTCACTCTATCAAGACAGATAATGGTCCAGCATA--TGGCTCCAAACGC----TTTGC 5759
        |: |:|| || ||||| || ||:|||||||||||||||::|:||--|||-----:| |:----||:||
  4979 TCATGGGTGTGCCTCAGGGGATAAAAACAGATAATGGTCCGACGTACATGG-----GAGGTCGGGTTCGC 5043

  5760 TGATTTTTGTAACCTATGGGGCATTCAGCACACTAGAGGCATACCCCATAACCCCACAGGTCAGGCGATG 5829
        |:||:|||:|: -|:||||| :| |||:|:::| || || |:||||::|||||:|||||:||:|||
  5044 AGGTTCTTGCAGG-TGTGGGGGGTAAAGCATGTCATTGGAATTCTTCATAGTCCCACGGGTCAAGCAATG 5112

  5830 ATTGAACGCGCACACCGTACT-CTAAAGGA--CCTGTTGTTAAAACAAA-AGGGGGGAGA 5885
        || |||| | || ||: | |||-:|||||:|--|||: ||---||||||:-|||:||:|||
  5113 ATAGAAAGAGCTCATAGAACTATTAAAGAATACCTAATG---AAACAAGCAGGAGGAAGA 5169
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	2499	2550	Copia-51_CCri-I	775	826	d	0.7692	1.5000	271

```
  2499 CGGTGTCTTAGATGTGGTAATTTTGGCCATTTCAAGAGTGAATGCCAGGCAC 2550
        |:|||||: ::|||||||||| | |||||||:|||||| :|||||:|:|||||
   775 CAGTGTTACGGATGTGGTAAATATGGCCACTTCAAGCGCGAATGTCGGGCAC 826
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	2593	2644	Copia-51_CCri-I	775	826	d	0.7692	1.7143	263

```
  2593 CAGTGTCTTAGATGTGGTAATTTTGGCCATTTCAAGAGTGAATGCAAGGCAC 2644
        ||||||: ::|||||||||| | |||||||:|||||| :|||||: :|||||
   775 CAGTGTTACGGATGTGGTAAATATGGCCACTTCAAGCGCGAATGTCGGGCAC 826
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	3298	4494	ERV2-12_UCy-I	3931	5124	d	0.6715	1.9080	1890

```
  3298 CACTGATGCAGGGAAACTATCGAAAACTGCTGCCATTGTGTGGAA--AACAGAGAAGCAGTGGCAGAAGA 3365
        ||| ||:||||||||: |||:|:||| || || |||::::||| |--|:|||:||: |--||| | | :
  3931 CACGGACGCAGGGAAGAGATCAAGAACAGCAGCAATTACATGGCAGGAGCAGGGAGTC--TGGAATCATG 3998

  3366 AAGTGCTAAAGGGAACTG-CTGAGGATACCTTGCAGACACTAGAACTTACCGCAGTATGT----TGGGCA 3430
        ||:| || | | || ||-|| ||-|||||:|||||||| ||:||:-|||--||||:-|||----|||||-
  3999 AAATTCTTACTGCAAATGACTTAG-ATACCCTGCAGACCCTGGAG-TTA--GCAGC-TGTGGTATGGGC- 4062

  3431 TTTAATCA--CTGGATGATGAGTTCATTGAATGTAGTAACAGATTCATTGTACGTTGCAGGTGTGGCCCA 3498
        |:|:|-||--||---||| |:| :| ||||||::| || |||||||||| |||||:|| |: ||||| |: |
  4063 TCTGA-CAGTCT---TGAAGGGGCCTTTGAACATTGTTACAGATTCTTTGTATGTAGTTGGTGTTGTGGA 4128

  3499 GCGCATTGAGGATGCAGCAATAAGAGAAACTG-GTAGGCCGAGATTAGTGCGATTGTTCCAACAGCTCCA 3567
        : | || |||||||||| || || |-||:| ||-| |: | |||||:| | :|:||||| |||:|:||
  4129 AAGAATAGAGGATGCTGCCATCA-AGGAAGTGCGGAACCAGAGACTGTTTGAACTGTTCATACAACTTCA 4197

  3568 GCAAGC--TA----TTCGACAGCGCAGCTTGCCGTATTGTGTAATTCACATACGGAGCCATCAGTGG-AG 3630
        : |||||--||----:||| |:|::------|| ||| |:| ||:||:||| |:||:||: |:|||-||
  4198 AAAAGCAGTAAAAATCCGAGAACAT------CCTTATGCTATCATCCATATAAGAAGTCACAAATGGGAG 4261

  3631 TTTGGGTCTGGGACAGGGCAATGCAAAGGCAGATGCACTAGTCTCTGCAGCAATAACGATTCG--CTGCC 3698
        ||||-|:|:|||| |||||||||||| :|||||||: :|| ||------||||||:||---||:--|| |:
  4262 ATTGG-TTTAGGAGAGGGCAATGCTCGGGCAGATAAGCTCGT------AGCAATGAC---TCAAACTTCT 4321
```

```
3699 CACTTA-----GCAAATTCGAGTCTGCCAGGATGGCGCATAGTCAAT--TCCACCAAAATGCTAAAGGTC 3761
     | :|||-----:||||:---| ||-||:|||: |||:|||--|| ||--|:|||||:||||| ||||| :
4322 CCTTTATCAGGACAAAC---ACTC-GCTAGGGAGGCACAT--TCTATGTTTCACCAGAATGCAAAAGGGT 4385

3762 TGATGA-GGGACTTTGAGCTCTCTCAGGCAGAGGCCTCTGGGATTGTGAGAACTTGCCCTCAATGCAGCC 3830
     |-|::|-|||| ||||:: | ||:|| ||||| ||| ||| || || |||:|||||:||:   ||:||:|
4386 T-ACAACGGGAGTTTGGAATATCCCATGCAGATGCCACTGCTATAGTTAGAGCTTGTCCCATTTGTAGTC 4454

3831 ACCAT-----GGGCC-TGGAATTGGCATGGG-AGTAAATCCACGTGGGTTAAAAGCC------CTA--GA 3885
     |:|||-----|||:|-||| || ||-|||||-||| ||:|||||--------|:|||------|||--||
4455 ATCATAATGGGGGTCATGGCATGGG-ATGGGGAGTTAACCCACG--------AGGCCTTTCATCTAATGA 4515

3886 GATATGGCAAATGGATGTCACACACGTACCCAGTTTTGGGAGGCTTAAGTACGTCCATGTCACAGTTGAC 3955
     | |  |||||:|||||||||:|| ||:||| :||:||||| | || ||:||:||:|||||:|| :| ||:
4516 GCTTTGGCAGATGGATGTTACTCATGTAAATAGCTTTGGTCGCCTGAAATATGTTCATGTTACTATAGAT 4585

3956 ACTTACTCGCGGTT-TGTATGGGCCACAGCACAAACAGGGGAAAGGGCTTTGCATGTTAAACGGCACCTG 4024
     || ||-| ||:: |-|:| ||||| ||:|| ||||:| |||||||::|| ||:|||||| | |:||::||
4586 ACATA-TAGCAAATATCTGGGCAACGGCTCAAGCTGGGGAAAAAGCATTACATGTTATAAGACATTTG 4654

4025 ACGCAGT-GTGTGGCAGTCATGGGAGTTCCAGAAACCA-TCAAAACAGATAATGGGCCTGCATATGCCAG 4092
     -:|:|||-|: | |||||:||||||||| ||-||:| |-||||:|||||:||||| ||||||||:::::|
4655 -TGTAGTTGCTTTGCAGTTATGGGAGTGCC-GAAGCAAATCAAGACAGACAATGGCCCTGCATACATTGG 4722

4093 TGAAAGTGTGAAAAAATGGTTTCAACAT--TGGGGAATTAAACATGTAACAGGGATTCCTCACTCCCCTA 4160
     ||: || |||:: |::|--|||:|| ||--|||||||||:|:|:|::| ||:|||:|  | ||:||:||:|
4723 TGGCAGGGTGGGTAGGT--TTTTAAAATCATGGGGAATCAAGCACATTACGGGAATAGCACATTCTCCCA 4790

4161 CCGGACAAGCTGTAGTTGAACGAACCAATAAAACATTAAAAGAATACTTGGATAAGTTTAAGGATGAATT 4230
     |:||:|||| :|||| ||| |::| |||::||| ||:||:::||:||||| ||:: ||:|||--:|||
4791 CTGGGCAAGCAATAGTGGAAAGGGCAAATGGAACCTTGAAAAGATATTTGGAAAAACATAGGGA--GATT 4858

4231 --AGATATTCAGGAGAAGCTAAACAAGGCACTCTTTGTAATGAATCATTTGTGTATTTTTGGGGAT---A 4295
     --||||:||||:||:|:|||||     ||||::|||||||| | |||||||||||||| ||||||||---:
4859 GGAGATGTTCAAGAAAGGCTAATGAAGGTGCTCTTTGTCCTTAATCATTTGTGTATATTTGGGGATTCGG 4928

4296 ATGCAGAACCTGCAGCTCTATTGCATGGTAGAGCTCTGCCCAAAATACAGCCCAACTGCACT------GT 4359
     | |:| |||||||::---|| |:||| :|:||--------|||||---||---|| ||-| |------|
4929 AGGTACCACCTGCGA---TAGTACATTATGGA---------CAAAA---AG---AAATG-AGTAAAAGGG 4980

4360 CAAGG---------TTACTTATAGGGATCCTAAAACAGGTGCATGGAAAGGCCCTGCCGATGTAATATTC 4420
     |||||---------|:|   |||||||:|||||||||||||:: ||| |::||| || :| || ||| :
4981 CAAGGAGGCATGGGTCAGGTATAGGGACCCTAAAACAGGTATTTGGCAGAACCCGGCAAAGGTCCTATAT 5050

4421 TTTGGGAGAGGCTATAACTGTGTTCTAACACCGACAGGACCTCAAT--GGATTCCGGCAAAGTGGACTAA 4488
     | ||:||:|| ||| :||||||:: || || |||||--:|||||--||:| ||:||:||||||||:|:
5051 TGGGGAAGGGGATATCTTTGTGTTTCCACCCCTACAGG--TTCAATTTGGGTGCCAGCGAAGTGGACCAG 5118

4489 GGCAGC 4494
     | ||||
5119 GCCAGC 5124
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	1964	2772	ERV2-12_UCy-I	2612	3420	d	0.6836	1.8254	1845

```
1964 GACGAGTCTGTTTGGGTGGAGCAATGGCCGTTGACAAAAGAGCGGCTGGAGATCGCTCATCAATTGGTAT 2033
     ||:|||:||:| |||||||::|||||||||| |||| ||::||: | ||| |: :|||||| :||||
2612 GATGAGCCTATATGGGTAAAGCAATGGCCTTTGAAAAGGGGAAAGTCTGCAACATGCTCATGCCCTGGTCA 2681

2034 CAGAACAAGTTGAGCAAGGCCATTTAAAAGAGTCTGTTAGTCCCTGGAACACCCCGATATTTGTCGTGCC 2103
     | |||||:   | |:||||| |||:|:||| ||||:: |||||:|||||:|||||| || ||||| :|:
2682 CTGAACAGTATCAACAAGGGCATCTGAAATTGTCTACAAGTCCTTGGAATACCCCTATCTTTGTGATAAA 2751

2104 AAAAAAGTCAGGGAAGTGGCGTTTGCTTCACGACTTGCGAAAGGTTAACGAGCAGATGCAGCCTATGGGA 2173
     :||||||||||||:||:|: |||||:| ||:|:|:|| :||||||:::|:|||||| |||| |||||
2752 GAAAAAGTCAGGAAAATATCGTTTGTTGCATGATTTACGTGAGGTTAATAAACAGATGGAGCCAATGGGT 2821

2174 GCAGTGCAGTCAGGTCTACCGAACCCGGCTATGTTACCTGAAAATTGGCCATTGCTGATAATAGACCTTA 2243
     ||| |:|||:|||| ||:|| ||:|| ||||||||:|| |||||||||:|| |||:|:|:|||||||||||:|
2822 GCACTACAGCCAGGACTGCCTAACCCAGCAATGTTACCTGAGGGATGGCCTCTGTTAATAATAGACCTCA 2891
```

```
2244 AAGACTGTTTTTTCACAATCCGTTTGCACCCTAATGATACTCAGAGGTTTGCGTTTACTCTGCCTCCGCT 2313
     |||||||:|||||:|||||  ||||||:    |:  |||  |: || |  |||||:|||||::||||-- |||
2892 AAGACTGCTTTTTTACAATAGCTTTGCATGAAAGGGATTCCAAGCGCTTTGCATTTACCTTGCC--AGCT 2959

2314 T--AACAGGGCGGAACCAGCGAAACGGTTTGAGTGGACGGTCCTGCCCCAAGGTATGAAGAACAGCCCCA 2381
     |--|||||:| ::: ||||    |:||:|||||:|||||  ||::|||||:|||||:||   : |||||||||
2960 TTGAACAGAGAAAGTCCAGATCAGCGATTTGAATGGACTGTTTTGCCTCAAGGCATTCGCAACAGCCCCA 3029

2382 CCTTGTGTCAGCTCTATGTAGCGGCTGCGCTAGCTCCACTGAGGCAAACATGGCCACATG-TACTAATTT 2450
     ||||||||||||||:||::|||    |:||::||    || :|||||:|||  :||||||||| |-||:||-|||
3030 CCTTGTGTCAGCTTTACATAGATTCCGCATTACAGCCTTTGAGACAACAGTGGCCACAGGCTATTA-TTT 3098

2451 ACCAATACCTAGATGATGTGGTTTT--CTGTCAGCAAC--AATCC-TTTACCTCTGAGCAAAC---TCAG 2512
     |||| ||: |:|||||||:|---|||--:||::--||||--|||| -|||||----|||| |||---|:||
3099 ACCACTATATGGATGATAT---TTTAATTGCT--CAACCTAATCAATTTAC----GAGCCAACAGGTTAG 3159

2513 -------CAAATCCT--TGACACCCTTTCTGCTT-TTGGACTTCAAATAGCACAGGAAAAGCTCCAGACT 2572
     -------|||| |||--||: :| ||||  ||||-||---------||||| | :||:||: |:|||-:|
3160 ATATGTACAAAACCTACTGGGGCGCTTTAGGCTTGTT---------ATAGCTCCAGAGAAAATTCAG-TT 3219

2573 AGC-CAGCCTTGGAAGTATTTAGGGTGGGC--TATCTCTGA-TTCAGTGATCCGTCCCCAGAAACT-GAC 2637
     |:|-| |||||||||:||::|:||:|||||-|:|||| :|-:::||||: |---||||:|||:|-||
3220 AACTCCTCCTTGGAAATACCTGGGATGGACATTGTCTCAAAGCTTGGTGACAC---CCCAAAAATTAGAA 3286

2638 CATATCAACAGAGGTTGTTACCCTGCATGATGCTCAGAAACTATTAGGGGATCTGCAATGGGTACGGCCA 2707
     |-|: |||| ||:|||||||::|: |||||||||||:|||:|::||||  |||:|:||||||| |  ::|||
3287 C-TGAAAACACAGATTGTTACTTTAAATGATGCTCAAAAATTGCTAGGCGATTTACAATGGCTTAAACCT 3355

2708 GTGGTAGGCTTACGGAATGAAGACCTTGCACCTCTGTT--GTCACTGTTGAAAGGCACGGACCCTAC 2772
     :|:||:|| :| | ||||||-| : ||| |:-||| ||--:| :|||||||:||||||:|||||| ||
3356 ATAGTGGGACTTCCGAATGA-GCTATTGGAT-TCTCTTAGGCCCTTGTTGAAGGGCACAGACCCAAC 3420
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	2866	3671	ERV2-12_UCy-I	2612	3417	d	0.6775	1.9024	1821

```
2866 GACGAGTCTGTTTGGGTGGAGCAATGGCCGTTGACAAAAGAGCGGCTGGAGATCGCTCATCAATTGGTAT 2935
     ||:|||:||:| |||||::||||||||||| |||| ||::||: | ||| |: :|||||| :|||||
2612 GATGAGCCTATATGGGTAAAGCAATGGCCTTTGAAAAGGGAAAGTCTGCAACATGCTCATGCCCTGGTCA 2681

2936 CAGAACAAGTTGAGCAAGGCCATTTAAAAGAGTCTGTTAGTCCNTGGAACACCCCGATATTTGTCGTGCC 3005
     | |||||:   | |:|||||  |||:|:||| |||||:: ||||| |||||:|||||| || ||||| :|:
2682 CTGAACAGTATCAACAAGGGCATCTGAAATTGTCTACAAGTCCTTGGAATACCCCTATCTTTGTGATAAA 2751

3006 AAAAAGTCAGGGAAGTGGCGTTTGCTTCACGACTTGCGAAAGGTTAACGAGCAGATGCAGCCTATGGGA 3075
     :||||||||||||||:||:||:|: ||||||:|| ||:|:||:|| :||||||||::|:||||||| |||||
2752 GAAAAAGTCAGGAAAATATCGTTTGTTGCATGATTTACGTGAGGTTAATAAACAGATGGAGCCAATGGGT 2821

3076 GCAGTGCAGTCAGGTCTACCGAACCCGGCTATGTTNCCTGAAAATTGGCCATTGCTGATAATAGACCTTA 3145
     ||| |:|||:||||| ||:|| |||||:|| ||||| ||||| |||||::: ||||| :||:|:||||||||||:|
2822 GCACTACAGCCAGGACTGCCTAACCCAGCAATGTTACCTGAGGGATGGCCTCTGTTAATAATAGACCTCA 2891

3146 AAGACTGTTTTTTTCACAATCCGTTTACACCCTAATGATACTCAGAGGTTTGCNTTNACTCTGCCTCCGCT 3215
     ||||||||:|||||:|||||  |||:||:    |: |||  |: || | ||||| || ||::|||||-- |||
2892 AAGACTGCTTTTTTACAATAGCTTTGCATGAAAGGGATTCCAAGCGCTTTGCATTTACCTTGCC--AGCT 2959

3216 T--AACAGGGCGGAACCAGCGAAACGGTTTGAGTGGACNGTCCTGCCCCAAGGNATGAAGAACAGCCCCA 3283
     |--|||||:| ::: ||||    |:||:|||||:|||||  ||::|||||:|||||| ||   : |||||||||
2960 TTGAACAGAGAAAGTCCAGATCAGCGATTTGAATGGACTGTTTTGCCTCAAGGCATTCGCAACAGCCCCA 3029

3284 CCTTGTGTCAGCTCTATGTAGCGGCTGCGCTAGCTCCACTNAGGCAAACATGGCCACATG-TACTAATTT 3352
     ||||||||||||||:||::|||    |:||::||    || :| ||:|||  :||||||||| |-||:||-|||
3030 CCTTGTGTCAGCTTTACATAGATTCCGCATTACAGCCTTTGAGACAACAGTGGCCACAGGCTATTA-TTT 3098

3353 ACCAATACCTAGATGATGTGGTTTT--CTGTCAGCAAC--AATCC-TTTACNTCTGAGCAAAC---TCAG 3414
     |||| ||: |:|||||||:|---|||--:||::--||||--|||| -|||||----|||| |||---|:||
3099 ACCACTATATGGATGATAT---TTTAATTGCT--CAACCTAATCAATTTAC----GAGCCAACAGGTTAG 3159

3415 -------CAAATCCT--TGACACCCTTTCTGCTT-TTGGACTTCAAATAGCACAGGAAAAGCTCCAGACT 3474
     -------|||| |||--||: :| ||||  ||||-||---------||||| | :||:||: |:|||-:|
3160 ATATGTACAAAACCTACTGGGGCGCTTTAGGCTTGTT---------ATAGCTCCAGAGAAAATTCAG-TT 3219
```

```
3475 AGC-CAGCCTTGGAAGTATTTAGGGTGGGC--TATCTCTGA-TTCAGTGATCCGTCCCCAGAAACT-GAC 3539
     |:|-|   |||||||||:||::|:||:|||:|--:|:|||  :|-:|::|||: |---||||:|||:|-||
3220 AACTCCTCCTTGGAAATACCTGGGATGGACATTGTCTCAAAGCTTGGTGACAC---CCCAAAAATTAGAA 3286

3540 CATATCNACAGAGGTTGTTACCCTGCATGATGCTCAGAAACTATTAGGGGATCTGCAATGGGTACGGCCA 3609
     |-|:   ||| ||:|||||||::|: |||||||||||:||||:|::|||| |||:|:||||||| |  ::||
3287 C-TGAAAACACAGATTGTTACTTTAAATGATGCTCAAAAATTGCTAGGCGATTTACAATGGCTTAAACCT 3355

3610 GTGGTAGGCTTACGGAATGAAGACCTTGCACCTCTGTT--GNCACTGTTGAAAGGCACGGACCC 3671
     :|:||:|| :| | ||||||-| : ||| |:-||| ||--| | :|||||||:|||||:|||||
3356 ATAGTGGGACTTCCGAATGA-GCTATTGGAT-TCTCTTAGGCCCTTGTTGAAGGGCACAGACCC 3417
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	2462	2551	ERV2-12_UCy-I	6711	6800	d	0.7111	1.6250	339

```
2462 TAGAACAAGCAGTATTACAAAATAGAGAAGCCCTAAAATTCCTGTTAATGATTCATGGTTACCAATGTGA 2531
     ||:| || ||||||:||||||||||||| |||| | :| ||::|::|| ||::|||||| :|: :||:|||
6711 TAAATCATGCAGTACTACAAAATAGAGCAGCCATTGATTTTTACTATTGGCCCATGGACATGGATATGA 6780

2532 TGAGTTTAAAGGAATGTGTT 2551
     ||||||:||||:|||||||
6781 GGAGTTTGAAGGGATGTGTT 6800
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	1906	2604	ERV2-11D_GG-I	1897	2601	d	0.6255	1.8966	468

```
1906 GGGTGTGTTTTCGCTGTGG-CAGACCAGGGCACGTTCGTAAACAATGCCCAGCTGGGCCA--GTGTGGTG 1972
     ||:|:|||||:||:|||||-||:| -||| ||| |||----| |||||:-|::| ||||--|| |||||
1897 GGATATGTTTCCGTTGTGGGCAAAA-AGGTCACTATCG----CCATGCCT-GTCGTGCCAAGGTCTGGTG 1960

1973 CACCCTGTGTCAAAATAGCAGTCATGCCGATGA-AGCGTGTAAGAGGCCGGGAAACGGGATAGC-GAGCG 2040
     ::  | |||:||||: :|||  |||||-||: |- ||:||:|||| | |:: |||||||||-|||-|||||
1961 TGAGCAGTGCCAAAGGGGCACGCATGC-GACCACTGCATGCAAGATGACAACAAACGGGA-AGCAGAGCG 2028

2041 CGAATGGGAGTCGCGCG--------AGGATAACAGTAGCTCCCAATGTTGNGAATGGGGCT-----CTCC 2097
     ||||  || :|||:|||--------||||-:||:|| : ||:||:|||:  :------|||-----||||
2029 CGAAGGGCCGCCGTGCGCTGACAGAAGGA-GACGGTCAGTCTCAGTGTCTCA------GCTTCCTGCTCC 2091

2098 CGCCACTACAGGGAGCCTCGGGA-TTGACTTGGCAACAACAGTAGACGTTGTCTTAACTGACACGTCTCC 2166
     || ||:-|::||   |||:||||-|:|||::||||||:||||||:|:||::|||||  :|: :||  :
2092 AGCAACC-CGAGGTTCCTTGGGAATCGATCTGGCAGCAGCAGTAAATGTCACCTTAAAGAATCAATCAGT 2160

2167 CCAAATGATTCCTACTGGG-----TGGC----------GGAAACCGAAAGACTCCTTTGGGGCGTTGTTG 2221
     |||| :|||||:|||||:|||||:-----|||----------||:|--- |||||-||--||:| || ||:|||
2161 GCAAAAAATTCCCACTGGAACCCATGGCCCCATATCTAGGGA---TAAAGA-TC--TTAGTGCTTTATTG 2224

2222 TTAGGTCGGTCGTCGGCAGGACTTAAAGGATTAGTGGTCTTACCAGGCTTAATTGACGCTGATTATACTG 2291
     ||||  :|||  ||:|| ||: | : |||::||:|:||:|:||  |:|| ||:|| ||||||||| |
2225 ATAGGGAGATCTTCAGCTGGGGTAGCAGGGCTAATAGTTTTGCCTGGGGTGATAGATGCAGATTATACAG 2294

2292 GGGAGGTAAAGATAGTAGCACACACCTTGCAACCCC-CCA-TGGTCNTCCCAGCGGGAAGCCGCATAGCN 2359
     |||||::|||| |:|:   || :|:|| ||--|||||-|||-|:::: |: | |:||| | | | ||||||
2295 GGGAAATAATGGTGTGTGCTTATACATT--AACCCCTCCACTAACTATTACTGTGGGTACCAGGATAGCA 2362

2360 CAGGTCGTGCCGCTGACTAATCTGCTGCAAACAATGTCCTTAGG---GAAACGTG-TGAGTAACAT--TC 2423
     ||: | ||-----------|:|:|:|----|| |:::||:|:| :---||:||-||-| ||| || |--
2363 CAATTGGT----------AGTTTAC----AAAAGCATCTTCATACACGAGAC-TGCTCAGTTACCTGAAA 2417

2424 GGGGTGATCGTGGTTTCGGCTCT--TCAGG--GCCAGTGGCGTGTCTGTCGCTGCAGCTAAAATCGCAGC 2489
     |||||||: | || |||||||:||:--:||:|--|||-|| |:| ::|| ::| ||| |:||| :||
2418 GGGGTGACAGAGGGTTCGGTTCCACCCAAGATGCC-GTTGTATCCTTGGTACACCAGATGAAAACTAGGC 2486

2490 CCATTTTGAAAGTCATTCTTTCCTATAATGGAGAGCGGTAC--CCCA---TTCAGCTCCTGCTAGACACG 2554
     ||||   |:: : | |::||: ||----:|||||| ||:|:||--:|||---|||||-|| ||:|:||||||
2487 CCATGGTAGTGCTAACCCTCGCC----GTGGAGCGCAGCACGGTCCAGGTTTCAG-TCATGTTGGACACG 2551

2555 GGGGCAGATGTCACAATGGTCAGCCAAACTCTG---TGGCCGCCGCATTGGCC 2604
     ||:|| ||:|| ||:|| :| ||||||---| |---||||||||| | :||||||
```

```
2552 GGAGCTGACGTGACGATTATAAGCCAA---CAGAAATGGCCGCGGAGTTGGCC 2601
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	1004	1702	ERV2-11D_GG-I	1897	2601	d	0.6246	1.8729	439

```
1004 GGGTGTGTTTTCGCTGTGG-CAGACCAGGGCACGTTCGTAAACAATGCCCAGCTGGGCCA--GTGTGGTG 1070
     ||:|:|||||:||:|||||-||:| -||| |||  |||----| |||||:-|::| ||||--|| |||||
1897 GGATATGTTTCCGTTGTGGGCAAAA-AGGTCACTATCG----CCATGCCT-GTCGTGCCAAGGTCTGGTG 1960

1071 CACCCTGTGTCAAAATAGCAGTCATGCCGATGA-AGCGTGTAAGAGGCCGGGAAACGGGATAGC-GAGCG 1138
     ::  | |||:||||: :||| |||||-||: |- ||:||:|||| | |:: |||||||||-|||-||||| 
1961 TGAGCAGTGCCAAAGGGGCACGCATGC-GACCACTGCATGCAAGATGACAACAAACGGGA-AGCAGAGCG 2028

1139 CGAATGGGAGTCGCGCG--------AGGATAACAGTAGCTCCCAATGTTGGGAATGGGGCTC----TCCC 1196
     |||| || |:||:|||---------||||-:||:|| : ||:||:|||:-----| :| :||----|||
2029 CGAAGGGCCGCCGTGCGCTGACAGAAGGA-GACGGTCAGTCTCAGTGTC-----TCAGCTTCCTGCTCCA 2092

1197 GCCACTACAGGGAGCCTCGGGA-TTGACTTGGCAACAACAGTAGACGTTGTCTTAACTGACACGTCTCCC 1265
     || ||:-|::||  |||:||||-|:|||::||||||:||:||||||:|:|||:::|||| :|: :|| :
2093 GCAACC-CGAGGTTCCTTGGGAATCGATCTGGCAGCAGCAGTAAATGTCACCTTAAAGAATCAATCAGTG 2161

1266 CAAATGATTCCTACTGGG-----TGGC----------GGAAACCGAAAGACTCCTTTGGGGCGTTGTTGT 1320
     |||| :|||||:|||||:-----||||----------||:|--- |||||-||--||:| || ||:||
2162 CAAAAAATTCCCACTGGAACCCATGGCCCCATATCTAGGGA---TAAAGA-TC--TTAGTGCTTTATTGA 2225

1321 TAGGTCGGTCGTCGGCAGGACTTAAAGGATTAGTGGTCTTACCAGGCTTAATTGACGCTGATTATACTGG 1390
     ||||  |:|| ||:|| ||: | :|||::||:||:||:||:|| |:|| ||:|| |||||||| ||
2226 TAGGGAGATCTTCAGCTGGGGTAGCAGGGCTAATAGTTTTGCCTGGGGTGATAGATGCAGATTATACAGG 2295

1391 GGAGGTAAAGATAGTAGCACACACCTTGCAACCCC-CCA-TGGTCGTCCCAGCGGGAAGCCGCATAGCTC 1458
     |||::||| |:|:    || :|:|| ||--||||||-|||-|:::::|: |  |:||| | | | |||| |
2296 GGAAATAATGGTGTGTGCTTATACATT--AACCCCTCCACTAACTATTACTGTGGGTACCAGGATAGCAC 2363

1459 AGGTCGTGCCGCTGACTAATCTGCTGCAAACAATGTCCTTAGG---GAAACGTG-TGAGTAACAT--TCG 1522
     |: | ||-----------|:|:|:|----|| |:::||:|:| :---||:||-||-| ||| || |--  |
2364 AATTGGT----------AGTTTAC----AAAAGCATCTTCATACACGAGAC-TGCTCAGTTACCTGAAAG 2418

1523 GGGTGATCGTGGTTTCGGCTCT--TCAGG--GCCAGTGGCGTGTCTGTCGCTGCAGCTAAAATCGCAGCC 1588
     ||||||: | ||| ||||||:||:--:||:|--|||-|| |::| ::|| ::|  ||| |:||| |  :|||
2419 GGGTGACAGAGGGTTCGGTTCCACCCAAGATGCC-GTTGTATCCTTGGTACACCAGATGAAAACTAGGCC 2487

1589 CATTTTGAAAGTCATTCTTTCCTATAATGGAGAGCGGTAC--CCCA---TTCAGCTCCTGCTAGACACGG 1653
     |||  |:: : | |::||: ||----:|||||  ||:|:||--:|||---|||||-|| ||:|:|||||||
2488 CATGGTAGTGCTAACCCTCGCC----GTGGAGCGCAGCACGGTCCAGGTTTCAG-TCATGTTGGACACGG 2552

1654 GGGCAGATGTCACAATGGTCAGCCAAACTCTG---TGGCCGCCGCATTGGCC 1702
     |:|| ||:|| ||:|| :| ||||||---| |---|||||||| | :||||||
2553 GAGCTGACGTGACGATTATAAGCCAA---CAGAAATGGCCGCGGAGTTGGCC 2601
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	2928	4144	ERV2-9_UCy-I	1948	3158	d	0.6548	1.9661	1431

```
2928 CGCTCCGCAACC-CATGGCAGCGCAGGAGTGGATTTGGAAAC---AG---CAGTAGATACCACGTTGCTC 2990
     |||:| |||||||-||-||||||| | |||  ||||::|||  |||---||---|||||------|||||||||:
1948 CGCCCAGCAACCGCA-GGCAGCTCCGGACTGGACCTGGCAACCTCAGACACAGTA-------ACGTTGCTT 2010

2991 ACCTCGGAGGTCCGTCT--TATCGACAGCAAT---------ATCAAAGGACCTCTGGGCCGTGGTTTGTG 3049
     : :|| :  ||:|:|:|--| :| |||| |||----------|:||--|||||||| ::-:--------:| |
2011 GATTCCACTGTTCATTTGCTCCCTACAGGAATCTTTGGCCCACCA--GGACCTCAAA---------CGAG 2069

3050 TGCTCTGTTGTTAGGTAGGTCTTCTACT----TCAAAGCAGGGCATTTTTGTGTTACCTGGTGTTATTGA 3115
     |||::|:|| ||||:|||||||:|| |||----||----||----||:|| |:||||| :|:|| || ||:|| ||
2070 TGCCTTGCTGGTAGGCAGGTCCTCAACTACCCTC----CAAGGACTCTTTGTCCTGCCAGGAGTCATAGA 2135

3116 TGCAGATTATGTAGGGGTGATTAAGATCATGGTCTATACACTAACGCCGCCTGTTTTTATTCC-CGGGGG 3184
     : ||||:| ||||||||| :|| ||:|||||::|: || |:  : ||:||: | :|:||||-|::||
2136 CTCAGACTCTGTAGGGGAAATAAAAATCATGGCTTGGACTCCCTTTCCACCCTGTACTGTTCCACAAGGT 2205

3185 GAGTCGTATTGCTCAGTTAGTTCCGTTT-----TATTCCTGCGTGCCAAGTCCTGGATCGCAG-GT--TA 3246
```

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        | :-||:||||| ||:||::|||| |||-----:| ||| :|:: || |||-----| |: ||-||--:|
2206 GCA-CGCATTGCGCAATTGATTCCCTTTGCACACAATCCGACACCCCCAGT-----AACAAAGTGTGACA 2269

3247 GAGGAGAAGGAGGGTTTGGCTCCACAGGGTCTCCAGAAGTGTATATGG---CATTAGATATTTTAAAAGG 3313
        |:||:|:||||||:|||||||||||: |:|||||||:|:|-|||||---|| |:|||||:|--||---
2270 CAAGAAAGGGAGGATTTGGCTCCACAGGAACCCCAGAAATAT-TATGGGTGCAGGAAATATCT--AA--- 2333

3314 CAAACCTGAAGTGGTGGTTACAGTGGTAGCTCCATC----TGGGGACTCTAGACAGATGAAAATGATG-- 3377
        :|||||-----|| || |||:| |||-|:|::||----:||||||---||-|||:||| ||| |::--
2334 TAAAC-----GTCCTGTTTATAMATGTA-CCCTGTCACTGCGGGGAC---AG-CAGGTGACAATCACAGG 2393

3378 -ATT---GATACAGGGGCTGACATAACCATAATCTCTACTGCCCAGTGGCCTCTGTCATGGCCTGTAGTT 3443
        -|||---||:||||| ||:||::||| ||| :|||||    ||| ||||||||:|: | |||||: | ::|
2394 AATTTTGGACACAGGTGCCGATGTAAGCATTGTCTCTCAGGCCAAGTGGCCCCCCACTTGGCCCCTCACT 2463

3444 GCAG---CACAGACAGGCATTTTTGGGATTGGAGG---TACC--CAGGCGACCAAAATAAGCCGGGATGT 3505
        | :|---||||:||---| |: :|||:|||||||:||---|| |--||| |-||||||:|------------
2464 GAGGTGTCACAAAC---CCTCACTGGAATTGGGGGAAATAGCTACAGTC-ACCAAAGT------------ 2517

3506 TGTTGCTTT-TTGCTTTC-----------CCGATGGT-GCCTGCGTGTCTACACGGCC--TTACATCAT 3559
        -----||||-|: | |||------------|:||:|||-|| |:-|: |||::| :|||--|||:|:--|
2518 -----CTTTATCTCGTTCAGGTGAAAGGACCTGACGGTCGCATA-GCCTCTGTAAAGCCATTTATAC--T 2579

3560 GACTGTCCC---AGTCACTCTCATTGGCA-GAGACATTCTTAGCCAGATGAGAGCTCAGCTGGTAACCCA 3625
        | |||| ||---:||-|||---:| || |-|||||::| ||| |||-|||:|:::||:|:-----||: ||
2580 GCCTGTGCCTATGGT-ACT---GTGGGGACGAGATGTGCTTTCCCA-ATGGGGACTTAA-----AATGCA 2639

3626 GCC---TTTTCAGGGGCGGCCATTGACGATG---GGCAGCCTTTGTTGAAATTAAAATGGAAATCAGAGA 3689
        |:|---|||||:|: | |||||||||-||::|---|:|| |||-----||||||||| |||||| | ||||
2640 GTCAGATTTTTAATTGGGGCCATTG-CGGCGCGTGACACCCT-----GAAATTAACCTGGAAAACTGAGA 2703

3690 AAGCTATTTGGATAGATCAATGGCCGCTAACA-----CAGGATAGGCTGCAAAAGGTTCAA-GAGTTAGT 3753
        | ||:|||||:|:|||||||||||| || ||-----||:: || ||-|||-----:||| -|| :| ||
2704 CACCTGTTTGGGTGGATCAATGGCCCCTTCCATTGCCCAAACTACGC-GCA-----CTCACTGACCTTGT 2767

3754 GGAAGAACAGCTGGCTGCAGGT-CACATTGTTCCATCAACAAGTTCCTGGAATACNCCAGTTTTTACTAT 3822
        ||||:|||||||-| | ||| -|: || ||:|| || || |||:|||||||: | || || |||::|||
2768 TCAAGAGCAGCTG-CAGAAGGGACGAATAGTCCCCTCTACCAGTCCCTGGAACTCACCTGTGTTTGTTAT 2836

3823 CCCNAAGAAAAGTGGTAAGTGGAGATTGCTTCAAGACCTTAGNGCAGTCAATGCAGTNATGGAGGATATG 3892
        :   ||: ||| |||:||||| | ||||:||||:||: | : |||:|||: || || ||||||:|||
2837 TAAAAAACAAACTGGCAAGTGGCGTTTGCTCCAAGATCTCCGCAAAGTTAATAATGTTATTGAGGACATG 2906

3893 GGGTCCTTACAGCCAGGAATGCCTTCACCTGTNATGATTCCTGAANGTTGGGACTTGTTAATNATTGATT 3962
        ||| ||:| ||||| || |:||||| || :: |||||:||: :| :||||| |:||| :|:| |||||||
2907 GGGACCCTTCAGCCTGGKTTACCTTCCCCAACCATGATCCCCCGAGATTGGCATTTGACAGTCATTGATT 2976

3963 TNAAAGATTGTTTCTTTACCATACCCTTGCATCCAGATGATGCTGAGAAGTTTGCNTTTTCAGTCCCCTC 4032
        | |||||:||:||:|||: :|| ||:||||||||| ||||||||| ||:||||| ||||| ||:||
2977 TGAAAGACTGCTTTTTTGATATTCCTTTGCATCCTGATGATGCTCCTAAATTTGCCTTTTCTGTTCCGAG 3046

4033 TATTAACAAGGCAGAGCC----TGCTAAAAGGTATCATTGGGTTGTTCTTCCTCAGGGCATGAGAAATTC 4098
        :|:||||:|- |||-||||----|||--:||:|||||:||||| :|:| || ||||| ||||:| ::|||
3047 CACTAATA-TGCA-AGCCCCCTTGC--AGAGATATCACTGGGTTTCTTTGCCACAGGGGATGAAATGCTC 3112

4099 TCCAGCCATGTGCCAAACATTTGTGGCATGGGCNCTNGAACCTGTT 4144
        |||:|:|||:|||||: :||:|| ||| ||:: || || ||::||
3113 GCCAACTATATGCCAGTGGTTCGTTGCAAGGATTCTTGACCCCATT 3158
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	6739	6988	ERV2-9_UCy-I	6579	6828	d	0.6440	1.7200	550

```
6739 CCATAATCCCAGCAATTGGCACAACACATGCATTAGATCTTCTTACCAAAATGGGGTGCTGGTTGGCCAA 6808
        |||| ||:||||| || ||||||::|||||||||:||:| :|:| | :|| | || ||||||:| || ||
6579 CCATTATTCCAGCTATAGGCACGGCACATGCACTAAAAACTTTAAATAACCTTGGCTGCTGGCTTGCAAA 6648

6809 AGAAGCCAATGCCACTAGTTTTGCCCTAGAAGAATTATTATTAGACAC--ACAAAGCAATAAGAAA-GCC 6875
        | ||:|:||:||:||||||:|||||:|||::|  ||: |:||:|| :||:||::--|||:  |---||||| |-||
6649 ACAAACTAACGCTACTAGCTCTGCTTTAACAGGCTTGCTAACAGATGTTGACAGTG---TAAGACATGCG 6715

6876 TTGCTGCAAAACCGTGCTGCAATAGACTTTCTGCTTTTGGTCAATGGGCATGGATGTCAAGAGTTTGAAG 6945
```

```
        ::||  |||||||  |  ||:||:||  ||||||:|||||:|:|  |:||:||:||  ||:  |:||  ||||||:|
6716 ACACTTCAAAACAGGGCCGCGATTGACTTTTTGCTTCTAGCCCACGGACACGGTTGCGAGGATTTTGAGG 6785

6946 GTCTCTGTTGCCTCAATTTCTCTGATCATTCTACCTCCATTCA 6988
        |::|  ||||||:  |  ||:::|:||  ||:  |:|||  :  ||:|||||
6786 GCTTATGTTGTATGAACCTTTCGGACAACTCTTTGTCTATTCA 6828
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	2955	3381	ERV2-9_UCy-I	2069	2495	d	0.6444	1.8028	464

```
2955 GTGCTCTGTTGTTAGGTAGGTCTTCTACT----TCAAAGCAGGGCATTTTTGTGTTACCTGGTGTTATTG 3020
        ||||:::||:||  ||||:|||||:||  |||----||----||:||    |:|||||  :|:||  ||  ||:||  |
2069 GTGCCTTGCTGGTAGGCAGGTCCTCAACTACCCTC----CAAGGACTCTTTGTCCTGCCAGGAGTCATAG 2134

3021 ATGCAGATTATGTAGGGGTGATTAAGATCATGGTCTATACACTAACGCCGCCTGTTTTTATTCC-CGGGG 3089
        |:  ||||:|  |||||||||  :||  ||:|||||||||::|:  ||  |:    :  ||:||:    |  :|:|||||-|::||
2135 ACTCAGACTCTGTAGGGGAAATAAAAATCATGGCTTGGACTCCCTTTCCACCCTGTACTGTTCCACAAGG 2204

3090 GGAGTCGTATTGCTCAGTTAGTTCCGTTT-----TATTCCTGCGTGCCAAGTCCTGGATCGCAG-GT--T 3151
        |  :-||:|||||  ||:||:::||||  |||-----:|  |||  :|::  ||  |||-----|  |:  ||-||--:
2205 TGCA-CGCATTGCGCAATTGATTCCCTTTGCACACAATCCGACACCCCCAGT-----AACAAAGTGTGAC 2268

3152 AGAGGAGAAGGAGGGTTTGGCTCCACAGGGTCTCCAGAAGTGTATATGG---CATTAGATATTTTAAAAG 3218
        |  |:||:|:|||||:|||||||||||||||:  |:||||||:|:|-|||||---||    |:|||||:|-||---
2269 ACAAGAAAGGGAGGATTTGGCTCCACAGGAACCCCAGAAATAT-TATGGGTGCAGGAAATATCT-AA--- 2333

3219 GCAAACCTGAAGTGGTGGTTACAGTGGTAGCTCCATC----TGGGGACTCTAGACAGATGAAAATGATG- 3283
        -:|||||-----||    ||  ||||:|    |||-|:|::||----:|||||||---||-|||:|||  |||  |::-
2334 -TAAAC-----GTCCTGTTTATAMATGTA-CCCTGTCACTGCGGGGAC---AG-CAGGTGACAATCACAG 2392

3284 --ATT---GATACAGGGGCTGACATAACCATAATCTCTACTGCCCAGTGGCCTCTGTCATGGCCTGTAGT 3348
        --|||---||:|||||  ||:||::|||  |||  :|||||    |||  |||||||||:|:    |  ||||||:  |  ::
2393 GAATTTTGGACACAGGTGCCGATGTAAGCATTGTCTCTCAGGCCAAGTGGCCCCCCACTTGGCCCCTCAC 2462

3349 TGCAG---CACAGACAGGCATTTTTGGGATTGGAGG 3381
        ||  :|---||||:||---|  |:  :|||:|||||:||
2463 TGAGGTGTCACAAAC---CCTCACTGGAATTGGGGG 2495
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	6294	6376	ERV2-9_UCy-I	6362	6444	d	0.6747	1.6875	260

```
6294 GTATTTTTAATTTGTGGATTTAGAGTCTGGAAAATGATTCCTAGACTTGCTGCAGGAGGCCCTTGCACCT 6363
        ||:||||||:||  ||||||    :|||||::|||||::  :||  ||  :|:       |:|::|||||||||||||||
6362 GTGTTTTTGATATGTGGAAACAGAGCTTGGAAGGGAATACCAGGGAGGTCCGTGGGAGGCCCTTGCACCT 6431

6364 TTGGAAAACTAAC 6376
        ||||:  :|:||||
6432 TTGGGCGATTAAC 6444
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	3530	4378	ERV2-17_UCy-I	3412	4258	d	0.6518	2.1508	1539

```
3530 CAGCCTTTTCAGGGGCGGCCATTGACGATGGGCAGCCT-TTGTTGAAATTAA--AATGGAAATCAGAGAA 3596
        ||||  |||||||  |  |::|||||||:||  ||    :||  |||:-|:  |::|||||||  --:::|  ||---|  ||:|
3412 CAGCATTTTCCGTGATGGCCACTGCAGAGCAGCCGCCCATCCTCAAAATTACCTGGTTGA---CTGAAAC 3478

3597 AGCTATTTGGATAGATCAATGGCCGCTAACACAGGATAGGCTGCAAAAGGTTCAAGAGTTAGTGGAAGAA 3666
        |  ||:|  |||||  ||  ||:|||||:  |:  ||  |:|    |||||||||||:|  |    |:|||||:  ||||:
3479 ACCTGTGTGGATTGAGCAGTGGCCAATGTCAGAAGAATGGCTGCAAATTGCTGACCAATTAGTACAAGAG 3548

3667 CAGCTGGCTGCAGGTCACATTGTTCCATCAACAAGTTCCTGGAATACTCCAGTTTTTACTATCCCTAAGA 3736
        ||:||  |  ||  ||  |||:||      |||||  ::  |||:|  ||||||:||:|:::|||||:|:::||||:||||
3549 CAACTTGAGGCTGGACACGTTCAGCCATCTGTCAGTCCGTGGAACACCCCGATTTTCATCGTCCCCAAGA 3618

3737 AAAGTGGTAAGTGGAGATTGCTTCAAGACCTTAGGGCAGTCAATG--CAGTTATGGAGGATATGGGGTCC 3804
        ||      ||  ||:||||||||||  |  ||  ||:|  ||:: |||  ||||--|||--|||  |:|    |||||  |:
3619 AATCAGGAAATGGAGATTGGTGCATGATTTAAGAAAAGTGAATGAGCAG--ATGCAAGCAATGGGTGCT 3686
```

```
3805 TTACAGCCAGGAATGCCTTCACCTGTAATGATTCCTGAATGTTGGGAC-TTGTTAATTATTGATTTGAAA 3873
     ||:|||||| ||||||||  ||||  :: |||||:||  ||  |||:||-|||||:-:||:|||:||||:
3687 TTGCAGCCTGGAATGCCAGCACCAACCATGATCCCACAAGGGTGGAACATTGTTG-TCATCGATCTGAAG 3755

3874 GATTGTTTCTTTACCATACCCTTGCATCCAGATGATGCTGAGAAGTTTGCATTTTCAGTCCCCTCTATTA 3943
     ||:|||||||||||||||  ||:::|  ||||||| | |||:|: || ::||:|| ||: | ||  || ||| |:|
3756 GACTGTTTCTTTACCATTCCTCTTCATCCACAAGATACCCAGCGATTCGCCTTCACTGTGCCATCTCTCA 3825

3944 ACAAGGCAGAGCCTGCTAAAAGGTATCATTGGGTTGTTCTTCCTCAGGGCATGAGAAATTCTCCAGCCAT 4013
     |||::::||:|:|| ||  |||  |:||| |  |||||| :|||:|||||:|| ||| | |||||||||::|||
3826 ACAGAACAAAACCAGCGAAACGATATGAGTGGGTTTCTCTCCCTCAAGGAATGCGCAATTCTCCGACCAT 3895

4014 GTGCCAAACATTTGTGGCATGGGCTCTTG-AACCTGTTAG-AAAAATGTTT--AAAGATCTGTTGATCTA 4079
     |||:||: ::||||||  |  |||||-||||-:||| :|| |- || || |||--|| |---:| ||||:||
3896 GTGTCAGCTGTTTGTTGACTGGGC-CTTGCGACCAATTCGTCAACATTTTTCCAACG---CGATGATTTA 3961

4080 CCAATATTTAGATGATATTTTGATTTCAGGTAAGAAGCT--TAGAAAGGAGTTTGTCTTGAAAGTGG--- 4144
     :|| ||: |:|||||:||||:| ||| |  : :||: |||:--:| |--||  : |  ||||||- |||---
3962 TCACTACATGGATGACATTCTCATTACCACCAAACAGCCACTGGCA--GATGCAGACTTGAA-TTGGCTC 4028

4145 -TAACAGAACAGTTAGGCCGCAGGGGTCTGACAATAGCCCCTGAGAAGATTCAGCTAACAGAGCCTTGGA 4213
     -|  ||  ||||--| |:|  |||  ||:-|||:|:| | ||  ||:||:|| ||||  | ||| ||:||||
4029 TTCTCACAAC--TGAAGAAGCATGGAT-TGATAGTGTCACCAGAAAAAATACAGCGATCAGCCCCCTGGA 4095

4214 AATATTTAGGATGGACAATATTAAAGTCATCTATTAAGCCACAAAAGATT----CACATTTCAACAGAGA 4279
     ||||:|||||| ||| ::||  :|:|  ||:  |||  ::||  ||:||:  ||----:|||| :|||||----
4096 AATACTTAGGCTGGCTGATCACAGATGCACAAATTCGACCCCAGAAACTTACTTTACATGCCAACA---- 4161

4280 TTCGCACTCTTAC-TGATGTTCAGAGATTGGTAGGAGATATACAGTGGGTCAGAACTCTGTGTGGGA-TT 4347
     ||: :|||-||||-|||||::||||||:|  | |||||: |:|||||||:  |  ||: |-|||:|||-|:
4162 TTTCTACT-TTACATGATGCCCAGAGACTTTTTGGAGACCTGCAGTGGGTTCGTACCAT-TGTAGGAATC 4229

4348 ACCAATGATGATCTCGAGCCGTTAGTTCGCC 4378
     |||||:|||||||||  |:||:||--||:|||
4230 ACCAACGATGATCTGCAACCATT--TTTGCC 4258
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	4927	4995	ERV2-17_UCy-I	4785	4853	d	0.7500	1.7500	227

```
4927 CCTGTCGAAGGGGAAACAGTTTTCACTGATGCAGG--GAAGAAATCTCATAAAG--CTGTTAGTACTTGG 4992
     ||  ||  |||||:::::|||||||:|||||||| ||--|||||----||| ||||--|||||   |:::||||
4785 CCAGTGGAAGGAAGGACAGTTTTTACTGATGCCGGCCGAAGA----TCAAAAAGGGCTGTGTGCGTTTGG 4850

4993 CAA 4995
     |||
4851 CAA 4853
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	4600	4631	LINE1-32_SBi	1578	1609	c	0.8750	1.3333	224

```
4600 AAATCTAGTTCTAATCCATTGAGGGTGCTAGA 4631
     |:||||||||||||||||||||:|||||| :|||
1609 AGATCTAGTTCTAATCCATTAAGGGTGGCAGA 1578
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	6040	6073	RNERVK23	5595	5628	d	0.8529	1.2500	226

```
6040 AAAAATCCCCTGACAGGACAATGGGAAGGTCCTG 6073
     ||::|||||:|| |||||||||||||||:||||||||
5595 AAGGATCCTCTCACAGGACAATGGAAAGGTCCTG 5628
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003595_INT#LTR@Gypsy	6428	6500	Gypsy-38B_NS-LTR	875	948	c	0.7432	1.6667	214

```
6428 TTTAGTTTAAGGCCTAATGTGTCTAGTTTTTGTAGCTGTTTTAGTCTCCTGCTT----GGTATTTTTCTT 6493
     ||  |||||:|:||:| -|| :|:|::||||||   |-|| |||||-||||||:||----|||||||||:||
 948 TTGAGTTTGAAGCTTT-TGGATTTGATTTTTGGTG-TGATTTAG-CTCCTGTTTTTGAGGTATTTTTTTT 882
```

```
6494 TGTCTTA 6500
     |||||||
 881 TGTCTTA 875
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003627_LTR#LTR@unknown	113	194	CATS	1771	1855	d	0.7500	2.2500	283

```
 113 AAACTAACTATATATATTTATACAGAAAA---GAGAAAATTAAAAGAAACTA-CAATATAACACACACAC 178
     ||:|||||||: |:|||||||  ||:::||||---||-|:|||||| ||||| ||-:||| ||||| |||||
1771 AAGCTAACTGGACATATTTTAACGAAAAACTTGA-AGAATTAATAGAAAATAATAATCTAACAAACACAG 1839
```

```
 179 AAGTTAGAAATAACAA 194
     ||:| ||||||||| |||
1840 AAATAAGAAATATCAA 1855
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003665_LTR#LTR@Gypsy	184	269	Nimb-1_PH	2137	2226	d	0.7683	2.5000	240

```
 184 TGCTGCTGCTGCCT---GCCCGG----GACTGCTTCTGGCTGNNTNGCTGCTGCTGCCTGCCCCGGACTG 246
     |||||| |||||||---||:| |----|:||||||||||||||   : ||  |||:|||||--------|:|
2137 TGCTGCGGCTGCCTCTGGCTCTGCTGCGGCTGCTTCTGGCTCTGCTGCGCCTGTTGCCT--------CCG 2198
```

```
 247 CTTCTG-----GCTGCTCGTGTTTCTGC 269
     ||||||-----|||||||| ||:||||||
2199 CTTCTGCTGGGGCTGCTCCTGCTTCTGC 2226
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00003992_INT#LTR@unknown	392	504	LTR3B_Ami	650	788	c	0.6638	1.8000	268

```
 392 CCCCNCNCNGGGGTNNCNNNCCCCACACTGGG--------GTCACTATCCCCACACTGGGGTCTCCA--- 450
     |||| | | ||||: |     :|||||||||||--------||||||::  ||:  | ||||||::|:||---
 788 CCCCTCTCTGGGGCCTCCGCGTCCACACTGGGACTTCTCAGTCACTGCGCCTTCTCTGGGGCTTTCAGCA 719
```

```
 451 ------TCCCCTTCTCAGGGGTTTCTATCCCCACACTGGGGTC---------ACTATCCCCTTCTCAGG 504
     ------:|||||::||:||| |::|::| |||:||||||| ||---------:||:|||||:||||| ||
 718 ACGCTGCCCCCTCTTCGGGGCTCCCCGTGCCCGCACTGGGCTCCTCGGTAAGGCTGTCCCCCTCTCTGG 650
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-57#LTR@ERVL	950	1062	LTR3B_Ami	649	787	d	0.6810	1.4783	258

```
 950 CCCTGAGAAGGGGATAGT---------GACCCCAGTGTGGGGATNGAAACCCCTGAGAAGGGGA------ 1004
     ||| |||||:|||||:||:---------|| |||||||:||| |: |::| |||:||::|||||:------
 649 CCCAGAGAGGGGGACAGCCTTACCGAGGAGCCCAGTGCGGGCACGGGGAGCCCCGAAGAGGGGGCAGCGT 718
```

```
1005 ---TGGAGACCCCAGTGTGGGGATAGTGAC--------CCCAGTGTGGGGATGGTGACCCTAATGAGGG 1062
     ---||:|::|||||| | :|| ::|||||:--------||||||||||: ::|| |:|||:|: |||||
 719 TGCTGAAAGCCCCAGAGAAGGCGCAGTGACTGAGAAGTCCCAGTGTGGACGCGGAGGCCCCAGAGAGGG 787
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004237_LTR#LTR@unknown	67	141	ERV3-5_NuM-LTR	190	265	d	0.7273	1.8000	281

```
  67 AGCTGGGCTGAGCTAGCTAACAGG-TATTCCATACCATATTACATCATCTCAAAAGG-TGTAANANCCAG 134
     |||||: ||:|:||:||:|| :||-||||||||||||||| |||||| | ||||::-|:||| | : ||
 190 AGCTGACCTAAACTGGCCAAAGGGATATTCCATACCATATGACATCATGTGAAAAAACTATAAAACTGAG 259
```

```
 135 TGGGAGT 141
     -||||||
 260 -GGGAGT 265
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004237_LTR#LTR@unknown	364	415	R_Av	23352	23403	d	0.7925	1.3333	202

```
  364 ACAT-AACTTGTGTAAGTGTGTGTTATA-TTGTAGTTTTCTCTTAATTTTCTCT 415
       ||||-|||||: |||||||:|||||| ||-||:|:|||||||||||--||||:|:|
23352 ACATCAACTTAAGTAAGTATGTGTTTTACTTATGGTTTTCTCTT--TTTTTTTT 23403
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004824_LTR#LTR@unknown	424	475	R_Av	23352	23403	d	0.7925	1.3333	202

```
  424 ACAT-AACTTGTGTAAGTGTGTGTTATA-TTGTAGTTTTCTCTTAATTTTCTCT 475
       ||||-|||||: |||||||:|||||| ||-||:|:|||||||||||--||||:|:|
23352 ACATCAACTTAAGTAAGTATGTGTTTTACTTATGGTTTTCTCTT--TTTTTTTT 23403
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004276_LTR#LTR@unknown	36	95	ERV2-12C_PMaj-LTR	209	270	c	0.7581	1.7143	214

```
  36 ACGACT--TCATAGAAGTTAATAGCAAAGGCCGTTTATTCATACGCTCA-CAAAACTTTTATA 95
      ||||||--|||:||||||-|||||::|| |||||||||||: ||: :|:|-|| | |||||||||
 270 ACGACTCTTCACAGAAGT-AATAGTGAACGCCGTTTATTTCTATCTTTAGCACACCTTTTATA 209
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004571_LTR#LTR@unknown	1	68	CR1-1_ACC	4264	4330	c	0.7941	1.8571	332

```
   1 TCATAGAATGGATTGGGTTGGAAAAGACCTCNGAGATCATCAAGTCCAACCCTTGATCCAACCCCACT 68
     |||||||||| : ||:|||||||||||||||: :|||||||:|||||||||| |:::-||| ||||||
4330 TCATAGAATCATTTAGGTTGGAAAAGACCTTCAAGATCATCGAGTCCAACCATCAA-CCATGCCCACT 4264
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004863_INT#LTR@unknown	593	883	EnSpm-1_TC	266	556	d	0.7203	2.1154	241

```
593 AGCTAGT-AACTGAAATGCTGCTGTTAT--GCAATGTAGTAAGC--TTAACTCAATATAGGAAGGGTATT 657
    |||||:|-|| ||||----||-||||||--|:|||----|||||--||||:| |||-||| ||---||||
266 AGCTAATTAAATGAA----TG-TGTTATAAGTAAT----TAAGCAATTAATTAAAT-TAGTAA---TATT 322

658 AGTTAACAATAAGCTATAAATGTAACTTAATT-------TTAATGACTTAAACTTAGACTAAATGAATAT 720
    |-||||:||||| :||| |-| ||| ||||||-------|||: || ||||--|||:--||| | ||||-
323 A-TTAATAATAATTATTA-TTTAAATTAATTAAGGGGTTTAGGGAATTAA--TTAA--TAATTAATA- 385

721 TACTTAGCTAATTAATACATNAACTTAACTTA----TTTTGC---TTAACATT-------TTAACTTTTT 776
    -|:|||: |||||||||-|| ||-|||| |||----||| :|---:||-|||-------||||:: ||
386 -ATTTAAGTAATTAATA-ATTAA-TTAAATTAGTAATTTAACAAATCAA-ATTATAGTAATTAATCAATT 451

777 AACACTATT--TAATTTTACTTAAAATTTCTACTTGCTTAA-CAAATTAAAATGTTATTTTATTAGCTTA 843
    || |:||||--||| |||| |-|||||||| | ||:|||-: ||||||::| ||||| ||||::| |
452 AAAATTATTAGTAAATTTAGT-AAAATTTAAAATTATTTAAATTAATTAAGGTTTTATTAAATTAATTAA 520

844 ACAACTTAATTTTTTGAA-CAAATGAAAAAACATTTTTGTA 883
    |:||:||||:|-----||-|||||||||||||::||||| |||
521 ATAATTAACT-----AATCAAATGAAAAAATGTTTTAGTA 556
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004863_INT#LTR@unknown	990	1060	BEL-4_DAn-LTR	165	241	c	0.7600	2.3333	219

```
990 ATCTTAACTAACTAATGCT-GTATAACTAAAATCATTATGTGTTT-TAATTTACT---TTGG-TAGTTTT 1053
    |||||||| |||||||||:|-|| ||: | |||||:||||| ||:|-||:|||||||---||||-:|||| |
241 ATCTTAAAGAACTAATGTTTGTTTAGGTCAAATTATTATCTGCTTATAGTTTACTAGTTTGGACAGTTGT 172

1054 AAAAGAG 1060
     |||| ||
```

```
171 AAAATAG 165
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00004863_INT#LTR@unknown	1217	1277	ERV17_MD_I	4872	4929	c	0.7797	2.0000	271

```
1217 ATCCATTGCTGACTTCAACCTGTGGAGACAGAAATAAAAACTTTTCTCCAAATTATTAAAA 1277
     ||||||:|:|| |:|::||||||||||||||| ||| |||  ||||||:||---| |||||||
4929 ATCCATCGTTGTCCTTGACCTGTGGAGACACAAAGAAACCCTTTTCCCC---TGATTAAAA 4872
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7126#Unknown	1609	1656	ERV17_MD_I	4882	4929	d	0.8125	1.7500	247

```
1609 GNGAAAAG--TTTCTATTTTTGTCTCCACAGGTTGAAGTCAGCGATGGAT 1656
     | ||||||--|||||--|| |||||||||||||||::|:| ||:|||||||||
4882 GGGAAAAGGGTTTCT--TTGTGTCTCCACAGGTCAAGGACAACGATGGAT 4929
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-26#LINE@CR1	7	477	CR1-C4	4015	4495	d	0.8484	2.0606	2878

```
   7 CAGCACAGGAAGNN-----ACCTGTTGGAGNNAGTCCAGAGNNGG-CCACNAAGATGATNAGAGGGNTGG 70
     |||||||:||||  -----|  |||||||||  :||||||||  ||-|||| |||||||| |||||| |||
4015 CAGCACAAGAAGGATGTGGAGCTGTTGGAGCGGGTCCAGAGGAGGGCCACGAAGATGATCAGAGGGCTGG 4084

  71 AGCACCTCTCCTATGAN---ANGNTGAGAGAATTGGGATTGTTCAGCCTGGAGAAGAGAAGGCTTNGGGG 137
     ||||||||||||||||| ---|  | ||||:||::||||  |||||||||:||||||||||||||||: ||||
4085 AGCACCTCTCCTATGAAGAAAGGTTGAGGGAGCTGGGCTTGTTCAGCTTGGAGAAGAGAAGGCTCCGGGG 4154

 138 TGACCTAATTGNNGCCTTCCAGTACCTGAAGGGAGCCTACAAGAAAGATGGAGAGGGACTTTTTACAAGG 207
     ||||| ||||  ||||||||||||:|||||||||||:||:||| |:|| ||:||  ||||||||||| ||
4155 AGACCTCATTGCGGCCTTCCAGTACTTGAAGGGAGCTTATAAGCAGGAGGGGGACCGACTTTTTACACGG 4224

 208 GCATGTAGTGACAGGACAAGGGGGAATGGCTTCAAACTGAAAGAGAGTAGGTTTAGATTAGATATTAGGA 277
     |  :|||||:||||||||||||||||||||||:|||||:|||||||:| ||:|||||:||||||:||||||
4225 TCTGATAGTGATAGGACAAGGGGGAATGGCTTTAAACTAAAAGAGGGGAGATTTAGGTTAGATGTTAGGA 4294

 278 AGAAATTCTTTACTGTGAGGGTGGTGAGGCACTGGAACAGGTTGCCCAGAGAAGCTGTGGATGCCCCATC 347
     ||||||||||||| |||||||||||||||||:|||| ||||||:|||||||||||||||||||||||||||
4295 AGAAATTCTTTACTCAGAGGGTGGTGAGGCGCTGGCACAGGCTGCCCAGAGAAGCTGTGGATGCCCCATC 4364

 348 CCTGGAAGTGTTCAAGGCCAGGTTGGATGGGGCTNTGAGCAACCTGGTCTAGTGGAAGGTGTCCCTGCCC 417
     ||||||:|:|||||||||||||||||||||||||: ||:||:||||:|||:|||||  ||:: ||||||||
4365 CCTGGAGGCGTTCAAGGCCAGGTTGGATGGGGCCCTGGGCAGCCTGATCTGGTGGNTGGCAGCCCTGCCC 4434

 418 ATGGCAGGGGG-TTGGAACTAGATGATCTTTAAGGTCCCTTCCAACCCAAACCATTCTATG 477
     |||||||||||-||||||||||||||||||||||||||||||||||:||:|||||||||||
4435 ATGGCAGGGGGGTTGGAACTAGATGATCTTTAAGGTCCCTTCCAACCTAAGCCATTCTATG 4495
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
TE_00005070_LTR#LTR@unknown	1	168	CR1-C4	4321	4491	d	0.8353	1.6250	962

```
   1 AGGCCCTGGCACAGG-TGCCCAGAGAAGCTGTGGCTGCCCCATCCCTGGGAGTGTCCAAGGCCAGGTTGG 69
     |||| ||||||||||-||||||||||||||||||| |||||||||||||||::|:||:|||||||||||||
4321 AGGCGCTGGCACAGGCTGCCCAGAGAAGCTGTGGATGCCCCATCCCTGGAGGCGTTCAAGGCCAGGTTGG 4390

  70 ACAGGGCTTGGAGCANCCTGGGCTGGTGGGAGGTGTCCCTGCCCATGGCAGGGGG--TGGNACTGGATGG 137
     |::|||||:: |:||| ||||: ||||||| ||:: |||||||||||||||||||||--||| |||:|||||:
4391 ATGGGGCCCTGGGCAGCCTGATCTGGTGGNTGGCAGCCCTGCCCATGGCAGGGGGGTTGGAACTAGATGA 4460

 138 GCTTTAAGGTCCCTTCCAACCCAAACCATTC 168
     ||||||||||||||||||||||:||:|||||||
4461 TCTTTAAGGTCCCTTCCAACCTAAGCCATTC 4491
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-100#Unknown	193	359	Gypsy-71_PTr-LTR	1185	1330	c	0.7200	1.7222	294

```
 193 CCCAGGGGAGAGGGAAAAGGGAAAAAGGGGACTGAAGATAGGGAAGACACAAACCCAACCTAACAAAACC 262
     ||||||:||||||||||||::::||   |||:|||---|||---||| ||-||||:|-------|: :|||||
1330 CCCAGGAGAGAGGGAAAAAAAACCAGGAGAC---AGA---GGACGA-ACAAGC-------AGAGAAACC 1275

 263 AAATGAANCAAACANACACAATTAAAAAACCTCAAAGA-AGGGGAACAANCATGAAACAATCTCACCCAGG 331
     |:| ||: -|||||  :  |  ||--|||||||||:|:|||-||:|||||-|: || |||||||||----|| |||:
1274 AGAGGAGA-AAACACGAAAAA--AAAAACCTTAGAGAGAGAGGAA-AGCCAGGAAACAA----ACACAGA 1213

 332 ------ACAGGAGAACCACCAACAACCGGAGGGA 359
     ------|||:||||||| |||------|:||||||
1212 GAGAGAACAAGAGAACAACC------CAGAGGGA 1185
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-102#Unknown	139	315	Rex1-1_HRo	3651	3797	d	0.7237	1.7222	256

```
 139 CAATTTGT--TTAGCTNACTTCATNATTTGTTGANCACTTGCTTTTTCACTTGTAGTTCTTTCACNTTTA 206
     |||||||:--||| :| |:||:|| |::||||- || ||:|||||---||| ||-||:|||:|---|||
3651 CAATTTGCCGTTACTTCATTTTATATTCCATTG-TCAATTACTTTT---CTTTTA-TTTTTTTA---TTA 3712

 207 CTACTTTATTCTTNTTCTGATGTNAATGTCACTAGCCGATTTTTTTTTTNANATTTTAGAATTAATCATT 276
     :||-||||||-|| ||||:|| |--------------|||||  ||||| | :||||||:-------||||
3713 TTA-TTTATT-TTATTCTAATTT--------------ATTTTATTTTTCATGTTTTAA-------CATT 3758

 277 TTTCTTTCTC----TTTTTGTTCCAGTGTTCTCCCCCTTATTT 315
     ||||||||||----|||||:||----|:||:||:| |||||||
3759 TTTCTTTCTCACTTTTTTTATT----TATTTTCTCACTTATTT 3797
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-102#Unknown	608	678	CR1-3_HM	157	225	d	0.7286	1.7000	217

```
 608 CAAATGAAAAAAAACT-CTCCAAATTATTAAAAGCTGACAACATACTTTTAAACAAGAGNAATAACAAAGA 676
     |||||:|||||||| -||:|:||||||||||||: :| ||||:---||||||||||::: || |||:||||
157 CAAATAAAAAAAAGAACTTCGAATTATTAAAAAAAAAAGAACAC---TTTAAACAAAGAAAAGAACGAAGA 223

677 AA 678
    ||
224 AA 225
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	1136	1239	ERV2-12_GG-I	1098	1199	d	0.7030	1.5882	311

```
1136 GCCTTTTGAGTGGAAGCTGTTGCAGCAGCTGCGTGCGACGGTCTCTCAATACCAG----CTGCATAGTGA 1201
     ||| :|||:|||||||:||||| :|:||||| || ||||||----|||: |||----|||||:| ||
1098 GCCGCTTGGGTGGAAGTTGTTGCCACAACTGCGGGCCACGGTC----AATGACAGTGGACTGCATGGGGA 1163

1202 ACCGGTAAAGCAAATGCTGGGATATGTCTTTAGCGCAG 1239
     :|| :|:||:||:|| :||:: |||:|--||:| ||||
1164 GCCTATGAAACAGATCTTGAACTATAT--TTGGGGCAG 1199
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	234	337	ERV2-12_GG-I	1098	1199	d	0.6931	1.6471	301

```
 234 GCCTTTTGAGTGGAAGCTGTTGCAGCAGCTGCGTGCGACGGTCTCTCANTACCAG----CTGCATAGTGA 299
     ||| :|||:|||||||:||||| :|:||||| || ||||||----| |: |||----|||||:| ||
1098 GCCGCTTGGGTGGAAGTTGTTGCCACAACTGCGGGCCACGGTC----AATGACAGTGGACTGCATGGGGA 1163

 300 ACCGGTAAAGCAAATGCTGGGATATGTCTTTAGCGCAG 337
     :|| :|:||:||:|| :||:: |||:|--||:| ||||
1164 GCCTATGAAACAGATCTTGAACTATAT--TTGGGGCAG 1199
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-25903#LTR@ERVK	2045	2624	ERV2-10_UCy-I	3725	4298	d	0.6789	1.9186	1367

```
2045 TTTTTAATTTGCGGAGATAGAGCATGGCCTGGTATCCCCAGTAATCCAGTTGGAGGCCCTTGCTATCTA- 2113
     |||:|  ||  |||||:|||||||||||||||||||||  :| ||| | || ||:|| ||||||||||-||-
3725 TTTCTCATATGCGGGGATAGAGCATGGCCTGGTATCCCAGGAAATGCTGTAGGGGGACCTTGCTAT-TAC 3793

2114 ----AGTTAACTTCCTCTGTTCAAGCCTACCATAGCTCAAATGCTGAACA--ACACCTTATG-GAAT--- 2173
     ----|||||||| |----||||::  |||| |||    ||||||:||||:||--|||| |:| |-||||---
3794 GGAAAGTTAACAT----TGTTTGCCCCTAGCATTCATCAAATACTGAGCAGGACACATCAGGAGAATTCA 3859

2174 CGCACCAAA-GCATTACGTAGTAAACGATCAGTGTACCAACTAGGGCCAAACTGTGATAGCA---GGGTA 2239
     || ::|||||-|| |||--|||:|--------------|||:||||||||:|||||:|-|| |---| ::|
3860 CGAGTCAAATGCTTTA--TAGCA--------------CAATTAGGGCCAGACTGTAA-AGAATATGTACA 3912

2240 ACCTTTTGGAGCACTCCCGTCAATATCATC---ACATCGATAATATCTGGAATAGGTACTTCA-AAATCT 2305
     ||--| |||:::| ||: ::|||||||||| ---|||||:  |:|: :||||||:||| | || ||-|:|:|
3913 AC--TATGGGATAAACCTTCTAATATCATAGCAACATTTTTGACTCCTGGAGTAGCTTCTGCACAAGCCC 3980

2306 TTACGGGTAATT-CGACAATTAGCTTGCTGGACTGCGAAAGAACTAAACATAACATCCAAAGTCCTTTCA 2374
     ||:|  --:|:||-|:|  |::||||||||||||||||||||| |||| || | ||:  | ||||| :||:|--||| |
3981 TTGCT--CAGTTACAAAAGCTAGCTTGCTGGACTGGGAAACAAATCAATCTCACATCAGAAAT--TTTAA 4046

2375 G--AATTGACCACTGATGTAGATGGCNTCAGGCATGCAGTCCTGCAAAATAGGGCGGCCATAGACTNCCT 2442
     |--||:|:||||: |||||  |||::| |:||:||| | | :|:||:|||||:||:|:|:||||||:| ::|
4047 GCGAACTAACCATAGATGTTGATAACATTAGACATCAACTATTACAGAATAGAGCAGCTATAGATTTTTT 4116

2443 GCTGTTAGCTCAAGGATATGGGTGCAAAGACTTTGAAAGAATGTGTTGCATGAATCTATCTGATCATTCC 2512
     ||||||:|| |||||||:||||| |||:|||| ||||||:|||||||||||| |||||:|||| ||:|:||:|
4117 GCTGTTGGCACAAGGACATGGTTGCGAAGAATTTGAAGGAATGTGTTGCCTGAATTTATCAGACCACTCT 4186

2513 CAATCTATACATAAAAGCCTTGAGCAGTTGCAAGAANGTTTCAAACAACTGACAGTTTCAACTTCTCCTT 2582
      |:|||||  ||:||||: :|  |   |||:|   |:|||  ::  |  ||: |::|||| :| ||||  :||:|
4187 GAGTCTATTCACAAAAAATTAGCCCAGCTTAAGGAAAACATGAAGAAGTTGACCATAGAAACTAACCCCT 4256

2583 TCAGTGATTGGCTGAAATCGTTGGGCATTACCGGGTGGTTAC 2624
     |::::|  ||||||:||  || ||:|||  ||:  ||||||:|||
4257 TTGACGCTTGGCTAAAMTCCTTAGGCWTTGGGGGGTGGCTAC 4298
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-103#LTR@ERVK	462	615	TguLTRK2e_I	1963	2116	d	0.6667	1.6154	275

```
 462 GGGGCATGCTTTGCATGGGTTACAGCTTGATATGCTAATGGGGCAAGGCCCGTATGCAGC-AACCCCCAG 530
     ||||  |: |:||  :||||: |  ||||: |||||||||:|: ||||||:|| ||:|||||||:|-||:|---||
1963 GGGGGACCCCTTTTATGGAGTCCAGCCAGATATGCTGACTGGGCAGGGACCATATGCAACCAATC---AG 2029

 531 G--CAGCT--CCAGTTTCCTGCCGAGGTCCATAGAGCGTCTGCAGAAGCTG-CCCATAAGGCATTACTGC 595
     |--||:||--||--||||||:|::||::| ||| :| :|||-:||| |::||-||||| |:|| ||:|| :
2030 GTACAACTTACC--TTTCCCGTTGAAATGCATCAATTGTC-ACAGCAATTGGCCCATCAAGCTTTGCTTT 2096

 596 --GTATCCCAACAGAGAAAAAG 615
     --|||-|| :|||-|||||||||
2097 TGGTA-CCAGACA-AGAAAAAG 2116
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-105#Unknown	434	495	Gypsy-31_MAc-I	7369	7435	d	0.7656	2.1667	220

```
 434 GGTCGCTGCCCCAGCCG--GGGCGGGCAGGCCGTGACGCTGCAGGTGGCGGT---GAGACTGGAGCA 495
     ||:||||||||| :||||--|||||  |||||||||:||:|| |:|| |||||---|| |:||||||||
7369 GGCCGCTGCCCAGGCCGAGGGGCGTGCAGGCCGTAACACTCCGGGATGCGGTAGCGATCCCGGAGCA 7435
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-114#Unknown	264	309	Copia-11_RC-I	3351	3397	c	0.7660	1.2500	228

```
 264 AAAGCCAGACTTCCCTCTTGTCCCT-TATTGGTGAATTTGTATCCCT 309
     |||||||:|::|:||| ||||::||-| |:||||||||||||:|||||||
3397 AAAGCCAAATCTTCCTATTGTTTCTGTCTCGGTGAATTTGCATCCCT 3351
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	590	661	Gypsy-22_CT-I	3937	4002	c	0.7500	1.3000	222

```
 590 GCAGCAGGAGCATTGCTTGCTGCTGAGCTCCAAGACAGGCTGCAAATGGTGGCACTG--CTTTGCTGCTG 657
     |||||||||||||--|||||| :|||||| ||:|:|:|:|-----||||:|:|-:||--||||| |::||
4002 GCAGCAGGAGCAT--CTTGCTTTTGAGCTGCAGGGCGGAC-----ATGGCGAC-TTGTTCTTTGATATTG 3941

 658 AGCA 661
     ||||
3940 AGCA 3937
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	1049	1084	Gypsy-4_DWil-I	3041	3079	c	0.8378	1.0000	216

```
1049 TCCCAGATGGCACAAAGTTAAACC---ACTGGAGCAAAC 1084
     |||||:|||||||:||:||||||:---||||||:|||||
3079 TCCCAAATGGCACGAAATTAAACTCGAACTGGAACAAAC 3041
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6256#Unknown	2166	2201	Gypsy-4_DWil-I	3041	3079	c	0.8378	1.0000	216

```
2166 TCCCAGATGGCACAAAGTTAAACC---ACTGGAGCAAAC 2201
     |||||:|||||||:||:||||||:---||||||:|||||
3079 TCCCAAATGGCACGAAATTAAACTCGAACTGGAACAAAC 3041
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	1140	1197	Gypsy-51_MLP-LTR	1494	1552	c	0.8246	1.2000	256

```
1140 AGCAGAAGCCTCCTAAAAAC------CCTCAAAGAAACCCAGCACAAGGGGCAGCTCTTGCTGA 1197
     ||:|||||:: ||||||:||------|:|||||||||||-||||||||||-||---|||||||||
1552 AGTAGAAGTTGCCTAAAGACTGCCTTCTTCAAAGAAACC-AGCACAAGGG-CA---CTTGCTGA 1494
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-117#Unknown	1712	1767	Gypsy-21_SM-I	12951	13007	c	0.7679	1.3750	200

```
 1712 TAATTGCTTGTTTTTTCAGTTTCTT---AATTCTTGTGATTTGTTTGTGCTTTTCATCC 1767
      ||||| :|||||| ||||:|||||||---| ||:||:||:|||--|||||:||||:||:|
13007 TAATTTTTTGTTATTTCGGTTTCTTTTTATTTTTTATGGTTT--TTGTGTTTTTTATTC 12951
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-119#Unknown	134	197	SMAR18	2420	2489	c	0.8235	3.5000	244

```
 134 ACAATTAAAAACAGAA--TATGA-TA-TAATACATATATATACAAATGTGAAAA---GAAANACAACAAT 196
     |||||||||||||| ||--|||||-||-|||||||||||||:|||| || | ||||---:||| ||||-|||
2489 ACAATTAAAAACACAAGTTATGAATAATAATACATATATGTACATATTTCAAAATTCAAAAAACAA-AAT 2421

 197 A 197
     |
2420 A 2420
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-119#Unknown	422	546	ERV3-3_ACD-LTR	152	283	c	0.6953	1.6000	323

```
422 CTCCACCTC--CCTCTCTTTTTATACNTCTTGATACTTCTTGATGATGTCAGATGATATGAAATACCTCT 489
    ||||-||||--|||-||||| :|| |:||: :|||    ||-|||::||| |||:|||||:|||||:|:||
283 CTCC-CCTCTTCCTC-CTTTTTCCACCTTTTATTGCTGAGTG-TGACATCATATGGTATGGAATATCCCT 217

490 TTGGTTG-CTTAAGTCAG--------GTGATGCTTGTCCCTTCTAATCTATGTCACATCCTTTGGG 546
    |||||||-:|||:|||||--------||||||:|| |:::|| |||| ||:|-||:||:| |||
```

216 TTGGTTGGTTTAGGTCAGCTGCCCTGGTGATGTTTCTTTTCTCACATCTTTGCC-CACCCCTAGGG 152

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	26	94	Gypsy20-VV_I	2234	2300	c	0.6957	1.4615	212

```
  26 AAACCCAAACTCAGGTTGCAAATCCAGACAAGGCTATTTCTGCTGTCCCTGCTACAACCACGACTGAAA 94
     |||::|| |||-|| |: ||||||:|-||||:||| ||||:||::||::| || |||:|:||||||||
2300 AAATTCACACT-AGCTCCCAAATCTA-ACAAAGCTTTTTCCACTACCTTTCCTCCAATCATGACTGAAA 2234
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	1514	1582	Gypsy20-VV_I	2234	2300	c	0.6957	1.4615	212

```
1514 AAACCCAAACTCAGGTTGCAAATCCAGACAAGGCTATTTCTGCTGTCCCTGCTACAACCACGACTGAAA 1582
     |||::|| |||-|| |: ||||||:|-||||:||| ||||:||::||::| || |||:|:||||||||
2300 AAATTCACACT-AGCTCCCAAATCTA-ACAAAGCTTTTTCCACTACCTTTCCTCCAATCATGACTGAAA 2234
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	1405	1468	Gypsy20-VV_I	2234	2301	c	0.7077	1.4167	210

```
1405 CAAACTCAGACTG-----CAAANCTGGACAAGGCTATTTCTGCTGTCCCTGCTACAACCACGACTGAAA 1468
     ||||:|||| |||:-----|||| ||:-||||:||| ||||:||::||::| || |||:|:||||||||
2301 CAAATTCACACTAGCTCCCAAATCTA-ACAAAGCTTTTTCCACTACCTTTCCTCCAATCATGACTGAAA 2234
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	465	646	MuDR-1_GAr	8001	8156	c	0.7546	1.9412	526

```
 465 GGAACGAGAAGAAGAAGAAGAGGAACAAGAAGAAGAAGAAAAAGAAGAAGAAGAAGAAGAAGCAGACGAA 534
     |||| |||||-|||||||:|||:||----||||||||||||:||||||||||||||||||||| ||| |||
8156 GGAAGGAGAA-AAGAAGGAGAAGA----GAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA 8092

 535 GGAGCAGCTGCGAGAGAGCAAGAAACTGCTGTGACGATGGAAGGAGCAACGGCACGAGAGCAAAGAGTAG 604
     ||||-----------||| |:||::| ||  ||::|| ||||||:|: ||--| | :|||:-|||||||---
8091 GGAG-----------GAGGAGGAGGCGGCATTGGTGAGGGAAGAAAAAA--GAAAAAGAA-AAAGAG--- 8039

 605 TCACAGCAGAGGAAGGAGCAACGGCGAGAGAAGGAAGAATAG 646
     --- || |||:|||||:|| |: ||-|||:||||||:|| ||
8038 ---AAGGAGAAGAAGAAGAAGAGG-GAGGGAAGGAAAAAAAG 8001
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	890	924	Harbinger-1_PGr	5150	5184	d	0.8571	1.6667	224

```
 890 TTCAGCCTCACCAAAGGCAACCCTCCTTTGGAGGT 924
     ||||||||||:|||:|||||||  |||:|||||||
5150 TTCAGCCTCATCAAGGGCAACCGACCTCTGGAGGT 5184
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	1207	1310	Gypsy-12_ATr-LTR	3135	3237	c	0.6765	1.9375	259

```
1207 GAGAGGGTCAGAAAGGAAGTGAGAGAGGTTCCACGGAGGAGTGGAAGAGTAAAAACACAGGTAGAGAGAA 1276
     |||||:|| |||:||::|| ||||||||----| :|::||| ||||||| :||:| | ||| ||||||:|
3237 GAGAGAGTGAGAGAGAGAGAGAGAGAGG----AAAGGAGAGAGGAAGAGAGAAGAGAGAGGGAGAGAGGA 3172

1277 TAGTACG---TGGGAGAGACGGACAGGAAATAATGAG 1310
     ||:: |--- |:|||||| ||| |||::| |: |||
3171 AAGCGAGAGAGGAGAGAGAGAGGGAGAGGGGAGAGAG 3135
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	2695	2798	Gypsy-12_ATr-LTR	3135	3237	c	0.6765	1.9375	259

```
2695 GAGAGGGTCAGAAAGGAAGTGAGAGAGGTTCCACGGAGGAGTGGAAGAGTAAAAACACAGGTAGAGAGAA 2764
     |||||:|| |||:||::|| ||||||||----| :|::||| ||||||| :||:| | ||| ||||||:|
3237 GAGAGAGTGAGAGAGAGAGAGAGAGAGG----AAAGGAGAGAGGAAGAGAGAAGAGAGAGGGAGAGAGGA 3172

2765 TAGTACG---TGGGAGAGACGGACAGGAAATAATGAG 2798
      ||:: |--- |:|||||| ||| |||::| |: |||
3171 AAGCGAGAGAGGAGAGAGAGGGAGAGGGGAGAGAGAG 3135
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-122#LTR@ERVL	2152	2199	Gypsy-129_GM-I	174	220	d	0.7292	1.0000	209

```
2152 TCTCGTTCTTATTCTCGTTCCAGTTCCCGTTCTCGTTCCCGTTCCCGT 2199
     |||:|||:||:|||||||||::-|||:::|||:|||||||::||||::||
 174 TCTTGTTTTTGTTCTCGTTTTT-GTTCTTGTTTTTCGTTCTTGTTCTTGT 220
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-150#Unknown	1929	1986	Copia-9_HAE-I	663	720	d	0.7586	2.3333	286

```
1929 AAANNTTCACTGGAAAATGTTACCAATGTGGTAAATTTGGGCACAAGGCTCANAATTG 1986
     |||   ||| | ||||:|||||||||:|||:::|||| |||||||||| ||| :||||
 663 AAAAGTTCTCGGGAAGATGTTACCGATGTAACAAATATGGGCACAAGCGTCAAGATTG 720
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-128#Unknown	1982	2039	Copia-9_HAE-I	663	720	d	0.7586	2.0000	280

```
1982 AAANNTTCACTGGAAAATGTTACCAATGTGGTAAATTTGGGCACAAGGCTCAGAATTG 2039
     |||   ||| | ||||:|||||||||:|||:::|||| |||||||||| |||::||||
 663 AAAAGTTCTCGGGAAGATGTTACCGATGTAACAAATATGGGCACAAGCGTCAAGATTG 720
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-129#Unknown	592	649	Copia-9_HAE-I	663	720	c	0.7586	2.0000	280

```
592 CAATTCTGAGCCTTGTGCCCAAATTTACCACATTGGTAACATTTTCCAGTGAANNTTT 649
    ||||::|||  |||||||||| ||||:::||||:|||||||||:|||| | ||| |||
720 CAATCTTGACGCTTGTGCCCATATTTGTTACATCGGTAACATCTTCCCGAGAACTTTT 663
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-138#Unknown	744	801	Copia-9_HAE-I	663	720	c	0.7586	2.0000	280

```
744 CAATTCTGAGCCTTGTGCCCAAATTTACCACATTGGTAACATTTTCCAGTGAANNTTT 801
    ||||::|||  |||||||||| ||||:::||||:|||||||||:|||| | ||| |||
720 CAATCTTGACGCTTGTGCCCATATTTGTTACATCGGTAACATCTTCCCGAGAACTTTT 663
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-143#Unknown	613	670	Copia-9_HAE-I	663	720	c	0.7586	2.0000	280

```
613 CAATTCTGAGCCTTGTGCCCAAATTTACCACATTGGTAACATTTTCCAGTGAANNTTT 670
    ||||::|||  |||||||||| ||||:::||||:|||||||||:|||| | ||| |||
720 CAATCTTGACGCTTGTGCCCATATTTGTTACATCGGTAACATCTTCCCGAGAACTTTT 663
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-98#Unknown	614	671	Copia-9_HAE-I	663	720	c	0.7586	1.7500	274

```
614 CAATTCTGAGCCTTGTGCCCAAATTTACCACATTGGTAACATTTTCCAGTGAANCTTT 671
    ||||::|||  |||||||||| ||||:::||||:|||||||||:|||| | ||| :|||
720 CAATCTTGACGCTTGTGCCCATATTTGTTACATCGGTAACATCTTCCCGAGAACTTTT 663
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

Name								

```
      rnd-1_family-98#Unknown        482   541   L1-30_ACar   1726   1784   c   0.7500   3.5000   202
```

```
 482 ACATTTTTGTTCCAGTTTGTCTGGGTTTTGATTTTTTGCATTNTGTGGTTTACAGCTTCT 541
     ||||||||| || :| ||| |||:| ||||||||||||||-| ||| |: | ||| |||:||||
1784 ACATTTTTCTTGTATTTTTTCTAGTTTTTGATTTTT-GGATTCTAAGCTTTCCAGTTTCT 1726
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-130#Unknown	257	384	Gypsy-18_MN-I	7680	7813	c	0.7164	1.5000	284

```
 257 AAAGCCACNCAAACCACCTAAGAGAAAAAAG-TA-TAAAAGCAATTG------GGCATGAGCAAAAACTG 318
     |||||:|- |||||:|||-|||: ||| ||-||-|||||:|||:||------:||-:||||||||-||
7813 AAAGCTA-ACAAACTACC-AAGAACAAACAGATACTAAAAACAACTGAAATAAGACA-AAGCAAAAA-TG 7748

 319 GGG-AGAAA--TGCCATCGTCTCTGNG-GGGGTAGCTGAGAGCAGCTGCCCTGT--CTCCTCCCACCTCT 382
     |||-|||||--||--|| ||:||| |-:||||||| :-||:||: ||:||||||--|||||||::-|:|||
7747 GGGCAGAAAATTG--ATACTCCCTGGGCAGGGTAGGC-AGGGCGCCTACCCTGTTACTCCTCTT-CTTCT 7682

 383 TC 384
     ||
7681 TC 7680
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-134#Unknown	83	400	TguLTRK2d_I	4899	5189	c	0.6815	1.9762	574

```
  83 AAAACACACTACAATAGGCAAAGCAA---TAGAACTAAGACAA-GTACAGTGACTAAAACAATTGTTAGG 148
     |||||||: ||:||:|: :|||::||---||:|: |||:| ||-|||||:|-||:|||||:|--:|||:|
5189 AAAACACGGTATAACAATTAAAATAACTATAAAGATAAAAAAAAGTACAAT-ACCAAAACGA--ATTAAG 5123

 149 CCTTTTTTCAGAAAATTGAATAACCAACCATTAAATCTTAGCCTTTTCAACCAAATATCAAAAGCAGATG 218
     :||||-----|| ----------|||:||| ||| |:||: || |:|||: ||||||| | ||---
5122 TCTTT-----GAC----------CCAGCCAGAAAAACCTAAAGAATTGAGCCAGTTATCAAATGGAG--- 5071

 219 ATGT----TACCATTAGCTTTTTCATATAGTCTTTTAGCTATCTTAAATCTGCATGAAAAGATACTGAAT 284
     -|||----||| :| ||:|||||||:| |||:||:||::|:: |||| | | :||:|| ||| ||||
5070 -TGTCCACTACGGTAAGTTTTTTCATGTTGTCCTTCAATTGCGTTAACTGTTTATAAATCGATTGAGAAT 5002

 285 GATCTGACAAATTCATGCAGCACATNCA-TCAAATTCNTCAAATCTAAGGCCTTGAGCTAAAAGCTGTGC 353
     |:|| |||||||||||||||||||| | -||||||||| ||: |:|:| | ||||| ||||||||||------
5001 GGTCAGACAAATTCATGCAGCACATGCCCTCAAATTCTTCGCACCCATGTCCTTGTGCTAAAG------ 4938

 354 TGAAAGCAAAGAAAATCAAAAGCAACTATATTTTGCAATAATGCATG 400
     --------|||:||||||||| |||:|| |:|||||:|: | :|||||
4937 --------AAGGAAATCAATTGCAGCTCTGTTTTGTAGAACCGCATG 4899
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-134#Unknown	703	875	Gypsy-12_SLy-LTR	1186	1349	c	0.7195	1.8421	259

```
 703 TCATTTATCATTTGTTGATCACTTGCTTTTTC--ACTTGTA-GTTCTTTCACTTTTACTACTTTATTCTT 769
     |:||||| |:|||| || ||:|:|--||||||||--|:|: |-|-|||||||||---||:|||||||| :|:||
1349 TTATTTTTTATTTTTTTATTATT--CTTTTTCTAATTCGAATGTTCTTTC---TTCACTACTTTTCTTTT 1285

 770 --TTTCNGATGTNAATGTCACTAGTGTTCTCCCCCGATTTTTT------TTTTTTTTGAAGTTTATAGAA 831
     --|||| ||-------|||||--||:|||| ||:| ||::||------||||| |||----|||| :
1284 CTTTTCTTAT-------TCAC--GTATTCTACCTCTTTTCCTTATTCCATTTTTATTG----TTATTATT 1228

 832 TTATTTTTATCATTTTTCTCTTTTTCTTTTTGCTTCTTCCAGT 875
     ||||||||||-||||||||| |:||||| |:|||-:|||||:||:|
1227 TTATTTTTT-TCATTTTATTTTTTTATCTTT-TTTCTTTCAAT 1186
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-134#Unknown	996	1073	EnSpm-3_ALy	3974	4057	d	0.7284	2.0000	203

```
 996 AACCTTAACCTTA--CTCTAATGACTTAAACCTTAA---CCAAATTAACATTACTCTGCTAACTCAATTA 1060
     ||||:|||||:||--|:||||-: |:|||||||:|||---|:|||||||| :||| | ||||:| |||||
```

```
3974 AACCCTAACCCTAAACCCTAA-ACCCTAAACCCTAAACTCTAAATTAAAGTTAAAATCCTAATTAAATTA 4042
```

```
1061 ACACTTTAA--CTCT 1073
     |  ||||||--||||
4043 AATCTTTAAAACTCT 4057
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-134#Unknown	1753	1896	MERMITEJ	1004	1148	c	0.7305	2.1538	259

```
1753 CCGTCTTTCTTCCTTGTGCCGATACCGGGACCCTTCGCAGGGCGGCGGG-GACGGCGGGCGGGA--GCCG 1819
     || |||||||:||::||-||||:|----|||------||:|||||||||||-|:||| |||||||:--||||
1148 CCCTCTTTCCTCTCTG-GCCGGT----GGA------GCGGGGCGGCGGGCGGCGGGGGGCGGGGCGGCCG 1090
```

```
1820 GAACCGCGCGGCGGCGGCCA-GGGC-----TGGGGGGGGGGGGGGGGGGGGGGGNNGGAGCGGG----AAC 1879
     |--| | |||||||||||| |:-||||-----:|| ||| ||:| |||| || || || ||||||----|:|
1089 G--CGGGGCGGCGGCGGGCGCGGGCGGCGGCGGCGGGCGGAGCGGGGCGGCGGGGCGGCGCGGGGCGGAGC 1022
```

```
1880 CGATCG-CGGCCAGCGCG 1896
     |::||-||| |||||||||
1021 AGGCCGGCGGGCAGCGCG 1004
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-138#Unknown	475	611	Penelope-73N1_LMi	197	323	d	0.7200	2.1667	236

```
475 TACAGCTTTTTGGCAATCTTAAACTGCACTTTAACTGAAAATTAACAGAATTTCAAACTTTTAGCTTTTT 544
    |:||||||||||----|: |||||----|||||||------|||||-||||-----||||||||  |||||
197 TGCAGCTTTTT----ACGTTAAA----ACTTTAA------ATTAA-AGAA-----AACTTTTATATTTTT 246
```

```
545 TCA-AACTAACAACATGCTTTTGAACT-----GAACTGTTCTTGTTTGNNNGNNNAGTATGAA-----TN 603
    ||:-||:|||||||||-||||| ||:|-----:|:||||| ||: ||:  :   |:|||:||-----|
247 TCGTAATTAACAACA-GCTTTGCAATTTGGCAAAGCTGTTGTTAATTACGAAAAAAATATAAAGTTTTC 315
```

```
604 TTTAATTT 611
    ||||||||
316 TTTAATTT 323
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-10372#Satellite	332	460	Copia-13B_DR-I	2013	2152	c	0.7068	1.6111	217

```
 332 GGCAG--AGCCAGGGAGGAG--GGAGAGAT-GTC---AGTGCAGGAAGGGGCCAGCGAGGTGGGGCAGCC 393
     |||||--||||||||| ||||--||||:| :-|||---:|||||||:|||: || |::|| ||:||||--
2152 GGCAGGGAGCCAGGGTGGAGCCGGAGGGTCCGTCCAGGGTGCAGGGAGGGAACACCAGGGAGGAGCAG-- 2085
```

```
 394 GGGGGATGCC-----GACAGCCTG-CAGGGAAAGGGGCAGGGCATGGACACCGTAGGACAGCC---TGGG 454
     |:||||:| |-----|| ||:|||:-|||||:|---:|||:||||-||| ::|| ||: ||||---||||
2084 GAGGGACGACCCAGGGAGAGTCTATCAGGGGA---GACAAGGCA-GGAGGTCGGTGGGGAGCCGGCTGGG 2019
```

```
 455 CTGGAG 460
     ||||||
2018 CTGGAG 2013
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-145#Unknown	542	625	Gypsy-6_IS-I	3937	4014	d	0.7711	3.2500	216

```
 542 TCTCTCTGCAGCACTGCCC-GCTTGCCAGGAGCTCCCTGTGTGCCAGGAGCCCGGCCCAGCTCAGCAGCA 610
     ||||||| |||||-:|||||-|:|:||| |-|||||||||  |||| --|||| |--|||||-||||| ||
3937 TCTCTCGGCAGC-TTGCCCTGTTCGCCCG-AGCTCCCTGACTGCCC--AGCCAG--CCAGC-CAGCATCA 3999
```

```
 611 CAGCAACAGCCCAGG 625
     | |||||||:| |||
4000 CTGCAACAGTCAAGG 4014
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-10372#Satellite	1018	1101	Gypsy-6_IS-I	3937	4014	c	0.7711	3.2500	216

```
1018 CCTGGGCTGTTGCTGTGCTGCTGAGCTGGGCCGGGCTCCTGGCACACAGGGAGCTCCTGGCAAGC-GGGC 1086
     ||| |:||||||| ||| |||||-|||||--| |||| --|||| ||||||||:||| -|||:|:|-|||| 
4014 CCTTGACTGTTGCAGTGATGCTG-GCTGG--CTGGCTG--GGCAGTCAGGGAGCTCG-GGCGAACAGGGC 3951

1087 AGTGCTGCAGAGAGA 1101
     |:-||||| |||||| 
3950 AA-GCTGCCGAGAGA 3937
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-152#Unknown	422	488	Copia-80_Mad-I	2574	2642	d	0.7391	1.6250	210

```
 422 CCTCCATCTCAGGC--CTCCCAAACCCCATCCC--ATCTT-CCTCCAAGCCCCATCCCAACCCTCCCAAT 486
     ||||:||||||||| |--||||| --:|||||:|--||||-:||||||-|:|||||:: ||||||:| || 
2574 CCTCTATCTCAGCCTTCTCCCT--CTCCATCTCCTATCTTATCTCCAA-CTCCATCTTCACCCTCTCCAT 2640

 487 NC 488
     | 
2641 CC 2642
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-152#Unknown	575	667	Gypsy-96_GM-I	708	798	c	0.6774	1.7333	227

```
575 GGGGGAATTGTGGGGGTTGTTGGATTGGGCCA--TTTTGGGGAGGGACTGAGTAATTCTGAGTTGGGATG 642
    ||:|::|:|||||::|| |||||||||||:||| |--|| ||| |: |||:||:|:|||  --||| :|| ||| 
798 GGAGAGACTGTGAAGGGTGTTGGATTAGGCGAGGTTGTGGTGGTGGATTGGGCAATA--GAGGCGGTATG 731

643 GAGCTATTTTGGGGTGGGATCGAGG 667
    || :|| |||:|-||||:-||||| 
730 GATTTAGGTTGAG-TGGGG-CGAGG 708
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-152#Unknown	1133	1394	TE-X-12_DR	576	833	c	0.6589	2.2647	518

```
1133 TCTTCCCACACTCGTCACACTTGTAAGGCCTCTCNCCGGTGTGGANNCGCCGGTGGGTGATGAGGTTG-- 1200
     |:|| ||:|||| :|||||||||||: | ::|||| ||:||||||| || ||| :: |:||||||-- 
 833 TTTTGCCGCACTGATCACACTTGTGTGKTTTCTCTCCAGTGTGGATCAGCATGTGTTCATTAAGGTTGAT 764

1201 GAGTTCTGGTTGAATCTCTTCCCGCAGTCGGTGCANTNGAAGGGCCTCTCCCCCGTGTG--------TGT 1262
     ||-|| ||--|||| ||||||||:|| | :||:|| | | ||::||||:|| |||||--------||| 
 763 GA-TTGTG--TGAAACTCTTCCCACACTGAGTACATGTGTACGGTTTCTCTCCAGTGTGAATCATCTTGT 697

1263 GCGCTGATGCACGAGGAGATCTGAGCTGGTCNGANACCTCTTCCCACACTCAGAACACTCGTAGGGACGT 1332
     |:|:|--| ||-----| :|:|| :|:|--| ||-|:|||| :|:|| | ||||||||||||| || : : 
 696 GTGTT--TTCA-----ATGTTTGTACCG--CTGA-ATCTCTTGTCGCAGTGTGAACACTCGTACGGTTTC 637

1333 TCCCCAGTGTGGATCNTCTNGTGGCNGATCAG-GTTGGAGCTNTGACTGAAGCCCTTCCCACA 1394
     ||:||||||||||| ||| ||| | |||:-||| -|||| |:|-|:||: :||||:|||| 
 636 TCTCCAGTGTGGATCCTCTGGTGCCGTTTCAATGTTC-AGCTCTAA-TAAAASTCTTCTCACA 576
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-21#LINE@CR1	1	559	CR1-YB2_Pass	3297	3857	d	0.9571	11.0000	4451

```
   1 AGCAGGTN-AGGGAGGTGATCCTGCCCCTCTACTCAGCCCTNGTGAGGCCACATCTGGAGTGCTGTGTCC 69
     ||||||| -||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||| 
3297 AGCAGGTCGAGGGAGGTGATCCTGCCCCTCTACTCAGCCCTGGTGAGGCCACATCTGGAGTGCTGTGTCC 3366

  70 AGTTCTGGGCTCCTCAGTACAAGAGAGACATGGAGCTCCTGGAGNNGGTCCAGNNGAGGGCNACAAAGAT 139
     ||||||||||||||||||| |||||||||||||||||||||||| ||||||| |||||| ||||||||| 
3367 AGTTCTGGGCTCCTCAGNACAAGAGAGACATGGAGCTCCTGGAGCGGGTCCAGCGGAGGGCNACAAAGAT 3436

 140 GATTAAGGGACTGGAGCATCTCTCTTANGAGGAAAGGCTGAGGGAGCTGGGCCTGTTCAGCCTCGAGAAG 209
     ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||| 
3437 GATTAAGGGACTGGAGCATCTCTCTTACGAGGAAAGGCTGAGGGAGCTGGGCCTGTTCAGCCTCGAGAAG 3506
```

```
 210 AGANGACTGAGAGGGGACCTCATCAATGTCTATAAGTATCTGAAGGGAGGGTGTCAAGAGGATGGAGCCA 279
     ||| |||||||||||||||||||||||||||||||:| |||||||||||||||||||||||||||||||||
3507 AGACGACTGAGAGGGGACCTCATCAATGTCTGTNAGTATCTGAAGGGAGGGTGTCAAGAGGATGGAGCCA 3576

 280 GGCTCTTCTCNGTGGTGCCAAGCAATAGGACAAGAGGCAANGGGCAGAAACTGATGCACAGGAAGTTCCA 349
     ||||||||||| ||||||||:||||||||||||||||||| ||||||||||||||||||||||||||||||
3577 GGCTCTTCTCGGTGGTGCCGAGCAATAGGACAAGAGGCAACGGGCAGAAACTGATGCACAGGAAGTTCCA 3646

 350 CCTGAACATGAGGAAGAACTTCTTTACTGTGNNG-TGACNGNGCACTGGAACAGATTGCCCAGAGAGGTT 418
     |||||||||||||||||||||||||||||||   |-|||| | |||||||||||||||||||||||||||
3647 CCTGAACATGAGGAAGAACTTCTTTACTGTGCGGGTGACCGAGCACTGGAACAGATTGCCCAGAGAGGTT 3716

 419 GTGGAGTCTCCCTCACTGGAGATATTCAAGAACCNTCTGGANNCAATCCTGTGCCATGTGCTCTAGGATG 488
     ||||||||||||||||||||||||||||||||| |||||| |||||||||||||||||||||||||||||
3717 GTGGAGTCTCCCTCACTGGAGATATTCAAGAACCGTCTGGACGCAATCCTGTGCCATGTGCTCTAGGATG 3786

 489 ACCCTGCTTGAGCAGGGAGGTTGGACCAGATGACCCACTGTGGTCCCTTCCAACCTNACCCATTCTGTGA 558
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
3787 ACCCTGCTTGAGCAGGGAGGTTGGACCAGATGACCCACTGTGGTCCCTTCCAACCTGACCCATTCTGTGA 3856

 559 T 559
     |
3857 T 3857
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-27#LINE@RTE-BovB	23	3997	AviRTE_GRu	3	3976	d	0.9701	1.5733	33974

```
 23 TCGNGGGGGAGAAGCTTGCGTGCCCTCATGAGGTTGAGAGCTATGCTGGAGGTGGTTTGTGCCNCCGGTA 92
    ||| ||||:|::|||||||| |||||||||| |||||||||||||:||| :|||||||||||| :|||||
  3 TCGTGGGGAAAGAGCTTGCCTGCCCTCATGATGTTGAGAGCTATGTTGGCAGTGGTTTGTGCCATCGGTA 72

 93 GGGTCTCCCATGCCAGACAGGTCTCAGCTGAAGGGTCAGACAAAGTGTGTCCACGGGCAGGATGGGCTCG 162
    |||||||||||||||||||||||||||||||||||||||||||||| |||||||:||||||||:||||| ||
 73 GGGTCTCCCATGCCAGACAGGTCTCAGCTGAAGGGTCAGACAAAGGGTGTCCATGGGCAGGGTGGGCACG 142

163 CTAGCCNTCTGGCAACCATCCTAGGAGAAGGACAACTCCAACCCCAAACCCGGGCAGATGGAGCTCGCTT 232
    ||||||  |||||||||||||||||||||||||:||||||||||||||||||:|||||||||||::||||
143 CTAGCCATCTGGCAACCATCCTAGGAGAAGAACAACTCCAACCCCAAACCTGGGCAGATGGAGCCTGCTT 212

233 AGCCCTGTAAGGCCATCCATCTAAGAGAAGGATACTCTAACCAAACCTACGTCCTGAGGTATTCACTGTC 302
    |||||||:|||:||||||||||||||||||||||||||||||||||||||||||||||| |||:||||||
213 AGCCCTGCAAGACCATCCATCTAAGAGAAGGATACTCTAACCAAACCTACGTCCTGAGGWMTTCGCTGTC 282

303 ACCGTCCAAGCTCGCTAGGCCGTGGCAGATGAACCTTAGGAGTAAAGGGTGGGGCCAGTTCTGCGCACGC 372
    ||:||||||||||||| |||||||| |||| ||||||||+|||||||||||||+|||||||||| |||
283 ACTGTCCAAGCTCGCTTGGCCGTGGMAGATSAACCTTAGGRGTAAAGGGTGGGGYCAGTTCTGCGCWCGC 352

373 TGTGCCTCACCTAAAAAATCCATTGCGCAGGCTTGAAGGGTTCACCCACATTGCAAAGCCCTGTAGCGAC 442
    |||||||||||||||||+ |||+|||||||+|| ||||||+ |||||||||||||||||||||||||||||
353 TGTGCCTCACCTAAAAAARKCCAYTGCGCAGRCTKGAAGGGYWCACCCACATTGCAAAGCCCTGTAGCGAC 422

443 AGGCGAGGGTCGAAAACGGCAGGTGATAGGAAGCAGCTGGAAGCCGCAGACCCAACCCTGCATGCAGGCG 512
    :  |||||||||||||:|||||||||||||||||||||||||||:||||||||||||||||||||||:|
423 CATCGAGGGTCGAAAATGGCAGGTGATAGGAAGCAGCTGGAAGCTGCAGACCCAACCCTGCATGCAGGTG 492

513 GTTCAGGATATTGGTCATTCGAGACTTGACCCCGGAGATGACAGTCTCTTGNGGCAGCATCCTGAACGAC 582
    |||||||||||:|||||:||||||-||||||||||||||||||||||||| |||||:|||||||:||:
493 GTTCAGGATATTGATCATTTGAGACT-GACCCCGGAGATGACAGTCTCTTGAGGCAGTATCCTGAATGAT 561

583 CAAGCAGCCTTTTCTAGGGACAGCACTGCTTGCTCCACACGGAGAGGGGCCTAGCAAAGGTGGCCTAAAC 652
    |||||||||||||||||||||||||||||||:||:|||:|||||||:||:||||||||||:|||||||
562 CAAGCAGCCTTTTCTAGGGACAGCACTGCTTACTCTACACAGAGAGGGGTCTGGCAAAGGTGACCTAAAC 631

653 AAAGCTCATCTCCACACCCGGTTGGATAACCGCGGCCAACCGGCATCTTCCATGCGGTCAAACAAAAACA 722
    |||||||||||||||||||:| |||||||||::|||||||||||||||||||||||:||:|||||||||
632 AAAGCTCATCTCCACACCTGTTTGGATAACCATGGCCAACCGGCATCTTCCATGCAGTTAAACAAAAACA 701

723 AAGAGATTTCAAAGGCATACACCTGCCTGCAAAGGTGTGCTCAAACTTACACTCGCATGTTGGAACATCA 792
    ||||||||||||||||||||||||||||||||||||||||:|:|||||||||||||||||||||||||||
702 AAGAGATTTCAAAGGCATACACCTGCCTGCAAAGGTGTGTTTAAACTTACACTCGCATGTTGGAACATCA 771
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 793 GAACCATGCTTGATACTGGGGATAGTGGACGTCCTGAGCGTCGTTCTGCTCTAATTGCCCACGAACTGTC  862
     ||||||||||||||||||||||||||||||:||||||||:|:||||||||||||||||:||||:|||||||
 772 GAACCATGCTTGATACTGGGGATAGTGGATGTCCTGAGCATTGTTCTGCTCTAATTGTCCACAAACTGTC  841

 863 ACGGCTCAACATTGACATTGCTGCTCTCAGTGAAGTTCGTCTTCATGAGGAAGGCAGCCTTAAAGAACAT  932
     |||:||||||||||:||||||||||||||||||||||||||||||||||||:|||||||||||||||||||
 842 ACGACTCAACATCGACATTGCTGCTCTCAGTGAAGTTCGTCTTCATGAGAAAGGCAGCCTTAAAGAACAT  911

 933 GGTGCCGGCTACACACTCTACTGGTCAGGCAAACCCAAAACCGAAAGACACCTTTCAGGAGTTGGCTTCA 1002
     |||||:||||||||||||||||||||||||||||||||||||||||||+||+||+||||||||||||||||
 912 GGTGCTGGCTACACACTCTACTGGTCAGGCAAACCCAAAACCGAAAGRCAYCTYTCAGGAGTTGGCTTCA  981

1003 TGATTAAAAACTCCATTGCCTCCAAACTTGAAAATCTGCCGACAGGTCATTCCGATCGCATTATGTCCTT 1072
     |||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||||
 982 TGATTAAAAACTCCATTGCCTCCAAACTTGAAAATTTGCCGACAGGTCATTCCGATCGCATTATGTCCTT 1051

1073 ACGCCTCCCTCTACACAACAAGCAACATGTTGTTCTTTTTAGCGTATATGCCCCAACTCTCCAAGCTGAC 1142
     ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1052 ACGCCTCCCACTACACAACAAGCAACATGTTGTTCTTTTTAGCGTATATGCCCCAACTCTCCAAGCTGAC 1121

1143 CCAGCGGAAAAAGACAAATTCTACACCGACCTGCGCCGCCTCACCCAAAATGTTCCTGCAGATGATAAGA 1212
     |||||||||||||||||||||||||||:||||||||||:|||||||||||||:||||||||||||||||||
1122 CCAGCGGAAAAAGACAAATTCTACACTGACCTGCGCCACCTCACCCAAAAGGTTCCTGCAGATGATAAGA 1191

1213 TCATAATCCTTGGTGACTTCAATGCCAGAGTAGGTAAGAACTCTGAAGCCTGGAAAGGAGTCCTGGGCAA 1282
     |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
1192 TCATAATCCTTGGTGACTTCAACGCCAGAGTAGGTAAGAACTCTGAAGCCTGGAAAGGAGTCCTGGGCAA 1261

1283 GCATGGCGTTGGAAACTGCAACGACAACGGACGCCTCCTGCTAGAGTTTTGTGCAGAACGGCAGCTCACC 1352
     ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||:|||||||||
1262 GCATGGCGTTGGAAACTGCAACGACAACGGATGCCTCCTGCTAGAGTTTTGTGCAGAACAGCAGCTCACC 1331

1353 ATCACCAACACTATCTTTCAACAGAAAGACAGCCTGAAGACAACCTGGATGCATCCTCGATCCAAGCACT 1422
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1332 ATCACCAACACTATCTTTCAACAGAAAGACAGCCTGAAGACAACCTGGATGCATCCTCGATCCAAGCACT 1401

1423 GGCACCTCATTGACTATATCTTAGTACAACAGAGAAATGTCAGCGATGTCCGTCATACTCGAGTGATGCC 1492
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1402 GGCACCTCATTGACTATATCTTAGTACAACAGAGAAATGTCAGCGATGTCCGTCATACTCGAGTGATGCC 1471

1493 GAGTGCAGAATGTCAAACAGACCATCGCCTTGTGCGTTGCAAACTTAACCTCCACTTCAAGCCCAAACCT 1562
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1472 GAGTGCAGAATGTCAAACAGACCATCGCCTTGTGCGTTGCAAACTTAACCTCCACTTCAAGCCCAAACCT 1541

1563 AAGAGAGGCGGCATTCCAAGGAGGAGGCTCCAAGTCAGCAATCTTCAAACAGCCACAGTGAGAGACAGCT 1632
     ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1542 AAGAGAGGCGGSATTCCAAGGAGGAGGCTCCAAGTCAGCAATCTTCAAACAGCCACAGTGAGAGACAGCT 1611

1633 TCCAGGTAAACCTTCAAACTAGACTTAAAGATAATCCCATAGATCCCTCTCCTGAAGCGCTTTGGCAACA 1702
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1612 TCCAGGTAAACCTTCAAACTAGACTTAAAGATAATCCCATAGATCCCTCTCCTGAAGCGCTTTGGCAACA 1681

1703 TATTAAAAATTGCATCCTGCAGTCCTCTGAAGAGTCCCTAGGGTTCTCCTCCAAGAAAAACAAAGACTGG 1772
     |||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1682 TATTAAAAGTTGCATCCTGCAGTCCTCTGAAGAGTCCCTAGGGTTCTCCTCCAAGAAAAACAAAGACTGG 1751

1773 TTTGATGAAAACAATCAAGAGATCCAGGAATTGTTGAAGAAGAAGAGAACTGCTCACCAAGCACACCTTG 1842
     |||||||||||||||||||||||+|||||||||||||||||||||||||||||||||||||||||||||||
1752 TTTGATGAAAACAATCAAGAGATYCAGGAATTGTTGAAGAAGAAGAGAACTGCTCACCAAGCACACCTTG 1821

1843 CTCAGCCATCTTGCCATATAAGAAAAGCCGCCTTTCGTCTTGCATGCAGTAAGCTCCAACAGAAACTTCG 1912
     ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||
1822 CTCAGCCATCTTGCCATATAAGAAAAGCTGCCTTTCGTCTTGCATGCAGTAAGCTCCAACAGAAACTTCG 1891

1913 AGACATCCAGAACAAATGGTGGCTCAACCTAGCAGAAAAGACACAACTATGCGCAGATTTGGGTGACCAA 1982
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||
1892 AGACATCCAGAACAAATGGTGGCTCAACCTAGCAGAAAAGACACAACTATGCGCAGACTTGGGTGACCAA 1961

1983 AGAGGATTCTATGAGGCCCTGAAAGCAGTGTACGGACCCACACACCAGGTTCAAAGCCCCCTACTCAGTG 2052
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1962 AGAGGATTCTATGAGGCCCTGAAAGCAGTGTACGGACCCACACACCAGGTTCAAAGCCCCCTACTCAGTG 2031
```

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2053 CAGATGGTCAAATGCTTCTAACAGATAAAACCTCCATCCTGAACCGATGGTCTGAGCACTTTCAGACTCT 2122
     |||||||||||||||||||| ||||||||||||||||||||||:||||||||||||||||||||||||||
2032 CAGATGGTCAAATGCTTCTCACAGATAAAACCTCCATCCTGAATCGATGGTCTGAGCACTTTCAGACTCT 2101

2123 CTTCAGTGCCAACCGTGTAGTCCAAGGCTCAGCAATTCAGCACATTACACAACAACCGGTGAAACATGAA 2192
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2102 CTTCAGTGCCAACCGTGTAGTCCAAGGCTCAGCAATTCAGCACATTACACAACAACCGGTGAAACATGAA 2171

2193 TTGGATGCAGCCCCTACTATGGGAGAGATACTCAAGGCCATACAACAGGTGAAAACTGGCAAGGCAGCTG 2262
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2172 TTGGATGCAGCCCCTACTATGGGAGAGATACTCAAGGCCATACAACAGGTGAAAACTGGCAAGGCAGCTG 2241

2263 GGGTTGATGGAATTCCACCTGAAATCTGGAAGCATGGAGGTCAAGCACTCCATGCCAAATTCCACGAGCT 2332
     ||||||||||||||||||||||||||||||||||||||||||||||||||:|||||:||||||||||
2242 GGGTTGATGGAATTCCACCTGAAATCTGGAAGCATGGAGGTCAAGCACTCCATGCTAAATTTCACGAGCT 2311

2333 TGTTGTGCGTTGCTGGGAACAAGGGAAACTACCACCAGATCTCCGTGATGCAGTCATCATCACCCTGTAC 2402
     |||||||||||||||||||||||| :|||||||||:|||||||||||||:||||||||||||||||||||
2312 TGTTGTGCGTTGCTGGGAACAAGGCGAACTACCATCAGATCTCCGTGACGCAGTCATCATCACCCTGTAC 2381

2403 AAGAAGAAAGGAGAAAAATCAGACTGCTCAAATTACCGAGGTATTACTTTGCTCTCCATTGCTGGTAAAA 2472
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2382 AAGAAGAAAGGAGAAAAATCAGACTGCTCAAATTACCGAGGTATTACTTTGCTCTCCATTGCTGGTAAAA 2451

2473 TCCTTGCAAGAATACTTCTGAACAGATTAGTACCCACTATTGCAGAAGATCTTCTACCTGAAAGCCAGTG 2542
     ||||||||||||||||||||||||||||||||||||:|||||||||| | |||||||||||||||||||
2452 TCCTTGCAAGAATACTTCTGAACAGATTAGTACCCGCTATTGCAGAASAWCTTCTACCTGAAAGCCAGTG 2521

2543 TGGTTTCAGAGCCAATAGGAGCACCACAGACATGGTGTTTGTTCTCAGACAACTGCAAGAGAAGTGTAGG 2612
     |||||||||||||||||||||||||||||||||||||+||||||||||||||||||||||||||||||||
2522 TGGTTTCAGAGCCAATAGGAGCACCACAGACATGGTRTTTGTTCTCAGACAACTGCAAGAGAAGTGTAGG 2591

2613 GAACAGAACAAAGGTCTCTATGTAACCTTCGTTGACCTCACCAAAGCTTTCGACACTGTGAGCAGAAAG 2682
     |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2592 GAACAGAACAAAGGWCTCTATGTAACCTTCGTTGACCTCACCAAAGCTTTCGACACTGTGAGCAGAAAG 2661

2683 GCCTGTGGCAGATCTTGGAACGTTTAGGATGTCCCCCCAAGTTCCTCAAAATGATCATCCTGCTACATGA 2752
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2662 GCCTGTGGCAGATCTTGGAACGTTTAGGATGTCCCCCCAAGTTCCTCAAAATGATCATCCTGCTACATGA 2731

2753 GGATCAGCGTGGACAAGTCAGATATGGCGATGCACTCTCTGAGCCCTTTCCAATAACCAATGGTGTGAAA 2822
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2732 GGATCAGCGTGGACAAGTCAGATATGGCGATGCACTCTCTGAGCCCTTTCCAATAACCAATGGTGTGAAA 2801

2823 CAAGGTTGCGTTCTTGCACCAACTCTATTCACAATCTTCTTCAGCATGATGCTCCAAAGAGCCACAGCAG 2892
     ||||||||:||||||||||||||||||||||||||||||||||||||||||||||||||||:||||
2802 CAAGGTTGTGTTCTTGCACCAACTCTATTCACAATCTTCTTCAGCATGATGCTCCAAAGAGCCACGGCAG 2871

2893 ACCTCGATGAAGAAAACGGCATCTACATCCGATATCGTACCGATGGAAGCCTATTCAACCTAAGGCGACT 2962
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2872 ACCTCGATGAAGAAAACGGCATCTACATCCGATATCGTACCGATGGAAGCCTATTCAACCTAAGGCGACT 2941

2963 GAAGGCCCACACCAAGACCCTGAATCACCTTGTCCGTGAGCTGCTTTTTGCTGATGATGCCGCCCTCGTT 3032
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
2942 GAAGGCCCACACCAAGACCCTGAATCACCTTGTCCGTGAGCTGCTTTTTGCTGATGATGCCGCCCTCGTT 3011

3033 GCTCACACAGAAGCAGCTCTGCAGCGCTTAACATCCTGCTTTGCAGAGGCTGCTGAGCTTTTTGGGCTGG 3102
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3012 GCTCACACAGAAGCAGCTCTGCAGCGCTTAACATCCTGCTTTGCAGAGGCTGCTGAGCTTTTTGGGCTGG 3081

3103 AAGTCAGCCTGAAGAAGACAGAAGTTCTCTACCAACCTGCACCTCAGGAAGTCTTCCATCATCCTCACAT 3172
     |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||
3082 AAGTCAGCCTGAAGAAGACAGAAGTTCTCTACCAACCTGCACCTCAAGAAGTCTTCCATCATCCTCACAT 3151

3173 CACCATAGGCAATTCAGAGCTTAAGTCAGTCCAGCAGTTCACCTATCTGGGAAGTATCATTTCCTCAGAC 3242
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3152 CACCATAGGCAATTCAGAGCTTAAGTCAGTCCAGCAGTTCACCTATCTGGGAAGTATCATTTCCTCAGAC 3221

3243 GGTAAGATCGACAAAGAGATAGACAACAGGCTAGCAAAGGCATACAGAGCCTTCGGAAAACTCCATAAAA 3312
     ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3222 GGTAAGATCGACAAAGAGATAGACAACAGGCTAGCAAAGGCATACAGAGCCTTCGGAAAACTCCATAAAA 3291

3313 GAGTCTGGTCCAATAAACACCTGAAGAAAAGTACAAAGATCAGTGTCTACAGAGCCATTGTACTGTCTAC 3382
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      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3292 GAGTCTGGTCCAATAAACACCTGAAGAAAAGTACAAAGATCAGTGTCTACAGAGCCATTGTACTGTCTAC 3361

3383 TCTTTTATATGGGTCTGAATCATGGGTCATCTACCGCCACCACCTGCGGCTTCTCGAACGCTTCCATCAG 3452
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3362 TCTTTTATATGGGTCTGAATCATGGGTCATCTACCGCCACCACCTGCGGCTTCTCGAACGCTTCCATCAG 3431

3453 CGCTGCCTCCGTTCAATCCTAAACATCCACTGGTCTGATTACGTGACCAATGTGTCTGTTCTTGAACAGG 3522
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3432 CGCTGCCTCCGTTCAATCCTAAACATCCACTGGTCTGATTACGTGACCAATGTGTCTGTTCTTGAACAGG 3501

3523 CAGGGGTCACCAGTATCGAGGCCATGCTGATGAGAACGCAGCTGCGCTGGGCAGGGCACGTCTCCAGGAT 3592
      |||||||||||||||||||||||||||||||||||:||||||:|||||||||||||||||||||||||||
3502 CAGGGGTCACCAGTATCGAGGCCATGCTGATGAGAATGCAGCTGTGCTGGGCAGGGCACGTCTCCAGGAT 3571

3593 GGAGGATCACCGCCTTCCGAAGATTGTGCTCTATGGTGAACTCGCCACCGGCTGCCGCAAGAGAGGAGCC 3662
      |||||||||||:||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
3572 GGAGGATCACCGCCTCCCAAAGATTGTGCTCTATGGTGAACTCGCCACCGGCTGCCGCAAGAGAGGAGCC 3641

3663 CCGAAGAAGAGATACAAGGACTCCCTGAAACAACACCTCAGCCTTGGCCATATTGACTGCCACCAATGGT 3732
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3642 CCGAAGAAGAGATACAAGGACTCCCTGAAACAACACCTCAGCCTTGGCCATATTGACTGCCACCAATGGT 3711

3733 CCACTCTGGCCTCCAATCGGGATTCATGGAGACACACCATTCACGACGCTGCTGCTTCCTTTGAGAATGC 3802
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3712 CCACTCTGGCCTCCAATCGGGATTCATGGAGACACACCATTCACGACGCTGCTGCTTCCTTTGAGAATGC 3781

3803 ACGGAGAGTCAGTCTTGAGGAGAAAAGACAACGCAGAAAGAACCGTTCCTCACCAATATCGCCAAAGGAG 3872
      |||  |||||||||||||||||||||||||||||||||||||||||||::||||||||:||  |:||||
3782 ACGCAGAGTCAGTCTTGAGGAGAAAAGACAACGCAGAAAGAACCGTTCCTTGCCAATATCACCTAGGGAG 3851

3873 ACGTTCCGCTGTGCCTTTTGTGACCGGACCTGCCTATCCCGTATCGGCCTTTTTAGCCACCAGCACGCTT 3942
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
3852 ACGTTCCGCTGTGCCTTTTGTGACCGGACCTGCCTATCCCGTATCGGCCTTTTTAGCCACCAGCACGCTT 3921

3943 GCAGCAAGCGTGGGTAGTGCCCTTCTCAAATCTTCGTTCGCGAAGCCTAGCCATG 3997
      |||||||||:||||||||||||||||||||||||||||||||||||| |||||||
3922 GCAGCAAGCATGGGTAGTGCCCTTCTCAAATCTTCGTTCGCGAAGCCAAGCCATG 3976
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-29#Unknown	558	664	Coprina_Cc1	21	127	c	0.8131	4.0000	558

```
558 TGGGTTAGGGGTACTCTTAGAGTTACGCTTAGAATTAGGGTTAGGGTTAGGGTTAGGGCTAGGGTTAGGG 627
    ||||||||||| ||   ||||:|||| | ||||::||||||||||||||||||||||:|||||||||||
127 TGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG 58

628 TTAGGCTAANCTTTTGTGTTAGGATTAGGCTTTGGGT 664
    ||||| | |   || | ||||||:||||| || ||||
 57 TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT 21
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-29#Unknown	199	304	Coprina_Cc1	21	127	c	0.8037	4.0000	521

```
199 TGGGTTAGGGGTACTCTTAGAGTTACGCTTAGAATTAGGGTTAGGGTT-GGGTTAGGGCTAGGGTTAGGG 267
    ||||||||||| ||   ||||:|||| | ||||::|||||||||||||-|||||||||:|||||||||||
127 TGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGG 58

268 TTAGGCTAANCTTTTGTGTTAGGATTAGGCTTTGGGT 304
    ||||| | |   || | ||||||:||||| || ||||
 57 TTAGGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT 21
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-29#Unknown	919	1022	TREP_CE	123	226	d	0.7500	6.5000	365

```
919 GGGTTAGGGGTACTCTTAGAGTTACGCTTAGAATTAGGGTTAGGGTTAGGGTTAGGGCTAGGGTTAGGGT 988
    || |||||| ||   ||||||: ||| ||||||: ||||| ||||| ||||| |||||  :|||| |||||  |
123 GGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGGCT 192
```

```
989 TAGGCTAANCTTTTGTGTTAGGATTAGGCTTTGG 1022
    ||||||| |   :|| |  ||||| |||||||| ||
193 TAGGCTTAGGCTTAGGCTTAGGCTTAGGCTTAGG 226
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-31#LINE@CR1	1	1123	CR1-2_ACC	2708	3852	d	0.8291	2.7612	7467

```
   1 TGGANTTNTGNAAAGNNTTTGACACNGTNNNNNANNA------TNTCTCTAAANTGNAGAGANATGGATT 64
     |||| || || ||:|  ||||||||| ||        |   |------| ||||||||| || ||||| |||||||
2708 TGGACTTCTGTAAGGCCTTTGACACGGTCCCCCACAACATCCTTCTCTCTAAATTGGAGAGATATGGATT 2777

  65 TGATGNATNNANNNNTNNNTGGATAAGNAATTGGCTGGATGGTTNCANNCAN-GNGTNNNNGTCNNC--- 130
     ||||| || |    |    ||||||:|| |||||||:|||||||||: ||  || -| ||    ||| |---
2778 TGATGGATGGACTGTTCGGTGGATGAGGAATTGGTTGGATGGTCGCATCCAGAGGGTAGTGGTCAACGGC 2847

 131 TNAATGTCCAAGTGGAGANCAGTGANNAGTGGTGTTCCTCAGGGGTNNGTATTGGGACNNGTNCTGTTTA 200
     | |||||||||::|||||| ||||||    |||||||||:||||||||||  |||:||||||  || |||||||
2848 TCAATGTCCAGATGGAGATCAGTGACAAGTGGTGTCCCTCAGGGGTCCGTACTGGGACCAGTACTGTTTA 2917

 201 ACATCTTTGTNAGTGACATGGACAGTGGGATTGAGTGCACCCTCAGCAAGTTTGCNGATGACACCAAGCT 270
     |:||||||::| |:||||||:|||||||||||:||||||||||||||||||||||||:||||||||||||||
2918 ATATCTTCATCAATGACATAGACAGTGGGATCGAGTGCACCCTCAGCAAGTTTGCAGATGACACCAAGCT 2987

 271 GTGTGGTGCAGTTGACACACTGGAGGGAAGGGATGCCATCCAGAGGGACCTGGACAGGCTTGAGAGGTGG 340
     | ||||||||:|||||||||::|: ||||||  :||||||||||||||||||||||||:|||||||:||||
2988 GAGTGGTGCGGTTGACATGCCTGAGGGACAGGATGCCATCCAGAGGGACCTGGACAAGCTTGAGAAGTGG 3057

 341 GCCTGTGNGAACCTCATGAAGTTCAACAAGGCCAAGTGCAAGGTCCTGCACCTGGGTCAGGGCAATCCCA 410
     |||::|| ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||:|||
3058 GCCCATGTGAACCTCATGAGGTTCAACAAGGCCAAGTGCAAGGTCCTGCACCTGGGTCAGGGCAACCCCC 3127

 411 AGCACAAATACAGGCTGGGNNGAGAATGGATTGAGAGCAGCCCTGAGGAGAAGGACTTGGGGGTGTTGGT 480
     :|:|: |||||||||||||||  :  ||| ||||||||||||||| ||||||||||||||||||||::||||
3128 GGTATCAATACAGGCTGGGGGATGAAGGGATTGAGAGCAGCCCTGCGGAGAAGGACTTGGGGGTACTGGT 3197

 481 GGATGAGAAGCTNNACATGACCNAGCAATGTGCACTTGCAGCCCAGAAAGCCAACCNTATCCTGGGCTGC 550
     ||||||:||||||  |||||| | :||||||||||:||:||||||||||||||||| |||||||||||||||
3198 GGATGAAAGCTGGACATGAGCTGGCAATGTGCGCTCGCAGCCCAGAAAGCCAACCGTATCCTGGGCTGC 3267

 551 ATCAAAAGCAGNNTGGCCAGCAGGTCNAGGGAGGTGATTCTNCCCCTCTACTCTNCTCTNNTGAGACCCC 620
     |||||||| || |||||||||||||| |||||||||||||| |||||||||||: |||| |||||||||
3268 ATCAAAAGAAGCGTGGCCAGCAGGTCGAGGGAGGTGATTCTGCCCCTCTACTCCGCTCTGGTGAGACCCC 3337

 621 ACCTGGAGTACTGCATCCAGCTCTGGGGNCCCCANCANAAGAANGANATGGACCTGTTGGAGNNAGTCCA 690
     |||||  |||||||:|||||||||||:| ||:|| || |:||| || |||||||||||||||  :|||||
3338 ACCTGCAGTACTGCGTCCAGCTCTGGAGTCCTCAGCACAGGAAAGACATGGACCTGTTGGAGCGGGTCCA 3407

 691 GAGGANGGCCANNAAGATGATCAGAGGGCTGGAGCACCTCTCCTATGAAGACAGGCTGAGAGAGTTGGGG 760
     ||||| ||||| ||:|||||||||||||| ||||:|||||||||:|||:|| ||||||||||||||||||
3408 GAGGAGGGCCACAAAAATGATCAGAGGGATGGAACACCTCTCCTGTGAGGAAAGGCTGAGAGAGTTGGGG 3477

 761 TTGTTCAGCCTGGAGAAGAGAAGGCTCNNGGGAGACCTTATAGCA-CCTTCCAGTACCTAAAGGGGGCNT 829
     |||||||||||||||||||||||||||  ||:||||||||| |||-||||:||||||:||||||||||| |
3478 TTGTTCAGCCTGGAGAAGAGAAGGCTCTGGGAAGACCTTATTGCAGCCTTTCAGTACTTAAAGGGGGCTT 3547

 830 A-AAGAAAGCTGGAGANGGACTTTT-----------GTNGTGATAGGACAAGGGNNAATGGNTTTAAACT 887
     |-|||||||| |||:|| :||||||-----------|| |:|||||||||||||| ||||| ||||||||
3548 ATAAGAAAGATGGGGACAGACTTTTTAGTAGGGCCTGTAGCGATAGGACAAGGGGTAATGGTTTTAAACT 3617

 888 NAAAGAGNNTAGNTTTAGATTAGATATNAGGAAGAAATTCTTTACTGTGAGGGTGGTGAGNCACTGGAAC 957
     |||||| ||| |||||:|||||| |||||||||||:||||| :|||||||||: |||||||| ||||||||
3618 AAAAGAGGGTAGATTTAGACTAGATATAAGGAAGAAATTTTTTACAATGAGGGTGGTGAAACACTGGAAC 3687

 958 AGGTTGNCCAGAGAAGTTGTGGATGCCCCATCCCTGGAAGTGTTCAAGNCCAGGTTGGATGNGGCTNTGA 1027
     |||||| ||||||||:|| ||:|||||||||||||||||:::||||| :|||||||| |||||:| |||| |||
3688 AGGTTGCCCAGAGAGGTGGTAGATGCCCCATCCCTGGAAACATTCAAGGTCAGGTTGGACGGGGCTCTGA 3757

1028 GCAACCTGGTCTAGTGGAANNTNTNCCTGCCCATGGCAGGNGNNTTGGAACTAGATGATCTTTAA-GGTC 1096
     |||||||||:||||||    ||| |  | | |||||:||| |||||| | |--|:|||||||||:||||||-||||
3758 GCAACCTGATCTAGTTGAAGATGTCCCTGCTCATTGCAGGGGGGTT--GGACTAGATGACCTTTAAAGGTC 3825
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1097 CCTTCCAACCCAAACCATTCTATGATT 1123
     |||||||||||||||:||||||||||||
3826 CCTTCCAACCCAAACTATTCTATGATT 3852
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-44#Unknown	1	593	TguLTR5d	1	595	d	0.9143	2.7222	4734

```
1   TGTGCTGGTTTTGGCTGGGGTAGAGTTAATTTTCTTCACAGTAGCTNGTATGGGGCTGTGTTTTGGATTT 70
    |||||||||||||||||||||:|||||||||||||||||||||||| ||||||||||||||||||||||||
1   TGTGCTGGTTTTGGCTGGGATAGAGTTAATTTTCTTCACAGTAGCTGGTATGGGGCTGTGTTTTGGATTT 70

71  GTGCTGAAAACAGTGTTGATAATACAGNGATGTTTTTGTTATTGCTGAGCAGNGCTTACACAGAGCCAAG 140
    ||||||:|||||||||||||||||:|||| |||||||| ||||||||||||||| |||||||||||:||||
71  GTGCTGGAAACAGTGTTGATAACACAGGGATGTTTTNGTTATTGCTGAGCAGCGCTTACACAGAGTCAAG 140

141 GCCTTTTCTGCTTCTCANACNNCCNCACNAGCGAGGAGGCTGGGGGTGCACAAGAAGTTGGGAGGGGACA 210
    |||||||||||||||||   |  || ||| |||||||||||||||||||||||:||:||||||||||||||
141 GCCTTTTCTGCTTCTCACCCCACCCCACCAGCGAGGAGGCTGGGGGTGCACAAGGAGCTGGGAGGGGACA 210

211 CAGCCNGGACAGCTGACCCCAACTGACCAAAGGGATATTCCANACCATATGGCATCATGCTCAGNATATA 280
    ||||| |||||||||||||||||||||||||||||||||||| ||||||||||:|||||||||| |||||
211 CAGCCGGGACAGCTGACCCCAACTGACCAAAGGGATATTCCATACCATATGGCGTCATGCTCAGCATATA 280

281 AAGCTGGGGGAAGAAGGAGGAAGGGGGG-ATNTTTGGAGTGATGGTGTTTGTCTTCCCAAGTCACNGTTA 349
    ||||||||||||||||||||||||||||-|: ||:||||||||||:|||||||||||||||||||| ||||
281 AAGCTGGGGGAAGAAGGAGGAAGGGGGGGACGTTCGGAGTGATGGCGTTTGTCTTCCCAAGTCACCGTTA 350

350 NGNGTGATGGAGCCCTGCTNTCCTGGAGATGGCTGAACACCTGCCTGCCCATGGGAAGCAGTGAATNAAT 419
    | ||||||||||||||||| ||||||:|||||||||||||||||||||||||||||||||:|||||| |||
351 CGCGTGATGGAGCCCTGCTTTCCTGGGGATGGCTGAACACCTGCCTGCCCATGGGAAGCGGTGAATGAAT 420

420 TCCTTGTTTTGCTTTGCTTGTGTGNGNNGCTTTTGCTTTNCCTATTAAACTGTCTTTATCTCAACCCANG 489
    |||||||||||||||||||||:||| |   ||||||||| ||||||||||||||||||||||||||||| |
421 TCCTTGTTTTGCTTTGCTTGCGTGCGCGGCTTTTGCTTTACCTATTAAACTGTCTTTATCTCAACCCACG 490

490 AGTTTTCTCACTTTTACCCTTCTGATTCTCTCCCCNATCCCACTGGNGGG-AGTGAGNGAGNGGCTGTGT 558
    |||||||||||||||||||||:|||||||||||| |||||||:|| |||-|||||| ||| ||||||||||
491 AGTTTTCTCACTTTTACCCTTCCGATTCTCTCCCCCATCCCACCGGGGGGGAGTGAGCGAGCGGCTGTGT 560

559 GGGGCTTNGTTGCTNGCTGGGGGTTAAACCATNACA 593
    ||||||| |:|||: |||||||||||||||||: |||
561 GGGGCTTAGCTGCCGGCTGGGGGTTAAACCACGACA 595
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Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-45#Unknown	1	594	TguLTR5d	1	595	d	0.9007	4.8333	4704

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1   TGTGCTGGTTTTGGCTGGGATAGAGTTAATTTTCTTCACAGTAGCTNGTATGGGGCTNTGTTTTGGATTT 70
    |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| |||||||||||
1   TGTGCTGGTTTTGGCTGGGATAGAGTTAATTTTCTTCACAGTAGCTGGTATGGGGCTGTGTTTTGGATTT 70

71  GTGCTGAAAACAGTGTTGATAACACAGGGATGTTTTNGTTATTGCTGAGCAGTGCTTACACAGAGTCAAG 140
    ||||||:|||||||||||||||||||||||||||||| ||||||||||||||||:|||||||||||||||
71  GTGCTGGAAACAGTGTTGATAACACAGGGATGTTTTNGTTATTGCTGAGCAGCGCTTACACAGAGTCAAG 140

141 GCCTTTTCTGCTTCTCANNCCACCCCACCAGNGAGGAGGCTGGGGGTGCACAAGAAGCTGGGAGGGGACA 210
    |||||||||||||||||  ||||||||||||| |||||||||||||||||||||:||||||||||||||||
141 GCCTTTTCTGCTTCTCACCCCACCCCACCAGCGAGGAGGCTGGGGGTGCACAAGGAGCTGGGAGGGGACA 210

211 CAGCCAGGACAGCTGACCCCAACTGACCAAAGGGATATTCCATACCATATGGCATCATGCTCAGCATATA 280
    |||||:|||||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||
211 CAGCCGGGACAGCTGACCCCAACTGACCAAAGGGATATTCCATACCATATGGCGTCATGCTCAGCATATA 280

281 AAGNTGGGGGAAGAAG-ANGNANNGGGGNANNTTNNGAGTGATGGNTTTGTCTTCCCAAGTNACNNTTA 349
    ||| |||||||||||||-| | |    |||| |   || ||||||||||| ||||||||||||||| |||
281 AAGCTGGGGGAAGAAGGAGGAAGGGGGGACGTTCGGAGTGATGGCGTTTGTCTTCCCAAGTCACCGTTA 350

350 NNNNTGATGGAGCCCTGCTNTCCTGGAGATGGCTGAACACCTGCCTGCCCATGGGAAGTNGTGAATNAAT 419
    |||||||||||||||||| ||||||:||||||||||||||||||||||||||||||||||: ||||||| |||
```

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351 CGCGTGATGGAGCCCTGCTTTCCTGGGGATGGCTGAACACCTGCCTGCCCATGGGAAGCGGTGAATGAAT 420

420 TCCTTGTTTTGCTTTGCTTGTNTGNANNGCTTTTGCTTTACCTATTAAACTGTCTTTATCTCAACCCATG 489
    |||||||||||||||||||||:||:||||||||||||||||||||||||||||||||||||||||||||:|
421 TCCTTGTTTTGCTTTGCTTGCGTGCGCGGCTTTTGCTTTACCTATTAAACTGTCTTTATCTCAACCCACG 490

490 AGTTTTCTCACTTTTACNCTTCCNATTCTCTNCCCCATCCCACNNNNGGGGGAGTGAGNNAGNAGCTGTGT 559
    |||||||||||||||||| ||||| |||||||| ||||||||||||      |||||||||| || :||||||||
491 AGTTTTCTCACTTTTACCCTTCCGATTCTCTCCCCCATCCCACCGGGGGGGGAGTGAGCGAGCGGCTGTGT 560

560 GGNGCTTAGTTGCNNGCTGGGGTTAAACCANNACA 594
    || |||||||:||| ||||||||||||||||| |||
561 GGGGCTTAGCTGCCGGCTGGGGTTAAACCACGACA 595
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-51#Unknown	1	589	TguLTR5d	1	590	d	0.9066	4.9091	4701

```
1 TGTGCTGGTTTTGGCTGGGATAGAGTTAATTTTCTTCACAGTAGCTGGTATGGGGCTGTGTTTTGGATTT 70
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 TGTGCTGGTTTTGGCTGGGATAGAGTTAATTTTCTTCACAGTAGCTGGTATGGGGCTGTGTTTTGGATTT 70

71 GTGCTGAAAACAGTGTTGATAANACAGNGATGTTTTNGTTATTGCTGAGCAGTGCTTACACAGAGTCAAG 140
   ||||||:||||||||||||||||| |||| ||||||||| ||||||||||||||:||||||||||||||||
71 GTGCTGGAAACAGTGTTGATAACACAGGGATGTTTTNGTTATTGCTGAGCAGCGCTTACACAGAGTCAAG 140

141 GCCTTTTCTGCTTCTCACNCNACCCCACCAGNGAGGAGGCTGGGGGTGCACAAGAAGTTGGGAGGGGACA 210
    |||||||||||||||||| | |||||||||| |||||||||||||||||||||:||:||||||||||||
141 GCCTTTTCTGCTTCTCACCCCACCCCACCAGCGAGGAGGCTGGGGGTGCACAAGGAGCTGGGAGGGGACA 210

211 CAGCCAGGACAGCTGACCCCAACTGACCAAAGGGATATTCCANACCATATGGCATCATGCTCAGNATATA 280
    |||||:||||||||||||||||||||||||||||||||||| ||||||||||:|||||||||| |||||
211 CAGCCGGGACAGCTGACCCCAACTGACCAAAGGGATATTCCATACCATATGGCGTCATGCTCAGCATATA 280

281 AAGCTGGGGGAAGAAGNAGGAAGGGGGGNNN-TTTGGAGTGATGGNNTTTGTCTTCCCAAGTNACNNTTA 349
    |||||||||||||||| |||||||||||    -||:||||||||||  |||||||||||||||| || |||
281 AAGCTGGGGGAAGAAGGAGGAAGGGGGGGACGTTCGGAGTGATGGCGTTTGTCTTCCCAAGTCACCGTTA 350

350 NNNNTGATGGAGCCCTGCTTTCCTGGNGATGGCTGAACACCTGCCTGCCCATGGGAAGNNGTGAATNAAT 419
    |||||||||||||||||||||| |||||||||||||||||||||||||||||||  |||||| |||
351 CGCGTGATGGAGCCCTGCTTTCCTGGGGATGGCTGAACACCTGCCTGCCCATGGGAAGCGGTGAATGAAT 420

420 TCCTTGTTTTGCTTTGCTTGTNTGNNNNGCTTTTGCTTTNCCTATTAAACTGTCTTTATCTCAACCCATG 489
    ||||||||||||||||||:||  |||||||||| ||||||||||||||||||||||||||||:|
421 TCCTTGTTTTGCTTTGCTTGCGTGCGCGGCTTTTGCTTTACCTATTAAACTGTCTTTATCTCAACCCACG 490

490 AGTTTTCTNACTTTTACCCTTCNNATTCTCTCCCCNATCCCACTNNGGGGGAGTGAGNNAGNGGCTGTGT 559
    |||||||| |||||||||||||| ||||||||||| |||||||: |||||||||| || ||||||||
491 AGTTTTCTCACTTTTACCCTTCCGATTCTCTCCCCCATCCCACCGGGGGGGGAGTGAGCGAGCGGCTGTGT 560

560 GGGGCTTAGTTGCNNGCTGNGGNTAAACCA 589
    |||||||||:||| |||| || |||||||
561 GGGGCTTAGCTGCCGGCTGGGGTTAAACCA 590
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-47#LTR@ERVL	1	595	TguLTR5b	1	596	d	0.9379	3.2727	4945

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1 TGTGCTGGTTTTGGCTGGGGTAGAGTTAATTTTCTTCACAGTGGCTNGTATGGGGCTGTGTTTTGGATTT 70
  |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
1 TGTGCTGGTTTTGGCTGGGGTAGAGTTAATTTTCTTCACAGTGGCTGGTATGGGGCTGTGTTTTGGATTT 70

71 GTGCTGAACACAGNGTTGATAATANAGAGATGTTTTTGTTATTGCTGAGCAGNGCTTACACAGAGCCAAG 140
   ||||||||||||| |||||||||| |||||||||||||||||||||||||| |||||||||||||||||
71 GTGCTGAACACAGGGTTGATAATACAGAGATGTTTTTGTTATTGCTGAGCAGGGCTTACACAGAGCCAAG 140

141 GCCTTTTCTGCTTTTCATACTGCCACACTGGCNAGGANGNTGGGGGTGCATGGGANGNTGGGAGGAGACA 210
    |||||||||||||||:|||||||||:||||| |||| | | |||||||||||||| |||||||||||||
141 GCCTTTTCTGCTTTTCGTACTGCCACGCTGGCGAGGAGGCTGGGGGTGCATGGGAGGCTGGGAGGAGACA 210

211 CAGCNAGGACAGGTGACCCNAACTGACCAAAGGGATATTCCANACCATATGACATCATGCTCAGTATATA 280
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         ||||| :|||||||||||||| ||||||||||||||||||||| |||||||||||||||||||||||||
211 CAGCCGGGACAGGTGACCCCAACTGACCAAAGGGATATTCCAGACCATATGACATCATGCTCAGTATATA 280

281 AAGNNGGGGGAAGAAGGAGGAAGGGGGG-ANNTTTGGAGTGATGGNGTTTGTCTTCCCAAGTCACNGTTA 349
    |||  |||||||||||||||||||||||-|  |||||||||||||||||||||||||||||||   ||||
281 AAGTGGGGGGAAGAAGGAGGAAGGGGGGGACGTTTGGAGTGATGGCGTTTGTCTTCCCAAGTCACCGTTA 350

350 NNTGTGATGGGGCCCTGCTNTCCTGGAGATGGCTGAACACCTGCCTGCCCATGGGAAGCAGTGAATTAAT 419
     :|||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
351 CGCGTGATGGGGCCCTGCTCTCCTGGAGATGGCTGAACACCTGCCTGCCCATGGGAAGCAGTGAATTAAT 420

420 TCCTTGTTTTGCTTTGCTTGTGTGTGNNGCTTTTGCTTTCCCTATTAAACTGTCTTTATCTCAACCCACG 489
    ||||||||||||||||||||||||||:| ||||||||||||||||||||||||||||||||||||||||
421 TCCTTGTTTTGCTTTGCTTGTGTGCGCGGCTTTTGCTTTCCCTATTAAACTGTCTTTATCTCAACCCACG 490

490 AGTTTTCTNGCTTTTACCCTTCCGATTCTCTCCCCNATCCCACTGGTGGGGGAGTGAGCAAGTGGCTGTG 559
    |||||||| ||||||||||||||||||||||||||| |||||:|||||||||||||||:||:|||||:|
491 AGTTTTCTAGCTTTTACCCTTCCGATTCTCTCCCCGATCCCGCTGGTGGGGGAGTGAGCGAGCGGCTGCG 560

560 TGGGGCTTGGTTGCTGGCTGGGGTTAAACCACAACA 595
    |||||||||:|||||||||||||||||||||:|||
561 TGGGGCTTGGCTGCTGGCTGGGGTTAAACCACGACA 596
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-52#LTR@ERVL	1	1113	ERV3-4_PMaj-LTR	1	1134	d	0.8286	8.8000	7112

```
1 TGTATTGGGTTTGCNTGGCNAGGTTTTGGTAGNNNGNNGNNTACAGGGGTGNCT-CTGTGAGAAGCTGCC 69
  ||||||||||||| |||| |||||||||||   |  |   |||||||||| ||-|||||||||||||||
1 TGTATTGGGTTTGCATGGCAAGGTTTTGGTAGCGGGGGGGCTACAGGGGTGGCTTCTGTGAGAAGCTGCC 70

70 AGAAGCTTCCCCNATGTCNNNCAGAGCCAATGCCAGNNNGCTCCAAGANNGACCNNCNNNTGGCCAAGGC 139
   ||||||||||| :|||| |||||||||||||||| ||||||:|| |||| | |||||||||||
71 AGAAGCTTCCCCCGTGTCCGACAGAGCCAATGCCAGCCGGCTCCAGGATGGACCCACTGCTGGCCAAGGC 140

140 NNAGCCNATCAGNNANNGTGGNAGNACCTCTGNGATAACANATTTAAGAAGGNNNAAAANNNNNTGNNNA 209
    |||| ||||| |  |||| || :|||||| |||||||| |||||||||     ::|    -|  |
141 TGAGCCCATCAGCGATGGTGGCAGTGCCTCTGGGATAACATATTTAAGAAGGAAGGGAAAAAA-GCACA 209

210 ANTGCNGCNAGAGANANGAGTGAGAATATGTGAGAGAAACANCTCTGCAGACACCAAGGTCAGTGNAGAA 279
    | ||| || :|||| | |||||||||||||||||||||||| |||||||||||||||||||||| ||||
210 ATTGCAGCTGGAGAGAGGAGTGAGAATATGTGAGAGAAACAGCTCTGCAGACACCAAGGTCAGTGCAGAA 279

280 GGNNN---AGGAGGTGCTCCAGGNNCNNGAGCAGAGATTCCCCTGCAGCCNNTGGTGNAGNCCATGGTGA 346
    || ---|||||||||||||| | |||||||||||||||||||||||| |||| || ||||||||
280 GGAGGGGCAGGAGGTGCTCCAGGCGCCAGAGCAGAGATTCCCCTGCAGCCCATGGTGCAGACCATGGTGA 349

347 GGCAGCTGTNCCNCTGCAGCCCATGGAGGTCCANNGNGGANCAGANATCCACCTGCAGCCNNTGGAGGAN 416
    |||||||| || ||||||||||||||||| |-||| |||| ||||||||||||| ||||||:
350 GGCAGCTGTGCCCCTGCAGCCCATGGAGGTCCATGG-GGAGCAGAGATCCACCTGCAGCCCATGGAGGGC 418

417 NCCANNCNNGAGCAGGTGGATGCNNNNAGNAGGCTGTGACCCNNTGGGAAGCCNNNNCTGGAGCAGGNTC 486
    ||| | ||||||| |||||| || |||||||||| |||||||| |||||||||| ||
419 CCCACACCAGAGCAGGKGGATGCCCAAAGGAGGCTGTGACCCCATGGGAAGCCCGTGCTGGAGCAGGCTC 488

487 CTGGCAGGNC-TGNN-CCNNTGGAGAGAGNAGCCCANNCTGGAGCAGGTTTNCTGGNAGGACTTG--ACC 552
    |||||||| |-|| -|| ||||||||| |||||| ||||||||||||| |||| |||||||||--|||
489 CTGGCAGGACCTGTGGCCCATGGAGAGAGGAGCCCACACTGGAGCAGGTTTGCTGGCAGGACTTGTGACC 558

553 CNNTGGGGNC-CANNCTGGAGCAGNCTGTTC-TGAAGGACTN-ACCCNNTGGAANGGACCCANNCTGNAG 619
    |    |||| |-|| ||||||||| ||||||-|||| -|||| ||||| ||| |||
559 CCTGGGGGACTCACGCTGGAGCAGCCTGTTCCTGAAGGACTGCACCCCGTGGAAGGGACCCACGCTGGAG 628

620 CAGTTNNTGAAGAACTGCAGCCNNTGGGAAGGACTCANNNTGGAGAAGTTCNTGGAGGACTGTCTCCNNT 689
    ||||| |||||||||||||||| |||||||||||| |||||||| |||||||: |||||||||||||| |
629 CAGTTTGTGAAGAACTGCAGCCCGTGGGAAGGACTCACGTTGGAGAAGTTTGTGGAGGACTGTCTCCCGT 698

690 GGGAGGGACCCCANNCTGGAGCAGGGGAAG--------GANTCCTCNCCCTGAGGAGGAAGGAGCAGCAG 751
    ||||||||||||| ||||||||||||||||--------|| ||||: ||||||||||||||||||:||||
699 GGGAGGGACCCCACACTGGAGCAGGGGAAGAGTGTGAGGAGTCCTTCCCCTGAGGAGGAAGGAGCGGCAG 768

752 ANACAACNTGTGATGAACTGACNNNNANCCCCCATTCCCNATCNCC-CTGNNCCNCTGGNGGGGGAGGAGGT 820
```

```
     | |||||| |||||||||||||||    |  ||||||||||| ||| ||-||| || ||||-|||:|||||||
769 AGACAACGTGTGATGAACTGACCACAACCCCCATTCCCCATCTCCTCTGCGCCACTGG-GGGAAGGAGGT 837

821 NNA---ANTNNGGANTNAAGTTAAGCCNNGGAAGAAGGGAGGGGTGGGGGGAAGGTGTTTT-AAGATTTG 886
      |---| |  ||| | |||||:|||| |||||||||||||||||||||||||||||||-||||||||
838 AGAGAAAATTGGGAGTGAAGTTGAGCCCGGGAAGAAGGGAGGGGTGGGGGGAAGGTGTTTTTAAGATTTG 907

887 NTTT-ATTTCTCATTATCCTACTCTGATTTGATTGGTAATAAATTAAANTAATTTCCCCAAGTNNAGTCT 955
     |||-|||||||||||||||||||||||||||||:|||||||||| ||||||||||||||:  |||||
908 GTTTTATTTCTCATTATCCTACTCTGATTTGATTGGCAATAAATTAAACTAATTTCCCCAAGCCGAGTCT 977

956 GTTTTGCCCATGACGGTAATTGGTGAGTGATCTCTCCCTGTCCTTATCTCAACCCATGAGCCTTTNGTTA 1025
    |||||||||:|||:|||||:|||||||||||||||||||||||||||||||||:||||||||| :|||
978 GTTTTGCCCGTGATGGTAACTGGTGAGTGATCTCTCCCTGTCCTTATCTCAACCCACGAGCCTTTCATTA 1047

1026 TATTTTCTCTCCCCTGTCCAGCTGAGGAGGGGAGTGATAGAGNNGCTTTGGTGGGCACCTGGCATCCAGC 1095
     :||||||||||||||||||||||||||||||||-|||||||||  ||||||||||||||||||||||||
1048 CATTTTCTCTCCCCTGTCCAGCTGAGGAGGG-AGTGATAGAGCGGCTTTGGTGGGCACCTGGCATCCAGC 1116

1096 CAGGGTCAACCCACCACA 1113
     ||||||||||||||||||
1117 CAGGGTCAACCCACCACA 1134
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-53#Unknown	180	214	Gypsy-62_MLP-I	3006	3040	d	0.8286	2.0000	226

```
 180 CCCCTCAGGCATCTGTATCACCCCCCAAAANATTG 214
     |||||||||:|||||||||:|||||||| | | ||:|
3006 CCCCTCAGGTATCTGTATTACCCCCCCACAGATCG 3040
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-53#Unknown	596	645	BEL-732_AA-I	2188	2234	c	0.8163	1.4000	247

```
 596 TTTTCAACATGTGTGTTGATAAGAAGCAGCTCTGTTCTTTCCTTTTGCTT 645
     |:|||||||||||||:|||||||--|||  :|||-:||||:|||||||||
2234 TCTTCAACATGTGCGTTGATAA--AGCCCTTCT-CTCTTCCCTTTTGCTT 2188
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-53#Unknown	710	751	Penelope-11_HM	2692	2732	c	0.8095	1.4000	211

```
 710 ATAAGTGTTTTAGGTGGCTGTGTTTCTAGTTAGTAGTTTTTT 751
     |:||||:||||| |||| |||:|||||||||||::|-|||||||
2732 ACAAGTATTTTATGTGGGTGTATTTCTAGTTGAT-GTTTTTT 2692
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-54#LTR@ERVL	70	114	EnSpm-N5_HM	3855	3898	c	0.8444	3.0000	229

```
 70 ATATATATATATATATATATATATATNAGTTAAGAACAGTTATCCTT 114
    ||||||||||||||||||||||||||  :| :|||| |||||-||||
3898 ATATATATATATATATATATATATATAGAGAAGAGTTA-CCTT 3855
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-54#LTR@ERVL	489	680	ERV3-3_UCy-I	254	430	d	0.6704	1.4324	476

```
489 ATTTGGGTGGTGTTCTCCAGGCTGTTTTCCTGCCGTAACCTAAGCTGCTACCTCTGGGGATTTAGTAATA 558
    ||||||:  :|||  ||| |  ||||||  |:||:| |||:|||:|||||||||| |||||||  :|::|:||:
254 ATTTGGAATATGTACTCAATTCTGTTTGCTTGTCCTAATCTAGGCTGCTACGTCTGGGGCCTCGGCAACT 323

559 GTACTGA-CCCTTGGGA--AGGAACAAAGGGGAGTGTTTTCTCCCAACCCTTCGCTCACTCCCCATTTAA 625
    ::||: |-|||:||||:--|||::: ||||---| || |||:|:|||||||:|||-------------|:
324 ACACCCAGCCCCTGGGGGGAGGGGTAAAG---ATTGATTTTTTCCAACCTTTC--------------AG 375

626 GTCTGTTACAACGGCTTTTGGGA-TGTTTAAATTCTCCCTNGATGCCAGAGATAGC 680
```

```
        |::||  :|||:|:|:|||||::|-||||-||:|||:|:||  ||||||||::||:|||
376 GCTTGACACAGCAGTTTTTGAAAATGTT-AAGTTCCCTCTGGATGCCAAGGACAGC 430
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-54#LTR@ERVL	796	914	hAT-N9_LCh	981	1106	c	0.7119	1.2500	309

```
 796 GGGAGAG-GAAGAGAGTC---AAACCCCCGATGTCA-----TAGTGAGGAAAAAAAAAGAAGAGAGTAAA 856
     ||||||||-||:||||||:|---:|:||||  ||---||-----:|||||||:|:|:|||----|||||  |:|
1106 GGGAGAGAGAGGAGAGCCCCTGAGCCCCAGA---CAGAAAACAGTGAGGGAGAGAAA----GAGAGGAGA 1044

 857 ACCCCTGACATCACAGTGAAGAGAGAGAA--------GGAAGAGGGTAAAACCCCTGATGTCACAG 914
     :|||||||| ::|-|||-:||:||||||||||--------|::|||||:| |:|:||||||||  |:|-|||
1043 GCCCCTGAGGCC-CAG-AAAAAGAGAGAAAACAGTGAGAGAGAGAGGAGAGCCCCTGAGGCC-CAG 981
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-54#LTR@ERVL	948	1535	TguERVL2_I-b_fAlb	781	1372	d	0.6808	1.7019	1895

```
 948 GTAAAACCCCT-GATGTCACAGTGACGCAGGACGAGGCTCAACCAGGGGGACAGTCCAAGCCTATGGAAG 1016
     ||:::||||||  |-|||||:|||  :  :: ||||  :   :||| |||||  :|||:||||  ||||  :::|  ||
 781 GTGGAACCCATAGATGTTACATCTGTCCAGGTTCCAGCTGAACCACAGGGGCAGTCACAGCCAGCAGCAG 850

1017 TTGCCCCTATCCAGAAA--AGGAAATATAAGACCAAACCAGTCCGTCCAGCGGAT---GATGAGGG-GGC 1080
     |:||||||||:|--:||||--||:||||  ||||||:  |||  ||:  |::|:||   :||---||| ||:-|| 
 851 TCGCCCCTGT--GGAAACTAGAAAATCTAAGATGAAAACAAAGCACCTAGWTAATAAGGATMAGAAAGGA 918

1081 GGCTGCACCTTCACAGCAGGCAG---ACCCAGAGCCTGAGATCATCACTGAGTCATTGTCNTTTGATAAC 1147
     ||----:||:|||||:| :||||---| |||||| :|||||||||||||||||||| :| || | :|| |::
 919 GG----GCCCTCACAACCAGCAGGGGAGCCAGAGGTTGAGATCATCACTGAGTCCCTSTCGTACGAAAGT 984

1148 CTCCGTGGTTTGCGGAAAGACATTGCTCGA---CACCCAGGCGAGCCCATCCTGACTTGGTTGATCCGAG 1214
     ||||||:|:|||||:|||||||||| :  |||--- :||---:||| |: |: ::||||||||:  :|:||:|
 985 CTCCGTAATCTGCGAAAAGACATTGTACGAHGGGGCC---GTGAGGCTTTTACAACTTGGTTACTTCGGG 1051

1215 TTTGGGACCTTATGGGTGAAANCCTACAACTGGATGGTGCTGAAGCCAGGTTTTTGGGGGCTGTGGCCCA 1284
     |:|||||||||||||||  :  | : :  |||||||||||||||:||||:|| |||  ||||||: |:  ||:||||
1052 TCTGGGACCTTATGGGAACAGGTGTACAACTGGATGGTACTGAGGCAAGGAATTTGGGACCCTTGACCCA 1121

1285 GGATGTGGCTATTGAACAGGTGTTTGTGAGGGAATCAAAGCCCCTTTCACTCTGGGCACGACTTCTAATG 1354
     |||: ::| |:| || |||||:|:||:|||||::|:: ||||||||| ||||||| +|::|||:|||||
1122 GGACTCAGGTGTGGATCAGGTATTCGTAAGGGAGCCAGGCCCCCTTTCCCTCTGGGARCAGCTTTTAATG 1191

1355 AGTGTAAGAGAGAAGTTTGTNTATAGAGAAATCCTGCAGGANCATCACATTAAGAAAAC-TTGGAAGACG 1423
     ||||||:|||||||:|||||| :|:|||||:|    |||||+| ||:|||   ||-|||  :|-:|||||||||
1192 AGTGTGAGAGAGAGGTTTGTCCACAGAGAGAGAATGCAGRAGCACCACCGTA-GAATGCGCTGGAAGACC 1260

1424 ATGGAAGAAGGAATTTTACGTCTGAGGGAGATGGCAATGATGGAAGTGCTTTTTGGAAGGGGTGGGCAAA 1493
      |  ||:|||||:||:: :|: |||||:||::||||||:|: |:||:||:|:|||||:|||||::||:|:
1261 CTTGAGGAAGGGATCCAGCAGCTGAGAGAAGTGGCAGTATTAGAGGTACTCTTTGGGAGGGACGGACAGC 1330

1494 CCAATAATGACCCTGACAAGGTCAGATGCACACCACATATGT 1535
       ::|:|||||||||||||||||||||:||||||    :||  ||||
1331 ATGACAATGACCCTGACAAGGTCAGGTGCACAGGGCAGATGT 1372
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-64#Unknown	577	663	Chapaev-8_HM	7241	7329	d	0.7619	1.6000	210

```
 577 TATATCTATATCTACATATATATATATATATCAGTT--AAGAACAGTTATCCTTCTTGTA-----TTAAA 639
     |||||  |||||  ||:||||||||||||||||||:|  ||--||:| ||: ||: ||:-------|||-----|||||
7241 TATATATATATATATATATATATATATATATTATTTTTAAAATCAAATAC-------GTAAAAAATTAAA 7303

 640 GT--TCCTTTTCTTAAATTTGATAAA 663
     ||--::|||||:||  |:|||||||:|
7304 GTGTTTTTTTTTTTTCAGTTTGATAGA 7329
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-68#Unknown	586	636	Tx1-5_FR	2375	2426	c	0.7885	1.8000	221

```
 586 TCCCGTGTTCCGCCGAGCTAAGAATGG--AAAAAATGTCCCCAAAACCAAAAG 636
     ||||-||| | || ||| :||||:||:--|||||::||||||||||||
2426 TCCC-TGTACAGCAGAGACAAGAGTGACAAAAAAACATCCCCAAAACCAAAAG 2375
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-79#LTR@ERVL	1	1047	TguLTRL4b	1	1064	d	0.8458	5.4074	6720

```
 1 TGTATTGGGTTTGCNTGGCNAGGTTTTGGTAGCNGGGGGGGCTACAGGGGTGGCTTCTGTGAGAAGCTGCC 70
   ||||||||||||||| |||| |||||||||||||| ||||||||||||||||||||||||||||||||||||
 1 TGTATTGGGTTTGCATGGCCAGGTTTTGGTAGCGGGGGGGGCTACAGGGGTGGCTTCTGTGAGAAGCTGCC 70

 71 AGAAGCTTCCCCCATGTCCNACAGAGCCAATGCCAGCTGGCTCCAGGANGGACCCGCCGCTGGCCAAGGC 140
    :|||||||||:|||||||| :|||||||||| |||| :|||||||:|| |||| ||||||||||||||||
 71 GGAAGCTTCCTCCATGTCCGGCAGAGCCAATNCCAGCNGGCTCCAAGACGGACGCGCCGCTGGCCAAGGC 140

141 TGAGCCCATCAGNAATGGTGGTAACNCCTCTGGGATAACATATTTAAGAAGGNNAAAAAGTTNNTGNNCA 210
    ||:||| ||||| |||||||||||| |||||| |||||||||||||||||||| ||||||||| || |||
141 TGGGCCAATCAGAAATGGTGGTAACGCCTCTGTGATAACATATTTAAGAAGGAAAAAAAGTTATTGCGCA 210

211 GNNGNAATTGCAGCCAGAGAAGAG---AGTGAGAANATGTGAGAG-AACAACTCTGCAGACACCAAGGTC 276
    |   | |||||||:||||||||||---:||||||| |||||||||-||||:|||||||||||||||||||
211 GNTGTAATTGCGGCCAGAGAAGAGCGGGGTGAGAATATGTGAGAGGAACAGCTCTGCAGACACCAAGGTC 280

277 AGTGNAGAAGGAGGGGNAGGAGGTGCTCCAGGNGCNNGAGCTGAGNTTCCCCTGCAGCCNNTGGTGNAGA 346
    |||| |||||||||||| |||||||||||||||| || ||||||||| ||||||||||||||| ||||| |||
281 AGTGGAGAAGGAGGGGCAGGAGGTGCTCCAGGCGCCGGAGCTGAGATTCCCCTGCAGCCCGTGGTGCAGA 350

347 CCATGGTGAGGCAGCTGTNCCCCTGCAGCCCATGGAGGTCCA--GNGGNGCAGAGATCCACCTGCAGCCC 414
    |||||||||||||||||| ||||||||||||||||||||||||--| |: |||||||||||||||||||||
351 CCATGGTGAGGCAGCTGTGCCCCTGCAGCCCATGGAGGTCCACGGGGATGCAGAGATCCACCTGCAGCCC 420

415 NTGGAGGAN-CCCANNCNGGAGCAGGTGGATGCCCNA-AGGAGGCTGTGACCCNNTGGGAAGCCCATGCT 482
     |||||||| -|||| | |||||||||||||||||:| |-||||||||||||| |||||||||:::|||
421 ATGGAGGAGACCCACGCCGGAGCAGGTGGATGCCTGAGAGGAGGCTGTGACCCCGTGGGAAGCCCGCGCT 490

483 GGAGCAGGNTCCTGGNNGG-ACCTGNNGNCCNNTGGAGAGAGNAGCCCANNCTGGAGCAGNCTGTNNCTG 551
    |||||||| |||||| ||-|||| | || |||||||| |||||| ||||||||| ||-| : |
491 GGAGCAGGCTCCTGGCAGGGACCTGCGGACCCGTGGAGAGAGGAGCCCACGCTGGAGCAGGCT-CCTGG 559

552 NANGNNTNN--ACCCNNTG--AGNGACCCANNCTGNAGCAGTTTGTGAAGAACTGNNGCCCNTGGGANGG 617
    | | | --|||| ||--|| |||||| ||| |||||||:|||:||||||| |||| ||||| ||
560 NAGGACTTGCGACCCCGTGGGAGGGACCCACGCTGCAGCAGTTCGTGGAGAACTGCTGCCCGTGGGATGG 629

618 ACTCANNNTGGAGAAGTTNNTGNAGGACTGTCTCCNNTGG-AGGGACCC-ANNCTGGAGCAGGGGAAGNA 685
    ||||| ||||||||||| || ||:|||||||| |||-|||||||||-| |||||||||||||||||| |
630 ACTCACGCTGGAGAAGTTCATGGAGAACTGTCTCCCGTGGGAGGGACCCCACGCTGGAGCAGGGGAAGGA 699

686 CNNCTCTCCCTGAGNAG-AGCAGANACAA--TGTGATGAACTGACNNTAACCCCCATTCCCNNTCTCCCT 752
    |   |||||||||| || ||-:||||| ||||--||||||||||| |||||||||||| |||||||
700 CTCCTCTCCCTGAGCAGCGGCAGAAACAACGTGTGATGAACTGACCATAACCCCCATTCCCGTCTCCCT 769

753 GNNCNNCTGGNGGGGAGGAGGTAGANCCTNGGAAGNAGGGAGGGGTGGNGG-AAGGTGTTTTTAAGATTT 821
    |   |   ||||--||||||||||| |-| ||||| ||||||||||| ||-|||||||||||||||:|||
770 GCGCCGCTGG--GGGAGGAGGTAGAGC-TGGGAAGGAGGGAGGGGTGGGGGGAAGGTGTTTTTAAGGTTT 836

822 NNTTTANTTCTCATTATCCTNCTCTGATTTNNTTGGTAATAAATTNAATTAATNCCC--AANTNGAGTCT 889
     |||| ||||||||||||| ||||||||| |||||||||||| ||:||||||||| |||||| | ||||||
837 ATTTTACTTCTCATTATCCTGCTCTGATTTTGTTAGTAATAAATTCAATTAATATCCCTAANTCGAGTCT 906

890 GTTTTGCCCATGANNGTAATTGGTGAGTGATCTCTCCCTGTCCTTATCTNAACNCATGAGCCTTTNNTTA 959
    |||||||||:|||   ||| |||||||||||||||||||| |||||||||| ||| |||||:||:|| |||
907 GTTTTGCCCGTGACGGTATTTGGTGAGTGATCTCTCCCGGTCCTTATCTCAACCCATGAACCCTTCGTTA 976

960 TATTTTCTCTCCCCTGTCCAGNTGAGGAGGGGAGTGATAGAGNNGCTTTGGTGGGCACCTGGCATCCAGC 1029
    |||||||||||||||||||||| || |||||||||||||||||  ||||||||||::||||||||||||||
977 TATTTTCTCTCCCCTGTCCAGCTGCGGAGGGGAGTGATAGAGCGGCTTTGGTGGGTGCCTGGCATCCAGC 1046

1030 CAGGGTCAACCCACCACA 1047
     |||||||||||||:|||
```

1047 CAGGGTCAACCCACTACA 1064

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-81#Unknown	339	370	hAT-N126_CPB	298	329	d	0.8750	1.3333	206

```
339 GAGGGGGTGGAACAGGGGTGGGATGGGGCTGG 370
    ||||||||:|||:||||||:||| ||||||||||
298 GAGGGGGCGGAGCAGGGGCGGGCTGGGGCTGG 329
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	1418	1509	ATHILA7A_I	282	373	c	0.7391	1.3077	238

```
1418 ATGTTTGGTCTCACTGACCATCTCCAGTTGGTTGA----CCCTTGGCTTGACCTTG--GCCT-TGACCAC 1480
     |||||||||-||||::::|   :-|||||:||||||||||----|:|||||-||||: |||--|| |-||||||||
 373 ATGTTTGG-CTCATCAAAGG-CTCCAATTGGTTGATGAGCTCTTGG-TTGATGTTGTGGCATATGACCAC 307

1481 CCCCACTGGTCTCCTTGACCACCCCCATT 1509
     |||||:|:|----||||:|||::|||||
 306 CCCCATTAG----CTTGGCCATTTCCATT 282
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	402	472	ATHILA7A_I	282	354	c	0.7606	1.2000	220

```
402 CTCCACTTGGTTGA----CCCTTGGCTTGAC--CATGGCCT-TGACCACCCCCATTGGTCTCCCTGACCA 464
    ||||| |||||||||----|:|||||-||||:--::|||| |-||||||||||||||||:|----|:||:|||
354 CTCCAATTGGTTGATGAGCTCTTGG-TTGATGTTGTGGCATATGACCACCCCCATTAG----CTTGGCCA 290

465 CCCCCATT 472
    :::|||||
289 TTTCCATT 282
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	2396	2451	ATHILA7A_I	293	354	d	0.7797	1.2857	212

```
2396 CCAGACCAATGGGGGTGGTCA-AGGCCATGG--TCAAGCCAAGGG----TCAACCAAGTGGAG 2451
     |||::|:|||||||||||||||-| ||||:::--||||-|||||:|----|||||||| |||||
 293 CCAAGCTAATGGGGGTGGTCATATGCCACAACATCAA-CCAAGAGCTCATCAACCAATTGGAG 354
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	106	160	ATHILA7A_I	293	353	d	0.7759	1.1250	209

```
106 CCAGACCAATGGGGGTGGTCA-AGGCCATGG--TCAAGCCAAGGG----TCAACCAACTGGA 160
    |||::|:|||||||||||||||-| ||||:::--||||-|||||:|----|||||||||:|||
293 CCAAGCTAATGGGGGTGGTCATATGCCACAACATCAA-CCAAGAGCTCATCAACCAATTGGA 353
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	1068	1251	Gypsy-29_CT-I	5942	6127	c	0.6995	1.9524	288

```
1068 CCATCAATGGGTGGTCAAGGAGATCAATGGGGGTGGTCAAGGCCATGGGGGTCATC-TGACCATCAATGG 1136
     ||||||--||||| :||| || ||||---- ||| :||| ||:||| :||||:|||-||::|||||-|||
6127 CCATCA--GGGTCATCACGGTCATCA----TGGTCATCATGGTCATCAGGGTTATCGTGGTCATCA-TGG 6065

1137 TCAACCAGACCAATGGGGGTGGTCAAGGCCATGGTCAA-GCCA--AGGGTC--AAC--CAAGTGGAGATG 1199
     |||-:|| | | || :|||| :||| ||:|||---|||-|:||--| ||||-- ||--:||||----|||
6064 TCA-TCATAGCCATTAGGGTCATCACGGTCAT---CAACGTCATCATGGTCTTCACGGTAAGT----ATG 6003

1200 G---TCAGTGAGACCA-----GTCATGGTGGTCAAGGCCATGAGGGTCATC-TGACCATCA 1251
     |---|||||| |:||-----:|||::||:|||| |||||| ||||||||||-||:::|||||
6002 GCCATCAGTGTCATCACTGCCATCACAGTAATCATGGCCATCAGGGTCATCCTGGTCATCA 5942
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	1547	1732	Gypsy-29_CT-I	5942	6129	d	0.6910	1.6154	267

```
1547 TGATGGTCAG-ATGACCCTCATGGCCTTGACCACCATGACTGGTCTCACTGACCATCTCCACTTGTGGCC 1615
     |||||::|||-|||||||| |||||| |||::||::|||-|||---|| |||: |----|||| :|||||
5942 TGATGACCAGGATGACCCTGATGGCCATGATTACTGTGA-TGG---CAGTGATGA----CACTGATGGCC 6003

1616 TTGACCACCC------CCATTGGTCTGGTTGACCATTGATGGTCA-GATGACCCCCATGGCC-------T 1671
      |: ::|||| ------||||-------| ||||-:||||||::|:-|||||||||: |||||:-------:
6004 ATACTTACCGTGAAGACCAT-------GATGAC-GTTGATGACCGTGATGACCCTAATGGCTATGATGAC 6065

1672 CCT--TGACCAC-----CCCCATTGATCTCCTTGACCACCCATTGATGGTTG-GATGACCCCCATGGCC 1732
     | |--|||||||||-----|||:: |||:| :  ||||||-----|||||:::|-|||||||||: ||||||
6066 CATGATGACCACGATAACCCTGATGACCATGATGACCA-----TGATGACCGTGATGACCCTGATGGCC 6129
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	868	934	Tx1-1_CPB	546	606	d	0.7846	1.5000	210

```
868 GACCCCCATGGCCTTGACCACCAT-GTTTGGTCTCCTTGACCACCCCCACTGGTCTCACTGACCATCT 934
    |||||||||: :||---||||:|||-|||--|:|:|||: |||||||||||||||-||-||| |||||||
546 GACCCCCACCACC---ACCATCATCGTT--GCCCCCTCCACCACCCCCACTGG-CT-ACTCACCATCT 606
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	1852	1918	Tx1-1_CPB	546	606	c	0.7846	1.5000	210

```
1852 AGATGGTCAGTGAGACCAGTGGGGGGTGGTCAAGGAGACCAAAC-ATGGTGGTCAAGGCCATGGGGGTC 1918
     ||||||| |||-||-||||||||||||||| :|||:|:|--|||-|||:||||---||: :|||||||||
 606 AGATGGTGAGT-AG-CCAGTGGGGGTGGTGGAGGGGGC--AACGATGATGGT---GGTGGTGGGGGTC 546
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	1411	1451	Gypsy-82_MLP-I	2596	2635	d	0.8049	1.4000	238

```
1411 TCCAGGAGACCATTGGGGGTGGTCAAGGAGACCCATCAAGG 1451
     |:||||| || :|||||||:|||:||||||||:||||-|||||
2596 TTCAGGCGAGTATTGGGGATGGCCAAGGAGGCCCA-CAAGG 2635
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-84#Unknown	1335	1373	Gypsy-82_MLP-I	2598	2635	c	0.8205	1.5000	237

```
1335 CCTTGATGGGTCTCCTTGACCACCCCCAATGGTCTCCTG 1373
     |||||-||||:|||||||:|||:||||||: || ||||
2635 CCTTG-TGGGCCTCCTTGGCCATCCCCAATACTCGCCTG 2598
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-88#Unknown	2296	2379	CR1-1_PMo	1905	1981	c	0.7470	1.7500	243

```
2296 AATGGGGGTGGTCAAGGAGGCCATGGGGGTCTTCT-GACCATCCCAGACCAATGGGGGTGGTCAGGGAGG 2364
     |||:|||| |||--||||-|:|| |||:|||||||||-| |||:||||-:||-:|||| |||- |||||--
1981 AATAGGGTTGG--AAGG-GACCTTGGAGGTCTTCTAGTCCACCCCA-ATCA-TAGGGTTGG-AAGGGA-- 1920

2365 CCATGAGGGTCTTCT 2379
     || ||::|||||||||
1919 CCTTGGAGGTCTTCT 1905
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-97#Unknown	24	72	Gypsy139-I_DR	3341	3390	d	0.7400	1.2000	205

```
24 CTTGATGGGTTGAGGGAAACGCCTCAGCCCCCTG-GAGGGGTGCTCCCAG 72
   ||||||| ||||:|:|:|||::||:| |||:|||-|::|||||||||:||
```

```
3341 CTTGATGTGTTGGGAGGAACATCTTACCCCTCTGCGGAGGGTGCTCCTAG 3390
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-97#Unknown	385	464	CR1-9_NVi	673	765	c	0.7805	2.3333	237

```
385 TCTATTTTTTAT------ACTTTATAACTTTCTTACAAAGCTTATTCCTTTATACATTCTAT------CT 442
    |||||||||| |------|| |:|:||||||||--|: |||||| |||:|| |||||||| |||------||
765 TCTATTTTTTCTTTTATAACATCACAACTTTC--ATCAAGCTTTTTCTTTAATACATTATATGCTTTGCT 698

443 TACA---TCTTATGCTAACAGCTAC 464
    |:||---|||| ||:|||| ||||
697 TGCACTTTCTTCTGTTAACATCTAC 673
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-98#Unknown	2127	2172	StubV_scSl1	5389	5433	d	0.8261	3.0000	213

```
2127 TTTCTAGTAAATTTNNCAATTCTGCT-CCGATTTTATTCCAAAATTC 2172
     |||||||| ||:||| --|||| ||:|-|||||||||||||||||| ||
5389 TTTCTAGGAAGTTTG--AATTATGTTGCCGATTTTATTCCAAAAATC 5433
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-1_family-99#Unknown	382	493	BEL-2_HMM-I	5525	5629	c	0.7431	1.9091	243

```
382 TTTCTATTTTTCTATACTTTAC-TTTCTTAAC-TTTACTTTCTTACAAAGCTTATTCCTTTATACATTCT 449
    ||| :|||||| || |||||||||-|||:|:|||-||||| ||-||||||----||||| ---:|| ||:|
5629 TTTACATTTTACTTTACTTTACATTTTTCAACCTTTACATT-TTACAA----TATTCA---ACACCTTTT 5568

450 ATCTTACATCTTATGCTAACAGCTACTTTGATTCTTAC-TTTATA 493
    | |||:||:|||| :| :||--|:|||||||||:||||-||||||
5567 TTATTATATTTTATTTTTGCA--TGCTTTGATTTTTACATTTATA 5525
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-4_family-336#Unknown	566	903	ERV3-3_PMaj-LTR	833	1175	d	0.6687	1.7222	588

```
566 CCTCGCCGGAGCCCNTGAGTCANCNCAGCNGC--TGCCTC-CCGAGGTGCGGCATCGCCTCCTGCTGTCT 632
    ||::|||||| || ||:||| | ||| | ||--||||| -|||:|: |: || ||||:|||||:| ||
833 CCCTGCCGGCGCGGGGGAATCATCGCACCCGCCCTGCCTGGCCGGGGAGCCACCAGCGCCCCCTGCCGGCT 902

633 GTAAATATAACTGCACTGAAGGGG---------------CAGAGATAGG----ACTTGATTTGT----TT 679
    ||: :: |||||||||:|:|||||---------------||||||-|||----||| |::|||||----:|
903 GTGCCCGGAACTGCACCGGAGGGGAAAGTGCCTGCGGCCCAGAGA-AGGCGTCACTGGGCTTGTGCTGCT 971

680 GAAAGTTTTGGTTACNGTGTTGCTGTTTGTTCTGTTCTGNTTTTNTTTNGGTTATACATATATATATTTG 749
    |   ||:|| |  |   ||| ||||||||||------||| :||-------||||||||| ||||||---|
972 GCTCCTTCTGCTGCCCTTGTGGCTGTTTGT------CTGCCTT-------GTTATACAGATATAT---TC 1025

750 TAGTAAAGAACTGTTATCCTTTTCTCTACATTTT---CTGATTAAAGTCTCTTAATTTCAAAGGTTGTGG 816
    |:|||||||:|||||||:|:|||::|:|:||:|---||||---|||:|:|||||||||||||:| :|:::
1026 TGGTAAAGAGCTGTTATTCCTTTTCCCATATCTTTGCCTGA---AAGCCCCTTAATTTCAAAGATAATAA 1092

817 TGGTTTTTGGGGAGAGG-----CCCCCTTCCTAGTCCAGAAGGNTTCCTCACTTTCCTTGATAGACATCT 881
    |-----||||:|:||:|-----| : :||:|:| ||||:::|: :|:|:|:||||||::|||||:||
1093 T-----TTGGAGGGAAGGGGGTCATATTTTCCATTCCAAGGGAGGTTCCCGCCTTCCTTGGCAGACACCT 1157

882 TGNTTTCTTTTAAACTGAGACA 903
     ----|||||:|||||::|||||
1158 G----TCTTTCAAACCAAGACA 1175
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-10335#Unknown	206	252	I-66_AAe	4938	4984	c	0.8125	2.3333	228

```
206 AAACCTGAAGA-TGAATTCAGAAGTTAGAGGAACAAGAGACAAGGAGA 252
    ||||:|||||||-|||||||| |-|:||||:||| ||||||||| ||||
```

```
4984 AAACTTGAAGACTGAATTCATA-GCTAGAAGAAAAAGAGACACTGAGA 4938
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	2285	5696	TguERV2_I	1712	5120	d	0.6870	1.9172	8020

```
2285 CAATGGAGTTTAGAGTAGATACGGGAGCGAGTTATTCGGCTGTGAATGAATTACGGGGACCACTAAGCGA 2354
     ||:|::||||:  :||:||||||||||:||  |   |||||  |:  ||||||||  ||:|::|||| | |  :|  ||
1712 CAGTAAAGTTCCTGGTGGATACGGGGGCCACGTATTCTGTACTGAATGATTTGCAAGGACAAATTGGGGA 1781

2355 ATCAAA--AGTACTAGTGGTGGGGGTGTCGGGGGAGGTAGAAGAAAGGGAATTCCTACGGCCACTGGATA 2422
     --||||--|::|  :|:|:|:|| ||||::  |:|||:|||  :|||:|   ||  ||||||||||::|| :|:||||-
1782 --CAAACAAACAACAATAGTCGGGGCAACAGGGAAGGAGGAAAATCGGCCATTCCTACAACCCTTAGAT- 1848

2423 TTAAGTTTGGGGGGAAAGAATTTGAT-CATCAGTTTTTATATTTGCCTAATAGTCCTGAATC----TTTA 2487
     :|:  |||| ||::: |||: ::|||:-||| |:|||::|:||| ||||||:|  |||||-|| ||----||||
1849 CTGTGTTTTGGAAATAAGGTCCTGACGCATGAATTCCTGTATGTGCCTGAGTGTCC-GATTCCCCTTTTA 1917

2488 CTCGGAAGAGATTTGCTTTCGGTG----TTGCAAGCAAAAATTATTTTTGAAAAAGACAGAG----TAAA 2549
     ---|| |||||||||::|---||::----|||-| |||: :|| |::||||||:|| |:-:|||----|||-
1918 ---GGTAGAGATTTATT---GGCAAAACTTG-ATGCAGTGATAACCTTTGAGAATGG-GGAGCTTTTAA- 1978

2550 ATTAGAAATACCGGAGGAAAATATAGCCAAACTGTTTGTGATTAAAGAGGTAGAGAAGGAAAC------- 2612
     --|::|||||||| ||:  ||| |:|| ||| | :||||||||:||:---------||||-------
1979 --TGAAAATACCTGAATCAAAGACAGGAAAAATTTTAATGATTAAGGAA----------AAACCAGCTCC 2036

2613 ---TGTGCCTCAGGAGATTGAACAGGCTGTAATACCCTTGGTATGGGAAACAGGAGCTCCAGGTAAATCG 2679
     ---|:|  |||  :|||::| |||  | || ||||| ||:|::||||||||||||||:| :: || || |||||
2037 CTCTATTCCTAGGGAAGTAGAAGATGCAGTAATTCCTTCAGTATGGGAAACAGATATACCTGGGAAATCT 2106

2680 AAAGCAGCAGAACCGGTGATA-GTGAAACTAAAAGAAGGAGCTCAGCCGGTACGTGTAAAACAGTACCCG 2748
     ||| :||||| |:||:::|-|:|-|| :||:|||||:|||||:|| |: :|||||: || ||||||||:||
2107 AAATTAGCACAGCCAAT-ACATGTTGAATTAAAGGAAGGGGCAAAAGCAGTACAGGTTAAACAGTATCCT 2175

2749 ATAAAACTGGAGGCTAGGAAGGGGGTAGCCCCCATGATTACCCAGTTTTTAAATTTAGGAATTTTGCGGG 2818
     |||||||::||:|| || ||||::|||:  || ||||: : |:||:|:|| |   :||||||: ::|
2176 ATAAAACCAGAAGCACGGCAGGGAATAGTAAAAATTATTGATAAATTCTTGAAATACCAAATTTTAGAAG 2245

2819 AATGTGAATCTGAATACAATACTCCCATTTTTCCTGTTAAAAAGCCAAATGGTAGTTACAGATTAGTACA 2888
     ||||||||| ||||| |||||||| ||:| ||||| || |::||:|| |||||||:: ||:|||:|||||:||
2246 AATGTGAATCGGAATATAATACACCTATATTCCAGTGAGGAAACCCAATGGTGAGTATAGACTAGTGCA 2315

2889 GGATTTAAGGGCAGTCAATTTAATCACCAAAGATATACATCCTGTCGTGGCTAACCCATACACTTTGCTA 2958
     |||||||:||:|||:| ||| ||| ||:|:|:|:|| :|||| || || ||:|:|:|| ||||| |||:||
2316 GGATTTGAGAGCAATAAATGAAATAACTAAGGACATTTATCCAGTGGTTGCCAATCCTTACACATTGTTA 2385

2959 ACATCTGTTTCTGAGAAATTTCAGTGGTTTACAGTAATTGACTTAAAGGATGCCTTCTTCTGCAT-CCCT 3027
     ||||||:||     |||| || |  |:||||||||||||||||::|||||:|||||||||:||||||||-|||:
2386 ACATCCGTGAAAGAGACATATAAATGGTTTACAGTAATTGATCTAAAAGATGCCTTTTTTCTGCATACCCC 2455

3028 CTGGCACTTGAAAGTCAACATATCTTTGCATTTGAATGGGAAAATCCGGACACCGGACGGAAATGCCAGC 3097
     :||:||  -|||||| :: |: | |||||  |||||:|||||||||||:|: | |||| |:||:  |||||
2456 TTGACAAA-GAAAGTAGGAACCTGTTTGCCTTTGAGTGGGAAAATCCAGGAAACGGAAGAAAGACCCAGC 2524

3098 TAACCTGGACCAGACTGCCCCAAGGATTTAAGTCATCA--CCGACCATTTTCGGTAACCAGTTAGCCAAA 3165
     | ||||||||| |:|| || ||||||||||:|||--| ||--|| ||| | ||||| |||||::|:|| ||:
2525 TCACCTGGACACGGCTCCCACAAGGATTCAAG--AACAGTCCNACCCTATTCGGAAACCAACTGGCAAAG 2592

3166 GAACTGGAGGAATGGAAGAC-----------CACCCAGGTAAAAGATTCTCCTTTCTCTTATGTGATACT 3224
     ||:|||||: |||| |:|-----------:||| ||: || |:-------------||: || |:||
2593 GAGCTGGAGACCTGGACGGCGAGGGGGCAAGTACCGAGAGAACAA--------------TACCTGCTGCT 2648

3225 ACAATACGTAGACGATAT-CTG-----CGTGGGGGCAACAG--ACCGTGAACTTTGCTGTAAAT-TGACC 3285
     |||:||:|| ||||||||-|||-----|:::|:|| :| ||--|||--------|||-:|||| -|:||
2649 ACAGTATGTTGACGATATACTGATAGCCACAGAGGAGAAAGCAACC--------TGC-ATAAAGGTAACA 2709

3286 ATTGCCCTATTGAATATGCTGGGACAGGCCGGTTATCGAGTTTCGAGGGAAAAGGCACAACTGGTAAAAC 3355
     ||:|   |  ||:||| ::||||||  ||| || ||| ::|| || |::|||||:||||||| | |: |||
2710 ATCGAGATTTTAAATTCACTGGGAATGGCAGGATATAAGGTATCTAAAGAAAAAGCACAAATTGCCCAAC 2779

3356 AGAAGGTAATTTACCTGGGCTGCGAAATCTCTCAAGGGGTTCGGCGT---TTGGGGGTTAACCGTATCAA 3422
     |||  ||:|||||||||||| ||:||||||| ||:|||||||| |||||---|:||| ---:|||| ::|||||||||: |
```

```
2780 AGACTGTGATTTACCTGGGATGTGAAATCTCACAAGGG---CAGCGAAAACTGGGTACTAACCGTATTCA 2846

3423 AGCAATCTGTGAAATCCCAGTACCACGTAATCACCATGAACTGAGATCTTTCCTAGGAATGATTGGCTGG 3492
     ||| ||:|||| ||:|||| :|| |: |||| ||:|:||| || ::||||| ||:|||: || |||
2847 AGCTATTTGTGCCATTCCAGAGCCCCAGAATCTACACGAGCTGCGAGTCTTCCTTGGGATGACAGGGTGG 2916

3493 TGCCGATTGTGGATTCCCAACTTTGGATTGACGGCTAAACCGCTGTACGAAGC--AGTAAAGAAACCGAA 3560
     ||||| :|||||||||: : :||| ||||:|:|: || ||||| |||||:||:||--||--|||| :| |
2917 TGCCGCCTGTGGATCATGGACTATGGACTAATTGCAAAACCCCTGTATGAGGCCCAG--AAGACGCAGCC 2984

3561 ATTCGAGTGGGAACACCCAGAAGAGAAAGCGTTCCGGGAGCTGAAGCAGGCTCTTAAGGAG-GCGCCAGC 3629
     |||::  ||||: | ||| |::||:|:|| |||| :|:|:|||| ||||-|||:| :| -|| || ||
2985 ATTTACCTGGGGCAAACCACAGAAGGAGGCTTTCCTCAAACTAAAGGAGGC-CTTGACAACTGCTCCTGC 3053

3630 CTTAGGTCTGCCGGACTTAAATAAGGATTTCCAACTGTACGTACACGAGAGACAGAAATTAGCCCTGGGA 3699
     ||:|| :|:|| ||:||: :||:|||||:||:|||| :|||||:||:||: | : :|:|| :|||||
3054 ATTGGGGTTACCTGATTTGTCCAAAGATTTTCAGCTGTTTGTACATGAAAGGATGCGTCTGGCATTGGGA 3123

3700 GTGCTTA-CACAGAAACTGGGATCATGGAAAAGGCCTGTTGGATATTTTTCCAAACAATTGGACACTGTA 3768
     ||-||||-| ||: : :||||| ||||||||||||||||| || || ||:|||||||||||||:| |||| :||
3124 GT-CTTAACCCAACGTTTGGGAAGCTGGAAAAGGCCGGTGGGCTACTTTTCCAAACAACTTGACAACGTC 3192

3769 AGCTGT-GGCTGGCCAGGATGCTTGCGGGCGGTGGCGGCTACCGTGATCCTAATCCGAGAAGCACGTAAG 3837
     ||-||:-|| ||||| |||::|||||||||:|| ||:|:||:||||||||:|| |:|||||| | |||
3193 AG-TGCCGGATGGCCTTCATGTCTGCGGGCAGTCGCAGCCACTGTGATCCTGATACAAGAAGCCAGGAAG 3261

3838 TTGACCCTGGGTAAGCACAT-GATCGTTTATGTGCCCCATATGGTGATTACGGTTTTGGAACAAAAGGGG 3906
     :| |||| |||| |:||||||-|||-||:|||||:|| |||||||||:|:||| || |||||:||:||||||
3262 CTCACCATGGGAAGGCACATAGAT-GTCTATGTACCACATATGGTAACTACTGTGTTGGAGCAGAAGGGG 3330

3907 GGTCATTGGCTGTCGTCCAGTCGAATGCTGCAGTATCAGGCTCTGTTAAGGGAACAGGACGATATTGAGC 3976
     ||:||||||||| || :| |||||||||| || |:| :|||: | |||| |||:||:||:|||:|--|:|
3331 GGCCATTGGCTCTCCCCGAGTCGAATGATGAAATTCCAGGTAATCTTAACGGAGCAAGATGATGT--AAC 3398

3977 --TAAAATTGACTAACCACCTTAACCCAGCAGAATTTCT-GCTGT-CAAC-CCAGGAGGAGGGAAAGCC- 4040
     --||||||  ::||||||||  ::|  |||||||||       :||:||-|--||-||||-:|  |:||-----||||||-
3399 ATTAAAAACAACTAACCTTTTGAACCCAGCCTTGTTCCTAG--GTACAACATCTGAAG-----AAAGCCC 3461

4041 ---GGAGCACGACTGTGTAGAAGTGATTGAACACACATATGCCAGTCGAGAAGACTTGAAGGATGAACCA 4107
     ---|||:|||||:|:|:||||||:|||| ||||||||| |:|||  : | |||  |||::|||| ||||  ||-
3462 ATTGGAACACGATTGCGTGGAAGTAATAGAACACACCTGTGCGGCTAGAGCAGATCTGAAAGATGTCCC- 3530

4108 TTGCCTG--AC--CCGGACTGGGAATTGTTTACAGACGGCTCCAGTTTTGTGGAGAATGGTACCAGGTAT 4173
     ---|||:--||--||:||||||||||:|||||||:|||||| |||||:||:|||||||||:|| :|||::|:
3531 ---CCTAGAACAGCCAGACTGGGAGTTGTTCACAGATGGAAGCAGTTTCATGGAGAACGGAATCAGACAC 3597

4174 GCCGGATATGCGGTAGTTCGGATACAACAA--------GTGGTAGAGGCAAAAGCGCTAGCCCCAGGAAC 4235
     ||:||||||||||||--------||||||--------|||||||||||||||||||||||::|: | |||:: ||
3598 GCTGGATATGCGGTA--------ACAACAATCAGTACAGTGGTAGAGGCAAAAGCATTGCCACCAAATAC 3659

4236 ATCGGCTCAAAAGGCAGAAGTATGGGCGCTGGTAA---GAGCATTAATATTAAGCCAGGGAAAAAGAGTA 4302
     ||| ||:||:|||||||||| |--|| :||| -|||---||||:|: |||||:  :|:||:||||::||:
3660 ATCCGCCCAGAAGGCAGAACT--GGTTGCTT-TAACCAGAGCACTAGAATTAAGTGAAGGGAAAAGGTG 3726

4303 AATATATATACTGATTCTAAATATGCCTTTGGAGTGGTCCATGTGCACGGGGCTTTGTGGAAGGAGAGGG 4372
     ||:||||: ||||||||| ||||||||:|| ||||||||:||||||||||:|||||::|:||||||:||: |||
3727 AACATATGGACTGATTCAAAATATGCATTTGGAGTAGTGCATGTGCATGGGGCCCTATGGAAAGAACGGG 3796

4373 GACT-TCTTAAT-TCACAGGGAT-CATCTATTAAGTATAAAGAGGAGATACTCCAGCTGTTAGAAGCAAT 4439
     | ||-:||  :|-|||-|||||-||:--||||::||  |||| | :|| || |||||| ||::|||||:|
3797 GCCTGTTTTCGTCTCA-AGGGATGCAC--ATTAAACATCAAGATGCAGTTCTGCAGCTGATAAGAGCAGT 3863

4440 CTACAAACCTGTGGCAGTGGCAATAATGCACATTAGAGGACATCAA-----AACGATTCCAGCAAAGAGT 4504
     :| |||||||| : ||||||||| ||||||||||| ||:|| |||||||-----||--:|||||--|||---|
3864 ACAAAAACCTGAACAAGTGGCAATTATGCACTGTAAAGCACATCAATCAGGAA--ACTCCA--AAA---T 3926

4505 CCATG--GGAAATCGATTGGCTGATCAGGTGGCAAGACAAGTAGCTCGGGAAGTTTGGACTCAAC----- 4567
     :::||--|||||||||| ||| |||::|::||| |||||:|: |||||||:::|:| :::||--|||-----
3927 TTGTGAGGGAAATCGAAAGGCAGATTGGACGGCTCGACAGGCTGCTCGAAAGGTGCAAAC--AACAATGG 3994

4568 ---TAGCTCTTTTACCATCCCGAGAAAACCCGGCTGCTGCATAT--ATGGAAGCTGTCCCTCAC------ 4626
     ---|:|::|:|||||-----------||||:----|: ||:|| |--|| || :|::|:|-|||------
3995 CATTGGTCCCTTTA-----------AAACT----TAATGTATCTCAATTCAATTTACCTC-CACAGCCGA 4048
```

```
4627 --TATTCTCCGGAAGATGATAAATTGGCTCAGATGCTGCAGGCAAAGAAGAACATCAAG--GGGTGGTAT 4692
     --|||||   |:||||||||| |||:|||  ||   |:||| | ||| |||||||--|| ||--|||||||||
4049 AATATTCAGCAGAAGATGAGAAACTGGGACATTTACTGAATGCACAGAAGAA--TCCAGAAGGGTGGTAT 4116

4693 GTCAC-GTCTACTGGACA---AGTGGT------CTTGCCAGTCAGAATCATGAAGCATGTTTTGGAAATA 4752
     || ||-|: :||-|||||---|||||------||||---------:| ||||:: | |||:|: ||||
4117 GTAACTGCACAC-GGACAGATAGTGGTACCCCCCTTG---------GTAATGAGAGAGGTTCTACAAATT 4176

4753 GAACATAACAAGTGCCATTGGGGAGCAGAAGCATTGGTAAGATTTCTTAAAAAAGAAATAT--TCTCGAA 4820
     :||||||||:|:||:||||||||| |||||:||||||||||:||||||--|||| |   || |--||||::
4177 AAACATAACGAATGTCATTGGGGTGCAGAGGCATTGGTAAAATTTCT--AAAACGTTATTTGGTCTCAGT 4244

4821 CCAGATGTTGACCCTGGCAAAA--AGGGTTAATG-CAATGTGTCCGGTATGTATTAAAAACAATCCAGTA 4887
      |::|||||:||  |||||||||--|:---|||||-||| ||||   |:| ||: | ||||||:||:|||||:
4245 ACGAATGTTAACAATGGCAAAATCAA---TAATGTCAAAGTGTGAGATTTGCTTGAAAAATAACCCAGTG 4311

4888 GTAAGGAGGCAAATTCAAATGGGAACTATTCGGGTGGGACCCCAACCTGGAGATTATTGGCAGGTGGATT 4957
     |: ||: |:||::: ||| |:|||| :|||||||||:||: :  |||| ||||||||||||||||||:||||
4312 GCTAGACGACAGGCACAACTAGGAAGGGTTCGGGTAGGGATAGAACCAGGAGATTATTGGCAGGTAGATT 4381

4958 TCTCAGAACTCCCAAAGGCAC-AGAATTTTAAATATTTATTAGTTTATGTCTGTACCTTTTCAGGATGGC 5026
     |: :|||||:| ||||:::| |-||:| :-||||||||||||   : ||: :||| ||||| |||||||
4382 TTGTAGAATTACCAAGAACTCGAGGATAC-AAATATTTGTTAGTAGGGGTTGATACATTTTCCGGATGGC 4450

5027 CAGAAGCCTTTCCTTGCAGAACAAATCAATCAAGGGAAGTA-TTAAAAACCCTGTTGA----AAGAAATC 5091
     |||||||:|||||:||:  | ||:||:||| |||::|||::|-||||:-----|| | |----|||||||||
4451 CAGAAGCCCTTCCCTGTCGCACGAACCAAGCAAAAGAAACAGTTAAG-----TGGTTACTACAAGAAATC 4515

5092 ATTCCCAGGTTTGGGATACCTTTGGGGTTATCCTCAGACAGAGGCCCACATTTCACGGCATGGGTAGTGC 5161
     |||||||:||:|||:|:|||:|:||| |||| ||||||:||:|| || |||||||::|| |||:||:
4516 ATTCCCAGATTCGGGGTGCCTCTAGGGATATCATCAGATAGGGGACCCCATTTCATAGCCACGGTGGTAA 4585

5162 AAGAAATCTCTAAGACCTTGGGGATTTCCTGGGACCTGCACACCCCCTGGCGGCCTCAGTCAAGTGGACA 5231
     |||||:|   ||:|  : :|||||:||   |:||||||||| ||||| || ||| :||:||||||||||||
4586 AAGAAGTAAGTAGGTTGCTGGGAATAACTTGGGACCTCCACACACCATGGAGACCCCAGTCAAGTGGACA 4655

5232 GGTAGAAAGAATGAACCAAACATTAAAGGGTCAAATTAAAAAGATTTGTCAGGAAACAGGAATCCAGTGG 5301
     |||:|:|||:||||||:|:|||||:|||||:| ||:|:|: ||:|| |||||:|||:| ::| | |||||||
4656 GGTGGAGAGGATGAATCAGACACTAAAAAGGCAGATCAGTAAAATATGTCAAGAAGCCAAACTGCAGTGG 4725

5302 CCACAGGCACTTCCTTTAGCATTGTTGAGGATCAGGATTAAGCCAAGGGAAAAGATTGGGTTA---AGTC 5368
     ||||||||| :| || ||||||||:||||:|||| |||| |||||| |||:: ::|||---||:|---||||
4726 CCACAGGCTTTACCAATAGCATTGCTGAGAATCCGGATAAAGCCTAGGAGTGGGAT---GTCAGTCAGTC 4792

5369 CATATGAAATTTTGTATGGCAAACCTTA------TCATG----CAG-CTACATATAAGGGGGACCCTCAC 5427
     | ||||||:|| |||||||||| ||||| ||------|| ||----||:-|:| ||||||-----------|||
4793 CTTATGAGATATTGTATGGGAAACCATACGAATCTCCTGGACCCAATCCAAATATA-----------CAC 4851

5428 CTGGTGGGCGATCAAGTGCTGTTAAATTATGTGTTGTC-CTTAAATAAGACTCTTACA-GCCATCAGGGG 5495
      | ::|||  :| ||:| : |:| ||:|||||  :|||||| :|||||-||:::-||:|||:| :||-| | ||-||:|
4852 GTCACGGGAAAACAGGAAGTATATAACTATGTTCTGTCTCTTGGG-AAAACTTTAGCACGACTTC-GGAG 4919

5496 AGCACTGCAGTGGAATCGACCTCTACCCCTGGAAAATCCGGCACACGATATCCTTCCTGGAGACCAGGTG 5565
     || ||  |||||||| :|| ||: |:|| ||:||||| |: ||:|:|| | ||| |||||| |||||
4920 CGCCCTCGTGTGGAATAGGCCGCTGACTCTCGAGAATCCTGTTCATGACATACATCCAGGAGACGAGGTG 4989

5566 TACATCAGGAATTGGTCAGAGGGACCACTGAAGGAAAAATGGGACGGACCTCACCAGGTGATCATGACAA 5635
     |||||:|:|||||||| ||:|:||||||||||:|||||:|||: :|||||:||:|||||: | ||||| |
4990 TACATTAAGAATTGGAATGAAGAACCACTGAAAGAAAAGTGGACTGGACCCCATCAGGTACTACTGACCA 5059

5636 CATATACTGCTGTAAAGGTCCAG--GGAGTCGACAACTGGATCCACTACACCAGAGTGAAGAA 5696
     | | :|| || || |||||--||--|||| |||  |||||| ||||||||: ||||||||||
5060 CCTTCACAGCAGTCAAGGT--AGCTGGAGTGGACTCCTGGATACACTACACTCGAGTGAAGAA 5120
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	6908	7498	TguERV2_I	6052	6646	d	0.7069	1.9221	1464

```
6908 TAATTGTAGG---TACCTCACAGTACAC-----AGCCCAGGAAATTTAGTGTGGGTATTGGGACATGG-A 6968
     || ||||||||---|||||- | |||||||||-----||:||||||| | || ||:|||||:| :::| ||||-|
6052 TACTTGTAGGATGTACC-AAGAGTACACTCCGAAGTCCAGGACAATTCGTATGGGCAACAAGTGATGGTA 6120
```

```
6969 CAATGGACTACACATTTGCCTATAGACGGATTGATTACACAAATAACTTTAGGGATTCCCACATTATGTC 7038
     | -|||||| || |||:|:|||:||||:||: ::| | | |||| ||||||| |:||:|| ||:||||
6121 CC-TGGACAACCCATCTACCTGTAGATGGGAAAGTAAAAGAAATTACTTTAGGCCTCCCTACTTTGTGTC 6189

7039 CCTATTGGAAAGAATCAAAATTAACCGAGGGAGAAAAAT-------------TAAGCACAA-ACGAAAT 7094
     |    |||||||:|:|| ||| |---|||||-|||:||-------------|||||-||||-||||:|
6190 CAATTTGGAAAAAGTCCCCATTTA---AGGGA-AAAGATGAACTTCTGCAGATAAGA-ACAAGACGAGAA 6254

7095 GTGGATCAAGATTTGCAGGATATAGGTTTAGATAAAGACCAATGGCATGAGCCTTCAGGAGGGGTAAAGT 7164
     ||---|| |:||------:||: |::: ||||:||-|||--||||| ||:||:|| :| ||:||:||:|
6255 GT---TCCAAAT------AATGAAAATCAAGATGAA-ACC--TGGCAAGAACCCTCTAGTGGAGTGAAAT 6312

7165 TTGGATGGGTCTTAGAATCCTTGTTTGCACAGGTTGCTTCT-------TATCGTAATCGAGAAATGTTAT 7227
     ||||:|||||:||||||:||:|||:|||-----||--|:| |-------|||||: ||| :||||||||:|
6313 TTGGGTGGGCCTTAGAGTCTTTGCTTG-----GT--CCTATAGCAAACTATCAGAATAAAGAAATGTTGT 6375

7228 ATAAATTGATGGGTCAGACTGAAAGGCTAGCTGCGGTGACTAGGAAAGGTTTTAAAGACATAAACATCCA 7297
     |:||||: |::||||||::|| ||:|:|||: ||| |||||||:|||| |||||||| ||||||:| ||
6376 ACAAACTTACAGGTCAGGTAGATAGACTGGCTAGGGTCACTAGGGAAGGATTTAAAGAACTAAACGTACA 6445

7298 ATTGCAAGCTACATCCAGGATGACGTTACAAAATCGAATGGCATTAGATATGTTACTTTTAAAAGAGCAT 7367
     |||:|||||:|| | |::||||| ||||||||||| |:||||||:||||:|||||||||
6446 ATTACAAGCCACCACAAAAATGACCNTACAAAATCGATTTGCCTTAGATTTGTTACTCCTGAAAGAGCAT 6515

7368 GGAGTTTGTGG----TTACCTGCATGATAAAGAT-GAGCACTGTTGTGTACACATCCCAAACGTTACCCA 7432
     ||||| |||||----|||-----| |: | ||||-|| ||:||:||:|:: |||||||||||:|| ||:
6516 GGAGTGTGTGGACTTTTA-----AAGGGACAGATTGATCATTGCTGCATCCACATCCCAAATGTAACTGC 6580

7433 AGAAGTGGAAAATGACATTAGCCAGCTGGAACAAATTGAGAGCA--AAGTTCATGAGACTCAAAAAGA 7498
     ||| ||:|||| |||||||||:|::|||:||:||||||||--||||||--|||| || ||:: ||:|||||
6581 AGATGTAGAATATGACATCAATCAGTTAAAACAAAT--AGAGCATGAAGTACAAGAAGAGCAGAAAGA 6646
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	1243	1431	TguERV2_I	1136	1324	d	0.7407	1.9600	771

```
1243 AAAGTCCCGTTCTCGCCGAATGATTTAATGATATGGAAACAGTCGGCGGGAGCGTATAGGGAGAATCCTG 1312
     ||:|| || ||:|| || : ||||||:|:|| |||||||||:||||| |||:| |||||||||:|||||||
1136 AAGGTACCTTTTTCCCCTGCGGATTTAGTAATTTGGAAACAATCGGCTGGAACTTATAGGGAAATCCTG 1205

1313 AAAAGGTAGCTCGGGTTGTGAAAATGGTAATTAAGACTCAAACACCTGATTGGAATGATTTGCAAGTTCT 1382
     | ||:||:|| :||| ||:|||||||:| || ||:|||||:| || ||||||:||||| |:|||||  |
1206 ATAAAGTGGCAAGAGTGGTAAAAATGATTATGAAAACTCAGAATCCAGATTGGGATGATATACAAGTAAT 1275

1383 GTTAGACACATTGATGGATTCCACGGAAAAGGAGATGGTTATTAAAACA 1431
     :|||||||||| :|:|||||||||:||:|:||:||:|||||||| ||||||:||
1276 ATTAGACACCCTAATGGATTCTACAGAGAAAGAGATGGTACTTAAAGCA 1324
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	537	835	TguERV2_I	352	659	d	0.6881	1.8780	533

```
537 TTCTCCTCTTGGATGTTTGTTAAAACATTGGAAA---GGTAACTTTGATCAGGA--TATGAAGAAGCAGA 601
    |||||||:| ||:||:||:|||: ||||||||||---|||||:||||: ||:||--||:: ||::|:|-|
352 TTCTCCTTTGGGGTGCTTATTAGCACATTGGAAACAAGGTAATTTTGGGCAAGACTTACATAGGGGTA-A 420

602 GTTTAATTGATTATTGTAAT-CATGTCTGGCCGGAATATG-----AAACGGGGGGAATGCAGTGGCCACG 665
    |||-|||||||||:||||||-||||-|||| -|||||:||||||||-----:|| | || |||-- |:|||||||
421 GTT-AATTGATTACTGTAATACATGG-TGGCCAGAATATGTCTTGGAAGGTGGTGAA--AAATGGCCACC 486

666 TAACGGTACTCTG---------ACTACT--GGAATTATTGCTCCTTT---AATGAGTTTCTTGAGGGAAA 721
    ||:|| || :||---------||||:|--| ||||: ||: :|||---||:|-------:||:|||||
487 GAATGGAACATTGCAACATAACACTATTTTGCAATTGATGTTGTTTTGTAAACG-------CGAAGGAAA 549

722 ATGATAAATGGGATGAAATACCTTACTTAGACCTTTTTTATTACCTTAGACAAAAGACAGATTGGCAAAA 791
    |||-------|||||||::| || | : | ||:: |||| :|||:| || | ||| |||| |||||:::
550 ATG-------GGATGAGGTTCCGTATATTGATTTGTTTTTCTACTTGCGAGATAAGCCAGAATGGCAGGT 612

792 AGAATGTGG-T--ATGTTGGTTTTGGAAACTGTAAAAAATGAGTGTG 835
    ||||||||-|--||| |:||| || | ||::||: :||:|||||||
```

613 TGAATGTGGATTGATGGTAGTTAAGGCATCTACAAGTGATAAGTGTG 659

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	6176	6292	TguERV2_I	5345	5461	d	0.7265	1.8667	379

```
6176 TGAAAATCTAGTTGTAGGCTTAATTAGAGATTTTG---GATTGATGCAAAATA-TATCACAAATAACTGC 6241
     |||:|||| ||:| :| || |||:||||:|||||||||||---:|---|||||:||:|-|| ||-:|||||||||
5345 TGAGAATGTAATGATTGGATTAGTTAAAGATTTTGCCAAA---ATGCAGAACACTAGCA-GAATAACTGC 5410

6242 CTGCCTACCTATGCCTCAGACTGCTGGAGATCCAATCCCTTGGGGAGTAAT 6292
     |||:||:|| ||:||| ||:| || |||||:||||| |||||||:| ||
5411 CTGTCTGCCAATACCTAAGGCAGCGGGAGACCCAATAAATTGGGGAATCAT 5461
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	307	436	LTR-12B_Crp	140	270	d	0.7419	1.6429	253

```
307 ACAATATTATTTTGTTGGCAAGTTTGGATATTTGGTTGGTTGGTTG------GTTGTAGCATTGTAT--C 368
    ||| | ||||||||| |:|||||||||------|||||||--|||| |:------||| ||-:|||||||||--:
140 ACATTTTTATTTTGGTAGCAAGTTT------TTGGTT--TTGGATATCCACTGTTTTA-TATTGTATAAT 200

369 TGTTAGAGTCTCTAACGATTTTAATTCTGGGGCTGTTTAT------GTTATCATTT--GCATTGATCTCT 430
    |:||||-||:| || :||||||| |:|-----|:||| |||------:||||||||||--|:|||||||:|:|
201 TATTAG-GTTTGTATTGATTTTTACT-----GTTGTATATTGTATTATTATCATTTTTGTATTGATTTTT 264

431 GTTGTT 436
    :|||||
265 ATTGTT 270
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	1105	1134	tRNA-Ala-GCY_	46	75	d	0.9000	1.5000	202

```
1105 CCCCGGGTTCGATCCCCAGGATCTCCACCA 1134
     ||||||||||:|||||||| |:|||||||||
  46 CCCCGGGTTCAATCCCCAGCACCTCCACCA 75
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	1575	1701	ERV1-1_GG-I	1701	1828	d	0.6772	1.6818	315

```
1575 TGAGGGAGTTCGGGATGGG--ATCCCGAAAACACTGAATTGGTCAAAGTTATATACAGTAAGGCAGGA-- 1640
     |||:||:| | |:||-|||--||||| ||:||| | |||||||| || |||| |:|||| ||:|||||:--
1701 TGAAGGGGATGGAGA-GGGCTATCCCCAAGACAATCAATTGGTCTAACTTATTTGCAGTCAGACAGGGTC 1769

1641 -GAAAGGGGAGTCTCCATCCGCATTTTTGGAGAGGCTTAAAGATACTGCTCGGAAGTATACT 1701
     -:||||---|:|| ||||||:| :||||||||| |:|:| |::||::|::: :|||:|||||
1770 CAAAAG---AATCACCATCTGAGTTTTTGGATAAGTTAAGGGACGCCATGAGAAAGCATACT 1828
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	1734	1897	ERV1-7_MM-I	1900	2062	d	0.7375	1.3913	472

```
1734 ACAGATGGCTTTGATATTTATAGGGCAGTCGCAGGA--GGATATTAGGAAAAAGCTGCAGAAGCTAGAA- 1800
     ||||-|||| :||::|||||||:: |||||--|| |--|||:|||||:|::|||||:|||||:||||||-
1900 ACAG-TGGCGCTGGCATTTATAAACCAGTC--AGCACTGGACATTAGAAGGAAGCTACAGAAACTAGAAA 1966

1801 -----GGGGAAGA---AATGCGAAATTTAGAAAAACTACTGGAAGTGGCATGGAAAGTATACAATAATAG 1862
     -----|||||||:|---| || ||:||||||---------|||:||||||||| :|||||:||| |||||:||
1967 GACTAGGGGAAAAGTCATTGAGAGATTTAG---------TGGGAGTGGCAGAGAAAGTGTACCATAACAG 2027

1863 GGAAAA-GGAGGTGACAAAGAAACAACAAG-CAGGGA 1897
     ||||| -:::||:|||-:|||||:-| :|||-|||||
2028 GGAAACTAAAGATGA-GAAGAAG-ATTAAGACAGGGA 2062
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

| rnd-5_family-1147#LTR@ERV1 | 1926 | 1985 | Copia-130_SB-I | 778 | 836 | d | 0.7705 | 2.2000 | 231 |

```
1926 GGGTAATGGGGGAAATGCTCGAGGTCGG-GGTCGCAGCCGGGGAAGAGGTGGAATTGGAAG 1985
     ||| || ||:||||||-||-|| | |||-|||||::|||||||||||:||| | |||||||:|
 778 GGGAAAGGGAGGAAAT-CT-GATGGCGGCGGTCGTGGCCGGGGAAGGGGTCGCATTGGAGG 836
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1147#LTR@ERV1	2042	2091	TguERV1_I	3922	3971	d	0.8400	1.6000	321

```
2042 ATCAATGTGCTTTTTGCAGGGGATTTGGCCACTGGAAAAATGAATGCCCA 2091
     |||||||||| |||||||||::||||| |||||||||:||: |:|||||||
3922 ATCAATGTGCATTTTGCAGGAAATTTGGACACTGGAAGAACCAGTGCCCA 3971
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	786	844	hAT-N56B_CPB	306	359	d	0.8679	2.0000	213

```
786 GGAGCGCTCCGGTGCCGCGCTGCCCGCAAGTTTGCCGGC----CGGCGCTGCGGCTGGGGGCG 844
    ||:||||||||||--||||||:||||||-------|||||----||| |||| |||||||||||
306 GGGGCGCTCCGG--CCGCGCCGCCCGC-------CCGGCACTCCGGGGCTGGGGCTGGGGGCG 359
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	1040	1363	Ag-Jock-1	1181	1471	c	0.7021	1.8182	751

```
1040 CCGCGGCTGCTGGGGCNGGGGCTGCCGCTCCTGCCCCTCCCGCCGCTTCNGGCGCTGCGGCTGCCGGAGC 1109
     |:|| |||||||| || | |||||:||| ||||: || |:||:||| | :|||||| |||||:| |||
1471 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCCGCTGCTGCTGCTGCTGCAGC 1402

1110 TGTTGCCGCCGGGACTGCTGCCGGCGCGGCTGCTGCCGCCGCCGTTCCCGGGTCCGCTGCNGCCCCCGGG 1179
     ||:|||:||:|---|||||||:| :|| |||||||||:||:||:||| |:|---|:||||| ||:------
1401 TGCTGCTGCTG---CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGTTGCTG---CTGCTGCT------ 1344

1180 TCCGCTCCCGCTGCTGCCGCTGCCCCTNCCGCCGCTGCTGCTGCTGCNGCCGNTCCTG------CTGCTG 1243
     ---||| |:|||||||||:|||||: || |:||:||||||||||||||| || | |:|||------||||||
1343 ---GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCAGTTTCTGTTGCAGCTGCTG 1277

1244 CCGCCGATTCCGCCACCCCTGCCGCTCCTGTTGCTCCTGCTGAGACTGTGTCCCGTCACGCCGGTCCCGA 1313
     |:||:|| |:|:::: ::|||:::||| |||:|||| |||||| :||||:----||--------------
1276 CTGCTGAAGCTGTTGGTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGTA----GT-------------- 1225

1314 TCCTGTCCCATCTGCTGCCGCTGCTGGGTTTCCTTTCGGTTCCGCTGCCG 1363
     |:||||: || ||||||||:|||| |------|| |:|||||:|:|||:|
1224 TTCTGTTGCAGCTGCTGCTGCTGAAG-------CTGTTGGTTCTGTTGCTG 1181
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	3089	3955	ERV2-15_PMaj-I	3396	4261	d	0.6790	1.9741	1355

```
3089 CACCACCCCTAACCTGG---ACAACTGATACACCTCTGTGGATCCCACAGTGGCCCATTAAAAAAGATAA 3155
     ||||| |||||| |||---|| ||| |---:||| |||||:| |||||||||:|| ||:||||:|| ||
3396 CACCAGCCCTAAAATGGCTCACCACTCA---GCCTGTGTGGGTACCACAGTGGTCCCTTGAAAAGGAGAA 3462

3156 ATTGCAGCATATTCATGA----TTTAATAAAAGAACAATTAAAT-AAAAACAGATTAGTTCCCACAAATA 3220
     |:|--||-||:::|-|:|----||||:|| |||||:||::||: |-||::|| ||-|| || | | |
3463 ACT--AG-ATGCCC-TAAAATCTTTAGTACAAGAGCAGCTAGCTCAAGGGCACAT-AGAACCATCTATGA 3527

3221 GCCCATGGAACTTTCC--TATTT-TCACAATCAAAAAATCCTCTGGAAAATGGAGACTCCTGCATGATTT 3287
     |||| |||||| ::||--|||||-|||:|| ||:|||||---||| |||||||||:::| || |||||:|
3528 GCCCTTGGAACACCCCAGTATTTGTCATAAAAAAGAAATC---TGGTAAATGGAGGTTGCTCCATGACCT 3594

3288 GAGAGAGGCAAATAATATAATAGAACCAATGGGAGCCCTCCAAGTAGGACTACCATCTCCTACCATGATT 3357
     :|||:|:::|||| |:| ||:|||| ||||| ||:- ||| :||| |:||||||||||| ||||||
3595 AAGAAAAATCAATTCTGTCATGGAAAGCATGGGCGCT-TGCAACCAGGTATGCCATCTCCTACAATGATT 3663

3358 CCAGAAAATTGGCCACTTGTAATATT--------GGATATTAAAGATTG-TTTCTTTAATATCTATCTTC 3418
     ||-------- |||||:|| :|:|||--------|||: | |||||||||-|||:|||| |||::: || |
```

```
3664 CC-------TGCCACCTGGGACATTCTGATTGTGGACCTAAAAGATTGGTTTTTTTACTATTCCACTAC 3725


3419 ATCCTAATGATGCACATAGATTTGCCTTTTCTATTCCAGCTATTAAT---GCTGAAGAGCCCGCCAAAAG 3485
     |:||  :|||||:| |   |::|||||:|||  :|  ||| |:||||||---||||-------|:|||: :|
3726 ACCCAGATGATACCCCAAAGTTTGCTTTTACAGTGCCATCCATTAATAATGCTG-------CACCAGTGG 3788

3486 A----TATCACTGGGCTGTCCTTCCCCAAGGTATGAGAAATAGCCCAACTATATGTCAAGCGGT----TG 3547
     |----|||||  |||:   ||:||  || ||:||  ||||:|||:|||||| || || ||:||-|:|||----||
3789 AGCGTTATCAATGGAAAGTTCTGCCACAGGGGATGAAAAACAGCCCCACAATTTGCCA-GTGGTACGTTG 3857

3548 TGTC---CAATATAATTGAGCCAGTTCGAAAGCAATTTCCAGAAGCCATCATATT-CCATTACACAGATG 3613
     :-||---|| | | ||-----||||   ||:|:|||||||||||::||-:|  |:||-|||||||||::||||
3858 C-TCAGGCACTMTCAT-----CAGTGAGAGAACAATTTCCAGGGGC-GTACTGTTACCATTACATGGATG 3920

3614 ATATTCTGATCAGCTGTAGTAGC----ACTGAAAAATTAAAATTGGTACATGAATCTGTAAAAG--AAGC 3677
     |||||:|:||-------||:|:|----||::|||||---:| :|  :|||-|| ||------||--||||
3921 ATATTTTAAT-------AGCAACCCCAACCAAAAAA---GACCTTTCACA-GATTC------AGCCAAGC 3973

3678 TCTG-TGTAGCCAT-----------GGACTAGAAGTGGCTCCAGAAAAAGAGCAAAGACGTCCCCATGG 3735
     -|||-||:|: |||-----------||:||: |:||||| ||||||||:| |||: ||  ::| || |||
3974 -CTGATGCAAGCATTAAAAACATTTGGGCTGCAGGTGGCACCAGAAAAGGTGCAGCAGCAACCACCCTGG 4042

3736 AAATACCTTGGTCT---GATAATAGATGAGAGAACAATCAGGCCTCAGGCAAT--AACCTTGTCCACCAG 3800
     ||||||||||| ||---:|||||:||| |||---| || :||| ||::|||||--|||:||--| ||||:
4043 AAATACCTTGGACTCAAAATAATGGATCAGA---CCATACAGCCACAAACAATTCAACTTT--CAACCAA 4107

3801 AATTAAAACATTAAATGATTTGCAATCATTATTAGGGAATATAAACTGGATAAGATCTTTTCTCGG---- 3866
     |||| |||| :|||||:||| ::||| |:| ||:|| | :|| |||||||:| |||:|:| ||| ||----
4108 AATTCAAACTCTAAACGATGCACAAAAACTTTTGGGTACCATCAACTGGGTCAGACCCTATCTAGGATTG 4177

3867 ----TCTTTCAACAGACTTTTTAGCTCCTTTGTTTCAACTCCTAAAAGGAGAGCCAGAATTAACATCTCC 3932
     ----:||: |||--------||:|| ||:||:|||-||||||||||||| || || ||::|||| ||:||
4178 ACCACCTCACAA--------TTGGCACCCTTATTT-AACTCCTAAAAGGTGATCCTGAGCTAACTTCCCC 4238

3933 TAGGCATTTAACACCAGAAGCAA 3955
     :||: | |||||| |||||:||||
4239 CAGAAAATTAACCCCAGAGGCAA 4261
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1373#LTR@ERVK	4243	4426	ERV2-15_PMaj-I	3989	4162	d	0.6554	2.0000	303

```
4243 AGAACAGTTAGGCCGCAGGGGNCTGACAATAGCCCCTGAGAAGATTCAGCTAACAGA-GCCTTGGAAATA 4311
     |:||||  ||:|||:|||||----------|:||  || ||:|||:| ||||-|:||: -:||:|||||||||
3989 AAAACATTTGGGCTGCAGG----------TGGCACCAGAAAAGGTGCAGC-AGCAACCACCCTGGAAATA 4047

4312 TTTAGGATGGACAATATTAAAGTCAT-CTATTAAGCCACAAAAGATTCACATTTCAACAGAGATTCGCAC 4380
     ::|  |||:   |  |||| |::|-|||  -|:||  |||||||||| :|||||  ||||||| :|:||||: ||
4048 CCTTGGACTCAAAATAATGGA-TCAGACCATACAGCCACAAACAATTCAACTTTCAACCAAAATTCAAAC 4116

4381 TCTTACTGATGTTCAGAGATTGGTAGGAGATATACAGTGGGTCAGA 4426
     ||| | :||||: ||:|:|:| :|| : :|| | ||||||||||
4117 TCTAAACGATGCACAAAAACTTTTGGGTACCATCAACTGGGTCAGA 4162
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1533#Unknown	1	51	MuDRx-4_PI	32	82	c	0.7885	1.5000	232

```
 1 TGTCCTA-GTTCAGCAGGTGGGACCAGTTTATCACTGTGTGGGTGTGACCAA 51
   || |||||-|||:|||||:||| |||| :||:|||||-:|:|||||||||||||
82 TGACCTACGTTTAGCAAGTGTGACCTATTCATCAC-ATATGGGTGTGACCAA 32
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-15382#Unknown	212	281	Gypsy-232_OS-LTR	1419	1495	d	0.7042	1.1875	258

```
 212 TCCCCACCCAGGTGCTCTGGTGAGGGCTCCTT---------GGCCCTTCTCCCCTTTCTGTTCTGTTATCC 273
     || |||||: |||||||-|||||||:|||||:|---------: ||||:|||||||:|:|:|||:|||:::::|
1419 TCGCCACCTTGGTGCTC-GGTGAGGACTCCCTCCTCCTCCACCCCTCCTCCCCCTCCCGTTTTGCCGCTT 1487
```

```
 274 CTCGTGGC 281
     |:||||||
1488 CCCGTGGC 1495
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-15382#Unknown	533	581	hAT-N20_TrPr	261	308	d	0.8125	1.2000	230

```
533 CTTCTCCCTTTCCCTCC-ACGCCGCACAGAAG--AGACCCTTTTCNTTTTAA 581
    |||||||:|:||||||||-||||:----|||||--||||::||||| |||||||
261 CTTCTCCTTCTCCCTCCCACGCT----AGAAGGAAGACTTTTTTCTTTTTAA 308
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1599#Unknown	449	494	ERV1-2_ACC-LTR	479	525	d	0.8298	1.1667	283

```
449 CATGTCTTTGGTGGAATTATCCCCCATGTT-CCCAGCGCTGAATAAA 494
    ||:| |||||||||:|:||:||||||:||:|-|||||||||||||||||
479 CACGACTTTGGTGGGACTACCCCCCGTGCTGCCCAGCGCTGAATAAA 525
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-16196#Unknown	6	79	hAT-N17_NS	225	302	d	0.7733	1.7143	211

```
  6 TAGAGA---AAAGCCAGAACTTAGGGGAT-TTTACTAAAAGCACCCAA--CTT--TCATGGGAGTTTCCA 67
    ||||||---||||:|||||:|----||||-|||||||:|| | ||||--|||--|| ||:||: ||:||
225 TAGAGATGGAAAGTCAGAATT----GGATCTTTACTAAGAGGAACCAAAACTTGATCTTGAGAAGTTTCA 290

 68 AGAGATAAGGTT 79
    |||||||:| |||
291 AGAGATGATGTT 302
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-16196#Unknown	246	293	ERV44_MD_I	4921	4967	d	0.7917	2.2500	217

```
 246 CATGAGGATGAAGAACAAAAATACGACCACCACCAGATGAAGTAACAG 293
     |||| :|||||| ::||||||||| ||||:|||||-||||||||| || ||
4921 CATGTAGATGACAGACAAAAATCCGACTACCAC-AGATGAAGAAAAG 4967
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	1891	2047	EnSpm-2_NS	2148	2318	c	0.7562	1.7059	487

```
1891 ATAAAGAAGAAAACAACGAGGATGA-----AGGAGA-CTACA----AAA--CCCA------CAGAGCCAC 1942
     ||:|||||||||:| :| |||:||||-----||:|||-||: |----|||--||||------|| ||:|:
2318 ATGAAGAAGAAGAGGAGAATGAGAAAAAGAAGAACTGAAGGGGAAATTCCCAGCATTTCACTGCTAT 2249

1943 CTCCGCAATTGGAAC---GAGAAGAAGAAGAAGAGGAACAAGAAGAAGAAGAAAAAGAAGAAGAAGAAGA 2009
     :| |||-:||:|||---||-|||||||||||||||:||| |||||||||||||||:|||||||||||||||
2248 TTGGGCA-CTGAAACAGTGA-AAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGA 2181

2010 AGAAGCAGACGAAGGAGCAGCTGCGAGAGAGCAAGAAA 2047
     ||||| :|| ||:||:| :|----|||-||| ||||||
2180 AGAAGAGGAGGAGGGGGGGG----GAG-GAGGAAGAAA 2148
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1704#LTR@ERVL	2086	2193	ATCOPIA26I	2612	2710	c	0.6990	1.9286	264

```
2086 AGAGTAGTCACAGCAGAGGAAGGAGCAACGGCGAGAGAAGGAAGAATAGTCACAGTAGAGGAGGGAGCAG 2155
     |||| ||| || || | |||:|| ||||:|||--||-|||||||: :|| ||---|| | |||:|| ||||:|:
2710 AGAGGAGTGACCGGAGAAGACGGAGTAAC--CG-GAGAAGACGGACTA---ACCGGAGAAGACGGAGTAA 2647

2156 CCGCCAGAGACGGAGGAGTGGTCACAAGAGATGGGGTA 2193
     |||---|||| |: |||||||::|: |::|||||||:|||
```

2646 CCG---GAGAAGACGGAGTGACCGGAGAAGATGGAGTA 2612

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1706#Unknown	1	1894	ERV3-22_PMaj-I	3440	5335	d	0.7780	1.4754	10184

```
    1 AACAGGCTTTCAAGCAGATTAAGCAAGAAATCGCACATGCCGTGGCTCTTGGACCAGTCAGGACGGGACC 70
      ||||:||:||::  |||||:|||||:||:||||| ||||| ||:||:||||| |||||||||||:|||||
 3440 AACAAGCCTTTGCCCAGATCAAGCAGGAGATCGCTCATGCAGTAGCCCTTGGCCCAGTCAGGACAGGACC 3509

   71 AGATGTGAAGAATGTACTTTATTCCACAGCTGGAGATAAAGGTCCCTCCTGGAGCCTCTGGCAAAAGGTG 140
      ||||||||||||:||:||:||:||:||::||||:||::: | ||||: |||||||||||:|||||:||||||
 3510 AGATGTGAAGAACGTGCTCTACTCTGCAGCCGGGAGCCATGGTCTGTCCTGGAGCCTTTGGCAGAAGGTG 3579

  141 CCTGGTGAGACACGAGGGCGACCACTTGGTTTCTGGAGCCGAAGCTACAAAGGCTCTGAGGCCAATTACA 210
      ||||| ||||| ||||| |||||||| || ||||||||:|||||||||||:||| ||:||:|||||:||||
 3580 CCTGGGGAGACTCGAGGCCGACCACTGGGATTCTGGAGTCGAAGCTACAGAGGGTCCGAAGCCAACTACA 3649

  211 CCCCTATGGAGAAGGAGATTCTAGCGGCGTATGAAGGCATACGAGCAGCCTCGGAGGTAATTGGTACTGA 280
      |:||:||::|||||||||:|||:||||||:|| |||||||| ||:| |:||| ||||||:|||||||:|| ||
 3650 CTCCCACAGAGAAGGAAATTTTAGCAGCCTATGAAGGAGTCCAAGCTGCCTCAGAGGTGATTGGCACAGA 3719

  281 AGCACAGCTTTTCCTGGCACCTCGACTACCGGTGTTAAGCTGGATGTTTAAGGGAAAAGTGCCCCCTACA 350
      |||||:||:||::|||||||:|||||||||||||||:::| ||||||||:||:| |||:|| |||:|:|||
 3720 AGCACAACTCCTCCTGGCACCCCGACTACCGGTGCTGGGGTGGATGTTCAAAGCAAAGGTTCCCTCCACC 3789

  351 CACCATGCCACCGATGCTACGTGGAGCAAGTGGATTGCTTTGATCACTCAACGTGTCCGAATTGGGAGCT 420
      |||||||||||||:|||||:||:|||||||||||||||||||:| ||||| ||:||:|:||| |||||:|: :
 3790 CACCATGCCACCAATGCCACATGGAGCAAGTGGATTGCCCTCATCACGCAGCGCGCCCGTATTGGAAAAC 3859

  421 CGAATCGCCCTGGAATTCTAGAAATTATAACCAATTGGCCTGAAGGTGGGAACTTCAGCCTGGCAGATGA 490
      |||||||||||||:|||:|:||:|| || || ||:||||| |||||||::|||||::|:|| :| |||||
 3860 CGAATCGCCCTGGGATTTTGGAGATAATTACAAACTGGCCAGAAGGTGAAAACTTTGGTCTCACTGATGA 3929

  491 AGAAGAAGAAGAGTCAGTGAGTCGAGCTGAAGAGGCTCCACCATATAATCAGCTGCCAGATGAAGAGACG 560
      |||:||: |:||:: ||||| ||:|||||||||:||||||||:||:||:||:|:||||||||| ||||:||:
 3930 AGAGGAGCAGGAACAAGTGACACGGGCTGAAGAAGCTCCACCGTACAACCAACTGCCAGCAGAAGAAACA 3999

  561 CGCTACGCCCTTTTCACCGATGGTTCTTGCCGTATCGTAGGGGGGAGCCGGAAGTGGAAAGCAGCTGTGT 630
      |||||:||:|| |||||:||||||||:||:|:||||||||||: ||:|||||||||||||||||||:||:|
 4000 CGCTATGCTCTGTTCACTGATGGTTCCTGTCGCATCGTAGGGATGAACCGGAAGTGGAAAGCAGCCGTAT 4069

  631 GGAGTCCCACCCAACAGGTGGCAGAAGCCACTGAGGGGAAAGGCGAATCGAGTCAGTTCGCAGAACTCAA 700
      ||||:|||||| |:|||||| |||||||||||:|||||::||||:|:|||:|:||:||::|:|| |||||
 4070 GGAGCCCCACACGACAGGTCGCAGAGGCCACTGAAGGAGAAGGTGGATCAAGCCAACTTGCTGAACTCAA 4139

  701 AGCTGTCCAATTGGCCCTAGACATTGCAGAAAGAGAAGGATGGCCAAGGCTCTACTTGTACACCGACTCA 770
      ||||||:||||:||||||:|||||||||:|||||:|||| ||||||||:||||||:| |||||:||:|||
 4140 AGCTGTTCAACTGGCCCTGGACATTGCTGAAAGAGAGAAGTGGCCAAAGCTCTACCTCTACACTGATTCA 4209

  771 TGGATGATAACAAATGCCCTCTGGGGATGGCTAAATCGATGGGAGAAAATGAATTGGAGGCGTAGAGGGA 840
      ||||||:|::| |||||:|| ||||||||||| ||||||||:| :|:||:|:||::: |||||| :|||:|||||:|
 4210 TGGATGGTGGCCAATGCTCTGTGGGGATGGCTGGAGAGGTGGAAAAAAGGCCAATTGGCAGCGCAGAGGAA 4279

  841 AGCCCATCTGGGCTGCAGATCTGTGGCAAGACATTGCTGCCAGAGTAAAGAAATTAAACGTGAGAGTCCG 910
      |:|| ||||||||||| |||:||:|||| |||| ||||||:||:|:|||||:||:|||||:|: :||||::||||||
 4280 AACCAATCTGGGCTGCTGATGAGTGGAAAGACATCGCTACCAGGGTAGAGAAACTGTCTGTGAAGGTCCG 4349

  911 CCATGTAGATGCCCATGTGCCCAAAGGTCGAGCTAACGAGGAGCAAGATAATAACAGACAGGCAGACCGA 980
      :|||||||||||||||||||||||::||||:|:||||:|||||||| : ||:||:::||||::||:|:::
 4350 TCATGTAGATGCCCATGTCCCCAAGAGTAGGGCTAATGAGGAGCACCGAAACAATGAGCAGGTGGATCAG 4419

  981 GCTGCACAGATCGAGGTGTCACAAGTAGACCTCGATTGGCAGCAAAAGGGAGAATTGTTCCTAGCTCAAT 1050
      ||||| |||| ||:|||||:|:||||:|:|||||:| |||||||:|| |||||||||||||:|||||:||
 4420 GCTGCAAAGATAGAAGTGTCAAAGATAGACTTAGATTGGCAACACAAGGGAGAGTTGTTCCTAGCTCGAT 4489

 1051 GGGCCCATGATGCTTCAGGCCATCAAGGCCGAGACGCAACCTATAAATGGGCTCGAGACCGAGGGGTGGA 1120
      |||||||||||||||:|||||:||:|||||:|: ||||:||| |||||:|||| |||||||||||||||||
 4490 GGGCCCATGATGCCTCAGGTCATCAGGGTAGAGATGCCACCTATAAGTGGGCACGAGACCGAGGGGTGGA 4559

 1121 TTTAACCATGGACAGTATTTCCCAGGTTATCCGNGATTGTGAAACCTGTGCTGCCATTAAGCAGGCAAAA 1190
      |||||||||||||||||||||||||:|||||||||: ||:|||||:|| |||||:|| ||:|||||||| ||:
```

```
4560 TTTAACCATGGACAGTATTTCTCAGGTTATCCATGACTGTGAGACGTGTGCCGCGATCAAGCAGGCCAAG 4629

1191 AGGTTGAAGCCCCTCTGGTATGGTGGACGCTGGGACAAGTATAAATACGGAGAGGCCTGGCAGGTTGACT 1260
     |||||||||| || ||||||:|||||:||:||| |||:||:||::||:|||:||||||||||:||||||
4630 CGGTTGAAGCCGCTATGGTACGGTGGGCGTTGGTCCAAATACAGGTATGGGGAGGCCTGGCAGATTGACT 4699

1261 ACATCACATTGCCACAGACTAGCCAAGGTAAGCGCTATGTGCTTACTATGGTTGAAGCGACCACTGGATG 1330
     ||||||||:|||| ||:||:|: |||||||:||||||||:||||||:|| ||||| ||||| |||||||||
4700 ACATCACACTGCCCCAAACCCGCCAAGGCAAGCGCTACGTGCTCACAATGGTAGAAGCCACCACTGGATG 4769

1331 GTTAGAGACATACTCAGTACCACATGCAACGGCCCGGAATACTATCTTGGGCCTTGAAAAACAGGTCCTG 1400
     |||:||:|| |||:| ||:|| ||||| || ||||||||:||:|||:|||| ||||||||:||||||||
4770 GTTGGAAACCTACCCTGTGCCTCATGCCACWGCCCGGAACACCATCCTGGGACTTGAAAAGCAGGTCCTT 4839

1401 TGGAGGCATGGCACTCCAGATCGCATTGAGTCAGATAATGGGACTCATTTCAAGAACAATCTAGTGGCCA 1470
     |||||||||||||||:|| || | |||||||||:||||||||||||||||||||||||::|| :|:: ||
4840 TGGAGGCATGGCACCCCTGAGAGGATTGAGTCAGACAATGGGACTCATTTCAAGAACAGCCTTATAAACA 4909

1471 CTTGGGCACGGGAGCATGGTATTGAATGGGTATATCACATTCCATATCATGCACCTGCTGCTGGAAAGGT 1540
      :||||| |||||:|||||:|||||:|||||:|:||:|:|| ||:|||||||| ||||| ||:||:||
4910 GCTGGGCTAGGGAACATGGCATTGAGTGGGTGTACCATATCCCCTACCATGCACCWGCTGCAGGGAAAGT 4979

1541 TGAAAGGTGCAATGGACTGTTAAAAACAACTCTGAAGGCACTGGGTGGAGGAACCTTCAAGAACTGGGAT 1610
     ||:|||||:||||||||||||||||||:||::||||:||:|||||||:||| |:||||||:||:|||||
4980 GGAGAGGTACAATGGACTGTTAAAAACCACCTTGAAAGCATTGGGTGGGGGATCTTTCAAAAATTGGGAG 5049

1611 AAGCANTTAGCCAAGGCCACCTGGTTGGTTAACACCAGAGGCTCTGTCAATCGAGCTGGTCCTGCCCAAG 1680
     |||| :|||| |||||||||||||||:||:||||||||||:||:::|||:||||| ||:||||||||||
5050 CAGCATCTAGCAAAGGCCACCTGGTTAGTCAACACCAGAGGTTCCACCAACCGAGCAGGCCCTGCCCAAT 5119

1681 CAGAATCCCTCCACACGGTAGATGGAGACAAAGTTCCAGCGATTCACTTGAGAGGCATGTTAGGGAAATC 1750
     | ||:::|||| ||:||:|||||::|||||||||||:||||:| ||: | ||||: ||:||||:||: |
5120 CTGAGCCCCTGCATACAGTAGACAGAGACAAAGTCCCAGTGGTACATGTCAGAGGTTTGCTAGGAAAGAC 5189

1751 TGTTTGGATTACTCCTCCTTCGGGCCAAGACAAACCCATTCGTGGGATTGTTTTTGCCCAAGGGTCCGGA 1820
     |||||||:| |:|| |:|||:| |||||||||||||||||||||||:||||:|||||:|||||::| ||
5190 AGTTTGGATCAATTCTACCTCGAGTACAGACAAACCCATTCGTGGGGTTGTCTTTGCTCAAGGACCAGGT 5259

1821 AACACCTGGTGGGTAATGAGGAAAGATGGTGAAATCCAGTGTGTGCCCCAAGGCAATCTAGCC-TTGGG- 1888
     :||| |||||||:||||| :||||||||| : ||: |::|||||:||:|:|| :||||:::::-|||||-
5260 TGCACATGGTGGATAATGCAGAAAGATGGAACAACACGATGTGTACCTCAGGGAGATCTGATTGTTGGGT 5329

1889 GAAAAA 1894
     ||||:|
5330 GAAAGA 5335
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-1706#Unknown	1936	2014	Gypsy-12_DRh-I	2448	2523	d	0.7500	1.7778	262

```
1936 ACCAGATGAGAAAGACCCAAACAAAG---CCGGTACTGGTATCCCATGATGTCCAACAATAAGGCAATCC 2002
     ||||: |||:|| || || |||||||---|||||||||||:|| || :||| ||-----|:||||||:|:-
2448 ACCAACTGAAAACGAGCCTAACAAAGGCACCGGTACTGGCATGCCCCGATTTC-----ACAAGGCAGTT- 2511

2003 TAAACTGTGAAC 2014
     |||||||::|||
2512 TAAACTGCAAAC 2523
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-17134#Unknown	149	245	EnSpm1_HV	5077	5166	d	0.6882	1.4444	272

```
149 GGGGGGGGNAAGATGCATAGGGGGAAGAAAGACAGGAGAAGAGTCCAGGACAGCAAGGAAAAAGAAGAGA 218
    ||:|::|: |||| ||| :||:|||||||||: ||:|:|||:----||:| |:-|||:|:|||:|:||||
5077 GGAGAAGAGAAGAAGCAAAAGGAGAAGAAAGGAAGAAAAAGG----AGAAGAA-AAGAAGAAAAAGGAGA 5141

219 TGAGAAAAGATGAGAATGNAAAGGTTA 245
    --|||||||||| ||:|| | ||||:|||
5142 --AGAAAAGAAGAAAAAGAAAAGATTA 5166
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

| rnd-5_family-18364#LTR@ERVK | 1288 | 1352 | HERVK9I | 1353 | 1417 | c | 0.8000 | 1.8333 | 312 |

```
1288 TCAAACTTNGAGCGACACTCTGA--GGCCCAATGCCTTCCCTTTTTACATTTATGACAGATATCGGG 1352
     ||||||||| |||:|||||||--||--:|||||||||::||||:|||||||||||| |||| || ||:||
1417 TCAAACTTAGAGTGACACT--GATTAGCCCAATGTTTTCCTTTTTTACATTTTGGACATATTTCAGG 1353
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	1360	1419	ERV2-11_UCy-I	2289	2349	c	0.7541	2.0000	249

```
1360 GGGGTTCTAG-CCGCCGGCCTTTTAGGACAGTTGGTTTTAAAATGTCCAAATTCCCCACAG 1419
     ||||||:|:|-: | :|:||| |: |||||||: || |||||||||||||||||||||||
2349 GGGGTTTTGGGTAGGTGACCTGTCTGGACAGTCCTTTATAAAATGTCCAAATTCCCCACAG 2289
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	1654	1711	Juno3_Av_I	2495	2557	d	0.7833	1.6667	223

```
1654 TGGCACTGTGCATTGGCAT----TG--GATATTGCAATTTGTTTAAAAATAATGTCCTGTACAT 1711
     |||||||||||||||:||||----||--|||||||:: ||||:||: ||| :||||||-|| ||||
2495 TGGCACTGTGCATTAGCATACATTGATGATATTATCATTTATTCCAAATCAATGTC-TGAACAT 2557
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	2157	2202	Tx1-15_BF	1192	1236	c	0.8043	1.1667	226

```
2157 TGCCTTTTTCGCATCTT-TAATTAAAGGGATGGGTAAAGGCTCCCAA 2202
     ||||||||||| ||||||-:|:|||||||||:||:--:||||||||:|||
1236 TGCCTTTTTCCCATCTTACAGTTAAAGGAATA--CAAAGGCTCTCAA 1192
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	2423	2473	Tx1-8_AMi	2312	2363	c	0.7692	1.8333	204

```
2423 GGGCGCCGCCATCTTGGGCCGGATGTTGACAACAGGAGGG-GGCGGGGCCAC 2473
     |||| ||||||| |||||| :|||||||| | ||:|:||:|-||||:||||:|
2363 GGGCTCCGCCAGCTTGGGGTGGATGTTGCCTACGGAAGAGCGGCGAGGCCGC 2312
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	2669	2714	TguLTRL2b5	371	417	d	0.7872	1.6000	200

```
2669 CAGAAACAGTGTCCA--AGTACGCCGGTGGAGCAGAGGGAGAGGGGGG 2714
     ||| :||:|||-|||--||||| ||||:|||| ||::||||||||||||
 371 CAGCGACGGTG-CCAGCAGTACNCCGGCGGAGGAGGAGGAGAGGGGGG 417
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18364#LTR@ERVK	3210	3245	Gypsy-13_CCO-I	1470	1504	c	0.8611	1.3333	220

```
3210 TCCCGAGGTGCTCTGGTCCGCCCGCTTCCTCCGAGG 3245
     |||||||||:|:||-|||:||| |||||||||||
1504 TCCCGAGGTGTTTTG-TCCACCCGATTCCTCCGAGG 1470
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-18768#Unknown	1	976	ERV3-5_PMaj-LTR	1	982	d	0.9266	2.9524	8080

```
1 TGTAAGGACTTAAAGAGCACAGTTGCCTGTCTCAAACACTGTTAAGGCCACAGAAGGACTTTGCCATGAG 70
  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
1 TGTAAGGACTTAAAGAGCACAGTTGCCTGTCTCAAACACTGTTAAGGCCACAGAAGGACTTTGCCATGAG 70

71 ATAAGCACAGAATGGAGNGACAGGATGGCGCTAACTCCAGGCCTGGNNGAGGCGAGATCTGGTTAGCACA 140
   |||||||||| |||| |||||||||||||||||||||||||||||||| ||||:|||||||||||||||||
71 ATAAGCACAGAAGGGAGCGACAGGATGGCGCTAACTCCAGGCCTGGCAGAGGTGAGATCTGGTTAGCACA 140
```

```
141 TCCTGGNTAATGCATCCAGACAAAAATTCCCACTGTGGCAAACTGTGTAAAGAAGCAACTGCTN-ATANG 209
    ||||||| |||:|||||||||||||||||||||||||||||||||||||||||||||||||| -||| :
141 TCCTGGGTAACGCATCCAGACAAAAATTCCCACTGTGGCAAACTGTGTAAAGAAGCAACTGCTCGATACA 210

210 CATATCACTNGTCAAACAAAGATCACCCCAAGTTATGGGACAGATGGCATCT--GTGACCACCAANGACC 277
    ||||||||| |||||||||||||||||||||||||||||||||||||||||||--|||||||||| :|||
211 CATATCACTGGTCAAACAAAGATCACCCCAAGTTATGGGACAGATGGCATCTACGTGACCACCACCAACC 280

278 ACCNAAGCCCCCC-AAATATGCCTCNNTGGATACCTGGAACTTGGACTGTAAGTTAAGCCACCACAGCAG 346
    --: ||||||||||-:||||||||||  |||||||||||||||||||||||||||||||||||||||:|
281 --TGAAGCCCCCCCGAATATGCCTCCGTGGATACCTGGAACTTGGACTGTAAGTTAAGCCACCACAGCGG 348

347 GAACTTGAGATAAGATAAAGGTGGTACTATTGTCTGGGTGTTATCTCAGACCTAGGGGGAGGTTAACAAA 416
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
349 GAACTTGAGATAAGATAAAGGTGGTACTATTGTCTGGGTGTTATCTCAGACCTAGGGGGAGGTTAACAAA 418

417 GCTGGGGGAGAAGAATGTATCACTGATAATGGACACAAAGAATGCAGAATTTATGGGCCACAAGGAAAGC 486
    ||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
419 GCTGGGGGAGAAGAATGTATCGCTGATAATGGACACAAAGAATGCAGAATTTATGGGCCACAAGGAAAGC 488

487 CAACTCAGCAACTGTGCTGAAATCAGCTCNGACTGGGTAAAAGGTAATTCTGGCAGGGGGAGATNNTGAC 556
    ||||||||||||||||||||||||||||-||||||||||||||||||||||||||||||||||:  :|||
489 CAACTCAGCAACTGTGCTGAAATCAGCTC-GACTGGGTAAAAGGTAATTCTGGCAGGGGGAGACTGCGAC 557

557 CACTGACTCACNGCCCACNNACNCAAGAAACCCACNGACTCAAAAGAAGAGAAAGACTGAGCATGNGGAC 626
    |||::|||||| |||||| || |||||||||||| :|||||||||||||||||||||||||||-|||||
558 CACCAACTCACAGCCCACCAACCCAAGAAACCCACCAACTCAAAAGAAGAGAAAGACTGAGCATG-GGAC 626

627 TAATTAGCATTAGAAGNGAGGGAATCATTTAACCAATAGAATAAGAGAACTGTGTAGCCAATGAGCATTA 696
    ||||||||||||||||| ||||||||| |||||||||||||-|||||||||||||||||||||||||||||
627 TAATTAGCATTAGAAGTGAGGGAATMATTTAACCAATAGA-TAAGAGAACTGTGTAGCCAATGAGCATTA 695

697 ATTCCTTTGTTTGCTAAAATGTATAAATAGTGAAAAGTTTTGAATNACCTTGGGACCCCCACCACCNAGA 766
    ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||||||||:|||
696 ATTCCTTTGTTTGCTAAAATGTATAAATAGTGAAAAGTTTTGAATGACCTTGGGACCCCCACCACTGAGA 765

767 AGCCCAGGGTGAAGAAGGACCAANGGGATGCTNCTGGATCCANNGNTGGTGACTATCTTCTGCTTGATCT 836
    ||||||||||||||||||||||| :|||:||| ||||||||| | ||||||||||||||||||||||||
766 AGCCCAGGGTGAAGAAGGACCAACAGGACGCTGCTGGATCCATGGGTGGTGACTATCTTCTGCTTGATCT 835

837 CTCTCTNNNN-CTTTCTATTTCTTT-CTAT-----CTCTCTACCTCACATTNATTGTTAAATAAAATCCN 899
    ||||||     -|||:|: |:|||||-||||-----|||||||||||||||| ||||||||||||||||
836 CTCTCTCTCCTCTTCCCCTCTCTTTTCTATTTCTTCTCTCTACCTCACATTCATTGTTAAATAAAATCCG 905

900 TANTATTGANTTNNGCATATGGTCTTGTTTGCACCTTAATTTGGGCAGAGGCATCTCTCANTAATCAGAT 969
    || ||||||| || |||||||||||||||||||||||||:||||||||||||||||||| |||||:|||
906 TACTATTGACTTCGGCATATGGTCTTGTTTGCACCTTAATTCGGGCAGAGGCATCTCTCAATAATCGGAT 975

970 CTTAACA 976
    |||||||
976 CTTAACA 982
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-2267#LTR@ERV1	1	758	ERV1-5_PMaj-LTR	4	765	d	0.9619	3.0000	6206

```
1 TGCAAAATGTGGAATATGTNAAAATTTTCTTAAGAAAGGATGTTCTTTGATGTTTGATCTTTGTATACTT 70
  ||||||||||||||||||||-||||||||||||||||||||||||||||||||||||||||||||||||||
4 TGCAAAATGTGGAATATGT-AAAATTTTCTTAAGAAAGGATGTTCTTTGATGTTTGATCTTTGTATACTT 72

71 TCAAGCCTAATCAACAAGAANGGAGATTTAATCCGTGAAACAGCAGCTAACAAGCTCTAAGTGATGTCCA 140
   ||||||||||||||||||||| |||||||||||:|||||||||||||||||||||||||||||||||||||
73 TCAAGCCTAATCAACAAGAAGGGAGATTTAATCTGTGAAACAGCAGCTAACAAGCTCTAAGTGATGTCCA 142

141 GGTGTTAGAAAAACAAATTACTTGTTGGTAGAATTGCCTTGTTAAGGTTTAGGGCTTGACATGCTTCANT 210
    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
143 GGTGTTAGAAAAACAAATTACTTGTTGGTAGAATTGCCTTGTTAAGGTTTAGGGCTKGACATGCTTCAGT 212

211 GATCTCAGACCTAGGGGGAGGTTAACAAAGCTTGGGAAGAAGGATGNNCCACTGATAGTGGACACAAAGA 280
    ||||||||||||||||||||||||||||||||||||||||||||||  |||||||||||||||||||||||
213 GATCTCAGACCTAGGGGGAGGTTAACAAAGCTTGGGAAGAAGGATGTACCACTGATAGTGGACACAAAGA 282
```

```
281 ATGCAGAATTTANGGGCCACAAGGACATTTGGCAGAACTCCCAAGATAAGGAAGAAACTAATAAAGCCAA 350
    ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
283 ATGCAGAATTTATGGGCCACAAGGACATTTGGCAGAACTCCCAAGATAAGGAAGAAACTAATAAAGCCAA 352

351 CTCAGCAACTGTGCTGAA-TCAGCTCCAACTGGGTAAAAGGTAATTCTGGCAGGGGGAGATCGTGACCAC 419
    |||||||||:||||||||||-|||||||||||||||||||||||||||||||||||||| |||||||||||
353 CTCAGCAATTGTGCTGAAATCAGCTCCAACTGGGTAAAAGGTAATTCTGGCAGGGGCAGATCGTGACCAC 422

420 CGACTCANN--CCACNGACC-AAGAAACCCACNGACCCAAAA-GAAGAGAAAGACTGAGCATGTGGACTA 485
    |:||||| --|||| ||||-|||||||||| |||:|||||-||||||||||||||||||:||||||
423 CAACTCACAGACCACCGACCCAAGAAACCCACCGACTCAAAAAGAAGAGAAAGACTGAGCATGCGGACTA 492

486 ATTAGCATGAGAAGCNAGAGAATCATTAACCAATAGAAGATAGAATACTAATTAATAAGAGAACTATGTA 555
    ||||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
493 ATTAGCATGAGAAGCGAGAGAATCATTAACCAATAGAAGATAGAATACTAATTAATAAGAGAACTATGTA 562

556 ACTTGTAGCCAATGAACACTAATTCCTTTGTTTGCTAAAATGTATAAATAGTAAAAGTTTTGATAGTTG 625
    |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
563 ACTTGTAGCCAATGAACACTAATTCCTTTGTTTGCTAAAATGTATAAATAGTAAAAGTTTTGATAGTTG 632

626 GTGTGCTTGATTTGTGGAATACCACTGAGCACCCAGGCTTGNGCAACTCTGAAATAAATAATCAATGTCT 695
    |||||||||||||||||||||||||||:|||||||||||||| |||||||||||||||||||||||||||
633 GTGTGCTTGATTTGTGGAATACCACCGAGCACCCAGGCTTGTGCAACTCTGAAATAAATAATCAATGTCT 702

696 CTCTNGAGTGTGTAATTATTGGCTTGTTGCACACCNGGTAACAAATCCNATTTTTGTGGACAA 758
    |||| |||||||||||||||||||||||||||||||| |||||::|||||| ||||||||||||
703 CTCTCGAGTGTGTAATTATTGGCTTGTTGCACACCAGGTAATGAATCCGATTTTTGTGGACAA 765
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-25903#LTR@ERVK	22	73	Copia-11_TC-I	1626	1677	c	0.7925	2.2500	218

```
  22 ACATCTGAGTG-ACTGATTGAAGCTTTAAGTTTGATCCCTCAGATTCNAGATT 73
     ||||||||||||-|||:||||||||||| : |||| ||:|-||: ||| |||||
1677 ACATCTGAGTGCACTAATTGAAGCTTTTGTTTTGCTCTC-CAATTTCTAGATT 1626
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-25903#LTR@ERVK	247	291	Gypsy-18_AG-I	2447	2496	d	0.8478	3.0000	236

```
 247 AACACTAGGATTGCAAGA-----CTTAAAAATGTTAGAATTTGTTTTTAT 291
     ||| ||||||||||||||-----|||||||||: ||||| || |||||:|
2447 AACCCTAGGATTGCAAGATGGTTCTTAAAAATGCAAGAATATGATTTTGT 2496
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-25903#LTR@ERVK	729	829	L2_AC_9	1029	1143	c	0.7170	1.7143	272

```
 729 AAAAGGGGGGGGGGAGAAGAGTGACAG--------TAANAGTGAATGACAGAGTGA-ATAATAGAGTGAA 789
     |:||:||||:|||||||||||||||| || ||--------||| |:|-|||:| |:|:|:|-| ||||:|:|:||
1143 AGAAAGGGGAGGGGAGAAGAGAGAGAGAGAAAAAATAATAAT-AATAAAAAAATAATAAAATAAAATAAA 1075

 790 --TGATAAATAAAAGTAGCTAAA-CAAAATGGACTA---TAGATGG 829
     --|:| ||||||||| |: ||||-:|||||||||| ||---|||||||
1074 AATAAAAAATAAAATAAAATAAAATAAAATGGAATAAAATAGATGG 1029
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	892	946	L2-21_CTe	203	255	d	0.7593	1.7143	222

```
 892 TGACAGTACTTGAGATGACTCTCTCTAGTCAGCATGCAGATGTCAGTGTCCCATC 946
     ||||||:|||| || |||||||||||:::||| :|||||: |||--||||:|||||
 203 TGACAGCACTGGATCTGACTCTCTCCGATCACTATGCAATTGT--GTGTTCCATC 255
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	1695	1808	hAT-2_PBa	2795	2892	c	0.7549	1.5455	244

```
1695 ATTCACTTAATTAGGCTAAAATAGGGTACAAGCATCACTTAAATGACTTAAACAAGCTATTTAGCTATGA 1764
     ||||||||||||| ||: |||||||---||---||||:|||::--||||---|||||:||| |||||----
2892 ATTCACTTAATTCGGTGAAAATAG---AC---CATCGCTTGG--GACT---ACAAGTTATATAGCT---- 2838

1765 TGTTACCAGTTCATTTCAAAGATT----GCAGGCTTAGATGTAGCTCA 1808
     |||----|:||| ||||||::|||----:||:||||-|| ||| ||:|
2837 TGT----AATTCTTTTCAAGAATTCCTCACAAGCTT-GAGGTATCTTA 2795
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	2106	2169	Copia-53_MN-I	3445	3505	d	0.8065	4.5000	249

```
2106 ACAATGCTTGCACAATGATGTTTTCATCAACTTTGCTCTCAGATTGGATT--CTTGAGAGGCATGT 2169
     |||||| || |||||----||||||||| |||||||||||||| || -|||||--||::| |||||||
3445 ACAATGGTTTCACAA----GTTTTCAACAACTTTGCTCTCCGAA-GGATTTACTCAATCGGCATGT 3505
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	3486	3556	Gypsy-23_GAr-LTR	386	456	c	0.7222	1.6364	239

```
3486 TTTTTCTCTCTCTCCAC-CACGAACAAGGGAAGGGAAAGCAGGAAGGAGACCATGTCTCTCTGCTCCTGT 3554
     ||||:||:|||||||| ||-|||| : ||||||::|||||-||| |:| |||||||||| |:|:|:| :|:|| |
 456 TTTTCCTTTCTCTCAACTCACGGCCAAGGGGGGGGAA-GCATGGATGAGACCATTTTTTTTTCTTTCTTT 388

3555 GC 3556
     ||
 387 GC 386
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	3812	3844	Gypsy-4_AC-I	2426	2462	d	0.9118	1.0000	248

```
3812 CCGCTCCACTCT----CAGCAAGGGCAGAGCCCAGCA 3844
     |||||||||||||:----|||||||||:||||||||||||
2426 CCGCTCCACTCCTTTACAGCAAGGACAGAGCCCAGCA 2462
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	4025	4073	Mariner-N1743_AMi	392	437	c	0.7959	1.1667	202

```
4025 CATGTGCTGCCTCCCCCGCACTCGCTCTGTCTGCTTGCCTGGCTACCCC 4073
     ||| |||||||||:|||-|||:|-|||||:||||:|||-||||:||:|||
 437 CATCTGCTGCCTCTCCC-CACCC-CTCTGCCTGCCTGC-TGGCCACTCC 392
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3138#Unknown	4311	4383	PtConagree_I	2899	2976	d	0.7333	1.2143	299

```
4311 GGGAGCAGCCTCAGTGTATCCC---CGCACCTGGGGAACAACCTCAGTGCATCCCTGTATCCGCC---GG 4374
     |||:|||||||||: |||:::||---:||:|||||||::||||||||| |:|-|:| :||||:|||---||
2899 GGGGGCAGCCTCAAGGTACTCCATATGCGCCTGGGGGGCAACCTCAGGGTA-CTCAATATCTGCCTGGGG 2967

4375 GACAGCCTC 4383
     |:||:||||
2968 GGCAACCTC 2976
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3181#Unknown	1796	1830	DIRS-6_CPB	2876	2911	d	0.8611	1.3333	209

```
1796 CTCCA-TTCTGCTCCACCCTCCCTTTCATCCCCTT 1830
     |||||-||||||||||| |||||||::||:|||||||
2876 CTCCAATTCTGCTCCTCCCTCCCTCCCACCCCCCTT 2911
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3181#Unknown	1840	1885	ERV2-3b_CPo-I	3169	3212	c	0.8043	1.7500	215

```
1840 TTGAGGTCACAGACTGTGTGTGTGGAGTCACTGGGGAACAGGTTGT 1885
     |||||-| |||:|||||:-||:|||:||| |||||||||| ||||||
3212 TTGAG-TAACAAACTGTA-GTATGGGGTCCCTGGGGAACTGGTTGT 3169
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6012#Unknown	1871	1936	HAT-18_Mad	3406	3469	d	0.8182	1.1667	243

```
1871 GACACTCTCAGGAACTTGAAGGTTTGAT-GATGAATTTTGCTTTTTTAGAGGTTTG--TTCAGTTTTCA 1936
     ||||-|||||--|||||||||: |||||-:|||||||||||:||||||--||:|||||:--||||:||||||
3406 GACA-TCTCA--AACTTGAAGAATTGATCAATGAATTTTACTTTTT--GAAGTTTAGTTTCAATTTTCA 3469
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-3861#Unknown	55	105	HAT-18_Mad	926	977	c	0.8039	1.3333	211

```
 55 ATACCACAAACAGCATTTATTGCAAT---ACCAACTAGCAAAAGAGAATAAAAA 105
    |||||| |||||||||:::||| ||||---|:|||:||--||||||:|||||||||
977 ATACCAAAAACAGCACCCATTCCAATTGTATCAATTA--AAAAGAAAATAAAAA 926
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-42824#Unknown	76	106	hAT-7_PM	780	810	d	0.9032	3.0000	223

```
 76 AACATATGGCCAGCCAATTAAACAAAAATTC 106
    || ||||:||||||||||||||||||||| ||
780 AAAATATAGCCAGCCAATTAAACAAAAGTC 810
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	202	272	Gypsy8-I_Dpse	244	303	d	0.7742	1.7143	206

```
202 AAGTGTGGGAGAGAAGGGCGAACGCGCCGAAGGGCTTGTCGACACCCCGGGCGTGGTGGGCTGTAAACAA 271
    |:|||||||||| | |||||||:| |:|------||:|:|||||||||||||||-----|:| :|||||||
244 AGGTGTGGGAGTGTCGGGCGAACAGGTC------CTCGCCGACACCCCGGGCG-----GACGATAAACAA 302

272 G 272
    |
303 G 303
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-439#LTR@ERVK	545	600	BEL-677_AA-I	2820	2877	d	0.7544	2.1667	220

```
 545 GAAGAAAGT--GGCTATGGCAGCTCACCATGCACTAGATGACAATGAGGACCAGCGTG 600
     |||||||||--|| ||| :||||||| |:|:|||| || |: |||||:|||: ||||
2820 GAAGAAAGTATGGGTATTACAGCTCAACGTACACTCGAGGGAAATGAAGACCGCCGTG 2877
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-4633#LINE@CR1	16	498	CR1-X3_Pass	3935	4421	c	0.7851	20.4000	3243

```
  16 AGAATAGAATAGAATATTTCAGTTGGAAGGGACCTACAATGATCATCTAGTCCAACTGCCTGACCACTTC 85
     |||||||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
4421 AGAATAGAATAGAATATTTCAGTTGGAAGGGACCTACAACGATCATCTAGTCCAACTGCCTGACCACTTC 4352

  86 AGGGCTGACCAAAAGTTAAAGCATGTTATTAAGGGCATTGTCCAAATGCCTCTTAAACACTGACAGGCTT 155
     |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
4351 AGGGCTGACCAAAAGTTAAAGCATGTTATTAAGGGCATTGTCCAAATGCCTCTTAAACACTGACAGGCTT 4282

 156 GGGGCATCNACCACCTCTCTAGGAAGCCTGTTCCAGNGTTTGACCACNCTCTNNGTAAAGAAATGCTTCC 225
     |||||||| ||||||||||||||||||||||||||| |||||||||| |||| |||||||||||||||||
4281 GGGGCATCGACCACCTCTCTAGGAAGCCTGTTCCAGTGTTTGACCACCCTCTCGGTAAAGAAATGCTTCC 4212
```

```
 226 TAATGTCNAGTCTAAANCTCCNCTGGTGCAGCTTTGAACCATTCCCANNNNTCCTNTCACTGNATNNCAN 295
     |||||||| |||||:||  |||| ||||:|||||||||||||||||||     |||| |||||| || ||
4211 TAATGTCCAGTCTGAACCTCCCCTGGCGCAGCTTTGAACCATTCCCACGCGTCCTGTCACTGGATACCAG 4142

 296 NNAGAAGAGNTCAGCNNNTCNNTNTCCANNTNCNCTNCTCAGGAAGCTGNANNGANCAATGAGGTNNNCC 365
      |||||||| |||||   ||  | |||| | | || |||||||||||| |  || |||||||||  ||
4141 GGAGAAGAGNTCAGCACCTCCCTCTCCACTTCCCCTCCTCAGGAAGCTGTAGAGAGCAATGAGGTCGCCC 4072

 366 CTCANNCTCNNNTTNNNNAAN--AGACAANCNCANANTCCTTAGNNGNTCNNNANANNACATNCNNTCCA 433
     ||||   |||    ||     ||  --|||||||  |  || | ||||:||  |  ||   |  |||| |  ||||
4071 CTCAGCCTCCTTTTCTCCAAACTAGACAAGCCCAGAGTCCTCAGCCGCTCCTCACAGGACATTCCTTCCA 4002

 434 GCNNTNTNANCANNTTNNTNNN--TNNTNTGNANANNNTNANGNACNTTNNNATNNTTNTNNAANNG 498
     ||  | | | ||  || ||  |   --| | ||| :   | ||| || ||  || ||  || |
4001 GCCCTTTCACCAGCTTTGTTGCCCTCCTCTGGACGCATTCAAGGACCTTCACATCCTTCTTAAATTG 3935
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	612	645	ERV1-7_Crp-I	1802	1836	d	0.8571	1.0000	204

```
 612 AACGGGAGTGCCCCCAGCCGAGAGAGA-GAGGGGG 645
     |:|||||||||||||||:||:|||:||||-|||||||
1802 AGCGGGAGTGCCCCCGGCTGAGGGAGAAGAGGGGG 1836
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	2133	2226	ERV2-11C_GG-I	1251	1344	d	0.8000	2.4286	446

```
2133 AAAGGCATTGCCTCCTGGATAT-TTCTTGATCTGTGGTAACAGAGCTTGGCCTGGGATACCTGCCCTGGC 2201
     ||||||||||| ||||-|||:||-||:||||||||||| :||||||| ||||  || || |||: || ||:
1251 AAAGGCATTGGCTCC-GGACATCTTTTTGATCTGTGGAGACAGAGCATGGCAGGGCATCCCTAGCCGGGT 1319

2202 AACAGGTGGACCATGTTATTTAGGA 2226
     :|:|||||||||| |||||||||||
1320 GATAGGTGGACCTTGTTATTTAGGA 1344
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	2388	2433	Helitron-1_HM	11321	11362	d	0.8605	5.0000	220

```
 2388 AAGCTACTGGATTCAAGAACAATTTAACATCATTGCCAAAATGCTT 2433
      |||  ||:|||  |||||----||||  |||||||||| |||||||||
11321 AAGATATTGGTTTCAA----AATTGAACATCATTGGCAAAATGCTT 11362
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-5294#LTR@ERVK	2809	2882	EnSpm-N16_SBi	802	869	c	0.7887	2.0000	207

```
2809 TTGTTAGTTTGAAAAAAGCTGAAAGTTTGAAATTCTGTAATTTTCAGTTAAAGTG-CA-GTTTAAAATTG 2876
     || |||:|||||  |||| :|||| :|||||||||-|| ||||||||---|||:||-||-|||||:||----
 869 TTCTTAATTTGATAAAATTTGAATATTTGAAATT-TGAAATTTTCA---AAAATGACAAGTTTGAA---- 808

2877 CCAAAA 2882
     ||||||
 807 CCAAAA 802
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6012#Unknown	1441	1507	BEL-1_CGi-I	574	647	c	0.7286	1.3333	249

```
1441 CTGTGCCCTCTCCTGCTCTCACAC---AC-TTTGGCTCTTCACTGTGGTTTTCTGCAACAGGGC---AGT 1503
     |||||:||||||:| ||::|:||||---||- :||||||||::|:|||:|:||||||||  |||||---||:
 647 CTGTGTCCTCTTCAGCCTTTACACGTAACAGCTGGCTCTCTATTGTAGCTTTCTGCACAAGGGCCTCAGC 578

1504 TTCC 1507
     ||||
```

577 TTCC 574

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6012#Unknown	3062	3215	CR1-J2_Pass	3385	3540	d	0.9161	2.4000	1058

```
3062 CAGATGACACCAGGCTGGGTGGGATTGNTGATCTG--GGAGGGCAGGAAGGCTCTGCAGAGGGGTCTGGA 3129
     ||||:||||||||:|:|||||||||| || |||||||--||||||||||||||||||||||||:|||||
3385 CAGACGACACCAAGTTGGGTGGGAGTGTTGATCTGCTGGAGGGCAGGAAGGCTCTGCAGAGGGATCTGGA 3454

3130 CAGGCTGGATCGATGGGCCCAGGCCAACTGGATGAGGTTCAACAAGGCCAAGTGCTGGGTCCTGCCCTGG 3199
     |||||||||||||||||||||| |||||||||| ||||||||||||||||||||:|||||||||| || |
3455 CAGGCTGGATCGATGGGCCGAGGCCAACTGTATGAGGTTCAACAAGGCCAAGTGCCGGGTCCTGCACTTG 3524

3200 GGTCACAACCACCCCA 3215
     |||||||| ||||||
3525 GGTCACAACAACCCCA 3540
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6742#Unknown	294	370	Harbinger-38_CCri	2527	2600	c	0.7105	1.4615	228

```
 294 GGTGCATGCAAACGAAGGGAAAGAGGGAGGGGAGGAGTGGCAAAAGGACCA-ATGGGAGAATGAGGTGGG 362
     |||||||||||---|::|:||:||||||||||||| | |-|||:|::|||| :-||| |:| : |:|:||:|
2600 GGTGCATGCA---GGGGAGAGAGAGGGAGGGGATGCG-GGCGAGGGGACGGGATGCGGGTGGGGGATGAG 2535

 363 CGGGGAAA 370
     ||||||||
2534 CGGGGAAA 2527
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-6995#Unknown	378	414	NonLTR-2_LVa	4112	4149	c	0.8947	1.0000	264

```
 378 GATACTGGG-GAAGTTGAAATTTATTCCTGTTTGTTCT 414
     |||||||:|-|||||||||||||||||:|||||||:|
4149 GATACTGAGAGAAGTTGAAATTTATTCTTGTTTGTTTT 4112
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	826	890	Helitron-2_CRe	10933	10994	d	0.7302	1.3636	215

```
  826 TGCGCCACAGCACACCACAGCAGCACCGTCGCTCCGCCCACCACCTCATCGCCTGGCAACA-GCAC 890
      ||||| :|||||----:||||||||||||||||: ||| ::|::|| ||:|||||::||||:-||||
10933 TGCGCAGCAGCA----GCAGCAGCACCGTCGCCACGCGTGCTGCCGCACCGCCTAACAACGCGCAC 10994
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	1001	1053	ATCOPIA9I	1928	1981	d	0.7593	2.0000	228

```
1001 ACTGCTGTCTTCCTCAGCCAGCTTCTTC-AACAGCAGCCAACGACAACCCTACT 1053
     |||||:: |||||||||| | |||||||-|||| ||||: :|||||:|:|||||
1928 ACTGCCAACTTCCTCAGCAATCTTCTTCCAACATCAGCTCTTGACAGCTCTACT 1981
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	1116	1145	EnSpm-N2_OES	834	863	c	0.9333	1.0000	231

```
1116 ACAAAAACAACAATTTTCTTCAAATAATCC 1145
     |||||||||||||||||||||::||||||||
 863 ACAAAAACAACAATTTTCTTTGAATAATCC 834
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	1261	1305	Copia-36_ALY-I	2239	2288	d	0.8478	1.5000	236

```
1261 AATTCTGATACATTACAGGCTTTTCCAGTCTTT-----TATGGTAGAAAC 1305
     ||  ||||||::  ||||||||:||||||||:|||-----||||||||||
2239 AAGTCTGATGTCTTACAGGTTTTTCCAGTTTTTGTCAATATGGTAGAAAC 2288
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	2182	2283	MacERV4_int	1879	1979	d	0.6863	1.7222	329

```
2182 CCAAGCATTTGTCCAAGATGCCAAAAGGGACTTCATTGGGCATCTGAATGCAGGTCCCTGTTTGACAAAA 2251
     |||:||  |||||:|||||:||:  |||::|||    ||:||||||  :|||||:|::||:   :  ::|||||:
1879 CCAGGCCTTTGCCCAAGGTGTAAAAGAGGAAGGCACTGGGCAAACGAATGTAAATCTAAAACTGACAGTC 1948

2252 AAGGGAATCCTTTATCCCCTAAGGCAGTGAAA 2283
     ||||:|||||||||||:||||:|-||||| ||||
1949 AAGGAAATCCTTTACCCCCCA-GGCAGGGAAA 1979
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	2284	2403	hAT-N6_OD	920	1032	d	0.6810	1.4500	220

```
2284 AAAACTC-AAAATTCGGGAAACTCCAATCTGAGCGCTCAGGACAGCGTGTAGACATAAATAGTCCAGCTC 2352
     ||||  ||-||||||:  |||  ||:||||||:| |||-|:||::|||:|  :    |: ||||:|||:|||--|:|
 920 AAAAATCGAAAATTTTGGACACCCCAATTTTAGC-CCCAAAACAACCCCAAACCATAGATAATCC--CCC 986

2353 A----ACAATCAGATACAACTGACTCCAGCATTTCTCAAAAGAAACCTCAAAAAA 2403
     |----|:||||::||:| -|||-:|||||-----:|:|||||--||||||:|||||
 987 ATTTGATAATCGAATGCT-CTG-TTCCA-----CCCCAAAA--AACCTCGAAAAA 1032
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	2801	3037	TguERVK3a_I	3111	3347	d	0.6842	1.9355	354

```
2801 TGGTTTGTTAGACACTGGGGCAGACGTCACAATTATCTCAACCAAAGATTGGCCAAGCACTTGGGGTACA 2870
     ||||:|  ||||||||||||| |||||||::|:||::|  |:|:|||||||||:- |:| |  ||| |:
3111 TGGTCTTTTAGACACTGGGGCCGACGTCACGGTCATTCCCTCTAAGGATTGGCCG-TCGCGTTGGGAATT 3179

2871 ACAAGACCACCTG--TGGACA--TCCAGGGAGTAGGAGGATCTCAA-----------ATCCCCCTTCAAA 2925
     ||||||| ---||--||||||--|:||:|| || |||||:|||||||----------|||-----| |||
3180 ACAAGACG---TGGCTGGACAAATTCAAGGTGTTGGAGGGTCTCAATTGGCGAAACAATC-----TAAAA 3241

2926 GCAGCTTGCCTCTTCTGGTCCAAGGCCCACAGGGTAA---GGTTGCATCATCAAAGCCT-TTTATATTGG 2991
     :||  |  |  |    :|| |||-----||||  :    |||:||---| ||:|||-----|  |||:-||::||||:|
3242 ACATCGTTCAATTTGTGG-----GGCCGGACGGGCAATCGGCTTACAT-----ACGCCCGTTCGTATTAG 3301

2992 ACATCCCACTGA--CTCTGTGGGGCAGAGATGTTATAACACAGTGGGG 3037
     |--|: :|| ||--|:|||||||||:|||||: | ||:| ||:||||||
3302 A--TTATACGGAACCCCTGTGGGGTAGAGACCTGATGGCCCAATGGGG 3347
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	4325	4386	L1MCA_5	843	906	d	0.7619	1.8571	239

```
4325 AACTAATAACCCATTTACCAGCAATTCCTTTTTTGCAGT---TTCTGTCTATCTCTCAACCAAAA 4386
     ||||||  ::||:||||||-|||:|||||||||  :  ||||---|:  |||||||  ||:||||||  ||||
 843 AACTAAAGGCCTATTTAC-AGCAGTTCCTTTTACCCAGTACATCATGTCTAGCTTTCAACAAAAA 906
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	4407	4970	TguERVK5_I	5181	5735	d	0.6624	2.0513	736

```
4407 AGACCCTTTGGAGAAGGCAGTTACTGTGTTCACAGATGGATCTGGTAAGA--CAGGCAATGCAGTAGTAG 4474
     |||  ||||||:|||  ---|||:|  |||   |  |||||  ||||||||||:||:|--||--|||   |:|||:||
5181 AGAACCTTTAGAT---GCAATAACTCTCTTCACTGATGGATCTGGCAAAAGTCA--CAAATCGGTAATAA 5245

4475 CCTGGTT----TGAAGAAGGAGAA--TGGAAAATAGATGCTCATCAAGTCGAGGGCTCATCTCAAATCGC 4538
     |:||||||----::||  ||    |:|:--|||:|| :|||||::||    ||||  ||:|||  || :||||:||:|:
5246 CTTGGTTGAACCAAACAACTAAAGCTTGGGAATCAGATGTCCAAATAGTAGAAGGATCTCCTCAGATTGT 5315
```

```
4539 TGAACTCTCGGCAGTGGTGAAAGCTTTTCGTCTATTTCCACAGCCATTGAATTTAGTATCAGATTCTGCC 4608
     ||||||: | || |||||| ::||||||||: || |||||||:|| || ||||||:| |||||||||||:
5316 TGAACTTGCTGCTGTGGTTCGGGCTTTTCAGCTCTTTCCACAACCTTTTAATTTAATTACAGATTCTGCT 5385

4609 TATGTGGTAGGTGTTGTAAGTCGCATAGAAA-AT-AGTTATCTAAAAGAACTAAATAATCAAAATTTGTT 4676
     ||||| |: ::||| || | |:  | ||||||:-||-|||--:|||||:||  |  |:|||||-:| ||||---
5386 TATGTTGCTAATGTGGTTAAAAGAATAGAAGGATCAGTT--TTAAAGGATGTTAGTAAT-GATATTT--- 5449

4677 TACACTGTTTAAAACATTGTTGCTTTTGATCCAAC------AGAGGAAAC--ATCCATTTTACATCACTC 4738
     ||:|::|||---::| || ||:::||||-|| ||||------| | ::|||--|||||| || ::|: |||
5450 TATATCGTT---GGCTTTCATGTCTTT-ATACAACTTTGCAATACAGAACTAATCCATATTTTGTTTCTC 5515

4739 ACATTAGATCACATACAGGTTTGC---CTGGCCCATTAACAGAAGGCAACGATATTGCTGACAGAGCT-A 4804
     ||||||||: | ||| |---||:||---|||| :: :||:::|||||| ||||----:|-----|||||-|
5516 ACATTAGGGCTCATTC---TTCGCTTCCTGGATTTCTAGTGGAAGGAAACG----CG-----AGAGCTGA 5573

4805 CAAATT--CAGCCTTTCCTGTTAATTCTGTACCAACACCGAACAATTTTGAGAAAGCAAAACTTTCTCAT 4872
     ||||||--||:: ||| :|: ||: || ||||||||------||| |||||||: ||||:|||:|  |||| 
5574 CAAATTGACAATGGTTATTTCAAACACTCTACCAA------ACATTTTTGAACAAGCGAAATTGAGTCAT 5637

4873 AATTTTTTCCACCAAAATTCAAAATCACT-----GAAAAATTGTTTTCATTATCTGA---TTCACAAGC 4934
     : :|||| :|||||||||: |: || ||||-----|||-----|||||: | | ||::|---|---|||||
5638 GCCTTTTATCACCAAAACGCGCAAGCACTTGTGCGAA-----TGTTTCAAATTTCCAAAAGT---CAAGC 5699

4935 AAAGTCTATTGTGTCTGCATGTCCAGACTGTCAATT 4970
     ||| ||||::|    ||| ||||| ||||||||::| 
5700 TAAGGCTATCATTAGTGCTTGTCCTGACTGTCAGCT 5735
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	4993	5591	ERV2-3_STr-I	5044	5644	d	0.6683	1.8804	886

```
4993 GGAGTTAATCCCAGAGGACTCA-GCCCTTTAG--ATCTGTGGCAAACTGATGTAACACATGTCCCACAAT 5059
     |||||:|||||:|||||||:| |-|||---||:--|| | ||||||:|: ||:|| ||||| | ||| |||
5044 GGAGTCAATCCTAGAGGATTGATGCC---TAACCATATTTGGCAGATGGACGTCACACACTTGCCAGAAT 5110

5060 TTGGCAGATTGAAATATGTACATGTGTCAGTAGACACTTGTTCNGG--TCTTATTGCAGCTACAGCACAT 5127
     |||| |:|||:|||||| |:||||| |||| ||:|||| ||| ||--:||: ||-:||| |   :-|||
5111 TTGGAAAATTAAAATATTTGCATGTTACAGTTGATACTTCTTCTGGATTTTTGATG-GGCTCCCTT-CAT 5178

5128 ACTGGAGAAAAAGCTCANGATGTTAAGAGGCATTTTTCTTCAGCATTT-GCTATTATGGGCATTCCAAAA 5196
     :|:|| ||||||||:|| | |||||||| :: |||| :|-| ||: ||||-||:|:|:||||||||||||||
5179 GCCGGCGAAAAAACTAAAGATGTTATAGCTCATTGCT-TACAAAATTTTGCCACTGTGGGCATTCCAAAA 5247

5197 CAAGTAAAAACAGATAATGGCCCAGCTTACATTTCTGCTTCCCTCAGAAAATTTT--TCAATATGTGGGG 5264
     ||: |||||||||||||||||:|| ||| ||||:|: |||:||||::|:|:| ||||||--||| :|| |||--
5248 CAGTTAAAAACAGATAATGCCCCTGGTTATACGTCTACTTCTTTTAAACAATTTTGCTCATCATTTGG-- 5315

5265 TGTAATTCACACCACTGGAATCCCTCACTCCCCACAAGGGCAAGGAATAATAGAGAGAACCCA-CAAATC 5333
     ::| |:|||:|: || |||||||||| :|| :|||||:||:||||| |||:| ||:|||:|:||-||||::
5316 CATTACTCATATAACAGGAATCCCATACAATCCACAGGGACAAGGCATAGTTGAAAGAGCTCATCAAACT 5385

5334 CTTAAAA-G-ACATGCTAAAAAAACAAGA-AAAGTCAGCTATAGATCTCTCTCCTCCAGA---ACGCTTA 5397
     ||||||-|-|| |::|||: || ||||-:::|:::| | :|:| | | |:|:|||:|---| :||||
5386 ATTAAAATGTACTTATTAAAGCAAAAAGACGGAATTGGGAAGGGGTATATATTCCCCAAAGATAAACTTA 5455

5398 AA-CAAGGCACTGTATGTTCTCAATTTTTTGAAT--AGACTACATGATGATGTTTCACCTGTTGGTCGTC 5464
     ||-:||--| || | |::||| ||:|||||:|||--:||:|-||| | ||:----------||:|| ---
5456 AAATAA--CCCTTTTTACTCTAAACTTTTTAAATTTGGATT-CATCAGGAC----------TTAGTG--- 5509

5465 ATTTTGCAGAT-GGAAAAT-----TAAAAACGGGG---GAGGCTAAGGTAAAATACAAGGATGTCCTGAC 5525
     ---:||||||| -|| | ||-----:|||||  | :----:|| :|||||||   :| ||:|||:|:||:|
5510 ---CTGCAGAAAGGCATATGTGTCCAAAAAATGTACATAAGCCCAAGGTACTTTGGAAAGATATTCTAAC 5576

5526 AGGAGAATGGCATGGTCCTGTCCCTCTAATTGTCTGGGGTCGAGGACACGC--ATGTATTTCAACAGG 5591
     |||| |||||| | ||||||||| ||| |||||||||||::::||:||:|:: :|:--:|||:||||  |||||
5577 AGGACAATGGAAAGGTCCTGACCCAGTAATTGTCTGGAATCGGGGGTCTGTTTGTGTGTTTCCACAGG 5644
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	5651	5724	Jockey-6_DK	425	489	d	0.8030	4.0000	266

```
5651 CAGCTCCAGCAACGCCAGACCCAGCAGCAGCTGCTCCAACACCAGCCGCAGGGAGCGATCCTCCAGCAGC 5720
     |||| |||||||:|: ||| ||||||||||||| |||||||:|| |||| |||---------|| |||||||||
 425 CAGCACCAGCAGCAGCAGCACCAGCAGCAGCAGCTCCAGCAGCAGCAGCA---------CCACCAGCAGC 485

5721 ATCA 5724
     | ||
 486 AGCA 489
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	5850	5926	Keno-5_XT	2618	2688	d	0.7361	1.4545	230

```
5850 ATTTGGTTAAACCTGGCACAATCTCT--GAGCACTGATTCTATCTGTCTGTCTACTCTAGACCCCTCTCA 5917
     |:|||||::||--||||| |||:|||--||| |:|||||:|||| | |:|:|||------|||:::|:| |
2618 ACTTGGTCGAA--TGGCAGAATTTCTTCGAGAATTGATTTTATGTTTTTATCT------GACCTTTTAA 2679

5918 CCCTTTTAA 5926
     |||||||||
2680 CCCTTTTAA 2688
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7082#LTR@ERVK	7215	7272	RETROFIT2_I	2833	2887	d	0.8070	4.5000	243

```
7215 GCTTTAGAAAATAAAAAAGGACGAGATGTGGCAATGCATTCTGAATACATGGCTTGGA 7272
     ||||||| ||||||||| || |--||:|||||-||||| || |||||||||:||||||| ||
2833 GCTTTACAAAATAATAATTG--GAAATGTG-CAATGGATGCTGAATATATGGCTTTGA 2887
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7126#Unknown	169	321	ERV2-12_PMaj-I	191	332	d	0.6875	1.7619	261

```
169 GGGTCGCT-CCCTCCCTCCTACCGGGGGTCTTGGCTTATTGAAAAGATGGAAGCCGAGACAGCTGCTGCG 237
    |||||||| -|||||||||:||-:||| | |:|---||------|||::|||||||::|:| : || || ||:
191 GGGTCGCGACCCTCCCCCC-GCCGTGTGCC---GC------AAAGAATGGAAGTTGGGTTTGCGGCAGCA 250

238 ATA-TGGCTTTTGCTGGGTATACTGGCTAAGCGAAGTGAGGCAGACAGTG----GGACATTCTTTAAAAA 302
    | |-: ||||---|||:|:|| | |:|||:|||:|:||:|||| ||| |----||||----:| :||||
251 AAAACTGCTT---CTGAGCATTATCGTTAAACGAGGCGAAGCAGTCAGGGAAAAGGAC----CTGGAAAA 313

303 GCTCGTTGTATGGGCTAAA 321
    ||||||| |||||||||:|
314 GCTCGTTTTATGGGCTAGA 332
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-7126#Unknown	644	804	hAT-1_MAc	231	400	d	0.6890	1.6400	430

```
644 CTGCCGCCCCTTTNCCC--CCTCAGCCCTGGCCACCACCGCTGCGGCTCCGGCTCTCGCCGCTTTTGGGG 711
    |||:|||-----| |||--||::*:|||| :|:::|||||||| ||||| ||||:|||:|||: : |
231 CTGTCGC-----TGCCCAACCCTAACCCTGCTCGTTGCCGCTGCCGCTCCCGCTCCCGCTGCTCGCCGCT 295

712 ACTGCTGCCCG--ACCGCC-CCAC----GCCGCTCCCGC--CCGCT---GCTGTTTTTTTTCNCTGCC-T 768
    :|:|||||:||--:||||:-||:|----|||||||||||--|||||---||||:|: :| :| |||||-:
296 GCCGCTGCTCGCTGCCGCTGCCGCTGTCGCCGCTCCCGCTCCCGCTCCCGCTGCTCGCTGCCGCTGCCGC 365

769 TGGGATCGCCGCT-TCTCCCCTCCCGCCGCCCCTCCC 804
    || --|||||||||-|| || ||||||||:|||| || ||
366 TGC--TCGCCGCTGTCGCCGCTCCCGCTGCCGCTNCC 400
```

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-9233#tRNA	6	64	ERI1	12	70	d	0.7288	1.7778	264

```
6 GTGGTGTAANGGAGAGCACTCTGGACTCTGAATCCCAAGGTCCTGAGTTCGAGTCTCAG 64
  ||||||:|: ||| |: || |||||:||| ||:| :|||||||||||||:| :|:|||
```

12 GTGGTGCAGTGGATAAAACACTGGATTCTCAACCATAAGGTCCTGAGTTCAATCCCCAG 70

Name	From	To	Name	From	To	Dir	Sim	Pos/Mm:Ts	Score
rnd-5_family-963#LTR@ERV1	498	639	ERV1-2_ACD-LTR	508	653	d	0.6986	1.5417	452

```
498 ATGTATAACT---TACTTGCATATAAACCAGTT--GTTAACTCGACCAGGTGTGCATGTTTTTGGAGGAG 562
    ||:|:||||||---||||-||||||||| | || :--|||: | ||-:|||||||:|||:| :||||| ||::
508 ATATGTAACTCTTTACT-GCATATAACCAAGGCAAGTTGCCGCG-TCAGGTGCGCACGACTTTGGCGGGA 575

563 CTATCCCCCATGC-ACCCGGGCCTGGAATAAACGTACCT-CTCTATAACCTCACTGGATANAGAGTCTTC 630
    |||:||||||:|||-:|||:|   |||-|||||||||:|||||-||:||:||:||:|:|||||: |: :|||||: :
576 CTACCCCCCGTGCTGCCCAGCGCTG-AATAAACATACCTACTTTACAATCTTACTGATTGTGGAGTCCGT 644

631 TTTCCNCAA 639
    ||||| |||
645 TTTCCGCAA 653
```

Masked Regions

```
>TE_00000002#MITE@unknown FRAGMENT 1 -> 131
TTAGCTCAGTTGGTTAAAACTTGGTTGTAATAATGCCAAGGTCATGGGTTCAATCCCCTGTGTGGGCCAT
TGACTTAAGAGTTGGACTCGATGATCCTTGTGGGTCCCTTCCAACTCAGAATAGTCTGTGA
>TE_00000010#MITE@unknown FRAGMENT 1 -> 299
CAGTTAAATGCCTCCCTGACATCCGATCCCGTCAGATCTCGGAAGCTAAGCAGGGTCAGCCCCGGTTAGT
ACTTGGATGGGAGACCTCCTGGGAAATGCCGGGCTGTAGGTTCTAGTCCTGAGGACTTCACTGTCACTGT
CCAAGCTCGCTCGGCCGTGGCAGATGAACCTCAGGACTTAAACGGTGGGGCCAGTTCTGCGCACGCTGAG
CCTCACCTAAAAAATCCACTGCGCAGGCTGGAAGGGCACACCCACGTGGGGAGAGCCCTTCCCAAATCTT
CGTTCGCGAAGCCGAGCCA
>TE_00000012#MITE@unknown FRAGMENT 157 -> 48
GGGTGCTGGGTTATACATCTGNNTTTTGTGGGTTAAAACCANTTTTTCTCTGTATCATTGTATTTATTGT
AATCTTTTTAGTAAATTGTAACTCTGACTTGTAATCTCTC
>TE_00000012#MITE@unknown FRAGMENT 603 -> 361
CTTCACACCANTGACTCAGCTGTGATAACTCCCCTCNGGGGGAGGCATTAGCACCTTCACACCCAGCCTGA
GGGGTCATGTCTGCTAATGGGCCATTAGGGACTGGCACAATAGGCAGNTGCAATGACCTAGACCATCAAA
GATTCCAAAAATATCCCATGACTCACAGAGTTAAATCACCCATTGTGAAACTCCCCGCCCTGGGGGAGGT
ACTGGGCATTCCCACCTGAACCTGAGCATATAT
>TE_00000022#MITE@unknown FRAGMENT 450 -> 218
AAAAGACTTTCAAAACAACATTAGTGGAGATAGATAGATAAAGTAGNNCCTTTATTAGAAGCTTCTAGGT
GCACACNAAAAGTATGNGCACNCNCNTCAGCCAAATGTTACAGTTTTTATAACTTTCAGTAATTAACATA
TNTGATATCTATANCCAACCCNTGGTACCATTTTCCCCTGGTGCCCACCCTCAGAACTCCTCAGAACTGC
CCCTTGGAGCCCCTCCAAGGGCT
>TE_00000023#MITE@unknown FRAGMENT 257 -> 138
AGGGGGTGGGGGGTCTTGGGCAGGCAGGCGAACCGGGCCAGACTGTGAGTCCCCAATTCCCAGCCAATAG
GAAGAGGGGGCAGGGACCTTTCGGCCGGGAAAGGGTATAAAAAGTTCTGT
>TE_00000028#MITE@unknown FRAGMENT 1 -> 574
TGTAGTGGGTCTGGCTGAGCCGGAATTTATTTTCCCATAGTAGCCCTTACAGTGCTGTGCTCTGCATTGG
TAGCTAGAGGAGTGTTGATAACANGCCCATGTTTTGGCTACTGCTGAGCACAGCACTGTAACATTCCTTC
TTCAGTCAGGGGCGAGATCCTGGGAGGGGACACAGGTAGGCCAGCTGACCCCACACTGACCAAGGGGATAT
TCCATACCATATGANGTCAACCCAGATATAAAGCTGAGGCAAGGAGCNGGAAGGAGGCATTCATTGTCTN
TAATGGCTGCCTGCTGACAACNNTTACGNGTGCTGGAGCTCTGCTTNTCAGAGAAGTGGCCGACCATCGC
TGCTTATGGGAAGTAGAGATTAACTGCTAGCTTCTGCTTTGTGTGTGTGCACNCTGCTTTNGNTTTTTTT
NCTTTTTGCATAAATATAAACTGCCTTATCGCAACCCACGGTTTGTGTTATTTCTTTTTCCTCCCACCTT
NCTCTCTCCCCTGTCCNGCTGGGAAGGGGAGTGATAGAGCAGCTGGGTGGGCACCTGGCGTTCAGCCAAG
GTGAACCCACCACA
>TE_00000032#MITE@unknown FRAGMENT 282 -> 382
AAGCCAGCTACCACGACCTGGCCACGCGCTGGGCAGCCCAACCTCTGGCGACAGGCTGTCGCTGTCTGGG
GTTGTTTACTTCTCCTTCTGGCTGCCCCAAG
>TE_00000033#MITE@unknown FRAGMENT 180 -> 225
CAGCTGACTGACCAATTATGGGATGACACGGTGTGGGAGAAAGTAG
>TE_00000034#MITE@unknown FRAGMENT 71 -> 308
ATTNGAAGCTTCCAAGGTGCACACCAAAAGCATGCACACACNTGATCAGGGATGTTACAGTTTTTATAAC
CTCCAGCCATTAGCATATATGATATCTATAGCCAACCTGGGGTACCAATTTCCCTTGGTGCCCACCCATA
GAGTNCTCAGAACTGCCCCTTGGAGAGGCTCTGGGCCCTCTCTATTGTTTTGTCTTCAAGCTATCTTGCA
GGTGTTTCTTCAAAACACCATGTCCTTG
>TE_00000036#MITE@unknown FRAGMENT 167 -> 237
AGAAGACAAAACATAAGAAGAAGGCCTAGAGGTCCTGGAAGATCTCCANGGGGCAGTTCTGAAGACCCCT
A
>TE_00000040#MITE@unknown FRAGMENT 84 -> 145
GAGGGGACAGGTATCATCTGACTTAAGCAGCCAAAGAGGTATTTCATATCATCTGACATCAT
```

```
>TE_00000068#MITE@unknown FRAGMENT 98 -> 1007
GNCCTGNNNTNNNTCAANATTTCATAAANNANTTGGANNAAGGNATACTAAGNAAGTTNNAGATGACANA
AAANTGGGAGGAGCTGTTGACTCCNNAAGNAGNNGCCCTGCAGAGAGACCTNNACAAATTAGAGNNNTGG
GCAATNACCCATATNNANCANNNNAAGTGCNNNNTCTGCANCTGGGGGNAACCCTNGANNNTNNAGACTG
GNAAGATGCTGGAAAGCAGTGCCANNGAAAGGGAGTCCTGGTNNATGGCAAGTTGAATATGAGTCAGCAG
TCCTGGCAGCCAGGAGGGCCAACCNTGTCCTGGGGGCATCAGGCANAGCATCNCCAGCNNGTCNAGGGAG
GGGATTGTCCNNCTCTGCTCTGCACTGGGGCNGCCTCACCTTGAATATTGTGTGCAGTTTTGGGCACCAC
AATATAAGAAAGATATTAAGCTATTAGAGAGTGTCCAAAGGAGGGCAANGAAGATGGTGAAGGGCCTTGA
GGGGAAGCCGTATGAGGAGCAGCTGAGGTCACTTGGTCTGTTCAGCCTGGAGAAGAGGAGACTGAGGGGA
GACCTCATTGCAGTTACAACTTCCTNGTGAGGGGAAGAGGAGGGGCAGGCACTGATCTCTTCTCTGTGGT
GACCAGTGACAGGACCCNAGGGAATGGCCTGAAGTTGTGTCAGGGGAGGTTTAGGTTGGATATTAGAAAA
AGGTTCTTCACCCAGAGGGTGGTTGGGCACTGGAACAGGCTCCCCAGGGAAGTGGTCACAGCACCAAGCC
TGACAGAGTTCAAGAAGCATTTGGACAATACTCTCAGGCACATGGTGTGACTCTTGGGGATGGTCCTGTG
CAGGGCCAGGAGTTGGACTNNATGATCCTTGTGGGTCCCTTCCAACTCAGCATATTCTGTGATTCTGTGA
>TE_00000071#MITE@unknown FRAGMENT 3 -> 236
TGNNAGAGNGNAGGNTTATNNGATATTNGGAAGAAATTCTTCCCTGTGAGGGTGNNAGGCCCTGNACAGG
TGCCCAGAGAAGCTGTGGCTGCCCCATCCCTGGAAGTGTCCAAGGCCAGGTTGGACAGGGCTTGGAGCAA
CCTGGGCTAGTGGAAGGTGTCCCTGCCCATGGCAGGGGGTGGAACNAGATGATCTTTAAGGTCCCTTCCA
ACCCAAACCATTCTGTGATTCTNT
>TE_00000073#MITE@unknown FRAGMENT 115 -> 49
TTTCTCTTTGTGCCATTGCATTTATTGTAATATTGTTATTAAATTGTAACTCTGACTTATAATCTCT
>TE_00000073#MITE@unknown FRAGMENT 421 -> 366
CAGTGTGGAACTCCCTGCCCTGGGGGAGGCACTGGGGGCTCCCACCTGNACCTGAG
>TE_00001107_LTR#LTR@unknown FRAGMENT 246 -> 359
CAAAACCAAACCAAAACAAATGAAACAGACAAATACAATTAAAGACTTCAGGAAAGGAGAACAAGCATGA
AACAATCTCACCACGTCCCGGGCTAGGAAAACCAACAGAAACAG
>TE_00001324_LTR#LTR@unknown FRAGMENT 349 -> 387
TCCTGCAGGGTGGGTGGTGTTTCTTTGTCCTTGCACAGA
>TE_00002464_LTR#LTR@unknown FRAGMENT 236 -> 60
GGGTGGGCTCCATGGGCTGGGAGGGCTTTGCCAAGGTGGGCATCGGGCACAGGGTGGGCTCCATGGGCTG
GGAGGGCTTTGCCAAGGTGGGCATCGGGCACAGGGTGGGCTCCANGGGCTGGGAGGGCTTTGCCAAGGTG
GGCATGGGCACAGGGTGGGCTCCANGGGCTGGNAGG
>TE_00002464_LTR#LTR@unknown FRAGMENT 472 -> 254
CAGGAGNAGAGGNGCCTCAGGCTGGGCCAGGGNGGNACAAGGAATTTCTNCCTGGAAAGGGTGGNCAGGC
ACTGGCAGGGGCTGCCCAGGGAGGTTTGGAGTGCCCAGCCCTGGAGGTGCCCAAGGCAGGACTGGCCGTG
GCACTCAGTGCTCTGGGCTGGGGGACAAGGTGGGCATCGGGCACAGGGTGGGCTCCATGGGCTGGGAGGG
CTTTGCCAA
>TE_00002563_LTR#LTR@unknown FRAGMENT 56 -> 107
AGGAGAGACAGGTATCACCTGACTTAAGCAACCAAAGAAATATTTCATACCA
>TE_00002563_LTR#LTR@unknown FRAGMENT 426 -> 353
TTATACAGAAAAGAGAAAATTAAAAGAAAACTACAATATAACACACACTTACACAAGTTAGATATAACAA
CAAT
>TE_00002676_LTR#LTR@unknown FRAGMENT 21 -> 317
GAGGGGCAGGCACTGANCTCTGCTCTGGGGCAGGGACAGCACCCAGGGAATGGCTGGAGCTGTGCCAGGG
CAGGGTCAGGTTGGATCTCAGGAAAAGGTTCTTCCCCCAGAGGGTGGTGGGCACTGACCAGGCTCCCCAG
GGCAGTGGGCACAGCCCCAAGGCTGCCAGAGCTCCAGGAGGGTTTGGATGATGCTCTGGGCACAGGGTGT
GACTCTTGGGGNGNCTGTGCAGGGCCAGGGGTTGGACTGGATGATCCTTGTGGGTCCCTTCCAGCTCAGC
ATATTCTGTGATTCTGT
>TE_00002809_LTR#LTR@Gypsy FRAGMENT 358 -> 311
CTCTCCCGGGTCACTGCCCCAGCCGGGGCAGGCAGGCCGTGACGGTGC
>TE_00002832_LTR#LTR@unknown FRAGMENT 1 -> 433
AGGCTGGAGAAGGGACTGGAGCACAAGTGCTGTGGGGAGAGGCTGAGGGAGCTGGGGGTGTTTAGCCTGG
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>rnd-1_family-44#Unknown FRAGMENT 1 -> 593
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Annotation of Repbase Sequences

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ID   ATCOPIA26I  repbase;     DNA;    PLN; 4605 BP.
XX
AC   AF072897;
XX
DT   18-NOV-1999 (Rel. 4.10, Created)
DT   23-AUG-2018 (Rel. 23.08, Last updated, Version 2)
XX
DE   Internal region of ATCOPIA26 LTR-retrotransposon.
XX
KW   Copia; LTR Retrotransposon; Transposable Element;
KW   LTR-retrotransposon; COPIA superfamily; copia-like polyprotein;
KW   internal portion; ATCOPIA26LTR; ATCOPIA26I.
XX
NM   ATCOPIA26I.
XX
OS   Arabidopsis thaliana
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC   Camelineae; Arabidopsis.
XX
RN   [1]
RP   1-4605
RA   Kapitonov V.V. and Jurka J.;
RT   "ATCOPIA26I.";
RL   Direct Submission to Repbase Update (31-OCT-1999).
XX
RN   [2]
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RA    Kapitonov V.V. and Jurka J.;
RT    "Molecular paleontology of transposable elements from Arabidopsis
RT    thaliana.";
RL    Genetica 107(1-3), 27-37 (1999).
XX
DR    GenBank; AF072897; Positions    55458    50854.
XX
CC    ATCOPIA26 is a recently active Copia-like LTR retrotransposon,
CC    it has 5 bp-long target-site duplication, and its LTRs,
CC    ATCOPIA26LTR, are 99% identical. Its internal region, ATCOPIA26I,
CC    encodes 1489-aa Copia-like polyprotein (position 138-4595).
XX
FH    Key             Location/Qualifiers
FT    CDS             138..4595
FT                    /product="ATCOPIA26I_1p"
FT                    /translation="MSTELALASSTTPARTETRRTISPYDLTSGDNPGTLI
FT                    SKPLLRGPNYDEWATNLRLALKARKKFGFADGSIPQPVETDPDFEDWTANN
FT                    ALVVSWMKLTIDETVSTSMSHLDDSHELWTHIQKRFGVKNGQHVQRLKTEL
FT                    ATCRQKGVAIETYYGCLSQLWCSLADYQQAKTMDDVRKEREEDKLHQFLMG
FT                    LDESVYGAVKSALLSRVPLPSLEEAYNALTQDEESKSLSRLHNERVDGVSF
FT                    AVQTTSRPRDSSENRVCSNCGRVGHLAEQCFKLIGYPPWLEEKLRLKNTAS
FT                    SSRGGLSSFKGKQSHGRGSSINHVASSGMAANVVTNSSLTSPLTSDDRIGL
FT                    SGLNDSQWKILQTILEERKSTLNDHQSGKYFLESWIIDSGATNHMTGSLAF
FT                    LRNVCDMPPVLIKLPDGRFTTATKQGSVQLGSSLDLQDVLFVDGLHCHLIS
FT                    VSQLTRTRRCIFQITDKVCIVQDRTTLMLIGAGRELNGLYFFRGVETAAAV
FT                    TSKALPSSQLWHQRLGHPSSKALHLLPFSDVTSSTFDSKTCEICIQAKHTR
FT                    DPFPLSSNKTSFAFELVHCDLWGLYRTTSICGSRYFLTLVDDYSRAVWLYL
FT                    LPSKQEAPKHLKNFIALVERQYTTNIKIIRSDNGSEFICLSDFFAQKGIIH
FT                    ETSCVGTPQQNGRVERKHRHILNVARALRFQSGLPIEFWSYCALTAAYLIN
FT                    RTPTPLLKGKTPFELIYNRPPPLQHIRIFGCICYVHNLKHGGDKFASRSHK
FT                    SIFLGYPFAKKGWRVYNIETGVVSVSRDVVFRETEFHFPISVMDSSPSLDP
FT                    VLVDSSELEEISMTPPVTPSSPATPSSPVTPSSPVTPSSPVSPSSPVTPSS
FT                    PVTPLSSTTTSAAIDTIEDITTDLEDSTSMDFFPDDEDEFSPTATESPASS
FT                    SSPVHPPAVQLELLGKGHRPKRPPVKLADYVTTLLHQPFPSATPYPLDNYI
FT                    SSSRFSDNYQAYILAITSGNEPRNYNEAMLDDHWKGAVSDEIGSLENLGTW
FT                    TVEDLPPGKKALGCKWVFRLKYKSDGTLERHKARLVVLGNNQTEGLDYTET
FT                    FAPVAKMVTVRAFLQQVVSLDWEVHQMDVHNAFLHGDLDEEVYMQFPPRFR
FT                    TGDKTKVCRLRKSLYGLKQAPRCWFAKLTSALKNYGFIQDISDYSLFIFHK
FT                    NGVRLHVLVYVDDLIITGTTIAVITEFKHYLSSCFYMKDLGILRYFLGIEV
FT                    ARSPEGIYLCQRKYALDIITETGLLGVKPASFPLEQNHKLAFATGETIDDP
FT                    LRYRRLVGRIIYLATTRPELSYVIHILSQFMHNPKPAHWEAALRVVRYLKS
FT                    SPGQGILLRANTPLVLSAWCDSDFGACPHSDRSLTGWFIQLGGSPLSWKTQ
FT                    KQNVISRSSAKAEYRAMAETVSEIIWIRELLPALGIPCTAPTTLHSDSLSA
FT                    ISLAANPVYHARTKHVRRDVHFIRDELVNGTIATKHVSTTSQLADILTKAL
FT                    GRKEFADFLAKLGICNLHIPA"
XX
SQ    Sequence 4605 BP; 1188 A; 1062 C; 913 G; 1442 T; 0 other;

//
ID    ATCOPIA9I    repbase;    DNA;    PLN; 4300 BP.
XX
AC    AC005396;
XX
DT    12-APR-1999 (Rel. 4.03, Created)
DT    23-AUG-2018 (Rel. 23.08, Last updated, Version 2)
XX
DE    Internal region of ATCOPIA9 LTR-retrotransposon.
XX
KW    Copia; LTR Retrotransposon; Transposable Element;
KW    LTR-retrotransposon; COPIA superfamily; internal region;
KW    ATCOPIA9LTR; ATCOPIA9I; internal portion.
XX
NM    ATCOPIA9I.
XX
OS    Arabidopsis thaliana
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC    Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC    Camelineae; Arabidopsis.
XX
RN    [1]
RP    1-4300
RA    Rounsley D.S., Lin X., Kaul S., Shea P.T., Fujii Y.C., Mason M.T.,
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 RA    Shen M., Ronning M.C., Fraser M.C. et al.;
 RT    "Arabidopsis thaliana chromosome II BAC T26I20 genomic
 RT    sequence.";
 RL    Unpublished.
 XX
 RN    [2]
 RP    1-4300
 RA    Rounsley D.S. and Lin X.;
 RT    "ATCOPIA9I.";
 RL    Direct Submission to Genbank (07-AUG-1998)The Institute for
 RL    Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850,
 RL    USA, rounsley@tigr.org.
 XX
 RN    [3]
 RP    1-4300
 RA    Rounsley D.S.;
 RT    "ATCOPIA9I.";
 RL    Direct Submission to Genbank (25-SEP-1998)The Institute for
 RL    Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850,
 RL    USA.
 XX
 RN    [4]
 RA    Kapitonov V.V. and Jurka J.;
 RT    "Molecular paleontology of transposable elements from Arabidopsis
 RT    thaliana.";
 RL    Genetica 107(1-3), 27-37 (1999).
 XX
 DR    GenBank; AC005396; Positions   47404   43105.
 XX
 CC    The authors [1-3] have wrongly presumed an intron in the ATCOPIA9
 CC    ORF; the ORF has been corrupted by several mutations; there is
 CC    1% divergence between ATCOPIA9 LTRs; ATCOPIA9 has 5 bp-long
 CC    target-site duplication (Kapitonov,V.V. and Jurka,J.) rather than
 CC    6 bp-long target originally reported [1-3].
 XX
 FH    Key             Location/Qualifiers
 FT    CDS             join(14..2830,2834..3643,3647..4297)
 FT                    /product="ATCOPIA9I_1p"
 FT                    /translation="MDQSMDLYTLPSLNISNCVTVKLTDRNYILWKSQFES
 FT                    FLSGQGLLGFVNGAYAAPTGTVSGPQDAGVTEAIPNPDYQAWFRSDQVVMS
 FT                    EDILSVVVGSKTSHEVWMNLAKHFNRISSSRIFELQRRLHSLSKEGKTMEE
 FT                    YLRYLKTICDQLASVGSPVAEKMKIFAMVHGLTREYEPLITSLEGTLDAFP
 FT                    GPSYEDVVYRLKNFDDRLQGYTVTDVSPHLAFNTFRSSNRGRGGRNNRGKG
 FT                    NFSTRGRGFQQQFSSSSSSVSASEKPMCQICGKRGHYALQCWHRFDDSYQH
 FT                    SEAAAAAFSALHITDVSDDSGWVPDSAATAHITNNSSRLQQMQPYLGNDTV
 FT                    MASDGNFLPITHIGSANLPSTSGNLPLKDVLVCPNIAKSLLSVSKLTKDYP
 FT                    CSFTFDADGVLVKDKATCKVLTKGSSTSEGLYKLENPKFQMFYSTRQVKAT
 FT                    DEVWHMRLGHPNPQVLQLLANKKAIQINKSTSKMCESCRLGKSSRLPFIAS
 FT                    DFIASRPLERVHCDLWGPAPVSSIQGFQYYVIFIDNRSRFCWFYPLKHKSD
 FT                    FCSLFMKFQSFVENLLQTKIGTFQSDGGGEFTSNRFLQHLQESGIQHYISC
 FT                    PHTPQQNGLAERKHRQLTERGLTLMFQSKAPQRFWVEAFFTANFLSNLLPT
 FT                    SALDSSTTPYQVLFGKAPDYSALRTFGCACFPTLRAYARNKFDPRSLKCIF
 FT                    LGYTEKYKGYRCFFPPTNRVYLSRHVLFDESSFPFIDTYTSLQHPSPTPMF
 FT                    DAWLKSFPSSSSPLENDQTAGFNSGASVPVITAQQTQPILSLKDGPNILLP
 FT                    EGEITVSSNNQDIEDEPICVTPLQTLSSEDNAKSSETLSMGSEECSECTAS
 FT                    FDLDPIGNNALSSSPRHDQLTSSIPRAATESTHPMTTRLKKGIIKLNQRYA
 FT                    LLTHKVSYPMPKTVTAALKDPKWTAAMIEEMGNCSTHTWTLVPLQPNMHVL
 FT                    GSKWVFRVKLNVDGSLDKYKARLVAQGFKQEEGIDYLETYSPVVRSATVRA
 FT                    VLHLSTIMNWELKQMDVKNGFLHGDLTETVYMKQPAGFIDKAHPDHVCLLH
 FT                    KALYGLKQAPRAWFDKFSKFLLSFGFVCSMSDPSLFVCVKNKDVIMLLLYV
 FT                    DDMVITGNSSKLLSSLLSELNKQFKMKDLGRLSYFLGIQAQFHSQGLFLSQ
 FT                    QKYAEDLLATAAMSNCSPVATPLPLQPERTPNQTELFDNPSYFRSLAGKLY
 FT                    LTLTRPDLQFSVNYVCQKMHAPTVSDFHHLKRILRYIRGTTTMGISFNKDT
 FT                    DCQLRAYSDSDHAGCHGTRRSTGGFCTFLGNNLISWSSRKQDSVAKSSTEA
 FT                    EYRSMSVTASEITWLVNLLRDLGVPQLQLPELFYDNLSAVYLTANPSFHAR
 FT                    TKHFATHYHYVREQVAFGELIVHHIPGYLQLADIFTKSLAKAPFESLRFKL
 FT                    GVDFPPSPSLRG"
 XX
 SQ    Sequence 4300 BP; 1183 A; 1028 C; 832 G; 1257 T; 0 other;

 //
 ID    ATHILA7A_I  repbase;    DNA;    PLN; 4754 BP.
 XX
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AC    AC005965;
XX
DT    27-DEC-2001 (Rel. 6.11, Created)
DT    27-DEC-2001 (Rel. 6.11, Last updated, Version 1)
XX
DE    ATHILA7A_I is an internal portion of ATHILA7A endogenous
DE    retrovirus.
XX
KW    Gypsy; LTR Retrotransposon; Transposable Element; ATHILA7A_I;
KW    ATHILA7LTR; Athila superfamily; Gypsy-like endogenous retrovirus;
KW    ORF1; internal portion; pol; reverse transcriptase.
XX
OS    Arabidopsis thaliana
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC    Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC    Camelineae; Arabidopsis.
XX
RN    [1]
RP    1-4754
RA    Kapitonov V.V. and Jurka J.;
RT    "The ATHILA7A subfamily.";
RL    Repbase Reports 1(4), 8-8 (2001).
XX
DR    GenBank; AC005965; Positions   72809   68056.
XX
CC    ATHILA7A_I is an internal portion of ATHILA7A endogenous
CC    retrovirus.
CC    It belongs to the Gypsy superfamily and is related to the
CC    ATHILA-like
CC    endogenous retroviruses. ATHILA7A is a subfamily of the ATHILA7
CC    family. ATHILA7A_I and ATHILA7_I share ~95% identical 1.6 kb 5'-
CC    and
CC    ~2 kb 3'-terminal portions.
CC    There are two well preserved copies of ATHILA7A_I present
CC    in the A. thaliana genome; they are 96% identical to each other
CC    and
CC    are flanked by the 2% divergent ATHILA7LTR long terminal repeats.
CC    ATHILA7A_I encodes well preserved remnants of a protein similar
CC    to
CC    the ATHILA ORF1 protein (it is present also in other ATHILA-like
CC    retroviruses that populate the O. sativa, H. vulgare and V. faba
CC    genomes). The protein, ATHILA7Ap, is 930-aa. One false stop codon
CC    present in the copy deposited in Repbase Update is corrected
CC    based
CC    on the second ATHILA7A copy and other ATHILA ORF1-like proteins
CC    deposited in GenBank.
XX
FH    Key           Location/Qualifiers
FT    CDS           join(255..650,650..3043)
FT                  /product="ATHILA7Ap"
FT                  /translation="MNEPEVGGHNGNGQANGGGHMPQHQPRAHQPIGAFDE
FT                  PNIRGNRNGIQAPPVENNNFEIKSSLINMVQSSKFHCLSMEDPLDHLDQFD
FT                  MLCSTVKINGISEDAFKLRLFPFSLGDRARIWEKNLPQGSITSWDQCKRAF
FT                  LLKFFSTTRTARLRNEISSFTQRSNKSFCEAWERFKGYKMQCPHHGFSKES
FT                  ILSTLYRGVLPKFRMLLDTASNANFLGQDIDDGLSLVENLAQSDGNYGEDY
FT                  DRTPRESNEMSNLHRKEIKALNEKIDKMILANQKPIHFVSESDVYQGYQEH
FT                  MEGCVERQEEVNYAIGQGYNKFNLNYRNHPNLSYRSNNVENPQDQSYPPLK
FT                  PPGFTQQPNYQPQPQRNFQPKPQAYHHNQHQGSSSNPPPQADTNALLRQIL
FT                  EGQGRGAIDLATQMKGMHTKVDDIYGELNAKIERLNVHVYSPSSSTSKHPM
FT                  GTLKGKSETNHKEFCNAIFINDFDMVENMSYTQSREDGRIDENEKAIEEIS
FT                  KLLYGSNVENLMVASDEKAKKSTNGNDMITKSVEKKEASRVEPLPYEPLLP
FT                  FPGRVLTKAKKKVFSSFKANMSRVGAPLPCVENLSQIPLHFKFIQAILENR
FT                  EKVEEIMRAFDSPITPQTEPKSIIKLEDPGKFTIPCSLGDLQLDDALCDSG
FT                  ASVNVMSLEMVKSLGVKDMNHHTSSIMFGDASSTTPLGLIEDYPLKVGDCI
FT                  VPTDFMIVEMKDTHKVPLILGTPFLNTVGANIDFPNKRVTLLHVNGNVSYP
FT                  IKPFSTKFCGTITNEEVKTKKEPKSLKDQLEIKVVNAKNREDFTVDEKILD
FT                  GECLHFLFDAQEESTKKKELGKAKMVLEKNKRMMKRTHPPTLDNSPNPTSS
FT                  MTLTLLRYNDGILEYRVKCKGRSNPFSSVKAILTPEFKEKGSKSVEELMKE
FT                  VLTLAFKGSTRSFTTPPITSLPKVHN"
XX
SQ    Sequence 4754 BP; 1555 A; 859 C; 965 G; 1375 T; 0 other;
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 //
 ID   Ag-Jock-1   repbase;    DNA;    INV; 4725 BP.
 XX
 AC   .
 XX
 DT   29-OCT-2010 (Rel. 15.10, Created)
 DT   29-OCT-2010 (Rel. 15.10, Last updated, Version 2)
 XX
 DE   A Jockey clade non-LTR retrotransposon family from Anopheles
 DE   gambilae.
 XX
 KW   Jockey; Non-LTR Retrotransposon; Transposable Element; Ag-Jock-1.
 XX
 OS   Anopheles gambiae
 OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
 OC   Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
 OC   Culicoidea; Culicidae; Anophelinae; Anopheles.
 XX
 RN   [1]
 RP   1-4725
 RA   Biedler J. and Tu Z.;
 RT   "Non-LTR Retrotransposons in the African Malaria Mosquito,
 RT   Anopheles gambiae: Unprecedented Diversity and Evidence of Recent
 RT   Activity.";
 RL   Molecular Biology and Evolution 20(11), 1811-1825 (2003).
 XX
 RN   [2]
 RP   1-4725
 RA   Kojima K.K. and Jurka J.;
 RT   "Jockey clade non-LTR retrotransposons from Anopheles gambiae.";
 RL   Direct Submission to Repbase Update (24-SEP-2010).
 XX
 DR   [2] (Consensus)
 XX
 CC   [2] Consensus update. This consensus is generated from 6
 CC   sequences with >98% identity.
 XX
 FH   Key           Location/Qualifiers
 FT   CDS           113..1726
 FT                 /product="Ag-Jock-1_1p"
 FT                 /translation="MSKWRTVPYHAGPAVRKKRVKRTPDLLAEMRRRKREE
 FT                 AQPESSTPASKKKGEIKITPATAGDVAVNAAMDGIDVPNTAEEENHRKEKI
 FT                 PPIVVSGLNEEEYGSLCDATQSGAIKASFSFASGNTCRINAASRDDHDKVK
 FT                 KLLENYTKEFYSHEFKADKPYQVVLKGLRFGSAEQVTVMLRDVKLQPSLVR
 FT                 EVKIGEGRGLSSKLFVVSFPKGAISLEELQKITHINYTTVKWERFQPKHRD
 FT                 VLQCLNCLNFGHGAKHCAMSPRCAKCAGNHRSKQCTKEMGDVHTCANCMGD
 FT                 HSPYNRNCPSRKQYLQKRYSTQNAPRRLVPAPIPTRSSWAEPLPWVGQYRK
 FT                 DSVCTCHGCPHGHQQQNQQLQQQQLQQKLQQQQQQQQQQQNQQLQQQQLQQK
 FT                 LQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQQLQQQQQRQQQQQQQQQ
 FT                 QQQQQQQQQQSLQCKYQIASASCSYSIPRKTHRQPAQDKLDQLRSRLSDEE
 FT                 DEEIKSQFGDIVRLWVEFKRLSKQCPRDQILMKMVEFITANF"
 FT   CDS           1731..4373
 FT                 /product="Ag-Jock-1_2p"
 FT                 /note="apurinic-like endonuclease and reverse
 FT                 transcriptase."
 FT                 /translation="MIKCATWNACSVLPKRLELIDFLNHEKIDLLAVTETH
 FT                 LKHNKTFFLPDHTVVRLDRPDQPKGGVLIAIRRTLAFKVLPLPNTHYIEAV
 FT                 GIEMLSAEGNFHFYAAYCPRQVSDTSGTSRLLKRDLQLLTRASRRFIVAGD
 FT                 LNARHQEWGNLRANRNGMILRELTQASACSVSFPFQPSFQNGNSYSTIDIF
 FT                 ISNITDRLDVPSTITALSSDHLPVVMNIVCPGTHATRQQRNYREADWPRFE
 FT                 RYITENISSAPPLLTIEDINTAITNVESCMKEAVDRFVPLIQVRHKVTELD
 FT                 ADTKRLIASKNSLRRTYQRTRNRTYYSLYRQVAKIVDARMVEVRNRQFSDR
 FT                 LKTLPKHSRPFWRLTKVLKDKRRPIPVLIDGGIPAFTPREKAVKLSVNFAQ
 FT                 AHRLSESMTSTYESRVADSISSLVSEPIEATNIERISSGELLGTIKYLVGY
 FT                 KAPGADGIFNIMLKHVGHSTVVLLTDVFNRCLELGYFPHLWKYAKVVPVLK
 FT                 PGKDPSLGSSYRPISLLGALSKLFERTIYTRMMAHCESNNVISEVQFGFRK
 FT                 HRSAAQQLQRVLDVVDSAKMRGKTTALALLDVEKAFDNVWHDGLIHKLRVQ
 FT                 GFPLYIVRLVQSYLSGRSSAVYIGSEKSDPYENNAGVPQGSILGPLLYNCY
 FT                 TADVPTLGANASLALYADDTAILYSAKPLRFIRAGLQRGLDSYVNFLKEWK
 FT                 IVVNNTKTQALIFPYKVGMTASNIIAKVGSLKMENNIIPWASEARYLGVIL
 FT                 DRRLTFKAHVGYIKTKTGHLFRMLYSLLKYNSGLSIENRLAIYGQIVLPSI
 FT                 TYGSIAWGRCSRTNMQTIQVIQNRFLKTIMGLPNRYPTRALHSETGFVPIK
 FT                 DKLSEIIECLKRKCRDSEVDIIRNLFSS"
```

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     XX
     SQ    Sequence 4725 BP; 1448 A; 1068 C; 1070 G; 1139 T; 0 other;

     //
     ID    AviRTE_GRu  repbase;     DNA;     VRT; 3976 BP.
     XX
     AC    .
     XX
     DT    23-APR-2016 (Rel. 21.05, Created)
     DT    24-APR-2016 (Rel. 21.05, Last updated, Version 1)
     XX
     DE    RTE non-LTR retrotransposon from Gymnopithys rufigula.
     XX
     KW    RTE; Non-LTR Retrotransposon; Transposable Element; AviRTE_GRu.
     XX
     OS    Gymnopithys rufigula
     OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
     OC    Coelurosauria; Aves; Neognathae; Passeriformes; Thamnophilidae;
     OC    Gymnopithys.
     XX
     RN    [1]
     RP    1-3976
     RA    Suh A., Witt C.C., Menger J., Sadanandan K.R., Podsiadlowski L.,
     RA    Gerth M., Weigert A., McGuire J.A., Mudge J. et al.;
     RT    "Ancient horizontal transfers of retrotransposons between birds
     RT    and ancestors of human pathogenic nematodes.";
     RL    nature communications 7, 11396-11396 (2016).
     XX
     DR    [1] (Consensus)
     XX
     CC    AviRTE is a novel RTE family present in some birds and nematodes.
     CC    Frequent horizontal transfer. Only distantly related to BovB.
     XX
     FH    Key            Location/Qualifiers
     FT    CDS            777..3935
     FT                   /product="AviRTE_GRu_1p"
     FT                   /translation="MLDTGDSGCPEHCSALIVHKLSRLNIDIAALSEVRLH
     FT                   EKGSLKEHGAGYTLYWSGKPKTERHLSGVGFMIKNSIASKLENLPTGHSDR
     FT                   IMSLRLPLHNKQHVVLFSVYAPTLQADPAEKDKFYTDLRHLTQKVPADDKI
     FT                   IILGDFNARVGKNSEAWKGVLGKHGVGNCNDNGCLLLEFCAEQQLTITNTI
     FT                   FQQKDSLKTTWMHPRSKHWHLIDYILVQQRNVSDVRHTRVMPSAECQTDHR
     FT                   LVRCKLNLHFKPKPKRGGIPRRRLQVSNLQTATVRDSFQVNLQTRLKDNPI
     FT                   DPSPEALWQHIKSCILQSSEESLGFSSKKNKDWFDENNQEIQELLKKKRTA
     FT                   HQAHLAQPSCHIRKAAFRLACSKLQQKLRDIQNKWWLNLAEKTQLCADLGD
     FT                   QRGFYEALKAVYGPTHQVQSPLLSADGQMLLTDKTSILNRWSEHFQTLFSA
     FT                   NRVVQGSAIQHITQQPVKHELDAAPTMGEILKAIQQVKTGKAAGVDGIPPE
     FT                   IWKHGGQALHAKFHELVVRCWEQGELPSDLRDAVIITLYKKKGEKSDCSNY
     FT                   RGITLLSIAGKILARILLNRLVPAIAEXLLPESQCGFRANRSTTDMVFVLR
     FT                   QLQEKCREQNKGLYVTFVDLTKAFDTVSRKGLWQILERLGCPPKFLKMIIL
     FT                   LHEDQRGQVRYGDALSEPFPITNGVKQGCVLAPTLFTIFFSMMLQRATADL
     FT                   DEENGIYIRYRTDGSLFNLRRLKAHTKTLNHLVRELLFADDAALVAHTEAA
     FT                   LQRLTSCFAEAAELFGLEVSLKKTEVLYQPAPQEVFHHPHITIGNSELKSV
     FT                   QQFTYLGSIISSDGKIDKEIDNRLAKAYRAFGKLHKRVWSNKHLKKSTKIS
     FT                   VYRAIVLSTLLYGSESWVIYRHHLRLLERFHQRCLRSILNIHWSDYVTNVS
     FT                   VLEQAGVTSIEAMLMRMQLCWAGHVSRMEDHRLPKIVLYGELATGCRKRGA
     FT                   PKKRYKDSLKQHLSLGHIDCHQWSTLASNRDSWRHTIHDAAASFENARRVS
     FT                   LEEKRQRRKNRSLPISPRETFRCAFCDRTCLSRIGLFSHQHACSKHG"
     XX
     SQ    Sequence 3976 BP; 1135 A; 1043 C; 896 G; 879 T; 23 other;

     //
     ID    BARBARA_TM_I repbase;    DNA;    PLN; 6759 BP.
     XX
     AC    AF326781;
     XX
     DT    16-OCT-2002 (Rel. 7.09, Created)
     DT    16-OCT-2002 (Rel. 7.09, Last updated, Version 1)
     XX
     DE    Triticum monococcum copia-type retrotransposon, BARBARA_TM_I,
     DE    internal region.
     XX
     KW    Copia; LTR Retrotransposon; Transposable Element; BARBARA_TM_I;
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KW    COPIA superfamily; TREP228; internal region;
KW    target site duplication; internal portion.
XX
OS    Triticum monococcum
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    BOP clade; Pooideae; Triticodae; Triticeae; Triticinae; Triticum.
XX
RN    [1]
RA    Wicker T., Stein N., Albar L., Feuillet C., Schlagenhauf E.
RA    and Keller B.;
RT    "Analysis of a contiguous 211 kb sequence in diploid wheat
RT    (Triticum monococcum L.) reveals multiple mechanisms of genome
RT    evolution.";
RL    Plant J 26(3), 307-316 (2001).
XX
RN    [2]
RA    Wicker T.;
RT    "Direct submission.";
RL    Direct Submission to Repbase Update (from TREP) (02-APR-2002)..
XX
DR    Genbank; AF326781; Positions  153050  159808.
XX
CC    Internal region of Copia-type BARBARA retrotransposon.
CC    5bp target site duplications.
XX
SQ    Sequence 6759 BP; 2045 A; 1444 C; 1507 G; 1763 T; 0 other;

//
ID    BEL-1_CGi-I repbase;    DNA;    INV; 6373 BP.
XX
AC    .
XX
DT    29-NOV-2012 (Rel. 18.01, Created)
DT    29-NOV-2012 (Rel. 18.01, Last updated, Version -1)
XX
DE    LTR retrotransposon from the Pacific oyster genome: internal
DE    portion.
XX
KW    BEL; LTR Retrotransposon; Transposable Element; BEL-1_CGi_;
KW    BEL-1_CGi-LTR; BEL-1_CGi-I.
XX
OS    Crassostrea gigas
OC    Eukaryota; Metazoa; Lophotrochozoa; Mollusca; Bivalvia;
OC    Pteriomorphia; Ostreoida; Ostreoidea; Ostreidae; Crassostrea.
XX
RN    [1]
RA    Zhang G., Fang X., Guo X., Li L., Luo R., Xu F., Yang P.,
RA    Zhang L., Wang X., Qi H., Xiong Z., Que H., Xie Y. et al.;
RT    "The oyster genome reveals stress adaptation and complexity of
RT    shell formation.";
RL    Nature 490(7418), 49-54 (2012).
XX
RN    [2]
RP    1-6373
RA    Jurka J.;
RT    "LTR retrotransposons from the Pacific oyster genome.";
RL    Repbase Reports 13(1), 682-682 (2013).
XX
DR    [2] (Consensus)
XX
CC    Positions [5303-5887] - Integrase core
CC    LTRs are 99% similar to each other.
XX
FH    Key            Location/Qualifiers
FT    CDS            8..2623
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FT                   /translation="MDPRTTRKLTEKGQGYFEDEVQRYSIKLARLHRLIDE
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XX
SQ   Sequence 6373 BP; 1974 A; 1328 C; 1390 G; 1626 T; 55 other;

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ID   BEL-2_HMM-I repbase;     DNA;     INV; 5827 BP.
XX
AC   CAEZ01008606;
XX
DT   31-MAR-2012 (Rel. 17.08, Created)
DT   31-MAR-2012 (Rel. 17.08, Last updated, Version -1)
XX
DE   LTR retrotransposon from the Heliconius melpomene melpomene
DE   genome: internal portion.
XX
KW   BEL; LTR Retrotransposon; Transposable Element; BEL-2_HMM_;
KW   BEL-2_HMM-LTR; BEL-2_HMM-I.
XX
OS   Heliconius melpomene melpomene
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Lepidoptera; Glossata;
OC   Ditrysia; Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini;
OC   Heliconius; Heliconius melpomene.
XX
RN   [1]
RG   The Heliconius Genome Consortium;
RT   "Butterfly genome reveals promiscuous exchange of mimicry
RT   adaptations among species.";
RL   Nature 487(7405), 94-98 (2012).
XX
RN   [2]
RP   1-5827
RA   Jurka J.;
RT   "LTR retrotransposons from the Heliconius melpomene melpomene
RT   genome.";
RL   Direct Submission to RU (30-MAR-2012).
XX
DR   Genome; CAEZ01008606; Positions   13656   19482.
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     XX
CC     Positions [4488-5090] - Integrase core
CC     'ATTAT' target site duplication
CC     LTRs are 100% similar to each other.
     XX
FH     Key             Location/Qualifiers
FT     CDS             231..5441
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FT                     /translation="MSQERIQTTAEQDKYLTTLQEVYNIIQKTQINLKKCP
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     XX
SQ     Sequence 5827 BP; 2189 A; 899 C; 1140 G; 1599 T; 0 other;


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ID     BEL-4_DAn-LTR repbase;     DNA;     INV; 414 BP.
     XX
AC     AAPP01018099;
     XX
DT     25-OCT-2011 (Rel. 17.03, Created)
DT     25-OCT-2011 (Rel. 17.03, Last updated, Version -1)
     XX
DE     LTR retrotransposon from fruit flies: long terminal repeat.
     XX
KW     BEL; LTR Retrotransposon; Transposable Element; BEL-4_DAn_;
KW     BEL-4_DAn-LTR; BEL-4_DAn-I.
     XX
OS     Drosophila ananassae
OC     Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC     Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
OC     Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
OC     melanogaster group; ananassae subgroup.
     XX
RN     [1]
RG     Drosophila 12 Genomes Consortium;
RT     "Evolution of genes and genomes on the Drosophila phylogeny.";
RL     Nature 450(7167), 203-218 (2007).
     XX
RN     [2]
RP     1-414
RA     Jurka J.;
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 RT    "LTR retrotransposons from fruit flies.";
 RL    Direct Submission to RU (25-OCT-2011).
 XX
 DR    Genome; AAPP01018099; Positions     8207     7794.
 XX
 SQ    Sequence 414 BP; 147 A; 93 C; 69 G; 105 T; 0 other;

 //
 ID   BEL-677_AA-I repbase;    DNA;    INV; 6169 BP.
 XX
 AC   .
 XX
 DT   26-NOV-2018 (Rel. 24.02, Created)
 DT   26-NOV-2018 (Rel. 24.02, Last updated, Version 1)
 XX
 DE   LTR retrotransposon from the yellow fever mosquito genome:
 DE   internal portion: a sample sequence.
 XX
 KW   BEL; LTR Retrotransposon; Transposable Element; BEL-677_;
 KW   BEL-677_AA-I; BEL-677_AA-LTR.
 XX
 OS   Aedes aegypti
 OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
 OC   Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
 OC   Culicoidea; Culicidae; Culicinae; Aedini; Aedes; Stegomyia.
 XX
 RN   [1]
 RP   1-6169
 RG   Nene, V., Wortman, J.R., Lawson, D., Haas, B., Kodira, C., Tu,
 RG   Z., Loftus, B., Xi, Z., Megy, K., Grabherr, M., et al;
 RT   "Genome Sequence of Aedes aegypti, a Major Arbovirus Vector.";
 RL   Science 316(5832), 1718-1723 (2007).
 XX
 RN   [2]
 RP   1-6169
 RA   Bao W.;
 RT   "LTR retrotransposons from the yellow fever mosquito genome.";
 RL   Direct Submission to Repbase Update (26-NOV-2018).
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 CC   A sampled sequence. Flanking LTRs are 99% similar to each
 CC   other.
 XX
 FH   Key             Location/Qualifiers
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XX
SQ     Sequence 6169 BP; 1808 A; 1362 C; 1579 G; 1420 T; 0 other;

//
ID     BEL-732_AA-I repbase;      DNA;      INV; 6578 BP.
XX
AC     .
XX
DT     29-NOV-2018 (Rel. 24.04, Created)
DT     29-NOV-2018 (Rel. 24.04, Last updated, Version 1)
XX
DE     LTR retrotransposon from the yellow fever mosquito genome:
DE     internal portion: consensus.
XX
KW     BEL; LTR Retrotransposon; Transposable Element; BEL-732_;
KW     BEL-732_AA-I; BEL-732_AA-LTR.
XX
OS     Aedes aegypti
OC     Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC     Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
OC     Culicoidea; Culicidae; Culicinae; Aedini; Aedes; Stegomyia.
XX
RN     [1]
RP     1-6578
RG     Nene, V., Wortman, J.R., Lawson, D., Haas, B., Kodira, C., Tu,
RG     Z., Loftus, B., Xi, Z., Megy, K., Grabherr, M., et al;
RT     "Genome Sequence of Aedes aegypti, a Major Arbovirus Vector.";
RL     Science 316(5832), 1718-1723 (2007).
XX
RN     [2]
RP     1-6578
RA     Bao W.;
RT     "LTR retrotransposons from the yellow fever mosquito genome.";
RL     Repbase Reports 19(4), 614-614 (2019).
XX
DR     [2] (Consensus)
XX
CC     Flanking LTRs are 99% similar to each other.
XX
FH     Key             Location/Qualifiers
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FT                      KEYLPQIRGRTKWFEDSPPIKPGDLVIVVDGGMRNSWVRGKVVRTYPGKDG
FT                      RIRVADVQINSKVLQRPVTNLAVVEVQRSDIAGQTSQQYGSG"
XX
SQ   Sequence 6578 BP; 1896 A; 1483 C; 1615 G; 1584 T; 0 other;


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ID   CATS          repbase;    DNA;    INV; 5117 BP.
XX
AC   .
XX
DT   11-SEP-2012 (Rel. 20.10, Created)
DT   11-SEP-2012 (Rel. 20.10, Last updated, Version 2)
XX
DE   Non-LTR retrotransposon CATS.
XX
KW   R1; Non-LTR Retrotransposon; Transposable Element; TRAS; CATS.
XX
OS   Bombyx mori
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Lepidoptera; Glossata;
OC   Ditrysia; Bombycoidea; Bombycidae; Bombycinae; Bombyx.
XX
RN   [1]
RA   Mita K., Kasahara M., Sasaki S., Nagayasu Y., Yamada T.,
RA   Kanamori H., Namiki N., Kitagawa M., Yamashita H. et al.;
RT   "The genome sequence of silkworm, Bombyx mori.";
RL   DNA Res 11(1), 27-35 (2004).
XX
RN   [2]
RA   Sakudoh T., Tsuchida K. and Kataoka H.;
RT   "BmStart1, a novel carotenoid-binding protein isoform from Bombyx
RT   mori, is orthologous to MLN64, a mammalian cholesterol
RT   transporter.";
RL   Biochem Biophys Res Commun 336(4), 1125-1135 (2005).
XX
RN   [3]
RP   1-5117
RA   Kojima K.K. and Jurka J.;
RT   "Consensus update.";
RL   Direct Submission to Repbase Update (11-SEP-2012).
XX
DR   [3] (Consensus)
XX
CC   ~98% identical to consensus. It is similar to the TRAS family of
CC   non-LTR retrotransposons.
XX
FH   Key             Location/Qualifiers
FT   CDS             2..985
FT                   /product="CATS_1p"
FT                   /translation="RYPCKWHTRALSEQLEKTPLYAAGHGSLDEHSQLLKE
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FT                   NKEEIEKLSEEIKKQRTEWKENRSYASVVSGTKEKERGNAEMHSVVISSDD
FT                   QNATGEDVFNKIRSTLNAKEEGIKIDRIRKVKDRKVIVGCESKEELVKIRE
FT                   TIKTKGKDLHLQEIRNKEPMVQLKDVLNYNKDEDIVRALINQNKHLLGDVS
FT                   VDSSTLKVKFRRRARNPLTSHVAIQVPPKLWKRLTEAGLVHIDVQRVRVED
FT                   QSPLIQCSRCLGYGHGKRFCREKIDACSHCGEAHHRSECADWMARVPPSCC
FT                   NCLKAKIGEAEHNAFSPECPVRKRWETLARSTVTYC"
FT   CDS             978..4700
FT                   /product="CATS_2p"
FT                   /note="apurinic-like endonuclease, reverse
FT                   transcriptase and ribonuclease H."
FT                   /translation="LIAKVDSRNPDQIIPPRGTVSTLVAQSNLQRKHLATS
FT                   EFLLEAKKRRVDVALLQEPYVGSQGRVRDHRGVRIFQGINGQGAVIKSAIA
FT                   VFNDGWVVTPCPSLTTTNITVVKIYTGIRNLVVVSFYFEPDKPIGPHLEQL
FT                   GKVVETLGSRGILIGGDTNAKSVWWGSVGTDARGEEVLGMLGEWGLQLLND
FT                   GQTPTFETVRGGKLLTSHIDITACSEDIIGLISDWKVDDTMASSDHNAITF
FT                   VIKKSKDKYTQAKSKTTRKYNTNKANWTYFNEKLEELIENNNLTNTEIRNI
FT                   KEKTKLDEVINKYTEVVTEASNSAIPLIKIKNSMNLPWWSEKLAKMKQGVA
FT                   TRRRRIRCAAPVRRAKVVREYLESKELYENEAKKAQIDSWKEFCKKQTKET
FT                   IWNGVYRMIGKVSVKKEDLPLIYRGQTLSEEESAKHLAENFYPEDKSEEDN
FT                   AEHQAIRKAADRINGGQDDDYQDPPFTVHEVLTAAESFNPKKAPGADGLTA
FT                   DICKQAIQKNPKLYLSLANRCLQLGHFPTIWKEATVVVLRKPGKEDYTDVK
FT                   SYRPIGLLPVMGKILEKMVVGRVKWYLLPRMSTRQFGFMPQRGTEDSLYTL
FT                   VNYIRDRLKEKTIVTAISLDIEGAFDSAWWPAIRVRLSEEECPKNLRRMVD
FT                   SYFESRTVRVRFAGREHLKGTTKGCVQGSIGGPIFWNLLLDPLLRELDRRG
FT                   VYCQAFADDIILVFDGETANIQRRANEVLSYVRDWGVRNKLKFAPHKTKAM
FT                   VITRRLKYDSPILHMGGVDIDLTNELKVLGLIIDNKLTFNRHVAEISKKAI
FT                   GFYRRLSRAARAAKIHWGLNPEILRTLYNAVVEPIMLYAASAWAPATRKKC
FT                   VRRRLNSVQRGFVQRMTKAYRTVSLNSTLLLAGVLPLDIRVREAAMLYETK
FT                   RGHSQAVVGDRGMERPVAFANLDHPARRKRWEYRSLTDGAELESHIRECPS
FT                   IFTDGSKIEGRVGAALSIWEGTGEIKTKKLKLGSYCTVYQAELLALLKATE
FT                   EVLSGGAATYNIFCDARSTLDVIASGESLHPLAFKITKNLKTITERNQEIR
FT                   LFWIKAHIGLEGNERADVLAKEAALSLKCKPHYDRCPVSFAKRTIRQGSVD
FT                   EWDLRYTTESTASVTKIFFPNVKSSYSIIRRLEVDSTLTQVFTGHGGLSQY
FT                   LHRFRCKESPACVCDPVNQESIVHVLIECPVHAKERFDTEQHIDLNIEVRN
FT                   LPLILADKKNRSKFIEYCKKVIRIVINRNKQ"
XX
SQ   Sequence 5117 BP; 1727 A; 1013 C; 1333 G; 1044 T; 0 other;

//
ID   CR1-1_ACC    repbase;    DNA;     VRT; 4343 BP.
XX
AC   .
XX
DT   05-NOV-2018 (Rel. 24.12, Created)
DT   05-NOV-2018 (Rel. 24.12, Last updated, Version 2)
XX
DE   Non-LTR retrotransposon from the golden eagle genome, consensus.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-1_ACC.
XX
OS   Aquila chrysaetos canadensis
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Falconiformes; Accipitridae;
OC   Accipitrinae; Aquila; Aquila chrysaetos.
XX
RN   [1]
RP   1-4343
RA   Kojima K.K.;
RT   "Non-LTR retrotransposons from the golden eagle genome.";
RL   Repbase Reports 19(12), 2728-2728 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~96% identical to consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             319..1404
FT                   /product="CR1-1_ACC_1p"
FT                   /note="SGNH_hydrolase."
FT                   /translation="MVATRVKAIVRKNVATQTELPCKRAAVQVSGCRECLS
FT                   LSLMTEGSGDTSCVRCDQVDDLLSLVAELKEEVERLRSIRECEREIDWWAH
FT                   TLPSLRQRQQMEAPQEAEVPLPSCHQAGGDLRDGGEWIQVPARGGRRIPSR
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FT                   SPSPSQLPLHNRYGALELEDQASEDQGVDEALSREVPRLSRAAPRILTSSE
FT                   KRKRRVIVVGDSLLRGTEGPICRPDPSHREVCCLPGARVKDITRKLPGLVR
FT                   TSDYYPLLVVQVGSDEIAERNPKAIKRDFRALGRLVEGSGAQVVFSSIPSV
FT                   AGKYTERNRKTHLVNTWLRGWCHRWNFGFFDHGEVYTAPGLLATDGIQLSQ
FT                   RGKRILAHEMAGLIERALN"
FT   CDS             1464..4262
FT                   /product="CR1-1_ACC_2p"
FT                   /note="apurinic-like endonuclease and reverse
FT                   transcriptase."
FT                   /translation="MPMLGVDSIAQLKCIYANARSMGNKQEELEAIVQQDR
FT                   YDLVAITETWWDDSHDWSAAMDGYKLFRRDRQGRRGGGVALYVRECFDCTE
FT                   LHDCDDKVECLWVRMRGKANKADIVLGVCYRPPDQVEETDESFYKRLAVVS
FT                   ESCALVLVGDFNFPDICWKYNTAVSKQSRRFLECVEDNFLTQLVGEPTRGG
FT                   ALLDLLFTNREGLVGGVMVGGRLGLSDHEMIEFSILGEARKVVSKTTTMDF
FT                   RRANFGLFKALVERVPWETVLKGKGVQEGWTFFKKEILMAQDQAIPMCRKS
FT                   NRRGKRPAWLNRELLLGVKKKRRVYHLWKKGRATWEEYRDLVRSYREKIRK
FT                   AKAQLELNLATIVRDNKKCFYKYVNSKKNPKENIYPLMDTEGNVATRDEEK
FT                   AEVLNAFFASVFNRETSYPQGTPPPELEGKDEEQNIPPLIQEEIVSDLLRH
FT                   LDTHKSMGPDGIHPRVLRELAEVLAKPLSIIYQRSWSTGEVPEDWRLANVT
FT                   PIYKKGRREDPGNYRPVSLTSVPGKIMEQFVLRALTWQVVQDKQGIRPSQHG
FT                   FTKGRSCLTNLISFYDQVTHLVDEGKAVDVIYLDFSKAFDTVSHGILLEKL
FT                   AAHGLDKCTLRWVKNWLDGRAQRVVVNGVKSSWRRVTSGVPQGSVLGPVLF
FT                   NIFINDLDEGIECTLSKFADDTKLGGRVDLLEGREALQRDLDRLDRWAEAN
FT                   RMKFNKAKCRVLHLGHSNPMQRYRLGEEWLESCPAEKDLGVLVDSRLNMSQ
FT                   QCAQVAKKANGILACIRNSVASRSREVIVPLYSALVRPHLEYCVQFWAPHY
FT                   RKDIEXLERVQRRATKLVRGLEHKSYEERLRELGLFSLEKRRLRGDLIALY
FT                   NYLKGGCSEVGAGLFCQVAGDRTRGNGLKLRQGRFRLDIRKNFFTERVVRH
FT                   WNRLPREVVESPSLEVFKKRVDGVLQDMV"
XX
SQ   Sequence 4343 BP; 1095 A; 942 C; 1402 G; 901 T; 3 other;

//
ID   CR1-1_PMo   repbase;    DNA;     VRT; 1984 BP.
XX
AC   .
XX
DT   20-APR-2011 (Rel. 16.04, Created)
DT   20-APR-2011 (Rel. 16.04, Last updated, Version 1)
XX
DE   CR1-type non-LTR retrotransposon: partial consensus sequence.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-1_PMo.
XX
OS   Python molurus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata;
OC   Toxicofera; Serpentes; Henophidia; Pythonidae; Python.
XX
RN   [1]
RP   1-1984
RA   Castoe T.A., Hall K., Pollock D. and Feschotte C.;
RT   "LINE elements from snakes.";
RL   Repbase Reports 11(4), 1417-1417 (2011).
XX
DR   [1] (Consensus)
XX
CC   Additional repetitive elements from snakes are available at:
CC   http://www.snakegenomics.org/SnakeGenomics/Processed_Data.html.
XX
SQ   Sequence 1984 BP; 698 A; 372 C; 490 G; 422 T; 2 other;

//
ID   CR1-2_ACC   repbase;    DNA;     VRT; 3867 BP.
XX
AC   .
XX
DT   05-NOV-2018 (Rel. 24.12, Created)
DT   05-NOV-2018 (Rel. 24.12, Last updated, Version 2)
XX
DE   Non-LTR retrotransposon from the golden eagle genome, consensus.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-2_ACC.
XX
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 OS    Aquila chrysaetos canadensis
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Falconiformes; Accipitridae;
 OC    Accipitrinae; Aquila; Aquila chrysaetos.
 XX
 RN    [1]
 RP    1-3867
 RA    Kojima K.K.;
 RT    "Non-LTR retrotransposons from the golden eagle genome.";
 RL    Repbase Reports 19(12), 2727-2727 (2019).
 XX
 DR    [1] (Consensus)
 XX
 CC    ~92% identical to consensus.
 XX
 FH    Key           Location/Qualifiers
 FT    CDS           142..693
 FT                  /product="CR1-2_ACC_1p"
 FT                  /note="SGNH_hydrolase."
 FT                  /translation="RSIYTRGVAKVRKAYPCITTTSTRKKRRVIVVGDPLL
 FT                  RGTEGPICRTDPPLREVCCLPGAQVKDITRKLXSLVLPSDYYPLLLLHVGS
 FT                  DEXAMHSPRAIKRDFRALGWLVRESGAQVIFSSILPVAGNDIGRNRWTQSI
 FT                  NTWLRGWCHHHSXGXFDNGMAYTAPGLLASDGIHPSQRGKRVFAH"
 FT    CDS           721..3768
 FT                  /product="CR1-2_ACC_2p"
 FT                  /note="apurinic-like endonuclease and reverse
 FT                  transcriptase."
 FT                  /translation="QSFKLDLKGEGDNIRLARDKLWDDTPRLEGRGASEGP
 FT                  QPVALRRAGYTGAHLKSYGDEPGAPEVIGANRETPVKYLKGIKGCSSKKVT
 FT                  RPTAQLKCLYTNARSMGNKQEELEATVLLESYDLVAITETWWDESHDWSAA
 FT                  IDGYRLFRRDRRGRRGGGVALYIKKWIDCEELSLKNSHEQVESLWVRIRDR
 FT                  GNKGNLVVGVYYRPPDQGEPIDEAFLLQLQEASRSQALVLLGDFNHPDICW
 FT                  KSSTASCRQSRRLLECIEDNFLSQVIDSPTRGDAILDLMVTNASELIGDVK
 FT                  IGGSLGCSDHALVEFAVLRDMGQAKSKVRTLNFRKAKFQLFKELVNRTPWE
 FT                  TALRDKGAEQSWQIFKDAFHRAQELSIPRCKKSGKEGKRLAWLSRDLLVKL
 FT                  KGKKEMHRQWKQGQVSWEEYRDAAWLCRDGVRKAKAQLELNLARDAKNNKK
 FT                  GFYRYVSQKRKVKESVPTLMNKTGKLVTTDEEKAEVLNNFFASVFTGNLSS
 FT                  HTSRVDGPQDRDWGSKVPPTVREDQVRDHLRNLNIHKSMGPDEMHPRVLRE
 FT                  LADVVAKPLSMIFEKSWQSGEVPGDWKKGNIAPIFKKGRKEDPGNYRPVSL
 FT                  TSVPGKIMEQILLEAMLRHMEDREVIRDSQHGFTKGKSCLTNLVAFYDGVT
 FT                  TSVDKGRAMDVIYLDFCKAFDTVPHNILLSKLERYGFDGWTVRWMRNWLDG
 FT                  RIQRVVVNGSMSRWRSVTSGVPQGSVLGPVLFNIFINDIDSGIECTLSKFA
 FT                  DDTKLSGAVDMPEGQDAIQRDLDKLEKWAHVNLMRFNKAKCKVLHLGQGNP
 FT                  RYQYRLGDEGIESSPAEKDLGVLVDEKLDMSWQCALAAQKANRILGCIKRS
 FT                  VASRSREVILPLYSALVRPHLQYCVQLWSPQHRKDMDLLERVQRRATKMIR
 FT                  GMEHLSCEERLRELGLFSLEKRRLWEDLIAAFQYLKGAYKKDGDRLFSRAC
 FT                  SDRTRGNGFKLKEGRFRLDIRKKFFTMRVVKHWNRLPREVVDAPSLETFKV
 FT                  RLDGALSNLI"
 XX
 SQ    Sequence 3867 BP; 1040 A; 857 C; 1162 G; 803 T; 5 other;

 //
 ID    CR1-3_HM      repbase;    DNA;     INV; 4733 BP.
 XX
 AC    .
 XX
 DT    11-DEC-2008 (Rel. 13.12, Created)
 DT    11-DEC-2008 (Rel. 13.12, Last updated, Version 1)
 XX
 DE    CR1-type family: consensus.
 XX
 KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-3_HM.
 XX
 OS    Hydra vulgaris
 OC    Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
 OC    Anthoathecata; Aplanulata; Hydridae; Hydra.
 XX
 RN    [1]
 RP    1-4733
 RA    Jurka J.;
 RT    "CR1 families from Hydra magnipapillata.";
 RL    Repbase Reports 8(12), 1831-1831 (2008).
```

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XX
DR    [1] (Consensus)
XX
CC
CC    This sequence was derived from sequence data generated by TIGR,
CC    J Craig Venter Institute.
XX
FH    Key             Location/Qualifiers
FT    CDS             931..4194
FT                    /product="CR1-3_HM_1p"
FT                    /translation="MKICHHCKFCNKKIKDNHRAIQCDCCSFWIHAKCIPV
FT                    DKHAYNMLSNDSSEWFCPNCISNNMPFGVLSDLELKSTLSCKNPSNKIKFH
FT                    EPPDYLKNLFKTMNNVFNPTTKCKYLDVNELNKSINPGTEIYLHLNISSLP
FT                    FHINDLSSFVGTINTPPMVIGITESNLYANDSNITDITIQGYNIEHCPTES
FT                    KKGGALLYLNSNLNYIVRSDLQIYATKFLESIFVEVIYPLKSNTIFGCIYR
FT                    HPSLNITEFLSIHFNPLLEKLSHEAKNIVLMGDFNIDLLNYRESQVISNYF
FT                    ESLCSHSLFPTIILPTRVTAKTKTLIDNIFMNSFPTDIVSGNLTISISDHM
FT                    AQFVCIPNNPPIKKKVKMFKRSFKKFDSDSFIQEISDINWELLIKDDDNIN
FT                    ESINFFLKTFEKILDRYAPYKELTKKQIKLQSKPWITSGILKSISNKNILY
FT                    KKFTRSKNVNTKNILFTKFKLYRNKISNLLRYSKKLYYASFFNNNINNVKN
FT                    TWKGIKEIINIKPSTSTKSFNLKINENVISDHTSVANIFNNYFTTIQDELL
FT                    KNTVPSKCAFGNFLKIPSINSFFIEPVTENEVANLIKDTLKNNKSLGPNSL
FT                    PTFLLKLVSHIISKPLCTMMNNSFKNGIFPEAFKVAKVIPIHKMGSYLDYS
FT                    NYRPISLLSNLSKLFEKAMFQRLEHFLEKHKFIYKHQYGFRNKHSTTHSLI
FT                    EITEKIRQAIDNKHFACGVFIDIRKAFDTVEHTILLEKLKHYGIRGIPFLW
FT                    FSSYLCNRTQFVSINGINSGLAKSFNGVPQGSVLGPLLFLIFINDLNVSLK
FT                    FSTAYHFADDTNLLLINKSLKKLNKNMNHDLANVVQWLRSNKLSLNSKKTE
FT                    IIIFKSAKTKINKQLNFRLSGQKINPVNSIKYLGIKIDSNLSFASHLQDLA
FT                    LKLSRSNGILAKIRHFVNHETLLNLYHAIFHSHLRYACQVWGQSKQLAFLR
FT                    LTYLQNKALKLIYFQHTNSNCSILYFLSKVLKLCDLIQLSNCLFVWNQNHN
FT                    NLPLTFINFFSYRENCKYILRSALNFKLSVPKYRTVHYGYESIQHKSIQTW
FT                    NNLPSQLKSLKSFSKFKTALFNHFLEKYSL*"
XX
SQ    Sequence 4733 BP; 1699 A; 744 C; 479 G; 1808 T; 3 other;


//
ID    CR1-9_NVi    repbase;    DNA;    INV; 4291 BP.
XX
AC    .
XX
DT    12-MAY-2009 (Rel. 14.05, Created)
DT    12-MAY-2009 (Rel. 14.05, Last updated, Version 1)
XX
DE    CR1-type non-LTR retrotransposon: consensus.
XX
KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-9_NVi.
XX
OS    Nasonia vitripennis
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita;
OC    Terebrantes; Chalcidoidea; Pteromalidae; Pteromalinae; Nasonia.
XX
RN    [1]
RP    1-4291
RA    Bao W. and Jurka J.;
RT    "CR1 families from Nasonia vitripennis.";
RL    Repbase Reports 9(5), 936-936 (2009).
XX
DR    [1] (Consensus)
XX
FH    Key             Location/Qualifiers
FT    CDS             join(6..680,677..1201)
FT                    /product="CR1-9_NVi_1p"
FT                    /translation="MESSSAGSVTSQTAIFYKCHPKVEVKTVICIICEEAF
FT                    HTSDFAKIDGAVKISGVLGLCPEHNQVDLTSKVNTNVLSNEAKIIIAQIKL
FT                    AHNLRKSDQLSVSEADSDDDDENSVKIDSNLKCENALLKELNKELKEKNKL
FT                    LRELLDKQKSEINSSKNKTYAQVISSAMPNNKPKRIPKIIVKNKDTKEFSI
FT                    DKINDVVAHYLIKDKSIQAKKLIKKXSEIIVDCRCMLTEESASKAYNVLKK
FT                    KLDESCDVIKEKIENXKVKVVGINNFETLDNKKIEDDINERNFSKFNKKCT
FT                    VLHSYNNSKTHLQSVILEIPAELYQHVRENKNRIFVGYQNCKVHDYCNIKP
FT                    CFNCGRYGHNGFKCTNNHTCLKCAGNHKTTDCTGNKLNCPNCIFSNNKYKG
FT                    TLRIN*"
FT    CDS             join(1201..2442,2403..4094)
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FT                   /product="CR1-9_NVi_2p"
FT                   /translation="MAQEFNFEDIYNIERDAENIRSLNKSISKKKNLILCV
FT                   NIRSLNANYEKLESFIESLVVKPIIIICTETWILQYPQYYQLQGYKSYYND
FT                   SKINRADGVMLYIKKNIQEITKIEVIDRLSVVSSDTFLESGEAIRISAMYR
FT                   CHDISKSEFTNSVRKFLSKQVNIKNQCIFGDFNIDIRDINYDKIGLAEKTI
FT                   AQEFLNNFFENEYIPFFRGITRPSQNSENGTCIDNCFAKVRNIELESFKLN
FT                   IPFNDHYPLFISINKFKIQKDYNQSACINYGKLINIAKRVEWDSLLQINDP
FT                   NQAINELISMIQSCVEKATDRKYSNKNKKDSVPKKKWITKAILISCKTKEM
FT                   LYNIWKKNPTNMKLKMDYKNYEKILSKVIKDAKYKYENNAIRKCSGNSRQL
FT                   WSIINDKLGKKRXKEDHLIVVRKKKKQGGSLDSIIVNDQKIEDKTTIANTM
FT                   NEYYCNVGIXLSNQIXKMDLEQLKLPVRNNYSIFINPTNMYEIQNIIIAMK
FT                   KKAGGVDNISAITIKTLSKHILKPLEYIFNLSIQQSIWPNALKQADIVPIY
FT                   KSGDNSCISNYRPISLTSNIAKIFEKIIYNRLYNFIMKHKIISDKQFGFIR
FT                   KRGTKDALNCLXNIIYRNLDKSKPIITAFLDLAKAFDTVDHSILLDKLERY
FT                   GVRGEALKLLISYLSDRKQCVKISNCKSEYKEITIGVPQGTILGPLFFILY
FT                   VNDLLIDMQNETILSYADDTVIISCDNSWTAAQERLNEYLRKVAIWLNLNK
FT                   LSLNVNKTVYIAYGNYCDSVPSTLNIKIGDNVINRVDSYRYLGLIIDYNMK
FT                   WDKHINYIIKSTRYLIFIFAKLKKFMDSKTLMLLYYAFFQSITNYGIIAWG
FT                   GAYNNYLNLIQGIQKKILRIINKNCYITQNQPLPIRQMFELECIVYHYNEL
FT                   RDRYIRSTNKTRNKNLPLPKIDKTVSKKSSYYVAVSVFNTLPNDLKDLSIS
FT                   KVSIKRKLKMFIGKNYFGCYIF*"
XX
SQ   Sequence 4291 BP; 1777 A; 538 C; 724 G; 1245 T; 7 other;


//
ID   CR1-C4      repbase;    DNA;     VRT; 4511 BP.
XX
AC   .
XX
DT   29-AUG-2008 (Rel. 13.08, Created)
DT   29-AUG-2008 (Rel. 13.08, Last updated, Version -1)
XX
DE   CR1 Non-LTR Retrotransposon from chicken.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; LINE; CR1-C4.
XX
OS   Gallus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
OC   Phasianidae; Phasianinae.
XX
RN   [1]
RP   1-4511
RA   Smit A.F.;
RT   "CR1-C4 - CR1 Non-LTR Retrotransposon from chicken.";
RL   Direct Submission to Repbase Update (05-AUG-2008).
XX
DR   [1] (Consensus)
XX
CC   18% (3end was B2C) GG000915 (part), GG000575, GG000077 (once was
CC   X1) general    update20040306.
XX
SQ   Sequence 4511 BP; 1131 A; 1014 C; 1471 G; 852 T; 43 other;


//
ID   CR1-E_Pass  repbase;    DNA;     VRT; 3085 BP.
XX
AC   .
XX
DT   08-JAN-2009 (Rel. 14.01, Created)
DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE   CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-E_Pass;
KW   LINE.
XX
OS   Passeriformes
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae.
XX
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 RN   [1]
 RP   1-3085
 RA   Smit A.F.;
 RT   "CR1-E_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
 RL   Repbase Reports 9(1), 45-45 (2009).
 XX
 DR   [1] (Consensus)
 XX
 CC   18% div. Minor subfamilies ignored. 83% similar to CR1-E in
 CC   chicken (consensus starts at poss 1418 in full chicken CR1-E
 CC   consensus, at very end of ORF1).
 XX
 SQ   Sequence 3085 BP; 828 A; 685 C; 968 G; 585 T; 19 other;

 //
 ID   CR1-J1_Pass repbase;     DNA;     VRT; 3993 BP.
 XX
 AC   .
 XX
 DT   08-JAN-2009 (Rel. 14.01, Created)
 DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
 XX
 DE   CR1 Non-LTR Retrotransposon from Passeriformes.
 XX
 KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-J1_Pass;
 KW   LINE.
 XX
 OS   Passeriformes
 OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC   Coelurosauria; Aves; Neognathae.
 XX
 RN   [1]
 RP   1-3993
 RA   Smit A.F.;
 RT   "CR1-J1_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
 RL   Repbase Reports 9(1), 47-47 (2009).
 XX
 DR   [1] (Consensus)
 XX
 CC   20% subst. Starts at pos ~250. gag 2-1045 (almost complete), pol
 CC   1030-3903, encoding proteins 60%/71% and 76%/85%
 CC   identical/similar to the CR1-F encoded gag and pol proteins,
 CC   respectively. Majority of copies (2 of 3) have one C at pos
 CC   3336-7 and one G at pos 3356-7 AG, causing a frameshift in the
 CC   pol gene. While the pol ORFs and proteins of CR1-J2 and CR1-J1
 CC   are very similar (92% from 1128 to end 3992), the gag region is
 CC   only 20% similar, and the encoded proteins are distant from each
 CC   other compared to gags from other subfamilies. One or the other
 CC   is therefore the product of a recombination. Since Je seems to
 CC   have a 170 bp insertion at the recombination point compared to
 CC   this and other subfamilies, it forms the most likely candidate.
 XX
 SQ   Sequence 3993 BP; 977 A; 892 C; 1318 G; 780 T; 26 other;

 //
 ID   CR1-J2_Pass repbase;     DNA;     VRT; 4277 BP.
 XX
 AC   .
 XX
 DT   08-JAN-2009 (Rel. 14.01, Created)
 DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
 XX
 DE   CR1 Non-LTR Retrotransposon from Passeriformes.
 XX
 KW   CR1; Non-LTR Retrotransposon; Transposable Element; CR1-J2_Pass;
 KW   LINE.
 XX
 OS   Passeriformes
 OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC   Coelurosauria; Aves; Neognathae.
 XX
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RN    [1]
RP    1-4277
RA    Smit A.F.;
RT    "CR1-J2_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 48-48 (2009).
XX
DR    [1] (Consensus)
XX
CC    23% ORFs: gag 64-1164, pol 1149-4184. The gag peptide is 68%/76%
CC    identica;/similar to CR1-X_gag; pol protein 76%/84% id/sim to
CC    CR1-H_pol and 83/87% to CR1-J1_Tgu_pol. The Ja/Je pol regions
CC    are 91-2% identical, but the gag regions of Je and Ja are 20%
CC    different, so that one has to be a recombination product. There
CC    may be some distinct subfamilies still to be worked out.
XX
SQ    Sequence 4277 BP; 1054 A; 980 C; 1397 G; 839 T; 7 other;

//
ID    CR1-J3_Pass repbase;    DNA;    VRT; 4266 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-J3_Pass;
KW    LINE.
XX
OS    Passeriformes
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae.
XX
RN    [1]
RP    1-4266
RA    Smit A.F.;
RT    "CR1-J3_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 49-49 (2009).
XX
DR    [1] (Consensus)
XX
CC    18% ORFS: gag 245-1318, pol 1303-4176 Build from 180 copies.
CC    First 500 bases copied from K3.
XX
SQ    Sequence 4266 BP; 1043 A; 934 C; 1376 G; 879 T; 34 other;

//
ID    CR1-X1_Pass repbase;    DNA;    VRT; 4428 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-X1_Pass;
KW    LINE.
XX
OS    Passeriformes
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae.
XX
RN    [1]
RP    1-4428
RA    Smit A.F.;
RT    "CR1-X1_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 50-50 (2009).
XX
DR    [1] (Consensus)
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XX
CC    subfamily1 17%. gag ORF (full) 311-1453, pol (1 frameshift)
CC    1618-4348, but, like the distantly related R1-YB2_Tgu,  there is
CC    a frameshift that appears tru in the consensus. The frameshift
CC    (2 bp missing) is at 3807, corresponding to pos 3239 of
CC    CR1-YB2_Pass. Notably, this is at a different, later spot then
CC    in CR1-YB2_Pass.With 600 copies of terminal 700 bp, coseg could
CC    find 2 or 3 subfamilies. These are at most 5-6% different from
CC    each other, and I get the impression that recombined copies have
CC    hopped around, so there is only one consensus. Absent at
CC    orthologous sites in chicken.
XX
SQ    Sequence 4428 BP; 1163 A; 1004 C; 1344 G; 899 T; 18 other;

//
ID    CR1-X3_Pass repbase;     DNA;     VRT; 4471 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-X3_Pass;
KW    LINE.
XX
OS    Passeriformes
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae.
XX
RN    [1]
RP    1-4471
RA    Smit A.F.;
RT    "CR1-X3_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 52-52 (2009).
XX
DR    [1] (Consensus)
XX
CC    21% Pos 1-1627 were not derived for this subfamily and are taken
CC    from CR1-X1. Complete pol ORF at pos 1421-4336 encodes a protein
CC    70% identical (80% sim) to chicken CR1-X pol. There are many CR1
CC    copies in chicken that match CR1-X3_Pass better than the current
CC    chicken CR1-X consensi, but many X3 copies are precisely absent
CC    and (so far) none are present at orthologous sites in chicken.
XX
SQ    Sequence 4471 BP; 1177 A; 938 C; 1330 G; 1006 T; 20 other;

//
ID    CR1-YB2_Pass repbase;     DNA;     VRT; 3871 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    CR1 Non-LTR Retrotransposon from Passeriformes.
XX
KW    CR1; Non-LTR Retrotransposon; Transposable Element; CR1-YB2_Pass;
KW    LINE.
XX
OS    Passeriformes
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae.
XX
RN    [1]
RP    1-3871
RA    Smit A.F.;
RT    "CR1-YB2_Pass - CR1 Non-LTR Retrotransposon from Passeriformes.";
RL    Repbase Reports 9(1), 54-54 (2009).
XX
```

```
 DR   [1] (Consensus)
 XX
 CC   15-18%. gag 1-805 (incomplete), pol 790-3782. Interesting story:
 CC   1) The pol is very close to that of chicken CR1-Y (79-80% at DNA
 CC   level), the gag is close to that of chicken CR1-X (78% at DNA
 CC   level) (chicken X & Y are only ~65% similar at the DNA level).
 CC   The junction is confirmed by many copies. This indicates a
 CC   recombination in the chicken or the finch lineage. Remember that
 CC   the chicken gag tree did not correspond to the pol tree, so a
 CC   recombination in the chicken lineage would make sense. 2) There
 CC   is a distinct frameshift in the pol (pos 2959-2969 in this
 CC   consensus, around AA 745 in related pols). The consensus is very
 CC   clear and the frameshift seems to break the RT region (make
 CC   sure), so the retrovirus must have had a frameshifting
 CC   mechanism. The frameshift is not in the closely (75-80%) related
 CC   CR1-Ya_Pass consensus.
 XX
 SQ   Sequence 3871 BP; 1054 A; 879 C; 1160 G; 745 T; 33 other;

 //
 ID   Chapaev-8_HM repbase;    DNA;    INV; 9037 BP.
 XX
 AC   .
 XX
 DT   27-FEB-2008 (Rel. 13.02, Created)
 DT   05-JAN-2017 (Rel. 22.01, Last updated, Version 2)
 XX
 DE   Autonomous Chapaev DNA transposon -a consensus sequence.
 XX
 KW   EnSpm/CACTA; DNA transposon; Transposable Element; Chapaev;
 KW   Chapaev-8_HM.
 XX
 NM   Chapaev-8_HM.
 XX
 OS   Hydra vulgaris
 OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
 OC   Anthoathecata; Aplanulata; Hydridae; Hydra.
 XX
 RN   [1]
 RP   1-9037
 RA   Kapitonov V.V. and Jurka J.;
 RT   "Autonomous Chapaev transposons from the hydra genome.";
 RL   Repbase Reports 8(2), 34-34 (2008).
 XX
 DR   [1] (Consensus)
 XX
 CC   Chapaev-8_HM is a young family of autonomous Chapaev DNA
 CC   transposons that were active in the hydra genome less than a few
 CC   million years ago (copies are ~2% divergent from their consensus
 CC   sequence). The consensus sequence was obtained based on a
 CC   multiple alignment of 15 incomplete copies; it codes for a 841-aa
 CC   Chapaev transposase (ten exons). The consensus sequence is
 CC   incomplete (its 3'-terminal portion in unknown). The Chapaev-8_HM
 CC   TPase forms a distinctive group of Chapaev TPases (including
 CC   Chapaev-3_HM, Chapaev-4_HM, Chapaev-6_HM, Chapaev-7_HM), whose
 CC   240-300-aa N-terminal portion composed of the Chapa zinc and RING
 CC   fingers is similar to the N-terminal portion of RAG1 (pos.
 CC   ~100-380). For instance, the N-terminal portion of the
 CC   Chapaev-8_HM transposase (pos. 4-245) is 27% identical to the
 CC   RAG1 N-terminal portion (E value <1e-14).
 CC   This sequence was derived from sequence data generated by TIGR,
 CC   J Craig Venter Institute.
 XX
 FH   Key            Location/Qualifiers
 FT   CDS            join(675..1694,1778..2070,2150..2359,2528..2770,
 FT                  2951..3027,3470..3672,3760..3900,4500..4568,
 FT                  5096..5270,5356..5660)
 FT                  /product="Chapaev-8_HMp"
 FT                  /note="Transposase."
 FT                  /translation="MEIHNKNLTLLCRVCGFLVGKKSYPIGTNQKNKIEKV
 FT                  FHVMLSDEQENVHPNKICHKCYNTINNVIKRMTSTTLHLSMNWKPHCDECF
 FT                  CCQQVEKLCKGLNFAKLLKQNKKLIGRPGIGEKVWSFSMIANIKKSIVTTH
 FT                  DSEIDIEELKNEFNPHLQLCQCNLCGKIPKQPVTLKKCEHLFCFFCIVENI
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FT                    KVKKLNETSCPKCKELILPEDLVTSVKTNSLLNMLTVECICKKKYNVMKEY
FT                    DLYTNHKSVCIDKSIVQAAPLLSPSISSFASNLASSSSFTVSTSSSTSYLF
FT                    NNNISEIFNLTVDNDIPRIVEDAALHVLKQKMAKDGGQVVEFKSGGSRPVL
FT                    FSLTPKAYVSSNQASNTTIRVRNASIKRHMKVISGTSNDAVCCQTSKLINS
FT                    FQAETKGLILDNLNTERVVISATNMVAMKADLCIPWEKLKTISKWLKSFNI
FT                    NTASHSSQRIVAEKLSGDDLVVENAPFTFEKEEKGTFEIKYVSWGYIENLP
FT                    MHILRHLDQLESCKRLHHHEFIPEKEIQIKIGGDYGGGSFKMTYQVANTLN
FT                    PNSKDNTIVFSIFEAKDYRVNVKVAMSRFEKQIEDLQKMKYKDNNIRVFVF
FT                    GDYQFLCALYGISGASGRHCCLFCYATASDMKFGEHKSSEIKDRTLEDLFL
FT                    DHERFIENGGLKKNAKNFNNVITEPILKIPLDQVSLPSLHMALGIYLNFFN
FT                    LFEEEVHQLDILIAAEAVKSNINFSEAYTTNIYNTLFGKHSFEFGQRPCTK
FT                    MLCNCIPKLVHEEGYSGTSVHQFAVEISNKYKQLFDKFAQCYKIFSSKNTI
FT                    TQDDLILLKKNINNLMQFYRLNWPEASVTPKLHMLEHHAIPFMEKWGAGFG
FT                    FYGEQGGESIHMEFNKLKTIYQSIPCPTLRLKSILKSHYQKTNPENMRLKP
FT                    CLKKKKRS"
XX
SQ     Sequence 9037 BP; 3334 A; 1159 C; 1221 G; 3323 T; 0 other;

//
ID     Copia-11_RC-I repbase;      DNA;      PLN; 4279 BP.
XX
AC     AASG02001408;
XX
DT     22-MAR-2011 (Rel. 19.09, Created)
DT     22-MAR-2011 (Rel. 19.09, Last updated, Version -1)
XX
DE     LTR retrotransposon from the castor oil plant genome: internal
DE     portion.
XX
KW     Copia; LTR Retrotransposon; Transposable Element; Copia-11_RC_;
KW     Copia-11_RC-LTR; Copia-11_RC-I.
XX
OS     Ricinus communis
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC     Pentapetalae; rosids; fabids; Malpighiales; Euphorbiaceae;
OC     Acalyphoideae; Acalypheae; Ricinus.
XX
RN     [1]
RA     Chan A.P., Crabtree J., Zhao Q., Lorenzi H., Orvis J., Puiu D.,
RA     Melake-Berhan A., Jones K.M., Redman J. et al.;
RT     "Draft genome sequence of the oilseed species Ricinus communis.";
RL     Nat Biotechnol 28(9), 951-956 (2010).
XX
RN     [2]
RP     1-4279
RA     Jurka J. and Kohany O.;
RT     "LTR retrotransposons from the castor oil plant genome.";
RL     Direct Submission to Repbase Update (22-MAR-2011).
XX
DR     Genome; AASG02001408; Positions   19462   23740.
XX
CC     Positions [1705-2187] - Integrase core
CC     'AGATA' target site duplication
CC     LTRs are 99% similar to each other.
XX
FH     Key           Location/Qualifiers
FT     CDS           880..3123
FT                   /product="Copia-11_RC-I_1p"
FT                   /translation="MVMRGRSTERGPSGSHNHGRSKSKSKKNYKCYNCGKK
FT                   GHLKKDCWSLKNSNPQGNVACTSDDGNVLCCEAAISTESRKRFADVWLLDS
FT                   GATYHMTSRREWFHHYEPILGGSVYSCEDNALKIIGIGTIRLKMHDGTVRT
FT                   IQGVRHVEGLKKNLLSLGQLDDLNCIIKVQKGIMKISRGALVIMKGEKIAA
FT                   NLYMFLGETVHEAEASVASSSSSERSAIVWHQKLGHMSEQGMKILAEKNLL
FT                   PGLTKVSLPFCEHCITSKQHRLQFNTSNSRSKDVLELVHSDVWQAPVSSLG
FT                   GAKYFVSFIDDYSRRCWVYPIKSKGDVFVIFKTYKARVELDSGNKIKCLRT
FT                   DNGGEYTGHEFNSFCKQEGIKRQFTTAYTPQQNGVAERMNKTLLERTRALL
FT                   GAAGLNKAFWAEAVNTACYVINRSPSTAIDQKTPMEMWTGKPVDYSNLHIF
FT                   GSPVYVMYNIQETTKLDPKSRKCLFLGYADGVKGYRLWDPTAHKVIISRDV
FT                   IFLEDKLKGEDDSTSKENSETTTIQVERKSTEEDSSEVAPEHEEEEPVEFE
FT                   EPAEVEESELGKGKRIKFTPTWHKDYDIGSNVAYCLLTEEGEPSTLQEAMS
FT                   SSDASQWMAAMQEEMEALHKNKTWELVPLPQGRKAIGNKWVFKIKRNSDDQ
FT                   VERFRARMVVKGYAQKEGIDFNEIFSPVVRLTTVRVVLAMCATFNLHLEQL
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FT                    DVKTAFLHGDLKEEIYMLQPEGFEEKGKRNLVCRLNKSLYGLKQAPRC"
XX
SQ   Sequence 4279 BP; 1405 A; 720 C; 1034 G; 1120 T; 0 other;

//
ID   Copia-11_TC-I repbase;    DNA;    PLN; 4114 BP.
XX
AC   CACC01006392;
XX
DT   18-JAN-2011 (Rel. 16.02, Created)
DT   18-JAN-2011 (Rel. 16.02, Last updated, Version -1)
XX
DE   LTR retrotransposon from the cocoa genome: internal portion.
XX
KW   Copia; LTR Retrotransposon; Transposable Element; Copia-11_TC_;
KW   Copia-11_TC-LTR; Copia-11_TC-I.
XX
OS   Theobroma cacao
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Malvales; Malvaceae;
OC   Byttnerioideae; Theobroma.
XX
RN   [1]
RP   1-4114
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from the cocoa genome.";
RL   Direct Submission to RU (18-JAN-2011).
XX
DR   Genome; CACC01006392; Positions   26379   30492.
XX
CC   Positions [1640-2140] - Integrase core
CC   'AATAC' target site duplication
CC   LTRs are 97% similar to each other.
CC   We thank Le Centre de coopération internationale en recherche
CC   agronomique pour le développement (CIRAD) for making the sequence
CC   data for Theobroma cacao available.
XX
FH   Key             Location/Qualifiers
FT   CDS             join(1244..2953,2957..4114)
FT                   /product="Copia-11_TC-I_1p"
FT                   /translation="MKSISNVMFVPEVAQNLLSVRQLIEDGYILLFKTNAC
FT                   TILDASGKELFSVEMRNKCFSVDWMKVKHKAYQCLSTNSEIWHRRLGQVNY
FT                   RSLMHMISNNLVEGLPSLTQTDRICSTCQYGKQCRVSFPKSRNWRAKQKLQ
FT                   LVHSDVEGPMKTLSLNGSLYYLIFVDDYTRYSWIFFMKHKYDVFNLFTKFV
FT                   AAVENESGSNLMILRTDNGGEFNSTEFKEFLARKGIKHKLMVAYNPQQNGV
FT                   CEHKNRTVMEMTRCLLFEKDLPKEFWAEAANVAVYLLNVLPTKALNVKCPY
FT                   EAWHGTKPSVAHLKVFGCICYAKIPDGKRTKLDPKSQLAIHLGCSNLSKGY
FT                   RLYDLKTKKVFVSRDVRFDEDLKWNWKTTAVEKSKSNNTTGDVNEGLKWNL
FT                   EIATDENNADGDENLFDDEESVDENDESLAVRGTRPLQEIYGRCIMAVIEP
FT                   NEVSKALKDEKWKEAMDAEMQMIARNRTWYLVDRPQGPKVSGVKWIFKTKL
FT                   NPDGSVNKLKARLVVKGYSQVQGVDFEETFAPVARYDTIRVLTALAVKENW
FT                   SIWHMDVKSAFLNGVISEDIYVEPEGYVVQGKEDKVCKLVKALYGLKQAPR
FT                   AWYDRIDSYMREKGFIRSNNEATLYVKKSGNAVKLIVSLYVDDLLITGPDD
FT                   EFLKEFKAQMKFEFDMTDLGKMSYFLGLEFQQLEGQICLYQSKYAEDLLKK
FT                   FKMNFCKPAPTPLTMGWKLSKDDGEIKTDARLYRSIIGCLLYLSATRPDIM
FT                   FATSLLSRFMQEPSEMHMKAAKRILRYIRGTTTFGLKFVKQDSNHLQGHCD
FT                   SDWAGSVDDSKSTTGYCFSFGSAIFSWNSRKQEVVAHSSAEAEYIAASSAT
FT                   NHVLWLRKLLDDLGFRQFIGTVLWVDNMSAISIAKNPVQHARTKHIRVKFH
FT                   SIREAVKNDEVVIKHCSTNDQVADIFTKSLNKDKYYYLRSKLGICEINSKE
FT                   V"
XX
SQ   Sequence 4114 BP; 1357 A; 654 C; 950 G; 1153 T; 0 other;

//
ID   Copia-130_SB-I repbase;    DNA;    PLN; 4364 BP.
XX
AC   ABXC01003225;
XX
DT   30-OCT-2009 (Rel. 14.10, Created)
DT   30-OCT-2009 (Rel. 14.10, Last updated, Version -1)
XX
DE   LTR retrotransposon from sorghum: internal portion.
```

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XX
KW    Copia; LTR Retrotransposon; Transposable Element; Copia-130_SB_;
KW    Copia-130_SB-LTR; Copia-130_SB-I.
XX
OS    Sorghum bicolor
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae;
OC    Sorghinae; Sorghum.
XX
RN    [1]
RP    1-4364
RA    Jurka J. and Kohany O.;
RT    "LTR retrotransposons from sorghum.";
RL    Repbase Reports 9(10), 2554-2554 (2009).
XX
DR    Genome; ABXC01003225; Positions    4836     473.
XX
CC    Positions [1711-2031] - Integrase core
CC    'GCTAG' target site duplication
CC    LTRs are 94% similar to each other.
XX
FH    Key           Location/Qualifiers
FT    CDS           322..2055
FT                  /product="Copia-130_SB-I_1p"
FT                  /translation="MQVAKKKTGKEVWDSLKTRFVGADRVRDARLQTLKSE
FT                  FDAIQMKEDDLLDPIVAKLTTMSVKYNSLGGSLDDAALVKKLFDIVPERFL
FT                  TVVAGIEQFFDLKTMAFDEAVGRLKAFEERTRRGSSSARSEDKQVLLTQAE
FT                  WEARQKTSGGESSGKGRKSDGGGRGRGRGRIGGRGGRGNGGDAGGDGTGKR
FT                  DKNHIKCFKCHKYGHYANRCPGEKKGDEAHHARVEEAAVLLAETEVPGPFK
FT                  RLSASTVQNGIVLNEPKVMPELHLTGGRSSSGDMWYLDNGASNHMTGDRQK
FT                  FKDLDSNITGKVRFGDDSTVEIEGMGTILFQGQSGDQWVLSEVYFIPKLHS
FT                  NLISLGQLTEVGHKVELDDDLLEVSEKNPRRLIMKVQRSGNRLYKIQLKTV
FT                  DPTCLMVNIGDDAWLWHGRLGHVNFRSLKYLASKGMATGVPQLNHPDQVCR
FT                  DCLTAKQTRFPFPKSAQWLAEEKLALVYVDLCGPITPVTTGGNKYFMLLVD
FT                  DYSRWMKVYLLKSKDAVEFFVRYKAEVENFTGSKIKTLRSDRGGEFLAGVF
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FT    CDS           2229..3797
FT                  /product="Copia-130_SB-Ip"
FT                  /translation="MFGCTAHAKNSAPHLKKLDDRSKALVYFGVEEGSKAH
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FT                  AVNLSTPQQSLFGGNISTPGSGDSSEPMRFRNLSEIYDETSEVELQEPESE
FT                  TENSDAEALLVDSGEPTCYREAAGHQEWLEAMKKEMESIEKNRTWELVKLP
FT                  VGKKPIGLKWVYKLKKNTEGEVVKHKARLVAKGYVFAPVARLDTVRFFLAL
FT                  AANLGWRVHHLDVKFAFLHGDLEEEVYVSQPEGFVVKGKEHCVLRLSKALY
FT                  GLKQAPRAWNVKLDNSLKKLGFSRCLSEQAVYTRGEGPDAVILGVYVDDLI
FT                  VTGGNPTKIKEFKDEMMSEFEMTDLGLLSHYLGIEVDQKDDYITVKQTSYA
FT                  KKVLGQFGMSGCNSTKTPMDPGSKLDADKGGEPVDSTEYRRMIGCLRYLLH
FT                  TRPDLSYSVGLASRFMERPTVMHVKAE"
XX
SQ    Sequence 4364 BP; 1265 A; 801 C; 1293 G; 1005 T; 0 other;

//
ID    Copia-13B_DR-I repbase;     DNA;     VRT; 2419 BP.
XX
AC    .
XX
DT    11-NOV-2013 (Rel. 19.05, Created)
DT    07-MAY-2014 (Rel. 19.05, Last updated, Version 1)
XX
DE    LTR retrotransposon from zebrafish: internal portion, consensus.
XX
KW    Copia; LTR Retrotransposon; Transposable Element; Nonautonomous;
KW    Copia-13B_DR-I.
XX
OS    Danio rerio
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC    Cypriniformes; Cyprinidae; Danio.
XX
RN    [1]
RA    Howe K., Clark M.D., Torroja C.F., Torrance J., Berthelot C.,
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RA    Muffato M., Collins J.E., Humphray S., McLaren K. et al.;
RT    "The zebrafish reference genome sequence and its relationship to
RT    the human genome.";
RL    Nature 496(7446), 498-503 (2013).
XX
RN    [2]
RP    1-2419
RA    Bao W. and Jurka J.;
RT    "LTR retrotransposons from zebrafish.";
RL    Repbase Reports 14(5), 1251-1251 (2014).
XX
DR    [2] (Consensus)
XX
FH    Key             Location/Qualifiers
FT    CDS             17..2314
FT                    /product="Copia-13B_DR-I_1p"
FT                    /translation="MRTQQKDDSFLSHMPQLLRLHALRQHGSELKEFAERF
FT                    RMAAEGLGFNDWALLNLLNFALDKPLYPLQIQRLVGYSYKQFVDHMVNQVA
FT                    HECRQERICSVLPPTDQPEPSSLLPPTEKRKLRRRNRSSSIVTPLLVTEPA
FT                    AAHPATTLAAASPSEAPATDTASVQQAVEYAAVSEEVASFPPPRPRKRRRR
FT                    KGSSTTTAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAP
FT                    ERPPVSAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAPE
FT                    RPPVSAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAPERPPVSAPAPER
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FT                    PFMSSCLFTPLSCVC"
XX
SQ    Sequence 2419 BP; 309 A; 1044 C; 614 G; 451 T; 1 other;


//
ID    Copia-32_BD-I repbase;    DNA;    PLN; 4552 BP.
XX
AC    ADDN01000536;
XX
DT    09-MAR-2010 (Rel. 15.03, Created)
DT    17-MAR-2010 (Rel. 15.03, Last updated, Version -1)
XX
DE    LTR retrotransposon from the purple false brome: internal
DE    portion.
XX
KW    Copia; LTR Retrotransposon; Transposable Element; Copia-32_BD_;
KW    Copia-32_BD-LTR; Copia-32_BD-I.
XX
OS    Brachypodium distachyon
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    BOP clade; Pooideae; Brachypodieae; Brachypodium.
XX
RN    [1]
RP    1-4552
RA    Jurka J. and Kohany O.;
RT    "LTR retrotransposons from the purple false brome.";
RL    Repbase Reports 10(3), 311-311 (2010).
XX
DR    Genome; ADDN01000536; Positions    64882    60331.
XX
CC    Positions [1673-2164] - Integrase core
CC    LTRs are 99% similar to each other.
XX
FH    Key             Location/Qualifiers
FT    CDS             53..3025
FT                    /product="Copia-32_BD-I_2p"
FT                    /translation="MTSPSTAAATAQSQLSGTLGAKTGGSVSIGSMATGPI
FT                    SVPSIAQLVTVKLSRDTHLLWKAQIVPILRGHQLLGYVDGEIETPPKHVPA
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FT                    ALERMFASQSRTRVAQIRRQLAKLQKKDLSMADYFARAKALGDQLAAAGRP
FT                    QSDEEMIVFILTGLDSSYDAFVTSINLQVDDMTLDEFYSHLLDHESFREAS
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FT                      HVGQSYIHTPHKPLLLQDVLHVPHTHKNLLSVHRLTRDNNVFIEFHPYYFL
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FT                      RMGHAGVSSSDHMDDDTAPETGTPSPAPAPDAPDSASATASPSHGAHADPA
FT                      ASDSAAAPVESSTPPAGSRSGPSADSLRSESPVFSPAATAAPDAPPPRCAL
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FT   CDS                2908..4542
FT                      /product="Copia-32_BD-I_1p"
FT                      /translation="MCTRRRDNTWRARIRTDGTIPYGLPRRRANIAISEPH
FT                      DHIEAASDTNWRRAMDEEHQALLDNRTWHLVPRPAHCNLIDSKWVFKLKYR
FT                      SDGSIDRYKARLVAKGFKQRYGVDYEETFSPVIKHTTIRLILSIAVSQDWC
FT                      LRQLDVKNAFLHGVLEEDVFMRQPPGYEDPTLPHFVCKLDKSLYGLKQSPR
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FT                      GMKDCKPASTPMAVAEKLSRDEGVKLPPNDATRYRSLVGALQYLTLTRPDI
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FT                      TAELIWFQSLLGELGVRQERAPVLWCDNLGATYLSANPVFHARTKHIEVDY
FT                      HFVRERVARKALEIRFVSTNDQVADGLTKPVGTQQLRQFCYHLNLVGSD"
XX
SQ   Sequence 4552 BP; 1059 A; 1291 C; 1109 G; 1093 T; 0 other;


//
ID   Copia-36_ALY-I repbase;    DNA;    PLN; 4687 BP.
XX
AC   ADBK01000448;
XX
DT   22-MAR-2011 (Rel. 18.02, Created)
DT   22-MAR-2011 (Rel. 18.02, Last updated, Version -1)
XX
DE   LTR retrotransposon from the Arabidopsis lyrata genome: internal
DE   portion.
XX
KW   Copia; LTR Retrotransposon; Transposable Element; Copia-36_ALY_;
KW   Copia-36_ALY-LTR; Copia-36_ALY-I.
XX
OS   Arabidopsis lyrata subsp. lyrata
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC   Camelineae; Arabidopsis; Arabidopsis lyrata.
XX
RN   [1]
RA   Hu T.T., Pattyn P., Bakker E.G., Cao J., Cheng J.F., Clark R.M.,
RA   Fahlgren N., Fawcett J.A., Grimwood J. et al.;
RT   "The Arabidopsis lyrata genome sequence and the basis of rapid
RT   genome size change.";
RL   Nat Genet 43(5), 476-481 (2011).
XX
RN   [2]
RP   1-4687
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from the Arabidopsis lyrata genome.";
RL   Direct Submission to Repbase Update (22-MAR-2011).
XX
DR   Genome; ADBK01000448; Positions  130542  135228.
XX
CC   Positions [2101-2592] - Integrase core
CC   LTRs are 92% similar to each other.
XX
FH   Key             Location/Qualifiers
FT   CDS             193..4671
FT                      /product="Copia-36_ALY-I_1p"
FT                      /translation="MGKRNCKSKYRRSLGLDSPESGTAVSPRSRGEASVPP
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FT                    YKLRHQLQSLHQGSLDLSSYHTQTQTLWEELSNIQVTPHTVEDLLAEKETN
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FT                    LTSAAFQVSQSQSSGTGAPSYPRKDRPYCTFCGKVGHVIDKCYKKHGYPTS
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FT                    DLPALHAWVIDSGATNHISHDQSSFLSFKPMNNTVNLPNGISVSIVGIGTI
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FT                    QSMQSILSLEKVKINADHHCKICHLSKQKHLPFVSKNKISENPFDLVHIDT
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FT                    YSELKVFGCLCYASTSPKNRHKFDPRARACAFIGYPNGYKGYKLLDIESNT
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FT                    YAARKGNSLPPNAVCKLQKSLYGLKQASRQWFLKFSTTLISLGFTQSYADH
FT                    TCFLKINATLFLCVLVYVDDIIIASNNDSEVDLLKSQLQSFFKLRDLGPLK
FT                    YFLGLEIARSSEGIHICQRKYALDLLDETGLLGCKPSSIPMDPHIKFSKDR
FT                    GGDLVDAESYRRLIGRLMYLQITRPDIAFAVNKLSQFSQAPRKSHQHALYK
FT                    ILHYVKGTIGQGLFYSSKAELQFQMFADADYDSCQDTRRSTSGFCLFLGTS
FT                    LISWKSKKQQVVSKSSAEAEYRSLSSSTDELVWITNFLQELQIPLSKPTML
FT                    FCDNTAAIHIATNAVFHERTKHIEKDCHSIRERLVAGLFQLFHVRTELQLA
FT                    DPFTKPLYPNQFHQLFSKMGLLNIFVPS"
XX
SQ   Sequence 4687 BP; 1202 A; 1026 C; 846 G; 1613 T; 0 other;

//
ID   Copia-51_CCri-I repbase;     DNA;     PLN; 4105 BP.
XX
AC   .
XX
DT   15-MAY-2013 (Rel. 18.10, Created)
DT   15-MAY-2013 (Rel. 18.10, Last updated, Version 1)
XX
DE   LTR retrotransposon from the red seaweed: internal portion.
XX
KW   Copia; LTR Retrotransposon; Transposable Element; Copia-51_CCri-I;
KW   Copia-51_CCri-LTR; Copia-51_CCri_.
XX
OS   Chondrus crispus
OC   Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
OC   Gigartinaceae; Chondrus.
XX
RN   [1]
RA   Collén J., Porcel B., Carré W., Ball S.G., Chaparro C., Tonon T.,
RA   Barbeyron T., Michel G., Noel B., Valentin K. et al.;
RT   "Genome structure and metabolic features in the red seaweed
RT   Chondrus crispus shed light on evolution of the Archaeplastida.";
RL   Proc Natl Acad Sci U S A 110(13), 5247-5252 (2013).
XX
RN   [2]
RP   1-4105
RA   Jurka J.;
RT   "LTR retrotransposons from the red seaweed.";
RL   Repbase Reports 13(10), 2336-2336 (2013).
XX
DR   [2] (Consensus)
XX
CC   Positions [1519-2013] - Integrase core
CC   LTRs are 99% similar to each other.
XX
FH   Key             Location/Qualifiers
FT   CDS             97..4083
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FT                   /translation="MDDELVSRRLHKFNAKRGEDFTLWSLRFEALLESRDL
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FT                        FNALVVSAYKNYEKTPTSLAEALLSKNRSKWIAAVEEEILCLKRNDTWKVV
FT                        QLPLSARAIDSKLVFVLKLKADGSVDRYKVRLVAKGFQEGHVDNVYAPVVD
FT                        FSTVRLVLAIMSQHGAFIHQLDVKSAFLNGKLDEEDNLYLNPPEGLELGVK
FT                        RGQALKMQKAMYGFKRAPKIWSKTWNAVMHRLKFVQLKSEECFYFIDIEGS
FT                        TVYVLVYVDDVLVVGITEGAVLTVKQMLMNEFRMTDLGVAKSFLGVEFVYT
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FT                        SKKQGGVALSSTEAEFISISECVKATKWLRMILKELSLLSDFPTVLYEDNT
FT                        GAIKWASGEKMAKHVHIRFHFVREAIMDGSINMCYCPTSXMIADALTKGLS
FT                        APRTLYLRQKLQIQECE"
XX
SQ      Sequence 4105 BP; 1214 A; 836 C; 1044 G; 1007 T; 4 other;


//
ID      Copia-53_MN-I repbase;      DNA;     PLN; 4543 BP.
XX
AC      ATGF01012833;
XX
DT      13-OCT-2013 (Rel. 20.12, Created)
DT      13-OCT-2013 (Rel. 20.12, Last updated, Version 1)
XX
DE      LTR retrotransposon from the mulberry tree: internal portion.
XX
KW      Copia; LTR Retrotransposon; Transposable Element; Copia-53_MN-I;
KW      Copia-53_MN-LTR; Copia-53_MN_.
XX
OS      Morus notabilis
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC      Pentapetalae; rosids; fabids; Rosales; Moraceae; Morus.
XX
RN      [1]
RP      1-4543
RA      Jurka J.;
RT      "LTR retrotransposons from the mulberry tree.";
RL      Direct Submission to Repbase Update (11-OCT-2013).
XX
DR      Genome; ATGF01012833; Positions   12127     7585.
XX
CC      Positions [1922-2314] - Integrase core
CC      LTRs are 98% similar to each other.
XX
FH      Key            Location/Qualifiers
FT      CDS            2396..4033
FT                     /product="Copia-53_MN-I_1p"
FT                     /translation="MLNNNKPSYTHLRTFGCLCYGSTLRAHRSKFSSRARS
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FT                     HDRVLPAFIPSQFIPSILPSPPSTPSSGSPSSPASSSCPHRVIKPPTYLSD
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FT                     IAGNNQVAVETIKSVIGKQFKIKDLESLKYFLGLEVARTAAGISVCQRKYA
FT                     LELLSEAGYLGCKPVSVPMEPNLKLSSEDGELLSAPTTYRRLIGKLIYLTI
FT                     TRPDLSYSVNRLSQYLAAPRVPHLQAAQRLLQYIKKAPGQGIFFSSESKL"
XX
SQ      Sequence 4543 BP; 1102 A; 1183 C; 795 G; 1463 T; 0 other;
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ID    Copia-80_Mad-I repbase;      DNA;      PLN; 4386 BP.
XX
AC    .
XX
DT    25-SEP-2010 (Rel. 15.10, Created)
DT    25-SEP-2010 (Rel. 15.11, Last updated, Version 0)
XX
DE    LTR retrotransposon from the apple genome: internal portion.
XX
KW    Copia; LTR Retrotransposon; Transposable Element; Copia-80_Mad_;
KW    Copia-80_Mad-LTR; Copia-80_Mad-I.
XX
NM    Copia-80_Mad-I.
XX
OS    Malus domestica
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC    Pentapetalae; rosids; fabids; Rosales; Rosaceae; Maloideae;
OC    Maleae; Malus.
XX
RN    [1]
RP    1-4386
RA    Jurka J.;
RT    "LTR retrotransposons from the apple genome.";
RL    Repbase Reports 10(10), 1698-1698 (2010).
XX
RN    [2]
RA    Velasco R., Zharkikh A., Affourtit J., Dhingra A., Cestaro A.,
RA    Kalyanaraman A., Fontana P., Bhatnagar S.K. et al.;
RT    "The genome of the domesticated apple (Malus x domestica
RT    Borkh).";
RL    Nat Genet 42(10), 833-839 (2010).
XX
DR    [1] (Consensus)
XX
CC    Positions [1779-2273] - Integrase core
CC    LTRs are 97% similar to each other.
XX
FH    Key           Location/Qualifiers
FT    CDS           216..2930
FT                  /product="Copia-80_Mad-I_2p"
FT                  /translation="MVPIKLTSTNYLTWSALFAPILRRYNLTGIIDGTMSA
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FT                  YYLIFVDDYTKYTWFFPLKSKSDVFDTFVQFKVLVETLLSTKIVILRSDSG
FT                  GEFLSLKFIKFLQEHGISHQLSCPHTPEQNGCAERKHRHLVETARTLLAAS
FT                  KVPHSYWVEAFATAIYLINRMPTTTNFSPWELLFHRSPDYTSLKIFGCRCF
FT                  PWLKPYTTSKLDPKSKECVFLGYSLNHKGYKCLDPSTGRVYLSRHVIFDED
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FT                  NKGKT"
XX
SQ   Sequence 4386 BP; 1046 A; 1129 C; 788 G; 1422 T; 1 other;

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ID   Copia-9_HAE-I repbase;     DNA;     PLN; 4191 BP.
XX
AC   .
XX
DT   21-MAR-2012 (Rel. 24.05, Created)
DT   21-MAR-2012 (Rel. 24.05, Last updated, Version -1)
XX
DE   LTR retrotransposon from the Hyaloperonospora arabidopsidis
DE   genome: internal portion.
XX
KW   Copia; LTR Retrotransposon; Transposable Element; Copia-9_HAE-I.
XX
OS   Hyaloperonospora arabidopsidis
OC   Eukaryota; Stramenopiles; Oomycetes; Peronosporales;
OC   Peronosporaceae; Hyaloperonospora.
XX
RN   [1]
RP   1-4191
RA   Jurka J. and Kojima K.K.;
RT   "LTR retrotransposons from the Hyaloperonospora arabidopsidis
RT   genome.";
RL   Repbase Reports 19(5), 793-793 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~96% identical to consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             5..4177
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FT                   /note="gag, integrase, reverse transcriptase and
FT                   ribonuclease H."
FT                   /translation="MSPTTPDAGDILREDNYFVWEFNARMRLAKKGLLEHL
FT                   DAMKAPEEGDASASTWKVNDMKAFAIVSTMISTNLQSMVRTAKTTAEAWDI
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FT                   HVLDGRMTTMTLPSRCDSEMHGHVGSTVEDPMFEIDDVTMIEEDQDSVEEV
FT                   SRSGQMAIGPSRRTSVQTSQETAMVPLGSVTNGQSQALVQVGGAGENFSDG
FT                   AEVCQERGTKRLRIGYEQACAAFETPATYEEALKSPHRDDWYKAIQAELKA
FT                   LHDKNTWTVKTQRPRQKVIGTKWVFALKRNELGEIERYKARLVALGYRQTY
FT                   GVDYMETYSPVANLNSIRVFLAVCCHKGMLIHQYDVDTAFLYGVLEEEVYV
FT                   YPPLGVRAGRDKVLKLNRSLYGLKQAAATWYKTISCVFVEMGFTSCAADSC
FT                   IFVKETKGSWIYAALYVDDLLIGAENTGAMDDVAAQLSSRFQMKILGGVRY
FT                   VLGIEVKYLRDSRRLKISQGSCISRMVKKFNQVDAKAVLNPSVEGQAMIKM
FT                   NEIDTRMKNRPYRSLVGSLLYVATGTRPDIAYAVCQLSRHLEFPHEEHWNA
FT                   AIRVLRYLKTTKSKGICYEGVSGNLQLSAYTDADWASDKCNRRSISGVLVM
FT                   INGAPVLFKSKMQQSVALSTAEAEYMALSLCVQEVLWTRSLLKEMQVQINY
FT                   AVTIHEDNQSAIAIAKNDGYQSRAKHIDIRYHFVREQVKDKIIDLQYTETK
FT                   SQLADFLTKPISTKKFESLLDKAKIRDF"
XX
SQ   Sequence 4191 BP; 1272 A; 847 C; 1162 G; 909 T; 1 other;

//
ID   Coprina_Cc1 repbase;     DNA;     PLN; 3033 BP.
XX
AC   .
XX
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DT   29-APR-2007 (Rel. 12.04, Created)
DT   17-MAY-2007 (Rel. 12.04, Last updated, Version 1)
XX
DE   Coprina_Cc1 is a Penelope-like retroelement.
XX
KW   Penelope; Non-LTR Retrotransposon; Transposable Element;
KW   Penelope-like element; reverse transcriptase; Coprina_Cc1.
XX
OS   Coprinopsis cinerea
OC   Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
OC   Agaricomycetes; Agaricomycetidae; Agaricales; Psathyrellaceae;
OC   Coprinopsis.
XX
RN   [1]
RP   1-3033
RA   Arkhipova I.R.;
RT   "Distribution and phylogeny of Penelope-like elements in
RT   eukaryotes.";
RL   Syst. Biol 55(6), 875-885 (2006).
XX
RN   [2]
RP   1-3033
RA   Gladyshev E.A. and Arkhipova I.R.;
RT   "Telomere-associated endonuclease-deficient Penelope-like
RT   retroelements in diverse eukaryotes.";
RL   Proc Natl Acad Sci U S A 104(22), 9352-9357 (2007)in press.
XX
DR   [2] (Consensus)
XX
CC   Coprina_Cc1 is a Penelope-like retroelement from the inky cap
CC   mushroom, Coprinus cinereus (aka Coprinopsis cinerea). Its single
CC   ORF contains homology to reverse transcriptases. No associated
CC   endonuclease has been found. Most copies are associated with
CC   telomeres and are 5' truncated by addition of reverse-complement
CC   C. cinereus telomeric repeats, (TAACCC)n.
XX
FH   Key             Location/Qualifiers
FT   CDS             127..2549
FT                   /product="Coprina_Cc1_1p"
FT                   /translation="TTPSLTAAPWQVEQTSEPPRKRRKTTEDVQRRPEQAE
FT                   EGRQGKGKGQLAVGVLPSDFRYDNPSSYPDWLLTVPYPVAISTILLNTPAR
FT                   ILEAAQFRNYVHLSPGVNVPLEYQYALSVGLRYMFPTPRNELLIRDAWKDF
FT                   ERRIRWRLFFTFSNEDNSLFDPDYEVPKQKSSAPPRLPAYLEHGLQRGELF
FT                   VNQTIAKIRRLPVEAPTYKSLKPNRDDLFEFLTSNNYVITGTDKNLGIAVS
FT                   ERTWIDERCKEILDVRSDYREIHIIQLNQICNEQCRQMELIAQLATATHPN
FT                   GKQLGEFFRSKITEKCSDTSGREYGDHTVPIFYGIPKIHKVPTKMRPIIPC
FT                   HSAIQNPAAKFVSKNLKFLIKESPTILHGSKDLAQKLSNVKLKPGRRWFFI
FT                   SGDVVAYYPNIPREDCLREVFKMWSDARFGRTLDDNDEGTAEHYEFSLMYN
FT                   ALMTGNKKLVFRYGSKYYEQIRGLAMGVADSPDLANLWGVRSEISCGVLTN
FT                   PLIEFYGRYIDDCLGVVYAHSEEEALSIAESIKIEGCTIEWTASEQYVHFL
FT                   DMTVYRDSYSQLQWQPFRKAGNHQERIPWISAHPLDVKRGTFLGEMSRLAT
FT                   LSSQYDTYREALHGLAALYTKRGYPSELVSKWLKDNASDKWEKRLSDRNHD
FT                   STGTDGVLVLKSTFNTAWNYFSARELGDTILGYWKTYAEKAKKDQLGGIHW
FT                   QQFSDNVGDFTDVPDELMSLFRTTKGLRYMPDVSKTNIWQRKVLVSRKRTR
FT                   NLFDLTSLWKKQVLSKLEEDILMDVDSDSDQMSVDTPSDRSDGIDPNFFIN
FT                   YTLGRT"
XX
SQ   Sequence 3033 BP; 816 A; 812 C; 679 G; 726 T; 0 other;

//
ID   DIRS-6_CPB  repbase;    DNA;    VRT; 6065 BP.
XX
AC   .
XX
DT   12-NOV-2012 (Rel. 18.07, Created)
DT   12-NOV-2012 (Rel. 18.07, Last updated, Version 1)
XX
DE   DIRS retrotransposon: consensus.
XX
KW   DIRS; LTR Retrotransposon; Transposable Element; DIRS-6_CPB.
XX
OS   Chrysemys picta bellii
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

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OC    Archelosauria; Testudines; Cryptodira; Durocryptodira;
OC    Testudinoidea; Emydidae; Chrysemys; Chrysemys picta.
XX
RN    [1]
RA    Shaffer H.B., Minx P., Warren D.E., Shedlock A.M., Thomson R.C.,
RA    Valenzuela N., Abramyan J., Amemiya C.T. et al.;
RT    "The western painted turtle genome, a model for the evolution of
RT    extreme physiological adaptations in a slowly evolving lineage.";
RL    Genome Biol 14(3), - (2013).
XX
RN    [2]
RP    1-5035
RA    Kojima K.K. and Jurka J.;
RT    "DIRS retrotransposons from the western painted turtle.";
RL    Repbase Reports 13(7), 1882-1882 (2013).
XX
DR    [2] (Consensus)
XX
CC    ~83% identical to consensus.
XX
SQ    Sequence 6065 BP; 1235 A; 1970 C; 1674 G; 1181 T; 5 other;

//
ID    ERI1         repbase;    DNA;    MAM; 289 BP.
XX
AC    .
XX
DT    06-SEP-2005 (Rel. 10.08, Created)
DT    30-MAR-2010 (Rel. 15.04, Last updated, Version 2)
XX
DE    SINE1 SINE from Erinaceus.
XX
KW    SINE2/tRNA; SINE; Non-LTR Retrotransposon; Transposable Element;
KW    Nonautonomous; SINE1; ERI1.
XX
NM    ERI1.
XX
OS    Erinaceus
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Laurasiatheria; Insectivora; Erinaceidae;
OC    Erinaceinae.
XX
RN    [1]
RP    1-289
RA    Smit A.F.;
RT    "ERI1 - SINE1 SINE from Erinaceus.";
RL    Direct Submission to Repbase Update (06-SEP-2005).
XX
DR    [1] (Consensus)
XX
CC    (bp 1-109 matches B2, bp 146-289matches L1 ORF2 fragment)
CC    Hedgehog  Insectivora; Erinaceidae; Erinaceinae;.
XX
SQ    Sequence 289 BP; 99 A; 61 C; 57 G; 72 T; 0 other;

//
ID    ERV1-1_GG-I repbase;    DNA;    VRT; 7104 BP.
XX
AC    .
XX
DT    06-FEB-2018 (Rel. 23.02, Created)
DT    06-FEB-2018 (Rel. 23.02, Last updated, Version 1)
XX
DE    LTR-Retrotransposons from chicken: Internal region, a consensus
DE    sequence.
XX
KW    ERV1; Endogenous Retrovirus; Transposable Element;
KW    LTR-retrotransposon; internal portion; ERV; ERV1-1_GG-I.
XX
OS    Gallus gallus
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
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 OC     Phasianidae; Phasianinae; Gallus.
 XX
 RN     [1]
 RP     1-7104
 RA     Bao W.;
 RT     "LTR retrotransposons from the chicken genome.";
 RL     Repbase Reports 18(2), 185-185 (2018).
 XX
 DR     [1] (Consensus)
 XX
 CC     Severall copies in the genome. the LTRs of the youngest one are
 CC     96% identical to each other.
 XX
 FH     Key            Location/Qualifiers
 FT     CDS            911..2095
 FT                    /product="ERV1-1_GG-I_1p"
 FT                    /translation="MKLYMQTCFSLSKIIPSGEDCGMGAPHDPFVLTLEKE
 FT                    RREKGENKVKRCCSSCSIGQQCIKIGNIRESEELLEHYQPPVETPPPQDGA
 FT                    QEGAQAPPGAQDGEQVPPGAQAPSEVQAPSGAQAPPDSPIASRTRSQQPLI
 FT                    IAPLREAVGPNGEPVLIKVPFSLFDLETWKSVAKGYQNDPLGVTRHFQFLI
 FT                    RQHKPDWSDIQLLLDQLTETEKQLILNTAQTLVEDSIQGRGKDVKDHFPLQ
 FT                    NPYWDPNTRAGRERLEMYREWVVKGMERAIPKTINWSNLFAVRQGPKESPS
 FT                    EFLDKLRDAMRKHTSLDPGSEESIQQLVSLFIGQSAGDIRRKLQKLKASAA
 FT                    RNLESLLEEALRVFSNREEVERRREKRMLIAVLQEAKRGEQNKVRKPLEKD
 FT                    Q"
 FT     CDS            join(2207..5323,5327..5734)
 FT                    /product="ERV1-1_GG-I_2p"
 FT                    /translation="REAGKSTLADSLVKLKLGSKQQSVEFLVDTGAIYSVL
 FT                    NEDLTPTSKEFVTIKGATAQPKRAYFLKPLEFKLGKQVGIHQFLYLPDSPH
 FT                    HLLGQDLLEQLRAEIRFESGKMKFKVKDDSFVKVLSLALITALEDSGIPKE
 FT                    IINQVYPGVWATEVPGRANNTSPIVIKVKQEAQTPQIKQYPLRAEDREGIQ
 FT                    PIIDQFIKYGLLVECESKYNTPILPVKKPDGSYRIVQDLRAINKIVEDLYP
 FT                    LVANPYTLLTRLSNELAWFTVLDLKDALFCLPLSPESQLLFAFEWENPKSG
 FT                    RRTQLTWTVLPQGFKNSPAIFGNQLAKDLEQWERPSGKGVLLQYVDDLLIA
 FT                    TETEELCIAWTISLLNFLGLNGHRVSPQKAQVAKQQVVYLGYGITAGLRTL
 FT                    GTVRKEAICQTPEPQTAKELRTFLGMTGWCRLWIHNYGLLVKPLFALLKTN
 FT                    PSVLTWDGETRRAFKLLKHELMQAPALGLPDTTKPFWLYSYEKQGIALGVL
 FT                    AQDLGPYRRAVAYFSKQLDEVSRGWPGYLRAVAALVLNVQEARKFTLGQKI
 FT                    TVLTSHTVSTVLEAKGGHWLSPQRFLKYQAILVEQDDVKIVVTNIINPASF
 FT                    LSGASGKSVTHDCLETIEAVCASWPDLKEELLEDAENSWYTDGSSYVRQGV
 FT                    RRMGYAITTDNEVMESGALTPNISAQKAEIIALIRTLEQAEGKRINIWTNS
 FT                    KYAFSMVHAHGVIWKERGLLSSQGKGIKNAKEILRLLEAVQLPEKVAIMHC
 FT                    KAHQKGKTPNEMGNAFADREAKRAAEEDPVKVQSLVPDGKIQIDNEPRYSK
 FT                    EDNNLIKDIGGQVGEGGWVTTPQGKIVVPTALLWAVVMAEHRKTHWGAEAL
 FT                    YKHLVQQIVARNLYTTIKQVTQQCEICLRNNPKSGYKISLGQIGRGNYPGQ
 FT                    QWQIDFSELPRKGGYRYTLVLTDTFSGWPEVFPCRTNKAREVTKVLLHEII
 FT                    PRFGVPATMSSDRGPHFIAKVVQQISTLLGIDWQLHTPYQLQSSGQVEKMN
 FT                    HLIKLQIVKLGQETGIPWPQAPPLALLRIRTKPTKEGLSPYEILYGRPYRV
 FT                    QKGISMQEGDEVLNEYMISLAKQLKKIEKAVFGARARGLDGPVHDALPGDY
 FT                    VYVKSLSDSPLEAKWEGPYQILLTTHTTTKVEGLAPWIHHTRLKKAPGPQW
 FT                    TAEERGPLKIRIRKHV"
 XX
 SQ     Sequence 7104 BP; 2261 A; 1386 C; 1841 G; 1616 T; 0 other;

 //
 ID     ERV1-2_ACC-LTR repbase;      DNA;     VRT; 575 BP.
 XX
 AC     .
 XX
 DT     17-OCT-2018 (Rel. 24.12, Created)
 DT     17-OCT-2018 (Rel. 24.12, Last updated, Version 2)
 XX
 DE     Endogenous retrovirus from the golden eagle genome, long terminal
 DE     repeat consensus.
 XX
 KW     ERV1; Endogenous Retrovirus; Transposable Element;
 KW     ERV1-2_ACC-LTR.
 XX
 OS     Aquila chrysaetos canadensis
 OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC     Coelurosauria; Aves; Neognathae; Falconiformes; Accipitridae;
 OC     Accipitrinae; Aquila; Aquila chrysaetos.
```

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   XX
   RN   [1]
   RP   1-575
   RA   Kojima K.K.;
   RT   "Endogenous retroviruses from the golden eagle genome.";
   RL   Repbase Reports 19(12), 2538-2538 (2019).
   XX
   DR   [1] (Consensus)
   XX
   CC   ~98% identical to consensus. 4-bp TSDs.
   XX
   SQ   Sequence 575 BP; 174 A; 120 C; 154 G; 126 T; 1 other;

   //
   ID   ERV1-2_ACD-LTR repbase;     DNA;     VRT; 657 BP.
   XX
   AC   .
   XX
   DT   06-NOV-2018 (Rel. 24.12, Created)
   DT   06-NOV-2018 (Rel. 24.12, Last updated, Version 2)
   XX
   DE   Endogenous retrovirus from the swan goose genome, long terminal
   DE   repeat consensus.
   XX
   KW   ERV1; Endogenous Retrovirus; Transposable Element;
   KW   ERV1-2_ACD-LTR.
   XX
   OS   Anser cygnoides domesticus
   OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
   OC   Coelurosauria; Aves; Neognathae; Galloanserae; Anseriformes;
   OC   Anatidae; Anser; Anser cygnoides.
   XX
   RN   [1]
   RP   1-657
   RA   Kojima K.K.;
   RT   "Endogenous retroviruses from the swan goose genome.";
   RL   Repbase Reports 19(12), 2554-2554 (2019).
   XX
   DR   [1] (Consensus)
   XX
   CC   ~97% identical to consensus. 4-bp TSDs.
   XX
   SQ   Sequence 657 BP; 199 A; 131 C; 163 G; 164 T; 0 other;

   //
   ID   ERV1-5_PMaj-LTR repbase;    DNA;     VRT; 767 BP.
   XX
   AC   .
   XX
   DT   17-OCT-2018 (Rel. 24.09, Created)
   DT   17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
   XX
   DE   Endogenous retrovirus from the great tit genome, long terminal
   DE   repeat consensus.
   XX
   KW   ERV1; Endogenous Retrovirus; Transposable Element;
   KW   ERV1-5_PMaj-LTR.
   XX
   OS   Parus major
   OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
   OC   Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
   XX
   RN   [1]
   RP   1-767
   RA   Kojima K.K.;
   RT   "Endogenous retroviruses from the great tit genome.";
   RL   Repbase Reports 19(9), 1778-1778 (2019).
   XX
   DR   [1] (Consensus)
   XX
   CC   ~88% identical to consensus. 4-bp TSDs. The consensus is ~97%
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 CC     identical to that of TguLTR12 from zebrafinch.
 XX
 SQ     Sequence 767 BP; 267 A; 131 C; 169 G; 199 T; 1 other;

 //
 ID     ERV1-6_MM-I repbase;    DNA;     ROD; 7499 BP.
 XX
 AC     .
 XX
 DT     15-OCT-2018 (Rel. 24.05, Created)
 DT     15-OCT-2018 (Rel. 24.05, Last updated, Version 1)
 XX
 DE     Internal portion of an ERV1-type endogenous retrovirus -
 DE     consensus.
 XX
 KW     ERV1; Endogenous Retrovirus; Transposable Element; ERV1-6_MM-I;
 KW     RLTR41B.
 XX
 OS     Mus musculus
 OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC     Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
 OC     Muroidea; Muridae; Murinae; Mus; Mus.
 XX
 RN     [1]
 RP     1-7499
 RA     Bao W.;
 RT     "Endogenous retrovirus from mouse.";
 RL     Repbase Reports 19(5), 775-775 (2019).
 XX
 DR     [1] (Consensus)
 XX
 CC     Consensus. Elements are ~90% identical to the consensus. LTR
 CC     region is RLTR41B-like.
 XX
 FH     Key             Location/Qualifiers
 FT     CDS             join(5589..6194,6198..6989)
 FT                     /product="ERV1-6_MM-I_3p"
 FT                     /translation="MRVLPLVLCLNILPLCFTSPGPHQPCNLTWQVINGVG
 FT                     DTIWSLSKVTTPSTWWPDLFPDIFKLAIGAPPGWDLGGYSDTQKAPSTSPL
 FT                     YVDKHQRDPWGGCSTRFDRSMLRTHPFYVCPGFHQRQSLNPKCGGRADFFC
 FT                     KSWSCETSGEAYWNPTSSWDYIKVKANYTLEPYVPGGKDVAECADWCHLLC
 FT                     ITFTEPGKQALETKGYTWGLRLYKERYDEGLLFTIKLIIETPYTPLGPNKV
 FT                     LAPVKINPRPSPSPHSHGTETPLKRVTETAPLNPPEQSHLTHLVQEAFRVI
 FT                     NSTNPEATKSCWLCYDVAPPYYEGMTFIKAVNHSDEATTCRWKQQSARLTL
 FT                     PAITGQGLCVGTVPHTHNSHNHLCNQTMSNIQSSYLHQTGGVHAPQGSPPV
 FT                     LTSKCSIIPKIFVCWYSWYQLLYYPYDDLLSHWDGGSTRTKRDLGITLSVL
 FT                     LGVGMGVVGIAMGSSALALHS"
 FT     CDS             join(439..1143,1026..1601)
 FT                     /product="ERV1-6_MM-I_1p"
 FT                     /translation="MGHGPSTPLSFTLEHWREVKTRAHNLSVDVKKNKWIT
 FT                     FCSSEWPTFQIGWPPEGSFSLPLILAVKRRIFGAGSKSHXDQVPYIIVWED
 FT                     LVTDPPPWVRPFVSFSGPMAVPILALQDRPKKEVLPTTDTDLLLDPPPPYP
 FT                     PSLLPQAAQAAGPLAPPVPPGEWGTRVLSLPGSEGPAQGTQPTGRQLLRGP
 FT                     IFCPSEPTVPLMNRVISPYNIGHFPRLIYIIGRLITPHFLRILRVAYGPPD
 FT                     EQGHQPLQYWPFSSADLYNWKTHNPSFSENPQGLTNLIESLLFSHQPTWDD
 FT                     CQQLLQVLFTTEEKQRILLEARKNVPGEDGHPSLLPVDIDAGFPLTRPNWD
 FT                     FNTPEGREHLKVYRQALMAGLRGAAHHPTNLTKVREVVQGPNESPSAFLER
 FT                     LMEAFRQFTPMILAVRSIRQQLLSPLSANLAEI"
 FT     CDS             join(1478..2185,2189..2533,2373..3395,3328..4374,
 FT                     4367..4918,4860..5324)
 FT                     /product="ERV1-6_MM-I_2p"
 FT                     /translation="VSLCLPRETHGGLSPIYPHDPSSEEHKATVTVTFISQ
 FT                     SSRDIRKKLQKLEGLQDRSLRELVQVAEKVYHNRESGEEKEERKQKEQEAR
 FT                     ELEREKRQXKNLHRILAAVVRXTREPSKTVPGNRREPLAKDQXAYCKEKGH
 FT                     WMRDCPKKKKKRGPHAPEKRPPGPKVLAMQEDSDWGRRDSDPLPEPRVTLK
 FT                     VEGKPTQFLVDTGAQHSVLLQTDGPISNKKSWVQGATGNKQYSWTTRTVDL
 FT                     GVGRVSHSFIVIPECPYPLLGRDLLTKIGAQIHFLPEGPQVKGQQGEPIQV
 FT                     LTMKLEDEYQLFEDRSQKVKDXDWWLQNYPQAWAETAGMGKAKNXPHPHPR
 FT                     PCRPESPIKMNINCLKTGVKKLKIWIGGCRTTHRHGQRLQGWGKPKITPTP
 FT                     TPVHVDLKAQSSPITVRQYPMSKEARDGIRPHILHLLQLGILWKCQSAWNT
 FT                     PLLPVQKPGTNDYRPVQDLREVNKQVTNLHPTVPNPYNLLSSLPPSRTWYT
 FT                     VLDLKDAFFCLSLATKSQEYFAFEWKDPDLGMTGQLTWTRLPQGFKNSPTI
 FT                     FDEALHQDLATFWAANPQVTLLQYVDDLLLAASSKDLCLQGTECLLTELGE
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FT                   LGYRTSAKKAQVCSQQVSYLGYLLKGGKRWLSEARKETVFHIPPPTNQKQV
FT                   REFLGTAGFCCLWIPGFAEIAAPLYPLTKNKQPFAWGEKEQRFQLHYTHSL
FT                   RTNSLLPGEKKSNGFDAIKTALMSAPALGLPDVTKPFHLFVAENKGIAKGV
FT                   LTQKLGPWKRPVVYLSKKLDPVAARWPACLRIVAVVAVLVKDADKLTMGQD
FT                   LVVSAPHALESVVCQPPDRWLTNARMTYYQTLLLNSDRITFAPPMGLNPAT
FT                   LLPDPDLEPPIHDCQQVLAEAHGWRKDLSDQPLADAEATWFTDGSSFLEGG
FT                   KWRVGAAMVDGQQIVWAQALPEGTSAQKAELIALTKALELGEGKKINIYMD
FT                   SRYAFATAHVHGAIYQQRGLLTSGGKEIKHKTEILALLKALHKPAKVSIIH
FT                   CPGHQKGDSPVARGNNLADQEARAVASRVAPVMVVWWSETQDHRDPSSGTL
FT                   LKIWQSSQKIPTTALIRERELWYVPSGKKILPQEQARTMIRQMHQWTHLGV
FT                   SKLTQTALRSKYYIPGLKHLVEQIVHSCVPCQKVNACRSKADPSKRPRGDK
FT                   PGAYWEVDFTEIKPGKYGYKYLLVFIDTFSGWVEAFPTKQETATVVVKKIL
FT                   EDIPPPIWSTXGNRILRRYWKTSPPPFGVPKVIGSDNGPAFIAKVSQGVAR
FT                   YLEVDWKLHCIYRPQSSGQVERMNRTLKETLTKLTMETGADWVVLLPLALF
FT                   RVRNTPSHFSLTPFEILYGTPVPLTLLGDIIEPTCHSNNDLYARLKGLQVV
FT                   RKKSMVPVGSCLRTWHA"
XX
SQ     Sequence 7499 BP; 1988 A; 1942 C; 1845 G; 1708 T; 16 other;

//
ID     ERV1-7_Crp-I repbase;     DNA;     VRT; 7161 BP.
XX
AC     .
XX
DT     22-OCT-2012 (Rel. 18.04, Created)
DT     10-SEP-2013 (Rel. 18.09, Last updated, Version 2)
XX
DE     LTR retrotransposon from the saltwater crocodile: internal
DE     portion.
XX
KW     ERV1; Endogenous Retrovirus; Transposable Element; ERV1-7_Crp-I.
XX
NM     ERV1-7_Crp-I.
XX
OS     Crocodylus porosus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Crocodylia; Longirostres;
OC     Crocodylidae; Crocodylus.
XX
RN     [1]
RP     1-7161
RG     International Crocodilian Genomes Working Group;
RT     "LTR retrotransposons from the saltwater crocodile.";
RL     Direct Submission to Repbase Update (22-OCT-2012).
XX
DR     [1] (Consensus)
XX
CC     ~92% identical to consensus.
XX
FH     Key            Location/Qualifiers
FT     CDS            5545..7131
FT                    /product="ERV1-7_Crp-I_2p"
FT                    /note="env."
FT                    /translation="MAKQLLCLLFLSFLPTTPSPFPEGVLTSSYQLANRTA
FT                    HSLNLSACWLCVSQRSWGTAIPAPPSLWGSLQASNSQWTRTHPKSDRGQSL
FT                    RGGEQALKSAWKFRDQPFTAKSPASGSIFGYITNHAENLYPICLQSNYTSH
FT                    QGSVYLGSIRPWQCNVTFSIQPPKFTTGGFNYSVFSPSQLENSSRPRQYSN
FT                    YSWGRPTNSHPALTKGGPNAILLYQSLQPQGQVLFDSSRGSIFFAPTNDTS
FT                    YKDPSLDPLLSATMAAQTLQAFVAKETRNGREVDLNPQRLYASAVFSSVLS
FT                    PASGVYWICGNRAYWVLPPGWQGTCSLGFVLPQIEVAPSGTPLPFQLQAVG
FT                    RLAKRVAPLLPLMAVVAVVAGATRMATGGTALGLQQELSQETAKALEKTGE
FT                    TLTLLQQQLDSLAGVVLQNRRALDLLTSGQGGTCLFLQEECCFYVNQSGQV
FT                    QENINEILQHASNIKSVGWGGWSGGPIQWLLSLLLPLIPVLVISLVILMCA
FT                    PHIIQALNRFISARMKTATQLQLVMFHKRQMRN"
FT     CDS            join(1992..3983,3987..5537)
FT                    /product="ERV1-7_Crp-I_1p"
FT                    /note="reverse transcriptase, ribonuclease H and
FT                    integrase."
FT                    /translation="TPGPRFQCSPRKPPPGGGSGKYVTVEGIEGKQSKLPM
FT                    CRPLLTKVGDNLLEHAFVYSPACPVALLGRDLLTKLQAEIFFRGDQMAVQL
FT                    PVKQGSNYQMALLGGESSAVGIEGLENVXPQVWADGTPARAKXVMPVRVRL
FT                    KEGEGPIRVKQYALNRQTRXGLKPLIEKFKGYGWLVEGSSPFNTPILGVPK
FT                    ADGTSYRLVQDLRAVNQKVLADHPVVPNPHTVLTQVPPNAKIXSVLGLRDA
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FT                    FFSIPLHEDSQRLFAFEWEDPDTRHKSQLMWTVLPQGFVSAPHIFGISLQK
FT                    DLEDWKQVHPDFTLIQYVDDLLIASPSLTKGKEATESLLNTLGERGYKVSR
FT                    EKAQICQSKVTFLGYEISKGARALSHDRILAIQNMPAPASPRELRAFLGLT
FT                    GFCRLWIPDYGGKAKALYDSLTKEGLADWKWTKGKQRSFELLKAALVQPPA
FT                    LMIPDGCKPYRLYVHENKGVASGVLTQPVGPTWKPVGYYSKVLDPVARGWP
FT                    ACLRAVAATATIVEEAQKIVMGTDMEVHTPHGVPQILGGEGGKFLNPXRQS
FT                    RYEIFLLSNPGLTFRHTTALNPATLLPEPGRPNHDCLEVLTQAILIRPDLT
FT                    DDPMENPDEELFVDRSSTMVDGKRHTGCAVVTLEAVVWKETLPSHWSAQAA
FT                    ELVALTWALELGEGKVNIYTDSRYAFTTVHAHGVLWKERGFVTASGQKIAN
FT                    GVQITRLLKALKLPREVAVVHVRAHGKASNEQQRRGNAKADVAXREAALMG
FT                    GEAHTQALSHLTTPLFEDRTPHYSVEEERMAKDGLATKNSEGWWIVPGGKV
FT                    IIXRPLLRELLMQLHSMTHMGGLAMGDLLIRQIVSPRLYLESQRVASQCLT
FT                    CQKVNPKPVGPPTPMGGRQWAHYPGQAWQIDFAELPKSGRHRYLLVMVDQL
FT                    TGWIEAFPTRTATASVVARTLLNEIVPRYSLPESIESDQGGHFVGKVTQEV
FT                    AKALGIRWKLHTPWRPQSSGQVERMNRTLKAMLTKICIETRLKWPQALPLA
FT                    LTRIRNTPRRGIKLSPYEIMFGMPPRVLPPGAREAVTFELGIAELRAYVIA
FT                    LQSVLTSLHRYTASFQRLPLDAPVHNFQPGDQVLVQQWRREPLSEKWEGPY
FT                    QVLLTTHSAVKLENHDRWIHHTRIKRYSGREADSSSLGEPAPEAGPPSEQE
FT                    ADTWTSEQAGDLTLRLKRSSKT"
XX
SQ     Sequence 7161 BP; 1893 A; 1817 C; 1911 G; 1510 T; 30 other;

//
ID     ERV1-7_MM-I repbase;      DNA;      ROD; 7785 BP.
XX
AC     .
XX
DT     15-OCT-2018 (Rel. 24.05, Created)
DT     15-OCT-2018 (Rel. 24.05, Last updated, Version 1)
XX
DE     Internal portion of an ERV1-type endogenous retrovirus -
DE     consensus.
XX
KW     ERV1; Endogenous Retrovirus; Transposable Element; ERV1-7_MM-I.
XX
OS     Mus musculus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
OC     Muroidea; Muridae; Murinae; Mus; Mus.
XX
RN     [1]
RP     1-7785
RA     Bao W.;
RT     "Endogenous retrovirus from mouse.";
RL     Repbase Reports 19(5), 776-776 (2019).
XX
DR     [1] (Consensus)
XX
CC     Consensus. Elements are ~86% identical to the consensus.
XX
SQ     Sequence 7785 BP; 2161 A; 1962 C; 1923 G; 1722 T; 17 other;

//
ID     ERV17_MD_I  repbase;      DNA;      MAM; 6935 BP.
XX
AC     .
XX
DT     17-NOV-2005 (Rel. 10.11, Created)
DT     17-NOV-2005 (Rel. 10.11, Last updated, Version 1)
XX
DE     ERV17_MD, a class 2 (HERVK) type endogenous retrovirus from
DE     Monodelphis domestica - consensus of LTR sequence.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element; Nonautonomous;
KW     ERV17_MD_I; ERV17_MD_LTR; Interspersed repeat.
XX
OS     Monodelphis domestica
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
XX
RN     [1]
RP     1-6935
RG     The Broad Institute of MIT and Harvard, Cambridge, MA, USA.
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 RG    Monodelphis domestica sequencing consortium;
 RT    "Monodelphis domestica WGS sequence.";
 RL     Initial data release, version 2.
 XX
 RN    [2]
 RP    1-6935
 RA    Gentles A. and Jurka J.;
 RT    "ERV17_MD, a class 2 (HERVK) type endogenous retrovirus from the
 RT    opossum M. domestica.";
 RL    Repbase Reports 5(11), 357-357 (2005).
 XX
 DR    [2] (Consensus)
 XX
 CC    Internal consensus of the class 2 ERV ERV17_MD. The LTR is
 CC    deposited as ERV17_MD_LTR. This consensus was reconstructed from
 CC    the June 2005 release of the 6.8X WGS sequence.
 XX
 FH    Key            Location/Qualifiers
 FT    CDS            1..1806
 FT                   /product="ERV17_MD_I_1p"
 FT                   /translation="IWRPKFRDINAIRNPDSFAGQRMTQSNGLCDNILDWV
 FT                   SRANLGQSQERSVFTGFLCSIIFSISFLCFVGYFSGGMGNSVPVLLQDGGW
 FT                   QAEHLIQAALTAHGVKVQKKMLKKFVGYVRQLAPWFPEGEIISSSEWERVG
 FT                   SKFGSEGETPPPDYAVIFNVIKSCIEDPEANKKMQAVLQMEVEEEDEEGEV
 FT                   SGEVGNQRKNISCPPFASGARLYPSLIQENFPETGTVFKNKPTVTSSGEMR
 FT                   QGQVGKFLRVAELEKALGDLDTGQAQLFPVLEDVNTQTRRFTPMPLKVLKE
 FT                   LKEACTKYGPQAAYTLSLLELIAAENLTPHDWKQVASVSLSQGQAVQWRAI
 FT                   WKEILEQERFRMEQTMMPGGAPTLDQLIGEGPNQFPQHQIGYIPQLYAVIA
 FT                   SAAIKAWKGMEGIPKLDFNKLRQKSDQAFEDYVAEVQKAVERTLGTVQGLE
 FT                   ELIKTIVKQNATPDYRQVLINLPASATLEDMIIKALEVKSQSHQARTQAAM
 FT                   VGAAVQQAMKSQGKGQIRCYGCGKLGHMKKNCWSNLSGTKPKPSQKCQKCY
 FT                   KGYHWNRDCRSGNGQGGLREAPTNNPRAFPAMYQTSLDWEKHQAPFRSTDQ
 FT                   PFQG"
 FT    CDS            2390..5080
 FT                   /product="ERV17_MD_I_2p"
 FT                   /translation="HGFFIGAVEELRAVPLTWKNDKPIWVDQWPLTASKLS
 FT                   ALKEIVQEQLTKGHIRPSTSPWNSPVFVIQKKSGKWRMLTDLRRVNESMEE
 FT                   MGALQPGLPVLSWIPINWKIWAIDLKDCFYTIPLQEKDCKRFAFSVPSINL
 FT                   QEPMDRYEWVILPQGMKNSPTMCQQYVDRALRSIRSKYPKVMMIHYMDDIL
 FT                   LAATTVEQLEALFPVLRQHLSEFNLVIAEEKIQKGEEISYLGSLIGPREIK
 FT                   PQKIQIRMDKLQTLNDFQKMLGDINWIRPFLKLTTEQLRPLFQLLEGDANL
 FT                   KSPRTLTPEAISALKNVEEALNTALLTRFDPQQPVEVKILRTPHVPTAAVV
 FT                   QRDKVILWIHSKSQSGKAIPLYPLLMGQIIKRAIKVVLQGIGQYPEVIHIP
 FT                   VTKAQLQDWIESYTEWASLLQFPCFFRPQTNLSPFWKIFNQYCIVSNPISN
 FT                   HPVDGPNIFVDANPQAAAIFSPPNQPMIFRTPFSSTQQNELAAALLALWKH
 FT                   PESFNLIVDSQYVAQALPKLTNAVIQSKRGTVNLIFSKLQHVLRDRLRSVY
 FT                   VLHVRSHTSLPGPIILGNHIVDQALEAPLLSFSSPAAEARKAHDKFHQSAR
 FT                   ALQKQFQITKAQARLIVKACPKCVPFQPASNKEGAQNPRGVHPLHIWQMDV
 FT                   THVNSFGLAKYVHVTIDTYSGFLWASALRSESARAVKTHCLLTFQTQGPPE
 FT                   ILKTDNGPAYTSEAFATFCRDWHITHITGIPYNPTGQAMIERANRTLKMVL
 FT                   VKQKGGAWRSPQDRLATAIFTINNLIWTQQITKAEKFFEHWHRMVPAQRED
 FT                   TLVPAGDSDYVMWKDENNTWYGPDRVLIRGKGFLCVSTGQGQRWIPRRWTR
 FT                   PILQSGENETSTSTKGQEKAPGATEKRETTDPVPGDSDEHSQHG"
 FT    CDS            5339..6934
 FT                   /product="ERV17_MD_I_3p"
 FT                   /translation="KTXPVCFEHPACIPLVNLTDHFYGAPNYTDKTGPHRV
 FT                   NEGWTFTAWGKISYYGWKGVLQNTRKDSGYLKNRSFIEQKTRQCSYVPEWD
 FT                   LPFSGKQSHGVFPPFLECDRHDLDMVKFHNVTFFSQHNDSACHNDSFPEAP
 FT                   DKRNHGCFIGGFATPGWRTSKMYNNRKVGYNYAKIPIAMKGVVVMAYRVLE
 FT                   FPGNIFTTYEGSTNPRHHYMTGSYNITACLEEDFAFMIGPQNSISIKWIGQ
 FT                   AWNITCLECNITECITQTPERYTVLVVRRPPLALLTARHSGGWYHSPADRA
 FT                   MERLSQLISSRKKRCISCIVLGIVALIAALTATTVSSVSLAQSVANVRVLE
 FT                   HDAEYLHGLAQNVTKALHIQQDINTRVFYALQQISKDVLLLTNQVEILAIK
 FT                   GKLRCDYRYSAFCLLPVKVNTSDAFEKIRNDLQGLWLKGNISENIQQLNHI
 FT                   IEEMDSSLAEDLYPEHIADSIYNWIKSGQSWLSPLAQMSITILTFILFIVI
 FT                   LLVLLPCLFQLLVSSLGRIGQVLTQHRVLLQNKKGE"
 XX
 SQ    Sequence 6935 BP; 2068 A; 1386 C; 1529 G; 1950 T; 2 other;

 //
 ID    ERV2-10_UCy-I repbase;    DNA;    VRT; 4434 BP.
 XX
 AC    .
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XX
DT   19-AUG-2019 (Rel. 24.08, Created)
DT   20-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE   Long terminal repeat of an ERV3 endogenous retrovirus from
DE   Uraeginthus cyanocephalus, internal portion.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element; ERV2-10_UCy-I.
XX
OS   Uraeginthus cyanocephalus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC   Estrildidae; Uraeginthus.
XX
RN   [1]
RP   1-4434
RA   Bao W.;
RT   "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL   Repbase Reports 19(8), 1552-1552 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~98% identical to the consensus.
XX
SQ   Sequence 4434 BP; 1345 A; 848 C; 1180 G; 1059 T; 2 other;

//
ID   ERV2-11C_GG-I repbase;    DNA;    VRT; 5749 BP.
XX
AC   .
XX
DT   05-FEB-2018 (Rel. 23.02, Created)
DT   05-FEB-2018 (Rel. 23.02, Last updated, Version 1)
XX
DE   LTR-Retrotransposons from chicken: Internal region, a smaple
DE   sequence.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element;
KW   LTR-retrotransposon; internal portion; ERV; ERV2-11C_GG-I.
XX
OS   Gallus gallus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
OC   Phasianidae; Phasianinae; Gallus.
XX
RN   [1]
RP   1-5749
RA   Bao W.;
RT   "LTR retrotransposons from the chicken genome.";
RL   Repbase Reports 18(2), 184-184 (2018).
XX
DR   [1] (Consensus)
XX
CC   one copy in the genome. LTRs are 92% identical to each other.
XX
SQ   Sequence 5749 BP; 1466 A; 1276 C; 1557 G; 1450 T; 0 other;

//
ID   ERV2-11D_GG-I repbase;    DNA;    VRT; 5894 BP.
XX
AC   .
XX
DT   06-FEB-2018 (Rel. 23.02, Created)
DT   06-FEB-2018 (Rel. 23.02, Last updated, Version 1)
XX
DE   LTR-Retrotransposons from chicken: Internal region, a smaple
DE   sequence.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element;
KW   LTR-retrotransposon; internal portion; ERV; ERV2-11D_GG-I.
XX
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 OS    Gallus gallus
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
 OC    Phasianidae; Phasianinae; Gallus.
 XX
 RN    [1]
 RP    1-5894
 RA    Bao W.;
 RT    "LTR retrotransposons from the chicken genome.";
 RL    Repbase Reports 18(2), 182-182 (2018).
 XX
 DR    [1] (Consensus)
 XX
 CC    one copy in the genome. LTRs are 96% identical to each other.
 XX
 FH    Key             Location/Qualifiers
 FT    CDS             join(169..852,855..2132)
 FT                    /product="ERV2-11D_GG-I_1p"
 FT                    /translation="MDVEFAAAQTLLLSILAKRGEPVKDKDLAKLVTWARE
 FT                    QGFLKSPLLVFIAAEWRDIGDHMWDCVISGGKDEKLPRPLGPVWRAVPNAL
 FT                    KAIRPPAERPPAASSGPSPDCAATATSAASARCSPRECSASRATLRTTAPA
 FT                    PRCPVGSWIAVSAPPEDEVPPQPAAATGSPGAEVHRAAVRPCQPPRRLPPP
 FT                    VCRRSLCRAAETGSRTRRRIYSLPNVIEFLRQRRDSLQTELGRQVGEAIQK
 FT                    LEGRRDSALNSGPIPPAQSVQQLIKQIPAVGSCASVTPSAALPDCTTAEGA
 FT                    PATERRWAGIIRGAVLEGEWQTAGALPRPLVQSPQGPRYEQHEWKVLQQAR
 FT                    KTVEENGIKSDAARMMFDWLFTADVNSPMDCANPARQLLAPSQVIIWQQEW
 FT                    ECFARVEAGRPCNQRDVLYGINPDMITGSGAYGNMEAQLMCPLQMHYLAAQ
 FT                    LARMAFNAVPDRQPRPSFAATRQGLTESYPQFVGRLWQVLANQAEMSEEAK
 FT                    QSMFKLLAFENANPSMKRLLATLPKDAGVGEMLDLASRAEQQRSEQVMANA
 FT                    MAQAIQPIMQLLAAAVARIGGKDGGCNPGICFRCGQKGHYRHACRAKVWCE
 FT                    QCQRGTHATTACKMTTNGKQSAKGRRALTEGDGQSQCLSFLLQQPEVPWES
 FT                    IWQQQ"
 XX
 SQ    Sequence 5894 BP; 1413 A; 1413 C; 1706 G; 1362 T; 0 other;

 //
 ID    ERV2-11_GG-I repbase;     DNA;     VRT; 5931 BP.
 XX
 AC    .
 XX
 DT    05-FEB-2018 (Rel. 23.02, Created)
 DT    05-FEB-2018 (Rel. 23.02, Last updated, Version 1)
 XX
 DE    LTR-Retrotransposons from chicken: Internal region, a smaple
 DE    sequence.
 XX
 KW    ERV2; Endogenous Retrovirus; Transposable Element;
 KW    LTR-retrotransposon; internal portion; ERV; ERV2-11_GG-I.
 XX
 OS    Gallus gallus
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
 OC    Phasianidae; Phasianinae; Gallus.
 XX
 RN    [1]
 RP    1-5931
 RA    Bao W.;
 RT    "LTR retrotransposons from the chicken genome.";
 RL    Repbase Reports 18(2), 181-181 (2018).
 XX
 DR    [1] (Consensus)
 XX
 CC    one copy in the genome. LTRs are 97% identical to each other.
 CC    TSDs are 6-bp long.
 XX
 FH    Key             Location/Qualifiers
 FT    CDS             join(1690..5172,5195..5491,5495..5716)
 FT                    /product="ERV2-11_GG-I_1p"
 FT                    /translation="MVFNAVPDMRPRPSFAATWQGLTESYPQFVDRLWKAL
 FT                    AGQADMSEEAKQSMFKLLAFENANPSMKRLLATLPKDAGVGEMLDLAGRAE
 FT                    QQRSRQVMANAVAQAIEPTTKLLAAAVTRISEKDGGQKSKIRFHCGQKGHF
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FT                    QRVCRAKVWCEQCQKDTHATTIRRMTKKTPAGVAGLIVLPEVIDADYTGEI
FT                    MVCAYTLTPPLTITAGTRIAQLIVYKRVSTHETAQLPERGDRGFGSTQDAV
FT                    VSLVDRMKTRPMIVLTLILEHDTFQVSVMLDTGADVTIISQQNWLRSWPLV
FT                    NTIDAVQGVGGSATPWCSLKTIKLRFPEGQEVATCPYAMPPPGRAERTHWK
FT                    RCSLTAQCNIVGSTFLGTATVSQLPTTRIPWKTDEPVWVEQWPLTRKRLTV
FT                    AHQLVKEQLEQGHIRPSIIPWNTSIYVIPKKSGKWRLLHNLRAVNEQMWAI
FT                    GALQPGLSTSTVLPQDWHILVIHLKDCFFTIPLQAVDTVCFAFTLPAINRG
FT                    EPAQRFEWAVLPQGMKNSPTVCQMYVHWALEPVCHAFPATVVYHYMDDILF
FT                    CRYKPFSPQDLEQISKLLLRRDVVVAPEKVQRSAPWRYLGWVDSERTIRPQ
FT                    KVTLTTNVQTVHDAQTLIGELQWVHALTGTRNDEMMPLMSLLRSTSPQAPV
FT                    HLSAEQRKCLQVLGNKLLSAHVDRRFPDVPTGVLVVSHPDSLFALLCQWLL
FT                    CHKETGERLPTDNPRGGTTTTTATTTMAVATIAKVKATERVSILEWVFLPH
FT                    TPPRSVWERTGVLAYLIKKARHRTVEISGQEPAFISLPLKADMQEWMLCNS
FT                    EHLQHALLGFPGAVSDCFPTDPRLRVIAKQRWLSRPKVSDRPIDSMTVYSD
FT                    AGKWTCKVACTWLEAGKWQSHTLQGVKGDSLQNLERAAVAWALTRWRDQCV
FT                    NIVSDALYVVGVVLRIEQALLKLPQNPRLAQIFLQVKRAIDDHSEPCSILH
FT                    IRSHLGTQGLGEGNARADALVSPLLRAPQDSFQAARSSHNMFHQSAKALRH
FT                    LFGLTDTEAKGIVWACSQCSQHGSRLGLGVNPKGLQACEIWQMDVTHMPEF
FT                    GRLKYVHVSLDTFSRMVWATAQAGEKAIHVVRHLTACFAVMGVPQGIKTDN
FT                    GPTYMGGRVRRFLQVWGVKHVIGILHSPTGQAMIERAHRTIKEYLMKQAGG
FT                    RDQVLFTLNFLSLVGDAELAPVIIHHSQIRMQSTPSVKVQYRKPTTGMWEG
FT                    PAPLLFNGRGYSCVSTGSGPLWVPSKWTKPAPNINNPSPPDVNNSDSGEQS
FT                    HGVQTSYTVPRLPGCDRYSLSRSQKTSHQEGLLDTGNFQEQLAVTRIRSAL
FT                    IVGSGTVSDPVWGRWYSYSSGY"
XX
SQ   Sequence 5931 BP; 1534 A; 1338 C; 1629 G; 1430 T; 0 other;

//
ID   ERV2-11_UCy-I repbase;     DNA;     VRT; 6838 BP.
XX
AC   .
XX
DT   19-AUG-2019 (Rel. 24.08, Created)
DT   20-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE   Long terminal repeat of an ERV3 endogenous retrovirus from
DE   Uraeginthus cyanocephalus, internal portion.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element; ERV2-11_UCy-I.
XX
OS   Uraeginthus cyanocephalus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC   Estrildidae; Uraeginthus.
XX
RN   [1]
RP   1-6838
RA   Bao W.;
RT   "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL   Repbase Reports 19(8), 1553-1553 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~92% identical to the consensus. LTR portion is UcyLTRK12.
XX
SQ   Sequence 6838 BP; 1993 A; 1913 C; 1376 G; 1538 T; 18 other;

//
ID   ERV2-12C_PMaj-LTR repbase;     DNA;     VRT; 293 BP.
XX
AC   .
XX
DT   21-AUG-2019 (Rel. 24.09, Created)
DT   21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
XX
DE   Endogenous retrovirus from the great tit genome, long terminal
DE   repeat consensus.
XX
KW   Endogenous Retrovirus; Transposable Element; ERV2-12B_PMaj-LTR;
KW   ERV2-12C_PMaj-LTR.
XX
OS   Parus major
```

```
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN     [1]
RP     1-293
RA     Kojima K.K.;
RT     "Endogenous retroviruses from the great tit genome.";
RL     Repbase Reports 19(9), 1770-1770 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~96% identical to consensus. The consensus is ~94% identical to
CC     that of ERV2-12B_PMaj-LTR.
XX
SQ     Sequence 293 BP; 101 A; 51 C; 60 G; 81 T; 0 other;

//
ID     ERV2-12_GG-I repbase;     DNA;     VRT; 7314 BP.
XX
AC     .
XX
DT     06-FEB-2018 (Rel. 23.02, Created)
DT     06-FEB-2018 (Rel. 23.02, Last updated, Version 1)
XX
DE     LTR-Retrotransposons from chicken: Internal region, a consensus
DE     sequence.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element;
KW     LTR-retrotransposon; internal portion; ERV; ERV2-12_GG-I.
XX
OS     Gallus gallus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
OC     Phasianidae; Phasianinae; Gallus.
XX
RN     [1]
RP     1-7314
RA     Bao W.;
RT     "LTR retrotransposons from the chicken genome.";
RL     Repbase Reports 18(2), 175-175 (2018).
XX
DR     [1] (Consensus)
XX
CC     severall copies in the genome. the LTRs of the youngest one are
CC     97% identical to each other.
XX
FH     Key             Location/Qualifiers
FT     CDS             join(280..4539,4518..4709,4713..5099,5103..5300)
FT                     /product="ERV2-12_GG-I_1p"
FT                     /translation="MAVRCGTYGLQCTMEREVALNLLQRFLEKRGVESGIV
FT                     KQVPGLIAYGKADGMFVHSEEFFEEEAWRKFGDTLWHKVIDEDKGAKKLMK
FT                     AWREVINCIKKHKVEKQVAATASRHLAGLPEDAGQIKPGCDYVPIPLSGAS
FT                     VPVRTSGLQEVGESANPSAPPLGSLGDESGDEAPDLYPPNPAGGDRNGSED
FT                     SRQAKGSYLMKCSEDPSLNRQAAAKVTTPRPVPSQPRPSRLDWAAVAREAM
FT                     GEGDMAMVEAVMQAFPIRYEQEGEGGLRGGYLPLGWKLLPQLRATVNDSGL
FT                     HGEPMKQILNYIWGSSVLVPEDIKVIVRMIMSQSEQLLWQAHWQRLCEISS
FT                     NTPRAEGDPLFGITVQQLMGMGPFATPDMQVHLGPDVCLEGMRTARQALEM
FT                     VKTSAPTPSYMSIKQGREETFASFIDKVTEAINRACVPDWMRAALLRQCAM
FT                     ENCNSSTRSILITLPIDATIEMMLERMSRVPTGPQALLVEAVRELGSKLAE
FT                     AQTQAFAALASLVGGGVPKGARPRRSQGLSCFHCGKEGHWRRDCRAKVWCE
FT                     NCNSANHSMLACRSSGNSGMSAKSRRAQTTMAAPVVSPXNGTPSNHSPPAA
FT                     VSHEPPPESPNYGPPRGGSLGLDLATATDVTVIDQKPVQVPSMATGPMIID
FT                     GSPVGCLLLGRSSTGLNGVTVLPGLIDADFTGVIQIVIQTLFPPVHIPTGS
FT                     RIAQLVPLPALTQSLQPESDMTRENKGFGSTGGLVMLTVPMKQRPVVTISL
FT                     YSAGLQRDIRALLDTGADITIVAQHCWPQSWPLECVDKGVEGVGGAVVVSR
FT                     SVRPIQIFIDGCYALTNWGTSPGGPRCFGSTRDSIDHARLGFSLAASVWVF
FT                     LIHLTWITDKPVWIEQWPLKKENLDNVIKLVAEQLQKGHIQPSTSPWNTPI
FT                     FVIKKKSGKYRLLHDLRAVNAQMQPMGALQPGLPNPAMIPENWHLLIVDLK
FT                     DCFFTIKIHPKDTSRFAFTVPATNKGAPAAQYEWTVLPQGMKNSPTLCQLF
FT                     VDAALEPIHKAWSHAVIYYYIDDILIAQSRPFTTDQELYLKRTLQSKGLVI
FT                     ALEKVQREPLWKYLGWVITQSHVRPQKLTLHTDIQTLNDAQKLLGDLQWLR
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FT                    PVVGLSNDDLNSLRPLLKGTDPAARISVSPEQRQIIERLAQTVVERSVDQR
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FT                    KAVATWCEDQQWRHRFLHAPLIFVAEKWCEIGDCMWDRVLQGKAKDATALG
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FT                    TTPGQPFCTWGEGVLLPTPRPYDPPLNYQPQPPAARVQTTPPPQQLLLHGL
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FT                    GSAKALPPDIFXICGNRAWQGIPSQVIGGHCYLGKLTMLAPTFVQFNISLS
FT                    NCSDRMKRALLTPECSDNTELLSFYRLLQGLXFFFLFFFFLNSFWLIKTAY
FT                    GIPCYKITLP"
XX
SQ   Sequence 7314 BP; 1871 A; 1705 C; 2002 G; 1732 T; 4 other;

//
ID   ERV2-12_PMaj-I repbase;      DNA;      VRT; 5387 BP.
XX
AC   .
XX
DT   21-AUG-2019 (Rel. 24.09, Created)
DT   21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
XX
DE   Endogenous retrovirus from the great tit genome, internal portion
DE   consensus.
XX
KW   Endogenous Retrovirus; Transposable Element; ERV2-12_PMaj-I.
XX
OS   Parus major
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN   [1]
RP   1-5387
RA   Kojima K.K.;
RT   "Endogenous retroviruses from the great tit genome.";
RL   Repbase Reports 19(9), 1722-1722 (2019).
XX
DR   [1] (Consensus)
XX
SQ   Sequence 5387 BP; 1606 A; 947 C; 1180 G; 1651 T; 3 other;

//
ID   ERV2-12_UCy-I repbase;     DNA;      VRT; 7095 BP.
XX
AC   .
XX
DT   19-AUG-2019 (Rel. 24.08, Created)
DT   21-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE   Long terminal repeat of an ERV3 endogenous retrovirus from
DE   Uraeginthus cyanocephalus, internal portion.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element; ERV2-12_UCy-I;
KW   ERV2-12_UCy-LTR.
XX
OS   Uraeginthus cyanocephalus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC   Estrildidae; Uraeginthus.
XX
RN   [1]
RP   1-7095
RA   Bao W.;
RT   "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL   Repbase Reports 19(8), 1554-1554 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~93% identical to the consensus.
XX
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```
SQ     Sequence 7095 BP; 2059 A; 1362 C; 1881 G; 1793 T; 0 other;

//
ID     ERV2-15_PMaj-I repbase;     DNA;     VRT; 6483 BP.
XX
AC     .
XX
DT     21-AUG-2019 (Rel. 24.09, Created)
DT     21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
XX
DE     Endogenous retrovirus from the great tit genome, internal portion
DE     consensus.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element;
KW     ERV2-15_PMaj-LTR; ERV2-15_PMaj-I.
XX
OS     Parus major
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN     [1]
RP     1-6483
RA     Kojima K.K.;
RT     "Endogenous retroviruses from the great tit genome.";
RL     Repbase Reports 19(9), 1724-1724 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~83% identical to consensus.
XX
SQ     Sequence 6483 BP; 1854 A; 1624 C; 1549 G; 1432 T; 24 other;

//
ID     ERV2-17_UCy-I repbase;     DNA;     VRT; 6421 BP.
XX
AC     .
XX
DT     19-AUG-2019 (Rel. 24.08, Created)
DT     22-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE     Long terminal repeat of an ERV3 endogenous retrovirus from
DE     Uraeginthus cyanocephalus, internal portion.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element; ERV2-17_UCy-I;
KW     ERV2-17_UCy-LTR.
XX
OS     Uraeginthus cyanocephalus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC     Estrildidae; Uraeginthus.
XX
RN     [1]
RP     1-6421
RA     Bao W.;
RT     "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL     Repbase Reports 19(8), 1558-1558 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~97% identical to the consensus.
XX
FH     Key             Location/Qualifiers
FT     CDS             425..2632
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FT                     /translation="MDGDLQASVRLLIHILSKRAEKVKEADLEQLVLWARN
FT                     RGKLQKPSLIFSEAEWRDLGQLLWDAVIEGGKDKKIVLEFGGIWKKVLRTL
FT                     QSMAAEKXAAEAAIQAFEQSASEQAGVRKPSRAEKFFSVXNMRPVWGQKVP
FT                     ISPSVKDCVASIEASARPGRAEPVSAGPSGSVAAAGAEVCPQTADVNGSEA
FT                     PRNETSPEVALPGPSGGGETPEEAGGVGDETGLSQEEEHRGGDQGGDQGGD
FT                     GTGVAPAPRPPAGAAAAAAAEEAACMRRGAARRYPAAANTPARFGGAGRNCA
FT                     SGMVEAATQTTTEQPPDTGSPHPTTVALRCPLPRSSDSDDSESDSPAVSCS
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FT                         FRSLAFENANSHTRTILATLPQGSPVDEMLVRAARAEQGNQTAAFAATVQD
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FT   CDS                   3300..6107
FT                         /product="ERV2-17_UCy-I_2p"
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FT                         HVQPSVSPWNTPIFIVPKKSGKWRLVHDLRKVNEQMQAMGALQPGMPAPTM
FT                         IPQGWNIVVIDLKDCFFTIPLHPQDTQRFAFTVPSLNRTKPAKRYEWVSLP
FT                         QGMRNSPTMCQLFVDWALRPIRQHFSNAMIYHYMDDILITTKQPLADADLN
FT                         WLFSQLKKHGLIVSPEKIQRSAPWKYLGWLITDAQIRPQKLTLHANISTLH
FT                         DAQRLFGDLQWVRTIVGITNDDLQPFLPWLHGSDANSPRVCTPEQQEALIR
FT                         VSEKLQRGWSARRIEHLPLSLFLSNADASPLAIVFQWQKKKRESQRGSTAI
FT                         MIEWVFLPVQPRSRVMGRTDALAALIRKGRDRILEMDGKEPADISVPVKNE
FT                         DLEWQLRHSTALQEALLGFTGVVHNRQPKGPMWHFVSRYQWLERPLCSLKP
FT                         VEGRTVFTDAGRRSKRAVCVWQQRGKWLEHLIRGDVEDSLQTLELKAVCWA
FT                         FQTWNKEPLNVVSDSLYVVGVVQRIEDALLRRTQNQRLGELFLQLRSVLKQ
FT                         RQHVFCIMHIRSHQCNRGLGEGNALADAAVSYAVHVPPQNSFERARNSHET
FT                         FHQNARAMHRQFQIPMNDAQGIVRACPQCSHHGPGLRLGTNPRGLKALEVW
FT                         QMDVTHVPEFGRLKYVHVTVDTYSRFIWATAQTGEKALHVKRHLFACFAVM
FT                         GVPVEIKTDNAPSXVGRQVAAFMQKWGVKHTTGIPHSSTGQAIVERANRTL
FT                         KEYLAKQKQSDETDVFNRLSKVLFTLNYLCLAEGREEPAVVIHHQAVKEGR
FT                         PQAIPGLYVYHKDMQTGEWRGPSPVLFNGRGYMCVSTGTGPVWVPSRFTRA
FT                         CPQAKIPTRSDKNVNDNSLPGTSHDNSNSDEN"
XX
SQ   Sequence 6421 BP; 1755 A; 1495 C; 1697 G; 1468 T; 6 other;

//
ID   ERV2-3_STr-I repbase;      DNA;      ROD; 7294 BP.
XX
AC   .
XX
DT   15-FEB-2010 (Rel. 15.12, Created)
DT   15-FEB-2010 (Rel. 15.12, Last updated, Version 3)
XX
DE   Internal portion of an ERV2-type endogenous retrovirus -
DE   consensus.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element; ERV2-3_STr-I.
XX
OS   Ictidomys tridecemlineatus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC   Sciuromorpha; Sciuridae; Xerinae; Marmotini; Ictidomys.
XX
RN   [1]
RP   1-7294
RA   Jurka J.;
RT   "Endogenous retroviruses from the thirteen-lined ground
RT   squirrel.";
RL   Repbase Reports 10(12), 2052-2052 (2010).
XX
DR   [1] (Consensus)
XX
CC   ~96% identical to consensus.
CC   This sequence was derived from sequence data generated by Broad
CC   Institute Mammalian Genome Project.
CC   We thank the Broad Institute Genome Sequencing Platform and
CC   Genome Sequencing and Analysis Program, Federica Di Palma, and
CC   Kerstin Lindblad-Toh for making the data for Spermophilus
CC   tridecemlineatus available.
XX
FH   Key             Location/Qualifiers
FT   CDS             69..2402
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FT                   /translation="MGSHSKFPLLFCFVFVLTCLSLEMSEREEKPLTSEEK
FT                   LFASEEQIGRKDGCICQEDRKAVIMILCGSLFIGFCLGFVWRHLVGLYYSR
FT                   NTGSAISKKQTERVLSKLLEEGSFPVKSRAVRAYVDIIQEYSPWLFKEELL
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FT                       LSPEGISVQSTAPPPYARRLPTPAVDSWDPETGSQVCPVFEVGGQRTYQGL
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FT                       AAAVKQALDARDINEQGQIVAAAVKQALDARDINEQGQIVAAAVKQALDAR
FT                       DINEQGQIVAAAVKQALDARPRTCYNCQQTGHFKRNCPVGGGFNETRYQTS
FT                       RIPGICPRCRRGRHWANECRSQTTIEGTPLYWANECRPQTTIEGTPLSKNE
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FT      CDS             3406..5697
FT                       /product="ERV2-3_STr-I_3p"
FT                       /translation="MVIMGPAQSGIPQLSALPKTWYVLVIDIKDCFFSIPI
FT                       HPEDSPRFAFTIPALNHEGPDQRYEWKVLPQGMANSPTMCQIYVNKVIQPL
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FT                       LLFIVLPTKNIPTGVFWQEGPLLWIHLSYSPNTILTRYPEAVGQLILKGIK
FT                       TAKAVFGISPHKIITPYTMNQIDELANELNTWAIIMCKSNVSFDNHLPSNP
FT                       LLSFWSLHPVIFPKMTRKTPIMNAPNIFTDGSNNGTAAIVTPDQTFTFLVP
FT                       KQSAQKVELNAVLQTFVMFKDSVFNLFSDSQYIVNAIVSLEDAGRISPSST
FT                       VFSLFSTIQSLIWDRKDPFFIGHIRAHTGLPGALSLGNDLADKTTRDIHIF
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FT      CDS             2120..3190
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FT                       GSTGVDWAMLSLNLDSRPMLKLNIQGHEFNGLLDTGADLSIISRQEWPKHW
FT                       PLQQATQXLRGLGVATNPDRSAMLLDWKDPEGCEGTIQPYVLDHLPVNLWG
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FT                       DRHGLDFHKGPLRQ"
FT
XX
SQ      Sequence 7294 BP; 2373 A; 1347 C; 1485 G; 2083 T; 6 other;

//
ID      ERV2-3b_CPo-I repbase;    DNA;     ROD; 7000 BP.
XX
AC      .
XX
DT      22-MAR-2011 (Rel. 16.05, Created)
DT      22-MAR-2011 (Rel. 16.05, Last updated, Version -1)
XX
DE      Internal portion of an ERV2-type endogenous retrovirus -
DE      consensus.
XX
KW      ERV2; Endogenous Retrovirus; Transposable Element;
KW      ERV2-3b_CPo-LTR; ERV2-3b_CPo-I.
XX
OS      Cavia porcellus
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
OC      Hystricomorpha; Caviidae; Cavia.
XX
RN      [1]
RP      1-7000
RA      Jurka J. and Walichiewicz K.;
RT      "Endogenous retroviruses from guinea pig.";
RL      Repbase Reports 11(5), 1488-1488 (2011).
XX
DR      [1] (Consensus)
XX
CC      ~100% identical to consensus.
CC      We thank the Broad Institute Genome Sequencing Platform and
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CC     Genome Sequencing and Analysis Program, Federica Di Palma, and
CC     Kerstin Lindblad-Toh for making the data for Cavia porcellus
CC     available.
XX
FH     Key            Location/Qualifiers
FT     CDS            20..1144
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FT                    RRTGTCERCGKGSHKAKDCRSIFDAQGNRISGRETTEPKNGQRGPSLRTGP
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FT     CDS            1156..1911
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FT                    NSDLKPLFDLLKGDPDIASPREFTPEARVALRKIEEALSTAALRRIDSEQP
FT                    FEVCLLQTVSQPTAVIWQKGPLLWVHPKVSPAKIIEHYPETVASLALEAHG
FT                    RAIQHFGSAPHAIRVPYTASQIKILTACIDTWAILRCVFLGEIDNQFPRDP
FT                    ILQFVTQHPVIFPKITASTPLTPATTIYTDGSKTGIGAYVVSGMPPISIQF
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FT                    NHSPAMEHCNPSPGNRGWVKWKDVLTGQWMGPDPVVSWNRGAVCVFPQEPG
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FT                    SFKCSNQPCFTGNCWNGSFPYAMLALRPPLMWVPFNESVWVHPVYQQDQLP
FT                    MLRRKRDFGITAALTALFVTLTATAVTAAVALTQSTLTAQAFTNLTDTTSL
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XX
SQ     Sequence 7000 BP; 1834 A; 1847 C; 1678 G; 1641 T; 0 other;

//
ID     ERV2-9_UCy-I repbase;     DNA;     VRT; 7077 BP.
XX
AC     .
XX
DT     19-AUG-2019 (Rel. 24.08, Created)
DT     20-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE     Long terminal repeat of an ERV3 endogenous retrovirus from
DE     Uraeginthus cyanocephalus, internal portion.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element; ERV2-9_UCy-I.
XX
OS     Uraeginthus cyanocephalus
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OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC     Estrildidae; Uraeginthus.
XX
RN     [1]
RP     1-7077
RA     Bao W.;
RT     "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL     Repbase Reports 19(8), 1551-1551 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~95% identical to the consensus.
XX
SQ     Sequence 7077 BP; 1820 A; 1694 C; 1683 G; 1863 T; 17 other;

//
ID     ERV3-18_PMaj-I repbase;     DNA;     VRT; 5296 BP.
XX
AC     .
XX
DT     21-AUG-2019 (Rel. 24.09, Created)
DT     21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
XX
DE     Endogenous retrovirus from the great tit genome, internal portion
DE     consensus.
XX
KW     ERV3; Endogenous Retrovirus; Transposable Element;
KW     ERV3-18_PMaj-I.
XX
OS     Parus major
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN     [1]
RP     1-5296
RA     Kojima K.K.;
RT     "Endogenous retroviruses from the great tit genome.";
RL     Repbase Reports 19(9), 1725-1725 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~93% identical to consensus.
XX
FH     Key           Location/Qualifiers
FT     CDS           121..1971
FT                   /product="ERV3-18_PMaj-I_1p"
FT                   /translation="MXSSLPRFGWHVVTAIFLPFAAPYLNMGPITKATVAI
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FT                   LTGISTLTPTPETGDAAPEPDTAPETRGAAPEPDTAPETGGAAPDPAPAPQ
FT                   PTSEMNHPEWVGVLVREIREMGQKLECISSAAGKPSPCLEEGESDGAAVEP
FT                   TDVTTVQVPAEPQGQSQPAAVAPVETRKSKMKSQHPVDKDKKGGPSQPTGE
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FT                   GWKTIEEGIQQLREVAVLEVLFGRGGQHDNDPDKVRCTGQMLWSLANLGPR
FT                   EYTTFIATINADNSRETVGSVATRLRNFESMVHGLQQAQVSAVIKELKEEM
FT                   REMREEMRKSSSHMAPVRVTSPKLQAQRPPARERGYTPRAELWFFLRDHGE
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FT                   /note="retropepsin, reverse transcriptase,
FT                   ribonuclease H and integrase."
FT                   /translation="RGPASSQEEARENRVFWTVWIRWPGTSEPQKYEALVD
FT                   TGAQCTLMPSGHVGAEPVSIAGVTGGSQQLTLLEAEVSLTGKEWQKHPIVT
FT                   GPEAPCILGIDFLRNGYYKDPKGLRWAFGIAAVEAEDIKQLNTLPGLSENP
FT                   SAVRLLKVEEQRVPIATSTVHRRQYRTNRDAVIPIHKMIRELESQGVVSKT
FT                   HSPFNSPIWPVRKSDREWRLTVDYRALNEVTPPLSAAVPDMLELQYELESK
FT                   AAKWYATIDIANAFFSIPLAAECRPQFAFTWRGVQYTWNRLPQGWKHSPTI
FT                   CHGLIQAALEKGEAPEHLQYIDDIIVWGNTAVEVFEKGEKIIQILLEAGFA
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FT                    IKKNKVKGPAREIQFLGVKWQDGRRQIPTEVINKITAMSPPTSKKETQAFL
FT                    GAIGFWKMHIPEYSQIVSPLYLVTRKKNDFHWGPEQQQAFAQIKQEIAHAV
FT                    ALGPVRTGPDVKNVLYSAAGNNGLSWSLWQKVPGETRGRPLGFWSRSYRGS
FT                    EANYTPTEKEILAAYEGVQAASEVIGTEAQLLLAPRLPVLGWMFKGKVPAT
FT                    HHATDATWSKWIALITQRARIGNPNRPGILEIITNWPEGENFGLTDEEEQE
FT                    QVTRAEEAPPYNQLPAEETRYALFTDGSCRIVGMNRKWKAAVWSPTRQVAE
FT                    ATEGEGGSSQLAELKAVQLALDIAEREKWPKLYLYTDSWMVANALWGWLER
FT                    WKRANWQHRGKPIWAADEWKDIATRVEKLSVKVRHVDAHVPKSRANEEHRN
FT                    NEQVDQAAKIEVSKTDLDWQHKGELFLARWAHDASGHQGRDATYKWARDRG
FT                    VDLTMDSISQVIHDCETCATIKQAKRLKPLWYGGRWSKYRYGEAWQIDYIT
FT                    LPQTRQGKRYVLTMVEATTGWLETYPVPHATARNTILGLEKQVLWRHGTPE
FT                    RIESDNGTHFKNSLINSWAREHGIEWVYHIPYHAPAAGKVERCNGLLKTSL
FT                    KALGGGTFKNWEINLAKATWLVNTRGSTNRAGPAQSEPFRTTDGDKVPVVH
FT                    MRGMLGKTVWVNSASSKDNPIRGVVFAQGPGCTWWVMQKDGETRCIPQGDL
FT                    VLG"
XX
SQ     Sequence 5296 BP; 1431 A; 1241 C; 1517 G; 1106 T; 1 other;


//
ID     ERV3-1_MUn-I repbase;      DNA;      VRT; 5618 BP.
XX
AC     .
XX
DT     14-DEC-2011 (Rel. 23.02, Created)
DT     14-DEC-2011 (Rel. 23.02, Last updated, Version -1)
XX
DE     LTR retrotransposon from the budgerigar genome: internal portion.
XX
KW     ERV3; Endogenous Retrovirus; Transposable Element; ERV3-1_MUn-I.
XX
OS     Melopsittacus undulatus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Psittaciformes; Psittaculidae;
OC     Melopsittacus.
XX
RN     [1]
RP     1-5618
RA     Jurka J. and Kohany O.;
RT     "LTR retrotransposons from the budgerigar genome.";
RL     Repbase Reports 18(2), 170-170 (2018).
XX
DR     [1] (Consensus)
XX
CC     Positions [4488-5003] - Integrase core
CC     LTRs are 94% similar to each other.
XX
FH     Key           Location/Qualifiers
FT     CDS           2151..5201
FT                   /product="ERV3-1_MUn-I_1p"
FT                   /note="reverse transcriptase, ribonuclease H and
FT                   interase."
FT                   /translation="MPSSCQGVEPIYISGVTGGSQELTVLEAEISLTGRKW
FT                   QKHPIVTGPEAPCILGIDYLRRGYFKDPKGYRWAFGIAALETEEIEQLSTL
FT                   PGLSEDPSVVGLLKVEEQQVPIATTTVHRRQYRTNRDSLIPIHKLIRRLES
FT                   QGVISRTRSPFNSPIWPVRKSNGEWRLTVDYRGLNEVTPPLSAAVPDMLEL
FT                   QYELESKAAKWYATIDIANAFFSIPLAAECRPQFAFTWRGVQFTWNRLPQG
FT                   WKHSPTICHGLIQTALEQGQAPEHLQYIDDIIVWGDTAEEVFEKGREIIQI
FT                   LLKAGFAIKRSKVKGPAREIQFLGIKWQDGRRQIPTDVINKITAMSPPTDK
FT                   KETQAFLGAVGFWRMHIPNYSSIVSPLYHVTRKKNDFKWGPEQQQAFEQIK
FT                   REIVHAVALGPVRTGPDVKNVLYTAAGENGPTWSLWQKAPGETRGRPLGFW
FT                   SRGYKGSEASYTPTEKEILAAYEGVRAASEVIGTEAQLLLAPRLPVLGWMF
FT                   KGRVSSTHHATDATWSKWAALITQRARIGNPSRPGILEVIMDWPEGKDFGM
FT                   SPEEEVMRAEEAPPYNKLSESEKQYALFTDGSCRIVGKHRRWKAAVWSPRR
FT                   QVAETAEGEGESSQFAEVKAIQLALDIAEREKWPVLYLYTDSWMVANALWG
FT                   WLQQWKQSNWQRRGKPIWAAALWQDIAARVQNLVVKVRHVDAHVPKSRATE
FT                   EHQNNQQVDKAAKIEVAQMDLDWQHKGELFLARWAHDTSGHQGRDATYRWA
FT                   RDRGVDLTMDTIAQVIHECETCAAIKQAKRLKPLWYGGRWLKYKYGEAWQI
FT                   DYITLPPTRQGKRHVLTMVEATTGWLETYAVPHATARNTILGLEKQILWRH
FT                   GTPERTESDNGTHFRNNLIGTWAKEHGIEWVYHIPYHAPASGKIERYNGLL
FT                   KTTLRAMGGGTFKHWDTHLPKATWLVNTRGSANRAGPAQSELLHTVEGDKV
FT                   PVVHMKNLLGKTVWVIPASGKGKPTRGIAFAQGPGYTWWVMREDGEVRCIP
FT                   QGDLILGENSQ"
```

```
 XX
 SQ    Sequence 5618 BP; 1576 A; 1293 C; 1505 G; 1241 T; 3 other;

 //
 ID    ERV3-22_PMaj-I repbase;    DNA;    VRT; 5478 BP.
 XX
 AC    .
 XX
 DT    21-AUG-2019 (Rel. 24.09, Created)
 DT    21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
 XX
 DE    Endogenous retrovirus from the great tit genome, internal portion
 DE    consensus.
 XX
 KW    ERV3; Endogenous Retrovirus; Transposable Element;
 KW    ERV3-22_PMaj-LTR; ERV3-22_PMaj-I.
 XX
 OS    Parus major
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
 XX
 RN    [1]
 RP    1-5478
 RA    Kojima K.K.;
 RT    "Endogenous retroviruses from the great tit genome.";
 RL    Repbase Reports 19(9), 1726-1726 (2019).
 XX
 DR    [1] (Consensus)
 XX
 CC    ~98% identical to consensus. 5-bp TSDs.
 XX
 FH    Key            Location/Qualifiers
 FT    CDS            316..2145
 FT                   /product="ERV3-22_PMaj-I_1p"
 FT                   /translation="MIYRKFIXVLESVPGMFGSWFLPRPSSTFWGFISNCT
 FT                   QFVRGGAGDEAFQPFLSFFSSESVTSLFENVQFPLSVKETTFLVFNLVSFL
 FT                   YTVCNFSRVRAEMSRGADETPAPEVDPGVENPEWCGEWEKMGRTLKEFSDP
 FT                   PAWEFSREQIQNPXEVGKYLEENCHDDSKEKNXIAISWALAYAYRTLLDTV
 FT                   GQQTGGRGQGDKSAATPVTQAAAKPAAKPDSEPKPAAKPDSEPKPMAVAPT
 FT                   TRGTKFXSKTDRPVDDDDGDAGEGPSTPPDIKPRVKATDTKSEGTSEPFSL
 FT                   KDLRGLRKDYTRRPDESIISWLVHLWDAAGEATVLDGTEARHLGSLSHDPV
 FT                   IDQGMMRGADPHSLWERVLGSVAQRYLCADDLYIQQTHWKTIEQGIQRLRE
 FT                   MAVVEIVFLDDLNTRNPDLVPCTSVMWRKLVRLGPQEYASALATMKRDDRE
 FT                   ETVLDMAKKLRAYADAVHGPTHARIAAVETRLQKLEDKIEENHKKLREEIK
 FT                   EDLLXISAVQTRSPGTQRRSSPDRERKYTPRAELWFFLRDCGENMKRWDGK
 FT                   STAALAKRVRELEDSKTQRGSSTKKKAAPVARSQTARYDDDDMSDPLEGTS
 FT                   KTDAQGKKDNQA"
 FT    CDS            2149..5328
 FT                   /product="ERV3-22_PMaj-I_2p"
 FT                   /note="retropepsin, reverse transcriptase,
 FT                   ribonuclease H and integrase."
 FT                   /translation="RGPASSQVEARENRVFWTVWIRWPGTSEPQKYEALVD
 FT                   TGAQCTLIPSRHVGAESVSIAGVTGGSQDFTLVEADVSLTGNEWKKHPIVT
 FT                   GPEAPCILGIDYLRSGYFKDPKGLRWAFGIAAVETEGVKQLNTLPGLSENP
 FT                   SAVGLLKVEEQRVPIATSTVHRRQYRTTRDAVIPIHKMIRELESQGVVSKT
 FT                   HSPFNSPIWPVRKSDREWRLTVDYRALNEVTPPLSAAVPDMLELQYELESK
 FT                   AAKWYATIDIANAFFSIPLAAECRPQFAFTWRGVQYTWNRLPQGWKHSPTI
 FT                   CHGLIQAALEKGEAPEHLQYIDDIIVWGNTAAEVFEKGEKIIQILLKAGFA
 FT                   IKKSKVKGPAREIQFLGVKWQDGRRQIPTDVINKITAMSPPTSKKETQAFL
 FT                   GAIGFWRMHIPEYSQIVSPLYLVTRKKNNFHWGPEQQQAFAQIKQEIAHAV
 FT                   ALGPVRTGPDVKNVLYSAAGSHGLSWSLWQKVPGETRGRPLGFWSRSYRGS
 FT                   EANYTPTEKEILAAYEGVQAASEVIGTEAQLLLAPRLPVLGWMFKAKVPST
 FT                   HHATNATWSKWIALITQRARIGKPNRPGILEIITNWPEGENFGLTDEEEQE
 FT                   QVTRAEEAPPYNQLPAEETRYALFTDGSCRIVGMNRKWKAAVWSPTRQVAE
 FT                   ATEGEGGSSQLAELKAVQLALDIAEREKWPKLYLYTDSWMVANALWGWLER
 FT                   WKKANWQRRGKPIWAADEWKDIATRVEKLSVKVRHVDAHVPKSRANEEHRN
 FT                   NEQVDQAAKIEVSKIDLDWQHKGELFLARWAHDASGHQGRDATYKWARDRG
 FT                   VDLTMDSISQVIHDCETCAAIKQAKRLKPLWYGGRWSKYRYGEAWQIDYIT
 FT                   LPQTRQGKRYVLTMVEATTGWLETYPVPHATARNTILGLEKQVLWRHGTPE
 FT                   RIESDNGTHFKNSLINSWAREHGIEWVYHIPYHAPAAGKVERYNGLLKTTL
 FT                   KALGGGSFKNWEQHLAKATWLVNTRGSTNRAGPAQSEPLHTVDRDKVPVVH
 FT                   VRGLLGKTVWINSTSSTDKPIRGVVFAQGPGPCTWWIMQKDGTTRCVPQGDL
```

```
FT                      IVG"
XX
SQ    Sequence 5478 BP; 1521 A; 1254 C; 1516 G; 1172 T; 15 other;

//
ID    ERV3-23_PMaj-I repbase;    DNA;    VRT; 3793 BP.
XX
AC    .
XX
DT    21-AUG-2019 (Rel. 24.09, Created)
DT    21-AUG-2019 (Rel. 24.09, Last updated, Version 2)
XX
DE    Endogenous retrovirus from the great tit genome, internal portion
DE    consensus.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    ERV3-23_PMaj-I.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN    [1]
RP    1-3793
RA    Kojima K.K.;
RT    "Endogenous retroviruses from the great tit genome.";
RL    Repbase Reports 19(9), 1727-1727 (2019).
XX
DR    [1] (Consensus)
XX
CC    ~86% identical to consensus.
XX
SQ    Sequence 3793 BP; 1078 A; 829 C; 1045 G; 831 T; 10 other;

//
ID    ERV3-28_PMaj-LTR repbase;    DNA;    VRT; 1038 BP.
XX
AC    .
XX
DT    17-OCT-2018 (Rel. 24.09, Created)
DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE    Endogenous retrovirus from the great tit genome, long terminal
DE    repeat consensus.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    ERV3-28_PMaj-LTR.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN    [1]
RP    1-1038
RA    Kojima K.K.;
RT    "Endogenous retroviruses from the great tit genome.";
RL    Repbase Reports 19(9), 1768-1768 (2019).
XX
DR    [1] (Consensus)
XX
CC    ~84% identical to consensus. 4 or 5-bp TSDs.
XX
SQ    Sequence 1038 BP; 282 A; 257 C; 219 G; 280 T; 0 other;

//
ID    ERV3-3_ACD-LTR repbase;    DNA;    VRT; 705 BP.
XX
AC    .
XX
DT    06-NOV-2018 (Rel. 24.12, Created)
DT    06-NOV-2018 (Rel. 24.12, Last updated, Version 2)
```

```
 XX
 DE    Endogenous retrovirus from the swan goose genome, long terminal
 DE    repeat consensus.
 XX
 KW    ERV3; Endogenous Retrovirus; Transposable Element;
 KW    ERV3-3_ACD-LTR.
 XX
 OS    Anser cygnoides domesticus
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Galloanserae; Anseriformes;
 OC    Anatidae; Anser; Anser cygnoides.
 XX
 RN    [1]
 RP    1-705
 RA    Kojima K.K.;
 RT    "Endogenous retroviruses from the swan goose genome.";
 RL    Repbase Reports 19(12), 2558-2558 (2019).
 XX
 DR    [1] (Consensus)
 XX
 CC    ~98% identical to consensus. 5-bp TSDs.
 XX
 SQ    Sequence 705 BP; 165 A; 169 C; 152 G; 219 T; 0 other;

 //
 ID    ERV3-3_PMaj-LTR repbase;    DNA;    VRT; 1175 BP.
 XX
 AC    .
 XX
 DT    17-OCT-2018 (Rel. 24.09, Created)
 DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
 XX
 DE    Endogenous retrovirus from the great tit genome, long terminal
 DE    repeat consensus.
 XX
 KW    ERV3; Endogenous Retrovirus; Transposable Element;
 KW    ERV3-3_PMaj-LTR.
 XX
 OS    Parus major
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
 XX
 RN    [1]
 RP    1-1175
 RA    Kojima K.K.;
 RT    "Endogenous retroviruses from the great tit genome.";
 RL    Repbase Reports 19(9), 1743-1743 (2019).
 XX
 DR    [1] (Consensus)
 XX
 CC    ~87% identical to consensus. 5-bp TSDs.
 XX
 SQ    Sequence 1175 BP; 187 A; 362 C; 336 G; 289 T; 1 other;

 //
 ID    ERV3-3_UCy-I repbase;    DNA;    VRT; 5130 BP.
 XX
 AC    .
 XX
 DT    01-AUG-2019 (Rel. 24.08, Created)
 DT    22-AUG-2019 (Rel. 24.08, Last updated, Version 1)
 XX
 DE    Long terminal repeat of an ERV3 endogenous retrovirus from
 DE    Uraeginthus cyanocephalus, internal portion.
 XX
 KW    ERV3; Endogenous Retrovirus; Transposable Element; ERV3-3_UCy-I;
 KW    ERV3-3_UCy-LTR.
 XX
 OS    Uraeginthus cyanocephalus
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
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OC     Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC     Estrildidae; Uraeginthus.
XX
RN     [1]
RP     1-5130
RA     Bao W.;
RT     "LTR-retrotransposons from Uraeginthus cyanocephalus.";
RL     Repbase Reports 19(8), 1539-1539 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~96% identical to the consensus.
XX
SQ     Sequence 5130 BP; 1449 A; 1228 C; 1369 G; 1084 T; 0 other;

//
ID     ERV3-4_PMaj-LTR repbase;     DNA;     VRT; 1134 BP.
XX
AC     .
XX
DT     17-OCT-2018 (Rel. 24.09, Created)
DT     17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE     Endogenous retrovirus from the great tit genome, long terminal
DE     repeat consensus.
XX
KW     ERV3; Endogenous Retrovirus; Transposable Element;
KW     ERV3-4_PMaj-LTR.
XX
OS     Parus major
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN     [1]
RP     1-1134
RA     Kojima K.K.;
RT     "Endogenous retroviruses from the great tit genome.";
RL     Repbase Reports 19(9), 1744-1744 (2019).
XX
DR     [1] (Consensus)
XX
CC     ~83% identical to consensus. 5-bp TSDs.
XX
SQ     Sequence 1134 BP; 263 A; 279 C; 371 G; 220 T; 1 other;

//
ID     ERV3-5_NuM-LTR repbase;     DNA;     VRT; 540 BP.
XX
AC     .
XX
DT     06-NOV-2018 (Created)
DT     06-NOV-2018 (Last updated, Version 2)
XX
DE     Endogenous retrovirus from the guineafowl genome, long terminal
DE     repeat consensus.
XX
KW     ERV3; Endogenous Retrovirus; Transposable Element; Nonautonomous;
KW     ERV3-5_NuM-LTR.
XX
OS     Numida meleagris
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
OC     Numididae; Numida.
XX
RN     [1]
RP     1-540
RA     Kojima K.K.;
RT     "Endogenous retroviruses from the guineafowl genome.";
RL     Direct Submission to RR (06-NOV-2018).
XX
DR     [1] (Consensus)
```

```
XX
CC    ~86% identical to consensus. 5-bp TSDs.
XX
SQ    Sequence 540 BP; 125 A; 107 C; 142 G; 166 T; 0 other;

//
ID    ERV3-5_PMaj-LTR repbase;     DNA;     VRT; 982 BP.
XX
AC    .
XX
DT    17-OCT-2018 (Rel. 24.09, Created)
DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE    Endogenous retrovirus from the great tit genome, long terminal
DE    repeat consensus.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    ERV3-5_PMaj-LTR.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN    [1]
RP    1-982
RA    Kojima K.K.;
RT    "Endogenous retroviruses from the great tit genome.";
RL    Repbase Reports 19(9), 1745-1745 (2019).
XX
DR    [1] (Consensus)
XX
CC    ~85% identical to consensus. 5-bp TSDs. The consensus is ~95%
CC    identical to that of TguLTR11.
XX
SQ    Sequence 982 BP; 303 A; 226 C; 226 G; 226 T; 1 other;

//
ID    ERV3-7_PMaj-LTR repbase;     DNA;     VRT; 741 BP.
XX
AC    .
XX
DT    17-OCT-2018 (Rel. 24.09, Created)
DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE    Endogenous retrovirus from the great tit genome, long terminal
DE    repeat consensus.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    ERV3-7_PMaj-LTR.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN    [1]
RP    1-741
RA    Kojima K.K.;
RT    "Endogenous retroviruses from the great tit genome.";
RL    Repbase Reports 19(9), 1747-1747 (2019).
XX
DR    [1] (Consensus)
XX
CC    ~92% identical to consensus. 5-bp TSDs.
XX
SQ    Sequence 741 BP; 188 A; 190 C; 144 G; 217 T; 2 other;

//
ID    ERV3-N2_MUn-LTR repbase;     DNA;     VRT; 564 BP.
XX
AC    .
XX
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DT   15-DEC-2011 (Rel. 23.02, Created)
DT   26-FEB-2018 (Rel. 23.03, Last updated, Version 4)
XX
DE   Long terminal repeat: consensus.
XX
KW   ERV3; Endogenous Retrovirus; Transposable Element;
KW   ERV3-N2_MUn-LTR.
XX
NM   LTR3-2_MUn.
XX
OS   Melopsittacus undulatus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Psittaciformes; Psittaculidae;
OC   Melopsittacus.
XX
RN   [1]
RP   1-564
RA   Jurka J.;
RT   "LTR retrotransposons from birds.";
RL   Repbase Reports 18(2), 168-168 (2018).
XX
RN   [2]
RP   1-564
RA   Bao W.;
RT   "Renamed sequence.";
RL   Direct Submission to Repbase Update (26-FEB-2018).
XX
DR   [2] (Consensus)
XX
CC   ~93% identical to consensus. 5bp TSD.
CC   [2]: Renamed.
XX
SQ   Sequence 564 BP; 111 A; 128 C; 168 G; 157 T; 0 other;

//
ID   ERV44_MD_I   repbase;    DNA;     MAM; 6127 BP.
XX
AC   .
XX
DT   16-JUN-2006 (Rel. 11.06, Created)
DT   16-JUN-2006 (Rel. 11.06, Last updated, Version 1)
XX
DE   ERV44_MD_I, consensus of internal sequence of class 1 ERV
DE   sequence from Monodelphis.
XX
KW   ERV1; Endogenous Retrovirus; Transposable Element;
KW   Interspersed repeat; nonautonomous; ERV44_MD_I.
XX
OS   Monodelphis domestica
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
XX
RN   [1]
RP   1-6127
RA   Broad Institute of Harvard . and MIT .;
RT   "Monodelphis sequencing consortium WGS sequence.";
RL   May 2006 assembly.
XX
RN   [2]
RP   1-6127
RA   Gentles A.;
RT   "ERV44_MD, a class 1 endogenous retrovirus from M. domestica.";
RL   Repbase Reports 6(6), 281-281 (2006).
XX
DR   [2] (Consensus)
XX
CC   The whole ERV sequence could not be completely reconstructed.
CC   Thus the LTR sequence is not unambiguously known, however this
CC   internal region seems to be highly associated with LTR5_MD, and
CC   thus may utilize is as an LTR.
XX
SQ   Sequence 6127 BP; 2386 A; 1144 C; 1078 G; 1517 T; 2 other;
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//
ID   EnSpm-1_TC  repbase;     DNA;     PLN; 7288 BP.
XX
AC   .
XX
DT   22-AUG-2014 (Rel. 19.09, Created)
DT   22-AUG-2014 (Rel. 19.09, Last updated, Version 1)
XX
DE   EnSpm DNA transposon from the cacao genome: consensus.
XX
KW   EnSpm/CACTA; DNA transposon; Transposable Element; EnSpm;
KW   EnSpm-1_TC.
XX
OS   Theobroma cacao
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Malvales; Malvaceae;
OC   Byttnerioideae; Theobroma.
XX
RN   [1]
RP   1-7288
RA   Argout X., Salse J., Aury J.M., Guiltinan M.J., Droc G., Gouzy J.,
RA   Allegre M., Chaparro C., Legavre T. et al.;
RG   et al;
RT   "The genome of Theobroma cacao.";
RL   Nat Genet 43(2), 101-108 (2011).
XX
RN   [2]
RP   1-7288
RA   Bao W. and Jurka J.;
RT   "DNA transposons from the cacao genome.";
RL   Repbase Reports 14(9), 2344-2344 (2014).
XX
DR   [2] (Consensus)
XX
CC   The 5'-end is not determined.
XX
FH   Key           Location/Qualifiers
FT   CDS           4085..4807
FT                 /product="EnSpm-1_TC_2p"
FT                 /translation="MARCFKGYYVNGYKFHTLDYGHNRKTMNSGVCIKGSC
FT                 YNDYDRDFYGLLVDIVELEYFGVNNRVVLFKCHWFDIDKGVRVDPVHGLVE
FT                 IRHNSILASNEPFVLAEQATQVYYTPYPSNKRDRRDWWAVFKTKARSRFPI
FT                 TDNEQSDGKMIDLNEGVYQEDEVSFNSRFDHTSIDLDNNTILVSGEYEEVN
FT                 TFVDVEHNEEDDEDDEAEGEYDETEEESDEEDENDIDDDEDENEENEFAVR
FT                 "
FT   CDS           join(1009..2541,2279..3310)
FT                 /product="EnSpm-1_TC_1p"
FT                 /translation="MFVLTSDNGRHHMSVIIFFLKMERDRSWMYSRVDSSG
FT                 FLRTEFVNGVDEFISFAFSQPRYVTENKIRCPCSRCMNSKFLVADKVREHL
FT                 FRKGFTGAYTIWDAHGESFHAGQSLGHFVGEQNEVVNEVRVENPYAEMVMD
FT                 ALRPEFQFNDETRDEPVFPEDPNPNAASFFSLLNDADAALWVGCDKHTKLS
FT                 AMSQLLNVKSEFNMSEACFNRLMHLVKEMLPSDESLPENFYRMKTQLKELG
FT                 LGYQKIHACKNNCVLFYNEYSELSYCPCCGHPRYKPNKSRGGREKKIPYKI
FT                 LRYFPLTPRLQRLYMSGKTAEHMTWHATHQSNDGVLRHPVDGEAWQHFNRT
FT                 HQSFAFEPRSVRLGLCSDGFSPFGPTTKPYSVWPVMLTVYNLPPWMCMKQP
FT                 YIFLSMVIPGRTSPGQNIDVFLRPLIDELKVLWDEGVVTYDAFTHQNFILR
FT                 AALLWTINDFPAYGMLSGWSTHGRLSCPYCMEHGKSFFLEYGRKPWFFLLS
FT                 STILADGSSFSSPKRKFCGTKGWSRTMPLLTKILFYEQHSYGPLMTSLHMV
FT                 CCPGGALMDVYHVHIAWNMERVSSWSTGGSLGFFYCHRQFLPMDHPFRRQR
FT                 DKFKKRVERDPPIPRLSGAEILERLESIPNITCGTKVGDQKLPGFGQTHNW
FT                 AKKSIFWELPYWQTNLIRHNLDVMHIERNVFDNIFNTMMDVPGKTKDNIKA
FT                 RRDLEVCCRRSELHLIANNGKLFKPKASYTLTKEQRKAVCAWVKQLRLPDG
FT                 FASNIAKCVNEQECKFYGMKSHDCHVFLQRLLPIALRDMVPHAIWSAIVEI
FT                 SHFFRDLCATELRVEHINAWEGKIVETICKLEKIFPRFFRLNGAFADPLAI
FT                 RS"
XX
SQ   Sequence 7288 BP; 2259 A; 1235 C; 1514 G; 2278 T; 2 other;

//
ID   EnSpm-2_NS  repbase;     DNA;     PLN; 14652 BP.
XX
```

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AC   .
XX
DT   06-OCT-2017 (Rel. 22.10, Created)
DT   06-OCT-2017 (Rel. 22.10, Last updated, Version 1)
XX
DE   DNA transposons from the wood tobacco, consensus.
XX
KW   EnSpm/CACTA; DNA transposon; Transposable Element; EnSpm-2_NS.
XX
OS   Nicotiana sylvestris
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
OC   Nicotianoideae; Nicotianeae; Nicotiana.
XX
RN   [1]
RP   1-14652
RA   Sierro N., Battey J.N., Ouadi S., Bovet L., Goepfert S.,
RA   Bakaher N., Peitsch M.C. and Ivanov N.V.;
RT   "Reference genomes and transcriptomes of Nicotiana sylvestris and
RT   Nicotiana tomentosiformis.";
RL    Genome Biol 14(6), - (2013).
XX
RN   [2]
RP   1-14652
RA   Bao W.;
RT   "DNA transposons from the wood tobacco.";
RL   Repbase Reports 17(10), 1226-1226 (2017).
XX
DR   [2] (Consensus)
XX
CC   ~97% identical to the consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             join(3814..5271,5385..6337,6432..7215)
FT                   /product="EnSpm-2_NS_1p"
FT                   /translation="MDLPRYSKEYIEGVQSFLDFAYSYGDPQGEEIQCPCA
FT                   KCCNIRWTRRNVVYDHLICYGFVQGYTRWINHGEWEISMNVNCDMDDNVCS
FT                   YDDIDGLLNDQFRNVAHAEGVYEGPNEDANKFYNLVDEASQELYPGCKGFS
FT                   RLSFTIRLYLLKCLHGWSNASFTSLLELLKEAMPDLNIPISYNKAKSMVKD
FT                   LGLDYEKIDACPNDCMLFRNDHKDDEYCHVCGASRYIKYPEVDSDLEASKK
FT                   GYRVPAKILRHFPLIPRLKRLFMCSKTADTLRWHDEERSKDGKLRHPADGQ
FT                   AWKDFDSLHSEFARDSRNLRLGLASDGFNPFRTMSISHSTWPVILMVYNLP
FT                   PWMCMKPEYCMLSLLIPGPRSPGNDIDVYLQPLIEELNVLWESGVETYDAS
FT                   RDQTFQMRAALLWTISDFPAYAMLSGWSTKGKLACPCCNYGTNSRYLKHSR
FT                   KMCYMDHRVFLPMDHPWRSNKRSFNGKIEFRPPPPLLKGTDHNSLRHNLDV
FT                   MHIEKNIVDNVIGTILDIPGKTKDHANARYDLKEMGIRKNLQPKDTKDGKR
FT                   TKFAKACFSMTNGEKSVFCGVLKTAKLPDGSASNISRCVQLDERKLSGYKT
FT                   HDAHFMLHYLLPIPVKSILPDHVAIPLIRLSSFFRRLCQXVITMEELDCLE
FT                   VEIRETTNQLERIFPPTFFDIMIHLPIHLANEVRLGGPVQNRWMYPPERYM
FT                   CTLKSYVRNRNYPEGSIAEAYLVEECLTLCSRYLHGGVKTRFNRRPRNNDE
FT                   YDSINAQSSSLFPNTGCPLGAKKSDPIVLDDMSLNQAHIYLLNNCDEVQEY
FT                   IREYEVEVSNQRRGSKWSKAKKHSQNFSQWFETRSLKEDVPDLIKQLSFGP
FT                   NSIAKRYSGYLINGYRFHARQRDARRKTQNSGVTLVAQTTSFASSKDKNPV
FT                   DANLTYYGRIVDIVELDYYGHFRVVLFKCDWYEVEEDIYGLTYVYFNKKCY
FT                   QNEPFVLASQVHQCFYVQDPYDQDRYYVMKTVPRDLFSISDELESNAPQCY
FT                   ENEPSEYLAGPSIPEDNGEVALVRSDVPATILDVPPEGFLAQQLEIESDEE
FT                   FDFEDTS*"
FT   CDS             join(7986..8012,8678..8745,9321..10111,10189..10436,
FT                   10580..10777,10878..10970,11073..11198)
FT                   /product="EnSpm-2_NS_2p"
FT                   /translation="MTSRYCYWVVYGHVPHCSTLNAIFSGYLNFSWMNQAA
FT                   ALKRKVLNPNKAQSPMKNIGFDFQYRSSAELAKKFQIKREKLASDCNDKAA
FT                   KEQALLGVKRKNYMPATLEGQSRQRLTQSDVSVQKLGRNRLPVYKSIQSSS
FT                   REDLNTSHNIASKGQIKQRSMQLEEPIQKQGMSKLXVPTSMIQSSAKVDPN
FT                   TLHMIRRTQGEGEKQLDIQELQNCKKVKTNSVLPSTSVNQFLKKYGIQVGG
FT                   EKHPDNHPENEVRFMSSPSIDEREIELDNFAAQDEVGDDEFIGDEDMNIDG
FT                   AAGGTSEKKRVRGKTTCKNIHARSFEEREEVTFDKGQAVGPTDKRVSDLTN
FT                   FLGTIARNPRFIPLVHTSWHAVSKDIKQRMWEYVNFLIPAEGEKWVMTGLR
FT                   DAWKRHKRNIKKKYFDKNATIEQMLQIRPNEIPEVQFRQLIEYWDNEDVQA
FT                   MCQLNSENRKKQKWRHRMGPINFARVRVALRATKENNEEPSKSEMFITTRT
FT                   KKGKEVHTDTQVAIVSHAAS*"
XX
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SQ     Sequence 14652 BP; 4322 A; 2374 C; 2894 G; 5048 T; 14 other;

//
ID     EnSpm-3_ALy repbase;     DNA;     PLN; 9131 BP.
XX
AC     .
XX
DT     22-MAR-2011 (Rel. 18.02, Created)
DT     22-MAR-2011 (Rel. 18.02, Last updated, Version -1)
XX
DE     EnSpm-type DNA transposon from Arabidopsis lyrata - a consensus.
XX
KW     EnSpm/CACTA; DNA transposon; Transposable Element; EnSpm;
KW     EnSpm-3_ALy.
XX
OS     Arabidopsis lyrata
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC     Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC     Camelineae; Arabidopsis.
XX
RN     [1]
RA     Hu T.T., Pattyn P., Bakker E.G., Cao J., Cheng J.F., Clark R.M.,
RA     Fahlgren N., Fawcett J.A., Grimwood J. et al.;
RT     "The Arabidopsis lyrata genome sequence and the basis of rapid
RT     genome size change.";
RL     Nat Genet 43(5), 476-481 (2011).
XX
RN     [2]
RP     1-9131
RA     Kojima K.K. and Jurka J.;
RT     "EnSpm DNA transposons from Arabidopsis lyrata.";
RL     Repbase Reports 13(2), 921-921 (2013).
XX
DR     [2] (Consensus)
XX
CC     This consensus is generated from 10 sequences with >96%
CC     identity. ~310-bp TIRs. The exon-intron structure was predicted
CC     with Softberry FGENESH.
XX
SQ     Sequence 9131 BP; 2949 A; 1392 C; 1930 G; 2860 T; 0 other;

//
ID     EnSpm-N16_SBi repbase;     DNA;     PLN; 4996 BP.
XX
AC     .
XX
DT     19-MAR-2010 (Rel. 15.06, Created)
DT     19-MAR-2010 (Rel. 15.06, Last updated, Version 1)
XX
DE     Non-autonomous EnSpm-type DNA transposon - consensus.
XX
KW     EnSpm/CACTA; DNA transposon; Transposable Element; Nonautonomous;
KW     EnSpm; EnSpm-N16_SBi.
XX
OS     Sorghum bicolor
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC     PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae;
OC     Sorghinae; Sorghum.
XX
RN     [1]
RP     1-4996
RA     Bao W. and Jurka J.;
RT     "Non-autonomous DNA transposons from Sorghum bicolor.";
RL     Repbase Reports 10(6), 847-847 (2010).
XX
DR     [1] (Consensus)
XX
CC     TIR is 14-bp long. The family sequences contain hairpin structure
CC     (Pos. 682-2306).
XX
SQ     Sequence 4996 BP; 1442 A; 861 C; 938 G; 1753 T; 2 other;
```

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   //
   ID    EnSpm-N2_OES repbase;     DNA;     PLN; 1787 BP.
   XX
   AC    .
   XX
   DT    16-APR-2019 (Rel. 24.11, Created)
   DT    16-APR-2019 (Rel. 24.11, Last updated, Version 1)
   XX
   DE    DNA transposons from the olive genome: consensus.
   XX
   KW    EnSpm/CACTA; DNA transposon; Transposable Element; Nonautonomous;
   KW    EnSpm-N2_OES.
   XX
   OS    Olea europaea subsp. europaea
   OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
   OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
   OC    Pentapetalae; asterids; lamiids; Lamiales; Oleaceae; Oleeae; Olea;
   OC    Olea europaea.
   XX
   RN    [1]
   RP    1-1787
   RA    Kojima K.K.;
   RT    "DNA transposons from the olive genome.";
   RL    Repbase Reports 19(11), 2145-2145 (2019).
   XX
   DR    [1] (Consensus)
   XX
   CC    ~93% identical to consensus.
   XX
   SQ    Sequence 1787 BP; 558 A; 305 C; 301 G; 623 T; 0 other;

   //
   ID    EnSpm-N5_HM repbase;     DNA;     INV; 4524 BP.
   XX
   AC    .
   XX
   DT    18-NOV-2015 (Rel. 20.12, Created)
   DT    18-NOV-2015 (Rel. 20.12, Last updated, Version 1)
   XX
   DE    DNA transposon from Hydra magnipapillata - consensus.
   XX
   KW    EnSpm/CACTA; DNA transposon; Transposable Element; Nonautonomous;
   KW    EnSpm-N5_HM.
   XX
   OS    Hydra vulgaris
   OC    Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
   OC    Anthoathecata; Aplanulata; Hydridae; Hydra.
   XX
   RN    [1]
   RP    1-1151
   RA    Bao W.;
   RT    "DNA transposons from Hydra magnipapillata.";
   RL    Repbase Reports 15(12), 3609-3609 (2015).
   XX
   DR    [1] (Consensus)
   XX
   CC    ~95% identical to the consensus.
   XX
   SQ    Sequence 4524 BP; 1839 A; 616 C; 522 G; 1547 T; 0 other;

   //
   ID    EnSpm1_HV   repbase;     DNA;     PLN; 10534 BP.
   XX
   AC    .
   XX
   DT    06-FEB-2003 (Rel. 8.01, Created)
   DT    17-AUG-2004 (Rel. 9.07, Last updated, Version 2)
   XX
   DE    En/Spm-like DNA transposon.
   XX
   KW    EnSpm/CACTA; DNA transposon; Transposable Element; CACTA; Caspar;
   KW    En/Spm superfamily; En/Spm1_HV; EnSpm1_HV; TREP749; transposase.
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 XX
 OS   Hordeum vulgare
 OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC   BOP clade; Pooideae; Triticodae; Triticeae; Hordeinae; Hordeum.
 XX
 RN   [1]
 RA   Wicker T.;
 RT   "Direct submission.";
 RL   Direct Submission to Repbase Update (from TREP) (JAN-2003)..
 XX
 SQ   Sequence 10534 BP; 3294 A; 2067 C; 2252 G; 2921 T; 0 other;


 //
 ID   GGERVL-A2-I repbase;     DNA;     VRT; 5717 BP.
 XX
 AC   .
 XX
 DT   16-SEP-2019 (Rel. 24.09, Created)
 DT   16-SEP-2019 (Rel. 24.09, Last updated, Version 2)
 XX
 DE   ERV3 Endogenous Retrovirus from chicken: internal portion
 DE   consensus.
 XX
 KW   ERV3; Endogenous Retrovirus; Transposable Element; GGLTR3B5;
 KW   GGERVL-A2-I.
 XX
 OS   Gallus
 OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC   Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
 OC   Phasianidae; Phasianinae.
 XX
 RN   [1]
 RP   1-5717
 RA   Kojima K.K.;
 RT   "Endogenous retroviruses from the domestic chicken genome.";
 RL   Repbase Reports 19(9), 1718-1718 (2019).
 XX
 DR   [1] (Consensus)
 XX
 CC   ~98% identical to consensus. Its LTR is GGLTR3B5. The consensus
 CC   is ~93% identical to GGERVL-A.
 XX
 FH   Key             Location/Qualifiers
 FT   CDS             217..2430
 FT                   /product="GGERVL-A2-I_1p"
 FT                   /note="gag."
 FT                   /translation="MILLSVLNQFVGRATNFTELVILKQVPSLSCESFMDC
 FT                   LNAHLTTLSISLNALFAIVIISLSIWNYRILKKSPPKPENTEWQGVWRDLG
 FT                   ETLERWTCSVSWNFTPEHLKDPESLNRYLRQRCCGLGRSEEAQMIWGLANA
 FT                   YRALFNTIPERERILEIERRIFLAEKESLWAERKGFQAEKDNLRAERENLQ
 FT                   AEKENLRAERENLQAEKENFRAERENLQAEKENLRSERDTLQFERNSLESE
 FT                   RDVLRTERDALQHAQFSLQSEITKIQSHQAKLESELSTLIIQRDRLRAELE
 FT                   SKSIGTDQPDQPQEAPESMSVAPVRGRKTKRISTQLEQKKEEEGVVEEAVN
 FT                   VREEEEGEVEEAGDVREEEERGPVEWLQGTGVPMPSIRLHAQTPRRAGSPE
 FT                   RAGGEQDIVTIVDRSLKMNEIRGLRKDFTRHPNEPIVTWLLRCWDSGANSV
 FT                   WLDSREARQLGGIARDSAIDRRISTCQNQAFTLWKRMLLAVREKHPFKDDL
 FT                   MPEKRKWTDMEKGIRYLRECAVVEMIYSPDFIPDEPDQEHDPERVRCTPNM
 FT                   WRTFTKTAPERYASTFAAMYGRGERRPLIDDLVNRLQDFELHLNPLRACVS
 FT                   AITRIVEKLDRIESKQEDIIDELSTKRDADGSMVDEDQNSQNPPLEELINL
 FT                   VSSRPTSSNISAIKRGRPPARGNDNGKTITRLALWRYLRDHGEDMKKWHKK
 FT                   PTSALQARIKELQDRSTTKVKSSKRVIAPVAADNQGNK"
 FT   CDS             2434..5610
 FT                   /product="GGERVL-A2-I_2p"
 FT                   /note="retropepsin, reverse transcriptase,
 FT                   ribonuclease H, and integrase."
 FT                   /translation="RGPAPSQEGERDNRVYWTVWIRWPGTSNPQKFKALVD
 FT                   TGAQCTLMPSSHQGTESIYIHGVTGGSQELTMLEAEISLTGKDWQKHPIVT
 FT                   GPGAPCILGIDYLRRGYFKDPKGYRWAFGIAAVDTEGVKQLSALPGLSEDP
 FT                   SVVGLLRVKEQQVPIATKTVHRRQYRTNRDSLLPIQKLIRQLESQGVISKT
 FT                   HSPFNSPIWPVRKASGEWRLTVDYRGLNEVTPPLSAAVPDMLELQYELESK
 FT                   AAKWYATTDIANAFFSIPLATECRPQFAFTWRGVQYTWNRLPQGWKHSPTI
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FT                   CHGLIQAALEQGGAPEHLQYIDDIIVWGNTAREVFEKGEQVIQILLSAGFA
FT                   IKRSKVKGPAQEIQFLGIKWQDGRRHIPTDVVDKITAMSPPTNKKETQSFL
FT                   GVVGFWRMHVPNYSLIVSPLYQVTRKKNDFTWGPEQQQAFEQIKQEIARAV
FT                   ALGPVRTEQDVKNILYTAAGEKGPTWSLWQRASGETRGRPLGFWSRAYRGS
FT                   EEHYTPTEKEILAAYEGVRAASEVVGTETQLLLAPRLPVLNWMFKGKVPST
FT                   HHATDATWSKWIALITQRARMGNLSRPGILEVIMDWPEGKKFGTSPGEEVS
FT                   RAKEAPPYNELPENEKKYALFTDGSCRIVGKHRRWKAAVWSPTRQVAEATE
FT                   GKGESSQFAEVKAIQLALDVAERERWPMLYLYTDSWMVANALWGWLQQWEQ
FT                   NNWQRRGKPVWAAELWKDIAARIKNMVVKVRHVDAHVPKNRATEEQQNNHQ
FT                   VDRAAKIEVAQIDLDWQNKSELFLARWAHETSGHQGRDATYKWARDRGVDL
FT                   TMDAIAQVIHDCETCAIIKQAKRMKPLWEEGRWQKYKYGEAWQVDYITLPR
FT                   SRNGKRYVLTMVEATTGWLETYAVPHATARNTILGLEKQVLWRHGTPERVE
FT                   SDNGTHFKNSLVNTWAKDHGIEWIYHIPYHAPASGKIERYNGLLKTMLKAM
FT                   GGGTFKHWEKHLAEATWLVNTRGSINRDGPASSLHTVKGDKVPVIHVKNML
FT                   GKAVWVLPASGKGKPLRGTVFAQGPGCTWWVMQKNGDVHCVPQGNLMMGER
FT                   NQ"
XX
SQ   Sequence 5717 BP; 1683 A; 1187 C; 1536 G; 1311 T; 0 other;

//
ID   GymnSINE    repbase;    DNA;    VRT; 302 BP.
XX
AC   .
XX
DT   23-APR-2016 (Rel. 21.05, Created)
DT   24-APR-2016 (Rel. 21.05, Last updated, Version 1)
XX
DE   SINE non-LTR retrotransposon from Gymnopithys rufigula.
XX
KW   SINE3/5S; SINE; Non-LTR Retrotransposon; Transposable Element;
KW   Nonautonomous; GymnSINE.
XX
OS   Gymnopithys rufigula
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Thamnophilidae;
OC   Gymnopithys.
XX
RN   [1]
RP   1-302
RA   Suh A., Witt C.C., Menger J., Sadanandan K.R., Podsiadlowski L.,
RA   Gerth M., Weigert A., McGuire J.A., Mudge J. et al.;
RT   "Ancient horizontal transfers of retrotransposons between birds
RT   and ancestors of human pathogenic nematodes.";
RL   nature communications 7, 11396-11396 (2016).
XX
DR   [1] (Consensus)
XX
CC   GymnSINE is mobilized by AviRTE in Gymnopithys rufigula.
CC   Positions 1-118 are 5S-rRNA-derived, positions 119-302 are
CC   AviRTE-derived.
XX
SQ   Sequence 302 BP; 75 A; 84 C; 75 G; 68 T; 0 other;

//
ID   Gypsy-129_GM-I repbase;    DNA;    PLN; 3510 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 17.03, Created)
DT   08-MAR-2012 (Rel. 17.03, Last updated, Version -1)
XX
DE   LTR retrotransposon from soybean: internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-129_GM_;
KW   Gypsy-129_GM-LTR; Gypsy-129_GM-I.
XX
OS   Glycine max
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae;
OC   Phaseoleae; Glycine; Soja.
XX
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```
RN    [1]
RA    Schmutz J., Cannon S.B., Schlueter J., Ma J., Mitros T.,
RA    Nelson W., Hyten D.L., Song Q., Thelen J.J. and Cheng J. et al.;
RT    "Genome sequence of the palaeopolyploid soybean.";
RL    Nature 463(7278), 178-183 (2010).
XX
RN    [2]
RP    1-3510
RA    Jurka J.;
RT    "LTR retrotransposons from soybean.";
RL    Repbase Reports 12(3), 351-351 (2012).
XX
DR    [2] (Consensus)
XX
CC    Positions [2801-3334] - Integrase core
CC    'CAAAT' target site duplication
CC    LTRs are 98% similar to each other.
XX
FH    Key           Location/Qualifiers
FT    CDS           983..3508
FT                  /product="Gypsy-129_GM-I_1p"
FT                  /translation="MAGAGDGGGEYHQLDGSQRLLLDVMTTQMQRLLNRNN
FT                  EELYGRIEGLENQLNQNAGRHYGGNRGGNDGPRQNRMEGQNRIEGVKLNVP
FT                  PFKGRSDPDAYLDWEMKIEHVFSCNDYTEEQKVKLAAAEFSDYALVWWNKN
FT                  QREMMREEGREIDTWTEMRRVMRKRYVPTSYSRTMRQKLQRLSQGSLTVEE
FT                  YYKEMEMALVRANIEEETEDTMARFLSGLNPDIRDVVELQEYVELDDLLHK
FT                  AVRVEQQLKRKIAARRNSSNTFNQNWTNRSKKEGGNSSSPSTQSPHGKSAV
FT                  SSAGTKHNSASSSNTGTRNIKCFKCLGRGHIASDCPTRRTMIMKADGEITS
FT                  ESEISEEEEVEEELEEEAMQGDMLMVRRLLGSQMQPLDDTQRENIFHTRCT
FT                  INGKLCSLIVDGGSCTNVASSRLVSKLNLDTKPHPRPYRLQWLSEDEEVKV
FT                  TQQVEVCLTIGRYNDRVLCDVVPMEATHILLGRPWQYDTKAVHDGFTNKIS
FT                  FQHHDQKIILKPLSPREVCDDQIRMREKREQEKEKSEAPKRNRKKKSDTRE
FT                  GKSDTHERKSDTHERKFNCLAKASEVRKVLLAREPLYLLYCKDSKVSADNS
FT                  NELTISASPSVEPLLQEFKDVFPKEIPHGLPPSRGIEHQIDLLPGASLPNR
FT                  PAYKSNPQETDVADLFFKEVVRLHGLPRSIVSDRDTKFLSHFWRTLWGRVG
FT                  LKLLFSTTCHPQTDGQTKHKDAQAKVEYVKRLHEQVKAQIAKKNESYAKQA
FT                  NKNRKKVVLEPGDWVWVHMRKERFPKQRKSKLQPRGDRPFQVLERINDNAY
FT                  KIDIPGEYGVSSSFNVADLTPFVAGDDSEHLRANAFQEGG"
XX
SQ    Sequence 3510 BP; 1080 A; 626 C; 840 G; 964 T; 0 other;

//
ID    Gypsy-12_ATr-LTR repbase;     DNA;     PLN; 4130 BP.
XX
AC    .
XX
DT    13-FEB-2014 (Rel. 20.04, Created)
DT    13-FEB-2014 (Rel. 20.04, Last updated, Version 1)
XX
DE    LTR retrotransposon from the Amborella trichopoda genome:
DE    internal portion, a consensus.
XX
KW    Gypsy; LTR Retrotransposon; Transposable Element;
KW    Gypsy-12_ATr-LTR.
XX
OS    Amborella trichopoda
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; basal Magnoliophyta; Amborellales;
OC    Amborellaceae; Amborella.
XX
RN    [1]
RT    "The Amborella genome and the evolution of flowering plants.";
RL    Science 342(6165), - (2013).
XX
RN    [2]
RP    1-4130
RA    Bao W. and Jurka J.;
RT    "LTR retrotransposons from the Amborella trichopoda genome.";
RL    Repbase Reports 15(4), 1414-1414 (2015).
XX
DR    [2] (Consensus)
XX
CC    ~90% identical to the consensus.
```

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  XX
  SQ     Sequence 4130 BP; 658 A; 1480 C; 532 G; 1460 T; 0 other;

  //
  ID     Gypsy-12_DRh-I repbase;      DNA;     INV; 4893 BP.
  XX
  AC     .
  XX
  DT     12-DEC-2011 (Rel. 17.08, Created)
  DT     12-DEC-2011 (Rel. 17.08, Last updated, Version -1)
  XX
  DE     LTR retrotransposon from the Drosophila rhopaloa genome: internal
  DE     portion.
  XX
  KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-12_DRh_;
  KW     Gypsy-12_DRh-LTR; Gypsy-12_DRh-I.
  XX
  OS     Drosophila rhopaloa
  OC     Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
  OC     Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
  OC     Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
  OC     melanogaster group; rhopaloa subgroup.
  XX
  RN     [1]
  RP     1-4893
  RA     Jurka J.;
  RT     "LTR retrotransposons from the Drosophila rhopaloa genome.";
  RL     Repbase Reports 12(8), 1573-1573 (2012).
  XX
  DR     [1] (Consensus)
  XX
  CC     Positions [1775-2197] - Reverse transcriptase
  CC     Positions [3245-3721] - Integrase core
  CC     LTRs are 93% similar to each other.
  CC     This consensus sequence was derived from the data released in
  CC     Genbank by the Baylor College of  Medicine Human Genome
  CC     Sequencing Center, prior to publication.
  XX
  FH     Key            Location/Qualifiers
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  FT                    ENQIAQMKQRETEPVREYAMGLRKLMQFTKLSEEAKLDRVYRNSRSKIKLY
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  FT     CDS            join(902..2947,2951..4810)
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  FT                    GKLFSVTFMILTEVAGGILLGMDFLAGVHSTLRCGNLELEIREPGGEEDQP
  FT                    ETNTEQEDTTGEPSEKEVQDFLETQRQVFEGMQGTSNITKHHIYLKDDKPI
  FT                    KQRYYPRNPKQQAIINEQVNELLALGLIEPSRSPYSAPVVLVRKKNNEWRM
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XX
SQ     Sequence 4893 BP; 1751 A; 1051 C; 1326 G; 764 T; 1 other;

//
ID   Gypsy-12_SLy-LTR repbase;     DNA;     PLN; 2030 BP.
XX
AC   .
XX
DT   31-AUG-2018 (Rel. 23.10, Created)
DT   31-AUG-2018 (Rel. 23.10, Last updated, Version 1)
XX
DE   LTR retrotransposon - long terminal repeat.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element;
KW   Gypsy-12_SLy-LTR.
XX
OS   Solanum lycopersicum
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
OC   Solanoideae; Solaneae; Solanum; Lycopersicon.
XX
RN   [1]
RP   1-2030
RA   Kojima K.K.;
RT   "LTR retrotransposons from the tomato genome.";
RL   Repbase Reports 18(10), 1160-1160 (2018).
XX
DR   [1] (Consensus)
XX
CC   ~95% identical to consensus.
CC   Similar to Ogre-SD1.
XX
SQ     Sequence 2030 BP; 894 A; 224 C; 263 G; 649 T; 0 other;

//
ID   Gypsy-13_CCO-I repbase;     DNA;     PLN; 5421 BP.
XX
AC   AACS02000012;
XX
DT   30-JAN-2011 (Rel. 16.02, Created)
DT   30-JAN-2011 (Rel. 16.02, Last updated, Version -1)
XX
DE   LTR retrotransposon from the mushroom Coprinopsis cinerea genome:
DE   internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-13_CCO_;
KW   Gypsy-13_CCO-LTR; Gypsy-13_CCO-I.
XX
OS   Coprinopsis cinerea
OC   Eukaryota; Fungi; Dikarya; Basidiomycota; Agaricomycotina;
OC   Agaricomycetes; Agaricomycetidae; Agaricales; Psathyrellaceae;
OC   Coprinopsis.
XX
RN   [1]
RP   1-5421
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from the mushroom Coprinopsis cinerea
RT   genome.";
RL   Direct Submission to RU (29-JAN-2011).
XX
DR   Genome; AACS02000012; Positions  324606  319186.
XX
CC   'CTTGC' target site duplication
CC   LTRs are 100% similar to each other.
XX
FH   Key              Location/Qualifiers
FT   CDS              128..5257
FT                    /product="Gypsy-13_CCO-I_1p"
FT                    /translation="MVDSLELRGRTLERTVPVRKARRTRKNQTTTTMDSPQ
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XX
SQ   Sequence 5421 BP; 1446 A; 1446 C; 1321 G; 1208 T; 0 other;


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ID   Gypsy-18_AG-I repbase;     DNA;     INV; 3956 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 21.07, Created)
DT   22-MAR-2011 (Rel. 21.07, Last updated, Version -1)
XX
DE   LTR retrotransposon from Anopheles gambiae: internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-18_AG_;
KW   Gypsy-18_AG-LTR; Gypsy-18_AG-I.
XX
OS   Anopheles gambiae
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
OC   Culicoidea; Culicidae; Anophelinae; Anopheles.
XX
RN   [1]
RP   1-3956
RA   Jurka J.;
RT   "LTR retrotransposons from Anopheles gambiae.";
RL   Repbase Reports 16(7), 1440-1440 (2016).
XX
DR   [1] (Consensus)
XX
CC   Positions [2993-3469] - Integrase core
CC   LTRs are 98% similar to each other.
XX
FH   Key             Location/Qualifiers
FT   CDS             1883..3955
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XX
SQ   Sequence 3956 BP; 1310 A; 740 C; 1128 G; 775 T; 3 other;

//
ID   Gypsy-18_MN-I repbase;    DNA;     PLN; 9360 BP.
XX
AC   ATGF01022208;
XX
DT   12-OCT-2013 (Rel. 20.11, Created)
DT   12-OCT-2013 (Rel. 20.11, Last updated, Version 1)
XX
DE   LTR retrotransposon from the mulberry tree: internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-18_MN-I;
KW   Gypsy-18_MN-LTR; Gypsy-18_MN_.
XX
OS   Morus notabilis
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Rosales; Moraceae; Morus.
XX
RN   [1]
RP   1-9360
RA   Jurka J.;
RT   "LTR retrotransposons from the mulberry tree.";
RL   Direct Submission to Repbase Update (11-OCT-2013).
XX
DR   Genome; ATGF01022208; Positions   93196  102555.
XX
CC   Positions [4905-5408] – Integrase core
CC   LTRs are 97% similar to each other.
XX
FH   Key             Location/Qualifiers
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XX
SQ     Sequence 9360 BP; 2755 A; 1930 C; 2291 G; 2384 T; 0 other;

//
ID     Gypsy-21_SM-I repbase;      DNA;      INV; 14614 BP.
XX
AC     AAWT01054580;
XX
DT     26-DEC-2011 (Rel. 23.04, Created)
DT     26-DEC-2011 (Rel. 23.04, Last updated, Version -1)
XX
DE     LTR retrotransposon from the Schmidtea mediterranea genome:
DE     internal portion.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-21_SM_;
KW     Gypsy-21_SM-LTR; Gypsy-21_SM-I.
XX
OS     Schmidtea mediterranea
OC     Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Seriata;
OC     Tricladida; Continenticola; Geoplanoidea; Dugesiidae; Schmidtea.
XX
RN     [1]
RP     1-14614
RA     Jurka J.;
RT     "LTR retrotransposons from the Schmidtea mediterranea genome.";
RL     Direct Submission to Repbase Update (26-DEC-2011).
XX
DR     Genome; AAWT01054580; Positions    26061    40674.
XX
CC     'ATAT' target site duplication
CC     LTRs are 99% similar to each other.
XX
FH     Key           Location/Qualifiers
FT     CDS           9643..10962
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FT                   IARENERSNGNETTTVTKQTNGNSELKRDIIEKSISKIEKEFEIPPRGLIK
FT                   VKTKRNLRINMLRNIRDSSPEDGEISETSSLMGEALQVSENEEQNKQIIRP
FT                   MNRWIYDRPFSPTEGEIKLINELIETIPETLINEEFINNEAFRRYMRNILQ
FT                   LEGTRGDVILEQEKPRVKAYLDKQKLEDITKFQILMQTPDFIERIWIKQPN
FT                   TDEIFDWIKERMGSSKKNDNLYYNGWLIKPDLHLVDALIWPGQPTYVTLEK
FT                   EKTVPDFGVWAEYAKNEFEINIKKNLQGATKRIFCKNREKLITQIIDQIHK
FT                   NWEILMYLKPVEMKVCIENLRDTVIHRHANYKNTTLIGRYGTHRVGKEKAK
FT                   ELKIKVKLPNEEQRTLKMSNKTRVNELIKIINEMIMEQTKDQSEDGMIEDV
FT                   AVKYLHHYLHEEDETYLYELGIWDDDQEIRIVPMEEARWGTDTTWKEMDEI
FT                   EKEGHQKSKRIIETYRQWRKDHRLKEKLSELDTNECKPTPWRKQWNEQEKR
FT                   WELKPGTIEEEPLEEEKVNNHEYRMKETENKTMSENECRKINVMKRQRSQP
FT                   VDIDETQIKLENDHCEKLIEILQQGARSQRRAATAHAKYMAENGENLENLR
FT                   ELVKEIEEYRRKNEWCPEVFDQVIRKWKHREWAQETQGKYKIKVFYPDQTS
FT                   EELEVHPTAKIKEVKRKLAYETPFHLQFHGRSLDNMLEVGVTPMVMGEINP
FT                   LKMAETLGIPLKRKEIKPKPIKASMSTPSMGGDKNETPKMFEGDEVMILND
FT                   NTDEEEELSPLVIKTPIKLPEIREEQPSTSYHQIEEQQGDEIEEMIIEMDI
FT                   EDKDFTPMKKCITQTHEAKDDIYLTQDWDEWLRKQNEESQRITLTNTTENE
FT                   TTKETGTSMEKRPRGRPKLVTENGEPKIKNQSKQQQWMTRLDKLEKIAYEM
FT                   RKIHPREESGTEWIRELLADMLIITSQPLRRLWQRNRASEDAKQLWYTVSS
FT                   IIPKLIKEKTKKMKLEWEEMRQIVAQLLTNTDDDEYRLVAFSYLVYNLMSL
FT                   ATSKIPNKQFMNKVELTAMIVQQEIEPGILQNGGWKQFINKPRKNEQVKPM
FT                   HVRLKALLNDFEHELPIKDIAMRNASIHSLMMTMMVWLMCTGATNGFLIFD
FT                   CDKAVLGDKYSLKDIKECRMAIPNNLTTIEKAITYHIYQESDFIRTKAKEC
FT                   AITRKTLAYHCGAHSHVSIINPGTEREILQVSGEQCKDLFSGGEMRLKEGV
FT                   VLKGKSGMIQVQSIFVAGVINSATGDCQGGKYTIKGELVTGVVVIETYTVE
FT                   LKEYEAQFDGATQVMKSNQMCQATDTVCKTGTSTIIYQANIHKCRMQFLKT
FT                   ALFDEVRGEVFEEDAEELQINDVNKIITRAGKIKARTRSQPLRTKQTPAAL
FT                   ITTEAEMGMRFIKGKITQKCGKMVYATNYPGLYAARQMLEQGIAAVAKDEV
FT                   KLYLYMNNKMDFLYHKGQESMQKVYHDLIRNDCQLNKEILKTTLRYE"
XX
SQ   Sequence 14614 BP; 6493 A; 2468 C; 2908 G; 2745 T; 0 other;

//
ID   Gypsy-22_CT-I repbase;     DNA;     INV; 4225 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 19.07, Created)
DT   22-MAR-2011 (Rel. 19.07, Last updated, Version -1)
XX
DE   LTR retrotransposon from Capitella teleta (a polychaete worm):
DE   internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-22_CT_;
KW   Gypsy-22_CT-LTR; Gypsy-22_CT-I.
XX
OS   Capitella teleta
OC   Eukaryota; Metazoa; Lophotrochozoa; Annelida; Polychaeta;
OC   Scolecida; Capitellida; Capitellidae; Capitella.
XX
RN   [1]
RA   Simakov O., Marletaz F., Cho S.J., Edsinger-Gonzales E.,
RA   Havlak P., Hellsten U., Kuo D.H., Larsson T. et al.;
RT   "Insights into bilaterian evolution from three spiralian
RT   genomes.";
RL   Nature 493(7433), 526-531 (2013).
XX
RN   [2]
RP   1-4225
RA   Jurka J.;
RT   "LTR retrotransposons from Capitella teleta (a polychaete
RT   worm).";
RL   Repbase Reports 14(7), 1951-1951 (2014).
XX
DR   [2] (Consensus)
```

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      XX
      CC    Positions [1619-1993] - Reverse transcriptase
      CC    Positions [3248-3754] - Integrase core
      CC    LTRs are 100% similar to each other.
      XX
      FH    Key           Location/Qualifiers
      FT    CDS           join(20..2206,2210..4162)
      FT                  /product="Gypsy-22_CT-I_1p"
      FT                  /translation="MTNQQRQYRPSLDWTPDTKLPQRFARWKEEMEDEILL
      FT                  FEGDEKSPKYICNFIKVCSGERGKAILQEIKLDQETKEYRNIISALEKQVK
      FT                  PTNEEISASYKYFYLRQGDLTLTEFYKQARDLVCAMNMDKDPLDKTLRNVL
      FT                  LNGLSSKEIYKECLKVDVGKLTSKAVMDIASNIQARNLMAEDLSMTAQQVL
      FT                  PENALTKGFPPLSSTPINRIRLQNHHPGASIQQKGCGWCGKQVRCSRNECP
      FT                  ANRSTCNNCGKIGHWGKVCRASSRKHPSFSKTKVHEIEDKHHETPHDDDDD
      FT                  AGDQESVSFHTLSTSSDPKAPHLRPMWFSTPDSSTVHLVEAEIDSGAGCNT
      FT                  IPLYLYNKTIGTGVRMEPATVKIKAYGDHSVKTIGSTLLRLRIGNQTLSRR
      FT                  FQVCDVRKHPIIGRHLSEEMGYIRFPPVKRPDLSSLPAVEKIYALRTGSSV
      FT                  EYVSIKKPTIQKQSTNSVTIEGRNHQLPITQEYVLKEFKDVFSGMGELPGG
      FT                  EYMVKLKPDAEPVQHAPRRVPEKKKLAYKAEIERLVREKVIVPVKQHSEWV
      FT                  NSAVSVDKPDGSIRLCLDPSDINKAIERNQYHMRSIDEISAELHGAKHFTL
      FT                  MDAKSGYWQVKLNEKSSFLTTFNTPWGKYRFLRLPFGLKVSSDVFQERLDS
      FT                  ILINSPGVTGIADDCLITGKTLQEHDLNLLHLLHLARLNNLKFNEKKLQFR
      FT                  TTSCKFFGQVLTPEGIKIDPDKVRAIQEMTPSNKQELESYLGLVNYLKRHS
      FT                  YQLTHLTKPFNDLMQKNAIFSWESSQDEAFQAIKKVITSAPVLEFYDVQAN
      FT                  HVIQTDASNKGFGAVLLQNDKPVIFAGRGLLPAEHNYSTIEKELAAIVFAL
      FT                  RRMHHFIHGGKVLVQTDHKPLVAMFNRQVHLSSIRQQRLLLKLHEYDVQME
      FT                  YLKGKNNVIADALSRLTASTEQIVEPDTVIPVHTITSTINASESRLERLRK
      FT                  ATASDSIMNQLSHYIVHGWPTHRHLSDPLTFDYWNYKSELSIEDGIIFKGD
      FT                  KLVIPEAERVSYTKDLHVGHLGEEKTLLRARQLVFWPNLTNDIRAVVSGCT
      FT                  TCQADRPALQREPMIPHEMPARPWEVVGIDFFEWNGSHYLLIADVFSKFPV
      FT                  IRGMTVTTTTKTIAVLKTVFGEYGVPQQIMTDQGPQFTSQEFQEFTNSYEI
      FT                  NTKHSSPRYPQSNGFIEAMVKTVKGILTRARDSGTDPQLAMLIYRTTPFKA
      FT                  GVASPSELLNGRRYQALIPMKERLSSCQEYSRERLLNNRQQVIDKYNEQAK
      FT                  NRSDLQEMQKVWFQKDPNRPRWEEATVVQVTDQPRSYVVQKEDGAQYQRTS
      FT                  RHVRPAAQKQDAPAAPKQDTPAAPKQDDASTEMTAAVAPPVVSESPQQTQP
      FT                  YMTRSGRVSRKPDRLQL"
      XX
      SQ    Sequence 4225 BP; 1343 A; 1029 C; 924 G; 927 T; 2 other;

      //
      ID   Gypsy-232_OS-LTR repbase;     DNA;     PLN; 3414 BP.
      XX
      AC    .
      XX
      DT    10-JAN-2018 (Rel. 23.04, Created)
      DT    30-JAN-2018 (Rel. 23.04, Last updated, Version 1)
      XX
      DE    LTR retrotransposon from the rice genome: long terminal repeat.
      XX
      KW    Gypsy; LTR Retrotransposon; Transposable Element;
      KW    Gypsy-232_OS-LTR.
      XX
      OS    Oryza sativa
      OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
      OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
      OC    BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
      XX
      RN    [1]
      RP    1-3414
      RA    Bao W.;
      RT    "LTR retrotransposons from the rice genome.";
      RL    Direct Submission to Repbase Update (30-JAN-2018).
      XX
      DR    [1] (Consensus)
      XX
      CC    Solo-LTR from a single locus.
      XX
      SQ    Sequence 3414 BP; 727 A; 1026 C; 715 G; 946 T; 0 other;

      //
      ID   Gypsy-23_GAr-LTR repbase;     DNA;     PLN; 3165 BP.
      XX
      AC    .
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XX
DT   01-JUN-2014 (Rel. 23.07, Created)
DT   01-JUN-2014 (Rel. 23.07, Last updated, Version 1)
XX
DE   LTR retrotransposon from the Gossypium arboreum genome: long
DE   terminal repeat.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element;
KW   Gypsy-23_GAr-LTR.
XX
OS   Gossypium arboreum
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Malvales; Malvaceae; Malvoideae;
OC   Gossypium.
XX
RN   [1]
RP   1-3165
RA   Jurka J.;
RT   "LTR retrotransposons from the Gossypium arboreum genome.";
RL   Repbase Reports 18(7), 800-800 (2018).
XX
DR   [1] (Consensus)
XX
CC   ~99% identical to consensus.
XX
SQ   Sequence 3165 BP; 928 A; 474 C; 742 G; 1021 T; 0 other;

//
ID   Gypsy-29_CT-I repbase;    DNA;    INV; 6477 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 19.07, Created)
DT   22-MAR-2011 (Rel. 19.07, Last updated, Version -1)
XX
DE   LTR retrotransposon from Capitella teleta (a polychaete worm):
DE   internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-29_CT_;
KW   Gypsy-29_CT-LTR; Gypsy-29_CT-I.
XX
OS   Capitella teleta
OC   Eukaryota; Metazoa; Lophotrochozoa; Annelida; Polychaeta;
OC   Scolecida; Capitellida; Capitellidae; Capitella.
XX
RN   [1]
RA   Simakov O., Marletaz F., Cho S.J., Edsinger-Gonzales E.,
RA   Havlak P., Hellsten U., Kuo D.H., Larsson T. et al.;
RT   "Insights into bilaterian evolution from three spiralian
RT   genomes.";
RL   Nature 493(7433), 526-531 (2013).
XX
RN   [2]
RP   1-6477
RA   Jurka J.;
RT   "LTR retrotransposons from Capitella teleta (a polychaete
RT   worm).";
RL   Repbase Reports 14(7), 1965-1965 (2014).
XX
DR   [2] (Consensus)
XX
CC   Positions [3716-4192] - Integrase core
CC   LTRs are 97% similar to each other.
XX
FH   Key             Location/Qualifiers
FT   CDS             210..1451
FT                   /product="Gypsy-29_CT-I_2p"
FT                   /translation="MSFKWVRSDLNNRLIRMPESETQTSPESLIYTNNIEN
FT                   ANNEDSSIASCNAGMEYDSFTGPQANETIRVKPEANGRRIRINEFTLESDE
FT                   GDTESDLEINRDEQDALKFFSAIADVSATERFIKRVGFCDGDKPSRTLEWL
FT                   RAIDRLPDNVQVEIALQTAESTIHSSLRELKNAKWPKIKTLLANRYVNANF
FT                   SEAQKEALDRLEQRPGEGLYNYITTFEVLLNEAYQALPLDQTSLIRTFLSG
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FT                   LSDRDMAKSVARKKLRTLPEVVKEVRRHYQDDDLLRPRKISKVHAIDKYEN
FT                   PQVSALSVVVTDLVNMQKETNAQIAALAKVETKPTPKSNYSCFRCGKPGHF
FT                   SRECRTKNTSVPPVKTMHQNASGQTCHRCRRPGHTFKNCRAGPPRSPCYCG
FT                   GSHWLFDCPKKSQTIPKSGN"
FT   CDS             1658..4786
FT                   /product="Gypsy-29_CT-I_1p"
FT                   /translation="MSITNHELPIRGMCNVRLAGLPIEVLVCESLGVDILI
FT                   GSDLCRSAVIDFKNGLLTLGNQKFPMQTVEKSCFSVVAVSCIPRAPQAVVN
FT                   DVIDAYRDIFSVKATPVNVARSLPPAVIDTGDHPPIKQPSYRMPLLKRQKV
FT                   EDCVTEMLRDGIIRPSDSAWASPITLAPKKDGTTRFCVDYRKINAITRKDA
FT                   HPLPLIQDVFDQVAGSKIFSTLDLRSGYWQVPMADSSISRTAFSCHLGLFE
FT                   FVRMPFGLTNAPAIFQRAMNKVLSGLIGRCCMVYLDDIVIFSRNPKEHAQH
FT                   LEQVFKRLRESGLQLKPSKCHFGLSQIDLLGHSVSADGIKPLSDRVEAIKT
FT                   LGPPKDLTSVRSFLGMAGYYRQFIPGFATLAAPLTDLTKSREPFRWGSEQQ
FT                   EAFDALKTALTQSPILVHPDVSKPYILYTDASNKAVGAILVQKDNEGVERV
FT                   ISYLSHKLSGAQLNWATIEKEAYAIIYALKKFHAYLWGAKFEIHTDHKPLR
FT                   SLFQSEIRSSKISRWSQQIQEFQAPILYHPGKLNIRADMLSRIAAIEPSTP
FT                   TPVVVPADIPDVWVTDRIDLHDLARRQKEQFCDAYVEASQETDESPYIVQG
FT                   SLLFTMAEPSRNAGRYLRLLLPQQFRQQVIDRCHAEVGHAAFLKTLARVQE
FT                   HYVWPGMRQHIKDYIRHCVLCNSLSPNHPAHPRGTVPVPPAPFHTWGIDLV
FT                   GPFPRDRRGRQYLLTCVDHLSGWCEAIPIASKKADTVQEAFIDNIVARYGV
FT                   PRYLISDNGGEMTSSNFENWLREFGISHRLTSPYHPQCNGMTERFNGTIQK
FT                   LLLKLTGGNPRKWTEYLASALYAYRITQGQAGISPYQAVFGQKPRLPRANP
FT                   SSQEEGERLQAIRLAERILREYRSKQKETYRENEPSRAKRLPPGTFVSVRI
FT                   LNPKKGETRWQPGYQVISSHDGALRVIELDTGNVVRINQRNVREIPESKPY
FT                   DEINPLPPLKNQTTFDYVSSEAKPIPVVEESYLPTRIPRGPKRPSNDQPNL
FT                   TTPSVPVPAVSAALAPSIVFPSDDWSSWCDFVFHFTH"
XX
SQ   Sequence 6477 BP; 1889 A; 1422 C; 1372 G; 1794 T; 0 other;

//
ID   Gypsy-31_MAc-I repbase;      DNA;      PLN; 9498 BP.
XX
AC   .
XX
DT   07-SEP-2018 (Rel. 24.04, Created)
DT   10-SEP-2018 (Rel. 24.04, Last updated, Version 1)
XX
DE   LTR retrotransposon from the wild banana Musa acuminata: internal
DE   portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-31_;
KW   nonautonomous; Gypsy-31_Mac-I.
XX
OS   Musa acuminata
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC   Musa.
XX
RN   [1]
RP   1-9498
RA   Bao W.;
RT   "LTR retrotransposons from the wild banana Musa acuminata.";
RL   Repbase Reports 19(4), 546-546 (2019).
XX
DR   [1] (Consensus)
XX
CC   Consensus. Elements are ~87% identical to the consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             join(686..5368,5372..5899,5915..6244)
FT                   /product="Gypsy-31_MAc-I_1p"
FT                   /translation="MEHVSAFRAQMALYGTSDALMCRAFPTTLRGPTRTWF
FT                   SRLRQSSVSSFDQLAGEFEQNFLASARPRPSMATLLMLSQREDESLSQFVA
FT                   RFATEIRGFPDAHPSLILQAFLMGLKPSRFFWSLIEKPPATISEMLQRANQ
FT                   YVAAEALVAGRRMEGKRPRAELSRGTTSAAPATPRRGLGRQELPLPRPPPL
FT                   PLNTSRTEIFLQIKETGLLQQPRPMKATHKDRSKYCRFHRDYGHDTEDCRD
FT                   LQNQIEALIRRGHLGRYLKSPEATPRPKGPVERQIDVISGGPAAGGSSSAA
FT                   RKAYARSTVEKRPRPELEPEITFGAGEAERSHHDDALVISIQIANARVKRV
FT                   MVDTGSSADVLYFDAFKKLGLTEGDLTPMTSALTGFTGDSISPLGTTVLPV
FT                   TIGEEPRAKTIMTTFMVVDLPSAYNVILGRPTLNKIKAVVSTYHRTIKFPT
FT                   SAGIGEARSDPGESRRCYLAAVTLPGKPRPTPVPDPREEPVPQVPLEPPEP
FT                   LIEVPLKRSRPDQTVKVGATLPEADQLHLIDFLRKNADMFAWSPEEMPGID
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FT                    PEVAQHRLNIDPEARPVRQRPRRFAPDRQKAIGDEVDRLIKAGFITEVKYP
FT                    RWLSNVVLVKKPNGSWRMCVDYTDLNRACPKDCYPLPRIDQLVDATAGHER
FT                    LTFMDAFSGYNQIRMATQDQEDTAFVTNRGAYCYKVMPFGLKNAGATYQRM
FT                    VDKLFKHQLGRNMEVYVDDMIVKSKVARTHLADLAETFQTLRRFNMRLNPA
FT                    KCVFGVSSGRFLGFVIHQRGIDANPEKVRAVTEMRSPRSAKEVQRLAGRLA
FT                    ALSRFVSRSGDKCLPFFRALRWADNFTWTSECEEAFEKLKACLARLPRLAS
FT                    PEPGETLGLYLAASAQAVSSVLVREIPPAQLPIHYVSHILGGPEARYSPIE
FT                    KLALALIKMARKLRPYFQAHTIKVITDQPLRQILSNFDASGRMLRWSVELS
FT                    EFDIQYSPRTAIKAQALADFISELTLEDHAVGRENDQNMWTLHVDGSSTSE
FT                    AAGVGLILKDPSGETYERSLQLQFRATNNEAEYEALLHGLRFALEMHVDDL
FT                    EVFSDSQLVTGHVNGSYEARDPTMVSYLMEAKRLAHRFNRLSVTRIPRAQN
FT                    MRADALARSASTRGPGSAPATESVAAPTIATHEVAETSSSPSWMEEILRYK
FT                    VGGEEPDDPVAARRLRRTQAWYCIIGGKLYRRAFSQPLLRCLAPSEAEVVL
FT                    AELHEGICGEHIGGRTLAFKTLRQGYYWPTMRQDAMSYVQQCPQCQRHARL
FT                    PHQPTVPLTPMDVAWPFAQWGLDLLGPFPPASGQRRFLIVGVDYFTKWVEA
FT                    EPLASITEKQVQSFTWKNIITRFGIPKAIVADNGTQFNNTKFKAYCQSYGI
FT                    QLKFSSVAHPQTNGQTEVMNRAILEGLKRRISGAHGAWVDELPSVLWAMRT
FT                    TPKTASGESPFSLAFGTEAILPPEMLFPTLRTSNYXQGDSEEGLRANLDLL
FT                    EEGRAKAHLRILSYKKAAAQIYNRRVRPRPIKIRDLILRRAEVSDPTRARG
FT                    KLAPNWEGPYRVYDMVREGTYRLETMEGSPLPRTWNAANLKKFYPRRLVGM
FT                    QKRYTGPAHPRLGKIASQNSKIKVLLNDRGDTHGGRAARPQARPEQKTKRE
FT                    GAQPLARGRSRGPIVEGDVRRHVDVLIRRVVDKRVRLQLQVRVLRPEASAG
FT                    HPVPILVRDPARPHQATLEPGGRFIPGDRLLNPFGQPQPLLLQGLLGGPGR
FT                    RPGGLDVLGEGQQLVIQPAFFQLGLGLQTSHLLTQCRGALFGRGNGLWTPLGS
FT                    QLQVLQPEGGVDLQLAPDHPPGVEDPVDQRHTVVLALHEDRCQHPRKRGSG
FT                    RGRKPLLTQMSDLAARSTSTSEVEL"
XX
SQ     Sequence 9498 BP; 2061 A; 3152 C; 2675 G; 1604 T; 6 other;

//
ID     Gypsy-38B_NS-LTR repbase;     DNA;     PLN; 2218 BP.
XX
AC     .
XX
DT     29-AUG-2017 (Rel. 22.10, Created)
DT     29-AUG-2017 (Rel. 22.10, Last updated, Version 1)
XX
DE     LTR retrotransposon from the wood tobacco: long terminal repeat.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-38B_;
KW     Gypsy-38B_NS-I; Gypsy-38B_NS-LTR.
XX
OS     Nicotiana sylvestris
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC     Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
OC     Nicotianoideae; Nicotianeae; Nicotiana.
XX
RN     [1]
RP     1-2218
RA     Sierro N., Battey J.N., Ouadi S., Bovet L., Goepfert S.,
RA     Bakaher N., Peitsch M.C. and Ivanov N.V.;
RT     "Reference genomes and transcriptomes of Nicotiana sylvestris and
RT     Nicotiana tomentosiformis.";
RL      Genome Biol 14(6), - (2013).
XX
RN     [2]
RP     1-2218
RA     Bao W.;
RT     "LTR retrotransposons from the wood tobacco.";
RL     Repbase Reports 17(10), 1232-1232 (2017).
XX
DR     [2] (Consensus)
XX
CC     ~91% identical to the consensus.
XX
SQ     Sequence 2218 BP; 872 A; 287 C; 362 G; 696 T; 1 other;

//
ID     Gypsy-4_AC-I repbase;     DNA;     INV; 3064 BP.
XX
AC     AASC02003433;
XX
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DT   18-JAN-2011 (Rel. 16.02, Created)
DT   18-JAN-2011 (Rel. 16.02, Last updated, Version -1)
XX
DE   LTR retrotransposon from Aplysia californica (California sea
DE   hare): internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-4_AC_;
KW   Gypsy-4_AC-LTR; Gypsy-4_AC-I.
XX
OS   Aplysia californica
OC   Eukaryota; Metazoa; Lophotrochozoa; Mollusca; Gastropoda;
OC   Heterobranchia; Euthyneura; Euopisthobranchia; Aplysiomorpha;
OC   Aplysioidea; Aplysiidae; Aplysia.
XX
RN   [1]
RP   1-3064
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from Aplysia californica (California sea
RT   hare).";
RL   Direct Submission to Repbase Update (02-FEB-2011).
XX
DR   Genome; AASC02003433; Positions    7204   10267.
XX
CC   Positions [2055-2534] - Integrase core
CC   'CGTCTC' target site duplication
CC   LTRs are 95% similar to each other.
XX
FH   Key             Location/Qualifiers
FT   CDS             987..2951
FT                   /product="Gypsy-4_AC-I_1p"
FT                   /translation="MSQSTGNEVSEVNRLQKGKFYRQGQSQGQGQGPKQKF
FT                   QRKENIGKKYHRCGRSPHDKQECPAKHAECYTCKKRGHFSTACRNKDKKSV
FT                   RQVEEIFLGTLQLENEYGVRAVQSNDDWWHAEITTIGKPVKYRVDTGADVT
FT                   VIPGRSFKKNSPLIKKTEKKLFGAGHQELQVKEVVRATLATRNTSSEQDLY
FT                   VVTNLNEPLLGRPAIEALKLLEEECELHARSVVEGFPASDKKLQEIREQQD
FT                   ADEICQKLKEYCQSSWPATTKGDPVMKPYWTSRDELAVEQCLLLYQCRIVI
FT                   PTILRQDILKRLHEGHQGIVKCRALARSSVWWPGLSQQIETLVTNCPDCEK
FT                   ERKVSPEPLKPTVTPDDPWQRVGMDLFVWKDHTYLLKVDYYSRWIEIAHLR
FT                   EPTASNVVEHCKSIFARYGVPEVVVSDNGFHFVAHEFQKFSQYYCLTNLRS
FT                   SPLHPQSNGEAERAVKTIKMLLSKSDDPYLALVNYRSTPLQQGQSPAELLM
FT                   GRKIRTRVPIFPEKLVPKGGERQVFRKIDAAFRQRQKQDYDRRHCAKPMSD
FT                   LSKGQPVWVKTPRDAKATVVQRSRDRSYLLKTDNGLKVRNRHQIRLRTEGD
FT                   DSSHLVIPRESSMLPHHQPELPAESLESDTTLHDTFTTSGYITKSGRHVRP
FT                   PQRLDL"
XX
SQ   Sequence 3064 BP; 1025 A; 597 C; 740 G; 702 T; 0 other;

//
ID   Gypsy-4_DWil-I repbase;    DNA;    INV; 5204 BP.
XX
AC   scaffold_181026;
XX
DT   05-MAR-2011 (Rel. 16.03, Created)
DT   05-MAR-2011 (Rel. 16.03, Last updated, Version -1)
XX
DE   LTR retrotransposon from fruit fly: internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-4_DWil_;
KW   Gypsy-4_DWil-LTR; Gypsy-4_DWil-I.
XX
OS   Drosophila willistoni
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
OC   willistoni group; willistoni subgroup.
XX
RN   [1]
RP   1-5204
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from fruit fly.";
RL   Direct Submission to RU (05-MAR-2011).
XX
DR   Genome; scaffold_181026; Positions  158411  153208.
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     XX
CC     Positions [2727-3314] - Reverse transcriptase
CC     Positions [4330-4806] - Integrase core
CC     'TATATA' target site duplication
CC     LTRs are 99% similar to each other.
     XX
FH     Key            Location/Qualifiers
FT     CDS            1206..3059
FT                    /product="Gypsy-4_DWil-I_2p"
FT                    /translation="MLYNEITELTVAGLKEKLKELNLSVKGNKPELRERLI
FT                    SYFDLDTNEESLYSEANTSIQGEVEEVEREVTMAFTLKDIRDSLTEFDGSN
FT                    KKDVLEWLSDFEGTAVTVQWNDLQKFIYGRQLLTGAAKLFVNSQEGLGRGR
FT                    LKSALQDEFTVKLSAKEVHKQLESRKKKYNESLVEYFYLMKSIAKRGSLDE
FT                    ESIVEYIIEGIPDSKMNKSVYYQARDLKELREKLTMYEKYASNQESKTKPR
FT                    FEKLQSRNTLEDFKCFKCGGKNHVAKNCKDNFKCFKCNQMGHKANQCEARN
FT                    TKETKKDNTNYQQMTLKFNRSFKNVPIGNGVLSALFDSGSDLSTISESTYK
FT                    EINPVNLNRECKEVIGVGGKKIRTLGFFNIKTELDGNAVEIDFHVVRDKDT
FT                    LYKGVIGNDVLENLNVTIGRKRIVFHKEDEIPKPISREVQTKTNISELQTT
FT                    FERIMTMTLDEDAPLEIDLIHLDEGIKSDILEMLKSYKPVKPTISPVEMKI
FT                    VVTDDIPISQRPRRLPYQDQVIVNQQIKEWMEPGIVRQSFSEYSSPVVLVS
FT                    KKDGKKRLCCDYRKLNQKIIKDNFPTALIDDVLHKLQRGKVFTTLDLCNGF
FT                    FHVPVDESSRKFTSFVPVRV"
FT     CDS            3352..5202
FT                    /product="Gypsy-4_DWil-I_1p"
FT                    /translation="MAVESYPIPTDKKGLQRFLGLTSYFRRFVKDFATIAR
FT                    PLTNMMKKDVPFMMNEEALASVRQLKVCLSNPPVLRLFDPMGITEVHCDAS
FT                    MYGYGAMLLQFNSEDQNFYPVEYMSRKTTPAEEKYHSYELEVLAIIQALSK
FT                    WRVYVLGKKIKIVTDCNAYAMTIKKKKVPLRVARWAIFLQDFDFEIEHRPG
FT                    TKMKHVDALSRIHCLLLENSLRHKIQQAQLLDEWINAVRKVLENGTYDDFY
FT                    LQYDILHKDLIKELIVIPSAMEREIITMAHRQGHFGIKKTIDVLGKDYYIS
FT                    NVASKFEVVIKSCVECIVSEQKHGRKEGFLNVIDKGDEPLTTFHLDHIGPM
FT                    ESTKKQYNHVLVIVDAFSKFVWLYLTKSTGSEEVVDRLQRQSEVFGNPKRF
FT                    ITDRGTAFTSNMFKEYCTSQKIQHLLIATGVPRGNGQVERLNRTVSTLLTK
FT                    LCAEEPKSWYKNVGRVQQFINSSPPRSTKISPFKILTGIEMRTTYDQELKS
FT                    QLEEELLIELQREKDEIRRLAKDNIAKIQEENRKSYNKFRKPETEYKVGDM
FT                    VAIKRTQFGAGLKLKKNYLGPYKIVRKLRHGRYSVEKIGDGEGPNRTNTVA
FT                    EYLKMWNPSFGTNEAVEWP"
     XX
SQ     Sequence 5204 BP; 1951 A; 802 C; 1153 G; 1298 T; 0 other;

     //
ID     Gypsy-51_MLP-LTR repbase;      DNA;      PLN; 1619 BP.
     XX
AC     AECX01002217;
     XX
DT     22-APR-2011 (Rel. 16.04, Created)
DT     22-APR-2011 (Rel. 16.04, Last updated, Version -1)
     XX
DE     LTR retrotransposon from the Melampsora larici-populina genome:
DE     long terminal repeat.
     XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-51_MLP_;
KW     Gypsy-51_MLP-I; Gypsy-51_MLP-LTR.
     XX
OS     Melampsora larici-populina
OC     Eukaryota; Fungi; Dikarya; Basidiomycota; Pucciniomycotina;
OC     Pucciniomycetes; Pucciniales; Melampsoraceae; Melampsora.
     XX
RN     [1]
RP     1-1619
RA     Jurka J. and Kohany O.;
RT     "LTR retrotransposons from the Melampsora larici-populina
RT     genome.";
RL     Direct Submission to RU (20-APR-2011).
     XX
DR     Genome; AECX01002217; Positions   36821   35203.
     XX
SQ     Sequence 1619 BP; 549 A; 220 C; 306 G; 544 T; 0 other;

     //
ID     Gypsy-62_MLP-I repbase;     DNA;      PLN; 6584 BP.
     XX
AC     AECX01001306;
```

```
XX
DT    22-APR-2011 (Rel. 16.04, Created)
DT    22-APR-2011 (Rel. 16.04, Last updated, Version -1)
XX
DE    LTR retrotransposon from the Melampsora larici-populina genome:
DE    internal portion.
XX
KW    Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-62_MLP_;
KW    Gypsy-62_MLP-LTR; Gypsy-62_MLP-I.
XX
OS    Melampsora larici-populina
OC    Eukaryota; Fungi; Dikarya; Basidiomycota; Pucciniomycotina;
OC    Pucciniomycetes; Pucciniales; Melampsoraceae; Melampsora.
XX
RN    [1]
RP    1-6584
RA    Jurka J. and Kohany O.;
RT    "LTR retrotransposons from the Melampsora larici-populina
RT    genome.";
RL    Direct Submission to RU (20-APR-2011).
XX
DR    Genome; AECX01001306; Positions    43142    36559.
XX
CC    Positions [4801-5151] - Integrase core
CC    'GATTA' target site duplication
CC    LTRs are 99% similar to each other.
XX
FH    Key           Location/Qualifiers
FT    CDS           656..3829
FT                  /product="Gypsy-62_MLP-I_2p"
FT                  /translation="MNPWREGRDSPAISSIFGRDLPPHQVPGSELSDPHAI
FT                  LLDSPRPHLINQFNRLPHSQSPVSRLAQGLNNLDFRTNSISFAHQPGHQNA
FT                  QIPQQHFTARMTGAAPAFHPQVFQQPLSFQPNHNHQQYPNQQSVPPIHNQF
FT                  VPNHFVPPPQAQYVHPQQQFQTGPIPPTHAYQVPLQQPIPQTTNQTAPLQR
FT                  PPSRMPNSYITDNRAPKICDNLRFFGDNKGLKQFLVEIHDELDQITLHDDK
FT                  MKINWIARHFTSPTSTPSSMQIWFMGLLERNAFQQGVQSLYGNLKSLDYVL
FT                  PELASLAIFLDELIYKFGDKNSDKTAREELDACKQGKLSIIDYNAKFEQLS
FT                  LHVKKSEEDKILQYVEGLHPSIQLEATRIAGWVRETDLLCKQAMALEAADI
FT                  LYLRSKVAHNHPHLRTPGESYRHPQHHQNPINQQTNGPVPMDINVNAVSLE
FT                  RSGSNPFPVIRRICNEKNLCYDCLKPYDDEHKCLRSLKGKQSCPNPYVCVK
FT                  EKLKVLCTSMKLPSDGRHTSPTQISAMQLEELEYAALPTEVIEETGRLVEA
FT                  YWESLGSPAYPLPSSSQSQPMSQDVQVDAIRIQSDVNRLRRFLIPLSIISQ
FT                  NLPVAIMALVDTGASDSFIDAEFADLHHLNLNKKFIPQNVLGFDGGPAKRV
FT                  TKEWCGLLSMNDVEGKETRLKAKLGVTKLGGGNDVILGLPWMEENGATLWM
FT                  NKNRRWLGIGEKVLSAVVVEEELVDLAVVYCEQDSLPISFSSSKAPTASTF
FT                  SQETPSITLNPTLAKFFPLNLPKSCTRYLHVFSPQVSVLPPHRSFDIAIEL
FT                  KPGCKPPFGGLYNLSPDEQSELKTYLNDQLSKGFVRPSKSPAAAPIFFVKV
FT                  PGKKNRPCVDYRGLNKITKRDSYLIPVMSWLLNQLRGCKFFAKIDLKVAFN
FT                  LLRVAKGDKWKTAFRTPWGLFEYTVMPFGLANAPAVFQRFIQWVLREYLDV
FT                  FCFVYLDDILIFSKNADEHELHIEQVLAKLSEHKLTASPEKCQFFAKEVIF
FT                  LGFVISTEGISMDPAKLKTIADWPFPQELTDLQRFLGFSNFYKQTFPESWV
FT                  P"
FT    CDS           4153..5151
FT                  /product="Gypsy-62_MLP-I_1p"
FT                  /translation="MGTKVPVTVLSDHANLRYFMTSQMLTPRQARWASFLG
FT                  EFNFEILHTPGKSNPTDPALRRSDFVCGKQDSARVILLGLREVKDIGVNAI
FT                  YISHPGHFNISSYMPVADELMVTIKHSYHADDLIAGIHPSFLHFLDGLWWW
FT                  RDRLYVPLALRISIIKQIHKSTIGGHWGTLKTLGLLTRSFGWPNARRDVLD
FT                  FIKGCSSCQQVKVDHRAPQGQLVPLPIPDRPWSTIGVDFIVKLPISDTFDS
FT                  VMVVVDHFSKVAHFVPAKESWSAEELAKAFVAQVFRFHGLPDAIVSDRGTT
FT                  LVSSFWTSVLKLLQISPAPSTAFHPQTDGQVERVRASPPRT"
XX
SQ    Sequence 6584 BP; 1812 A; 1448 C; 1394 G; 1930 T; 0 other;

//
ID    Gypsy-65_PIT-I repbase;    DNA;    PLN; 12051 BP.
XX
AC    .
XX
DT    22-MAR-2011 (Rel. 19.08, Created)
DT    22-MAR-2011 (Rel. 19.08, Last updated, Version -1)
XX
DE    LTR retrotransposon from the Phytophthora infestans genome:
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DE     internal portion.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-65_PIT_;
KW     Gypsy-65_PIT-LTR; Gypsy-65_PIT-I.
XX
OS     Phytophthora infestans
OC     Eukaryota; Stramenopiles; Oomycetes; Peronosporales;
OC     Phytophthora.
XX
RN     [1]
RP     1-12051
RA     Jurka J.;
RT     "LTR retrotransposons from the Phytophthora infestans genome.";
RL     Repbase Reports 14(8), 2297-2297 (2014).
XX
DR     [1] (Consensus)
XX
CC     Positions [7559-8038] - Integrase core
CC     LTRs are 97% similar to each other.
XX
FH     Key            Location/Qualifiers
FT     CDS            742..2619
FT                    /product="Gypsy-65_PIT-I_1p"
FT                    /translation="MSTPARSGGTPARSVATPARSTTASARSMTTPAKSAS
FT                    TPAKSVSTPARSIAASARSGTPSNDSRLQALVEESVERVLRKLTLSRESSA
FT                    GTPRSRTAGPDARYTPGSARLERTELERPSSAHRIEYQRPPIPRAPTPAKT
FT                    SMSVGMPLGPVPAYRGVPPKEISPYGNGMVGGAPRTGALYSQYQSMTQPTA
FT                    GWGQGGALPAWPAAPVAPTHEYPNLPTLGMPLAAGGASPSYMRNQGLEGSA
FT                    GSRGAEYRREGVPERADYPRRAAPYVGIPNELRNAVKVIVPFYSETATNER
FT                    AAAFWRSFERCTYGMDSLMRLTAFEQCLRGKVGQEWWYNARIDSFETLRVK
FT                    FHNRFICQTPAQLWNRLKNAKRSRGESAEEWGDRISTMCEALNYHEPRMRY
FT                    EFFLDGLRNKQMKAVLNGNMVATIREACDLLIYKNLHMPVEEEDEFADDGT
FT                    PVTRSNNANSTQSQMLQQLQLMNQSMQKQLQGAGVQQGYISAVVPPVPPAQ
FT                    GVPTPVGNASSTPNASTPGNAPSNLGPLRIRLGPDTRTTEGEVVCGRCGRV
FT                    GCGRETCPRGQGRCNRCNELGHFSMECNWPRPQGSYRNGERRRMECFLCGE
FT                    KSHSVAKCPSLDRLRSLTQNATAGNATA"
FT     CDS            5560..6921
FT                    /product="Gypsy-65_PIT-I_3p"
FT                    /translation="MESEIQEYLDLGLIRPSTSPWASPVLMIRKPDGGIRF
FT                    CIDYRKLNAVTVKDSYPMPLIDDILDVLGNASLFSTMDIASGYWNVPMDPG
FT                    SVEKTAFTSKFGLYEWLVMPFGLCNAVPAFERLMENVLVDLKWRTCLVYLD
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FT                    TGIMPNPEKAKAVMNIERPHDLHTVRAFLGLTSYFRRYIPGFAAIAAPLER
FT                    LKQKDVPFQWNDDCEVAFRQLQRALVKPPILVYPNFKARFKLFVDSSHLAV
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FT                    ERIPRATER"
FT     CDS            7166..8821
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FT                    /translation="MRALKAFLKDGALALDPQLRVTVLKMSPHYLIRNGVL
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FT                    NGTLMGMLRMFVNETQTDWDVYLPRVLFAYRTAYHEGLGDTPFFSLYGRDP
FT                    VLPIDLAFLNTGKDWKSNEVAVYRRKLYLSLRDSRRLVERQLLKAQDRHEQ
FT                    RLDKQVKVSYEEGDAVWVYQFFRARAGERRTKKLAFSWHGPYRVVGQVGEN
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FT                    LQEGDLPPTSFVERLNVGGEETAFSGVSSPIVDVLAKRVEKREVQYLVLTA
FT                    TYETFWLSRAALAPEFGTLIRAFEDADRRKRGLPELRRSARLVEANADVDN
FT                    AEILF"
XX
SQ     Sequence 12051 BP; 2628 A; 3138 C; 4038 G; 2231 T; 16 other;

//
ID     Gypsy-6_IS-I repbase;     DNA;     INV; 4087 BP.
XX
AC     ABJB010051582;
XX
DT     14-FEB-2011 (Rel. 16.02, Created)
DT     14-FEB-2011 (Rel. 16.02, Last updated, Version -1)
XX
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DE    LTR retrotransposon from the black-legged tick genome: internal
DE    portion.
XX
KW    Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-6_IS_;
KW    Gypsy-6_IS-LTR; Gypsy-6_IS-I.
XX
OS    Ixodes scapularis
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Chelicerata; Arachnida;
OC    Acari; Parasitiformes; Ixodida; Ixodoidea; Ixodidae; Ixodinae;
OC    Ixodes.
XX
RN    [1]
RP    1-4087
RA    Jurka J. and Kohany O.;
RT    "LTR retrotransposons from the black-legged tick genome.";
RL    Direct Submission to RU (14-FEB-2011).
XX
DR    Genome; ABJB010051582; Positions   21519   17433.
XX
CC    Positions [3193-3660] - Integrase core
CC    'GTTAC' target site duplication
CC    LTRs are 97% similar to each other.
XX
FH    Key           Location/Qualifiers
FT    CDS           133..4074
FT                  /product="Gypsy-6_IS-I_1p"
FT                  /translation="MNASSQASQPPPQPPPPYHLSAPEPFTFVPEHWTTWK
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FT                  QDSVCRALKNYVQTTWPKTKKQVHQECLPYWQFKNKLTLHEGILMRGQRYL
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FT                  ESQRPETVILKSKSIFARHGIPETVVTDNGPQFRSEFLCFARNWGFKHVTS
FT                  SPKHAQSNGCAEAAVKIAKTKLTKSFDPYRALLAYRATPLENGFSPADLLF
FT                  GRRLRTHVPISAELLRPSVPDHHQVEDFEHKARKRQAINYDRRHAVRDQPE
FT                  FQPSQRVWITDLKRAGTVLNKAETPCYCWIGTDQGIIRRNAKFLVIDRRRC
FT                  NFEEDLISLGSLPCSPELPDCPASQPASLQQSRSGPTSRSGRPLRPPCRYG
FT                  YD"
XX
SQ    Sequence 4087 BP; 1091 A; 1098 C; 1057 G; 841 T; 0 other;

//
ID    Gypsy-71_PTr-LTR repbase;     DNA;      PLN; 2188 BP.
XX
AC    .
XX
DT    15-DEC-2009 (Rel. 15.02, Created)
DT    15-DEC-2009 (Rel. 16.11, Last updated, Version 2)
XX
DE    Gypsy-type LTR retrotransposon from Populus trichocarpa: long
DE    terminal repeat.
XX
KW    Gypsy; LTR Retrotransposon; Transposable Element;
KW    Interspersed repeat; Gypsy-71_PTr-LTR.
XX
NM    Gypsy-71_PTr-LTR.
XX
OS    Populus trichocarpa
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OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC     Pentapetalae; rosids; fabids; Malpighiales; Salicaceae; Saliceae;
OC     Populus.
XX
RN     [1]
RA     Tuskan G.A., DiFazio S., Jansson S., Bohlmann J., Grigoriev I.,
RA     Hellsten U., Putnam N., Ralph S., Rombauts S. et al.;
RT     "The genome of black cottonwood, Populus trichocarpa (Torr. &
RT     Gray).";
RL     Science 313(5793), 1596-1604 (2006).
XX
RN     [2]
RP     1-2188
RA     Kojima K. and Jurka J.;
RT     "LTR retrotransposons from cottonwood.";
RL     Repbase Reports 10(2), 179-179 (2010).
XX
DR     [2] (Consensus)
XX
CC     ~82% identity to consensus. 5-bp TSDs. Similar to Ogre-PT1_LTR
CC     and Ogre-PT2_LTR.
XX
SQ     Sequence 2188 BP; 526 A; 486 C; 365 G; 811 T; 0 other;

//
ID     Gypsy-82_MLP-I repbase;      DNA;      PLN; 10260 BP.
XX
AC     AECX01001127;
XX
DT     22-APR-2011 (Rel. 16.04, Created)
DT     22-APR-2011 (Rel. 16.04, Last updated, Version -1)
XX
DE     LTR retrotransposon from the Melampsora larici-populina genome:
DE     internal portion.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-82_MLP_;
KW     Gypsy-82_MLP-LTR; Gypsy-82_MLP-I.
XX
OS     Melampsora larici-populina
OC     Eukaryota; Fungi; Dikarya; Basidiomycota; Pucciniomycotina;
OC     Pucciniomycetes; Pucciniales; Melampsoraceae; Melampsora.
XX
RN     [1]
RP     1-10260
RA     Jurka J. and Kohany O.;
RT     "LTR retrotransposons from the Melampsora larici-populina
RT     genome.";
RL     Direct Submission to RU (20-APR-2011).
XX
DR     Genome; AECX01001127; Positions    44906    34647.
XX
CC     Positions [8204-8725] - Integrase core
CC     LTRs are 98% similar to each other.
XX
FH     Key            Location/Qualifiers
FT     CDS            2055..4853
FT                    /product="Gypsy-82_MLP-I_3p"
FT                    /translation="MSSRASQPPSRASSASTRGSTRSKRSVEPTSRGTRGT
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FT                    SSSSCTVLPADKGGRGGPTSPSNQQSQARLGRSESCRQQLELQASIGDGQG
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FT                    QRLFNQSYLVSNLNSQISSSVVSASNSQLDLDELITRKSYAIYEKVENIKP
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FT                    SYEFKNQEQHQTAYEDVKVKFAELKEKFSEIQEIKKIILEIKRDSQDEIKD
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FT                    DKQLRLPIKDPYNKIEELLTKFGKHETHVSSTIDEIKEDTNITKIRENLNE
FT                    QQQQFESSMMKSYHSLQENIKENHEQLTKELLKQQDIQMKSFTEQMLKQQV
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FT   CDS               join(4871..6946,6950..9361)
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FT                     /translation="MDPLVVVSHLATAFTGTAAQWYMDKRKTRGSMTWNEW
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FT                     KIYLNRPRRPFIENRATFRDDKLQGPSSTRVQPSTSERKPSRACPNCGSKD
FT                     PKHQWRGCKDKKINVIEEDTEESDNMNDEFDFQGGQLSGDSSSDSEGENSP
FT                     NQHQQNVCMIDTHEDNEKSINILQAEADVPHSWQDDMQMGNTIDARLLKSK
FT                     PAEGMAHTLGHHAMARALVNNCKVPILLDSGASCSIVGKHFLSEIIPDWQE
FT                     RIMPSSHVKFSGVGSKLHALGVISLPVIFPHVKQSIRINAEFVVMENANNK
FT                     YFILGAENLSQYGFDIFHSKERYFTIGNNNKSIKFALMQHKEILSIKPDNT
FT                     MESPTNEDIHQLRGKLLESEFGPNLTYSQKEDIIQMVIKYKDQFGLGEQPL
FT                     GVIKNYPVKIELTIDKPYPPILRKGAYPASPRSRKEIEKHIEELLKMGIIR
FT                     KVGSDEEVDITSPVLIAWHNDKSRLCGDFRALNQYTKPDRYPLPRIDQSLT
FT                     NLFNAKYITLMDIMKGFHQNIVEICSRKYLRIICHLGIFEYIRMPFGIKNA
FT                     PAFLQRMMDTEFSKELREGWLKVYIDDIIVFHTTWEEHLEAMEVLLRAKAM
FT                     GMTISLKKCHFGFEECKALGHRVSGLWVSVDQNSVAAVLQKPCPKDKQELS
FT                     SFLGFTSYYRAHIPNFGIITRSLYKLYAKGVVFEMTKERIDAVNKIKHILT
FT                     TAPILFHPDFEKPFKLYVDASIEGLGAALHQTQIIDGKPKEGPIVFISRKL
FT                     TDTESRYSSPQLEALALVWALEKLHYYLDGSYFEVITDCTGVRSLTNLKSP
FT                     SRHMSRWMMAIQEYKPFMTITHRPGKFHNNADGLSRMALPNDSSNPAWEPE
FT                     EMERDIPVMGISLCELSEEFFDEVKTSYQKNSNTAKITRILSAQNTDLSLS
FT                     STLKQPWKDGLAQGKISLESDLLYFREKHTANLVIINAEHIQQTLHVCHDE
FT                     FMSGHLSEDRTVDRIKSTAWWPNWRQDVEEYVKTCERCQKANKATGKRFGL
FT                     LQRIEEPMYAWEVINMDFVTGLPPSLINNYNCVLVIVDRFSKRTRFLPCYK
FT                     EATAMYIALLFWERLISDVGLPQIIISDRDPKFTSEFWKSLHTLIGTTLAL
FT                     STTYHPQTDGLSERNISTLTEIIRRYCTEGLCYTDKDGHTHDWHTLLPALE
FT                     LAYNSSIHSTTGKKPFEVERGYCPRLPKDQIKNKNVEFHPTSLSFFDMLGK
FT                     ARARAAQCIEDSVTYNQERWNKTHKEPKFVVGEQVLLLTTNFTNLQGPKKL
FT                     QDQFVGPFVILEFHGSNAVEVALTEEFGRKHPVFPISLIKKFHASDKSKFP
FT                     DREIPKKTPIRFETDGEKIFSHIIKQREIQVNGKSSTLYLVRYKNRSADED
FT                     EWLPADKVPNGKTTLRDFRAQKRAHKPSEKK"
XX
SQ   Sequence 10260 BP; 3865 A; 2009 C; 1757 G; 2629 T; 0 other;

//
ID   Gypsy-96_GM-I repbase;    DNA;     PLN; 4542 BP.
XX
AC   ACUP01006069;
XX
DT   08-MAR-2012 (Rel. 17.03, Created)
DT   08-MAR-2012 (Rel. 17.03, Last updated, Version -1)
XX
DE   LTR retrotransposon from soybean: internal portion.
XX
KW   Gypsy; LTR Retrotransposon; Transposable Element; Gypsy-96_GM_;
KW   Gypsy-96_GM-LTR; Gypsy-96_GM-I.
XX
OS   Glycine max
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae;
OC   Phaseoleae; Glycine; Soja.
XX
RN   [1]
RA   Schmutz J., Cannon S.B., Schlueter J., Ma J., Mitros T.,
RA   Nelson W., Hyten D.L., Song Q., Thelen J.J., Cheng J. et al.;
RT   "Genome sequence of the palaeopolyploid soybean.";
RL   Nature 463(7278), 178-183 (2010).
XX
RN   [2]
RP   1-4542
RA   Jurka J. and Kohany O.;
RT   "LTR retrotransposons from soybean.";
RL   Direct Submission to RU (22-MAR-2011).
XX
DR   Genome; ACUP01006069; Positions   23623    19082.
XX
CC   Positions [3434-3928] - Integrase core
```

```
CC      'AGATC' target site duplication
CC      LTRs are 96% similar to each other.
XX
FH      Key             Location/Qualifiers
FT      CDS             3170..4540
FT                      /product="Gypsy-96_GM-I_1p"
FT                      /translation="MQRNFSYRAGILYFQERIFIPREAAIIPSLLEEYHSS
FT                      PLGGHSGIKATISRLSAVFYWPGMYADVKNFINSCSICHYNKYSTQPLYGL
FT                      LQPLPVPQQVWEDISMDFITNLPASSNKTVIWVVVDRLTKYAHFIALPTHF
FT                      TTSYLASMFLSEIHRLHGTLKTIVSDRDRIFISKFWKELFKSLGTTLAFSS
FT                      SYHPQTDGQIEVLNRCLETYLRCFFSEEPQQWTRFLSLAEFWYNTSHHSAI
FT                      GMTPFEALYGRAPPSLTSYVAGSSKIAAIDENFAKRSDILQLLKNNLHRAQ
FT                      HRMIQQVNSKRKDKEFAEGDWVYLKLQPYRQVSVHRRSSQKLAKRFYGPFR
FT                      ILHRIGPVAYELELPSTVRIHPVFHVSLLKPCIKTPDTQILPLPVTVVVAP
FT                      SGTKPQAIIGRRTIPQEHDSREEVLVHWEGQMPAEATWESRAAIVRSFPDF
FT                      DLKGKIYFGDMG"
FT      CDS             join(24..1955,1959..2915)
FT                      /product="Gypsy-96_GM-I_2p"
FT                      /translation="MNTRSQDLQQLQESIAALTTAFQEFKVHQDQRHESYL
FT                      SNFEHLQTKSDSSSSSSTQPTDQTIKLPKLILQPFDGSNPMEWLFQAEQFF
FT                      NHYSITPTQRLSRISCYMTGDALGWYQWMHNNHLISTWEEFTRAMELRFGP
FT                      SAYENHQQALFKLQQTATVPEYQRDFERLCNRVTSLPHHSILDCFISGLRP
FT                      EIQHELAILQPVTISQAIGLAKLVESKLLASKTSFTYSPRPTQPKSIPPLL
FT                      PNPPPQPRLIQHPSQSLLALPAPPSPKPTTPQIRLLSKTEMDDRQAKGLCF
FT                      NCDERYHRGHRCKNKGMLQLLSPDDPPDPHSDPISADVPPLTNSETTPPTP
FT                      SAFLLHSETPPTYTNPEQFHLSLQAVSGQPSPRTLRFYARINGHYVSVLVD
FT                      IGSSHNIIQPRVATFLRLPTQNLPSFTVMVGNGAHLKCDGLCTDVPLTVAE
FT                      HCFVVSLYVLPIQGADIVLGVQWLQTLGPFVSDYTIPSMQFYHNGVLVTLP
FT                      GTTSPSLSLATLPQLNRMIHTASVATLHTITMLPVDSSPPPSTPQTHSLSR
FT                      DEQPTLASFHPDITQVLHRYSPIFSIPHGLPPNRPHDHHIHLKPHSNPINI
FT                      KPYRYPHFQKESMTSMIADMLQQGIIRPSTSPYSSPVLLVKKKDGSCFCVD
FT                      YRALNAITIRDRFPIPTIDELLDELKGAQFFSKINLRSGYHQIRLAQEDIP
FT                      KTGFRTFDGHYEFLVMPFGLTNAPSTFQAAMNDLLRPFLRKFALVFFDDIL
FT                      IYSPTWSAHQIHLQQVLRLLLDNHFYAKLSKCNFGVCSVDYLGHIISGNGV
FT                      HADPTKVQDILAWPTPKSLTALRAFLGLTGFYRRFVQHYATIAGPLTDLLK
FT                      APTLMWTSKAEEAFTKLKHAMTNLPVLALLDFNLPFEVTTDASSVAVGVVL
FT                      SQQGHPIAYFSRKMCPRLCSSSAYVRELFAVTEAIKKWRQYLLGNSSAFIR
FT                      ITKVSRLY"
XX
SQ      Sequence 4542 BP; 1227 A; 1227 C; 773 G; 1315 T; 0 other;

//
ID      Gypsy103-I_Dr repbase;    DNA;    VRT; 4286 BP.
XX
AC      .
XX
DT      21-APR-2009 (Rel. 14.05, Created)
DT      21-APR-2009 (Rel. 14.05, Last updated, Version 1)
XX
DE      An internal portion of the Gypsy-103_DR LTR retrotransposon - a
DE      consensus sequence.
XX
KW      Gypsy; LTR Retrotransposon; Transposable Element;
KW      Interspersed repeat; Gypsy superfamily; endogenous retrovirus;
KW      gag; reverse transcriptase; integrase; Gypsy-103_DR;
KW      Gypsy-103-I_DR; Gypsy-103-LTR_DR; Gypsy103-I_DR.
XX
OS      Danio rerio
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC      Cypriniformes; Cyprinidae; Danio.
XX
RN      [1]
RP      1-4286
RA      Dib M.R. and Naveira H.F.;
RT      "Gypsy103_DR, a family of LTR retrotransposons from zebrafish.";
RL      Repbase Reports 9(5), 942-942 (2009).
XX
DR      [1] (Consensus)
XX
CC      Gypsy103-I_DR is an internal portion of the Gypsy103_DR LTR
CC      retrotransposon that belongs to the Gypsy superfamily. Its long
CC      terminal repeat is deposited in Repbase as Gypsy103-LTR_DR.
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CC     Gypsy103_DR is characterized by 4-bp target site duplications.
CC     The internal portion encodes one polyprotein the 1422-aa
CC     polyprotein Gypsy103_DR1p (pos. 19-4284) composed of the gag,
CC     protease, reverse transcriptase, and integrase domains. Some
CC     insertions fairly recent, according to the hight identity between
CC     their flanking LTRs. Consensus obtained after the alignment of at
CC     least five independent insertions bearing at least 85% Homology
CC     over at least 1000bp.
XX
FH     Key            Location/Qualifiers
FT     CDS            19..4284
FT                    /product="Gypsy103-I_Dr_1p"
FT                    /note="Polyprotein."
FT                    /translation="MDAAGSDTVRTAVTQQGALLGQHEARLTNTTREVEFL
FT                    ANQVAELTALVQDLQHEAAQGGPLRHHDPEPRCNNPPPYNGDPNSCRAFLS
FT                    QCAVVFTLQPRTYASEESKVAFVLTLLTGKARDWGTSVWETRAPCCASFED
FT                    FRQEMVRLFDRSVRGQEAADQLARLRQAGQSVTEYAIAFKTLAASCDWNEG
FT                    ACRSMFRAGLQDDIQDELATQDLPQDLDDLVNMALRIEGRLHRRRQRLTVR
FT                    PPWRVEDSRPVLAAEASGSAPMDPEPMQVGRLRLTPLQRQQRFVQGLCLYC
FT                    GKPGHFAVACPLKRQASPVKRGILVSTTPFLHSSSRTLLPVSVHFSDSSNS
FT                    CSALVDSGAEGNFMDSSLAALWGIPAIPLPDPIPARSLNGSLITTVSHSTP
FT                    PINLTVSGNHHEVTTLLLLDSPSASIVLGHPWLVKHGPHVDWSGNAILSWS
FT                    QYCLSSCLGSAPFPVSVSSVLQAEAADLTGVPVEYHGLRQVFNKSRATSLP
FT                    PHRPYDCAIELLPGTSPPKGHLFSLSGPEREAMDRYINESLKTGLIRPSSS
FT                    PAGAGFFFVKKKDGSLRPCIDYRGLNDITVKNRYPLPLMSSAFELLQGAKV
FT                    FTKLDLRNAYHLVRIREGDEWKTAFNTPTGHFEYRVLPFGLTNAPAVFQAL
FT                    VNDVLRDMVNRFVFVYLDDILIFSPCLQIHIQHVRQVLQRLLENQLYVKAE
FT                    KCVFHAQSIPFLGFIISAGEIQADPCKIRAVAEWPTPDSRKALQRFLGFAN
FT                    FYRRFIRNFGQIAAPLTALTSPKVWFKWNSDAQEAFDELKSRFVSAPVLSI
FT                    PDPEQQFIVEVDASDVGVGAVLSQRSCLDGKVHPCAFFSHRLNPSERNYDV
FT                    GNRELLAVRLALGEWRHWLEGAAQPFLVWTDHKNLEYIRSARRLTPRQARW
FT                    ALFFDRFKFTLSFRPGTKNVKPDALSRLFEVPGKEKSVDAILPKEMVVASI
FT                    SWDIERRVEKAIQKISVPGRVPAGRLFVPTRLRSEVIQWGHSSRLACHPGV
FT                    RRSLALIHQRFWWPSMAKDVRQFVAACSVCAQNKTSNAPPVGLLRPLPIPS
FT                    RPWSHVALDFVTGLPESKGNTVILTVVDRFSKSVHFIPLPKLPSAKETAQV
FT                    VIDHVFRIHGLPVNVVSDRGPQFVSRFWKEFCRQIGASTSLSSGFHPQTNG
FT                    QSERANQDLERTLRCLASHNPSSWCQQLSWVEYAHNSLPSSATGLSPFECS
FT                    IGFQPPLFPSQEPEAAVPSALAFVRRCRRTWRKAREALVRVGRRTKAAADQ
FT                    HRTPAPHYICGQRVWLSTKDLPLRVPSRKLAPRFGPYQITKVLSPVVVRL
FT                    KLPPKLGRVHPIFHVSRVKPVMYSPLVPSAPSPPPPQLVDGLPAYTVRRLL
FT                    DVRPRGRGFQYLVDWEGYGPEERSWVPARDILDQALVEDFHRRRGKPLPAA
FT                    PGGARRGG"
XX
SQ     Sequence 4286 BP; 877 A; 1218 C; 1091 G; 1100 T; 0 other;

//
ID     Gypsy139-I_DR repbase;    DNA;    VRT; 4231 BP.
XX
AC     chr15;
XX
DT     10-OCT-2008 (Rel. 13.10, Created)
DT     10-OCT-2008 (Rel. 13.10, Last updated, Version 1)
XX
DE     LTR retrotransposon from zebrafish: internal portion.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy139-I_DR;
KW     Gypsy139-LTR_DR; Gypsy139_DR.
XX
OS     Danio rerio
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC     Cypriniformes; Cyprinidae; Danio.
XX
RN     [1]
RP     1-4231
RA     Jurka J. and Kohany O.;
RT     "LTR retrotransposons from zebrafish.";
RL     Repbase Reports 8(10), 1539-1539 (2008).
XX
DR     Genome; chr15; Positions 31060996 31065226.
XX
CC     Positions [2937-3359] - Reverse transcriptase
CC     Positions [1833-2309] - Integrase core
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CC      'GTAAC' target site duplication
CC      LTRs are 99% similar to each other.
CC      This sequence was derived from sequence data generated by the
CC      Danio rerio Sequencing Group at the Sanger Institute.
XX
FH      Key             Location/Qualifiers
FT      CDS             157..1818
FT                      /product="Gypsy139-I_DR_1p"
FT                      /translation="MEDIMRRLSEITTRQQLFTEQLSVRQQRIEERLFQMA
FT                      EHLPLPEARASAHRHLTKLGDLDDIDAYLHTFEVIAKREEWPESEWAQILA
FT                      PFLTGESQRAYFSLDSPQNEDYTVLKGEILARVGLSPVRAAQQFATWAYEE
FT                      GAPVRAQAAQLSKLARLWLLGGSPTATQVAEKVVIERLLRALPRRLRGPVS
FT                      MRNPASLAALVEAVELAEATLTRDIIERAAVPSRRVNSPWRQVESASRPVS
FT                      RPAVPSPADEPMPTEPVNSTARAWLAGCIVHRTLPSGAPSRRVKLEGKTIT
FT                      AVLDTGSSVTLVQPGLIKPRVGSKATIPITCVHGDTRYVPAQRVTIAAGNG
FT                      AWPLEVGIVADLPVPLLLGRDWPGFEELLSLPAATPFQTRRRPRARTQRVR
FT                      QPALLATESDRGGECSNQSSNVFMDLFQQVSRGGSFGQAQREDDTLRNCWS
FT                      QVRVVEGQERLPAPHPLPHFIIQNGLLYCVAERREERRTLLVVPKSKTSTI
FT                      LELAHTHPMAGHLGAANTIQRIRDRFHWPGLNGEVKRYCQACPTCQKTAPQ
FT                      RPPPPVP"
FT      CDS             1767..4229
FT                      /product="Gypsy139-I_DR_2p"
FT                      /translation="MPDVPENCSPTSPPPSPLIPLPIIEVPFDRIGLDLIG
FT                      PLPKSSRGHEHILVILDYATRYPEAIPLRKATSNAIAKELFLLCSRVGIPS
FT                      EILTDQGTPFMSRLMADLCHLLKVKQLRTSVYHPQTDGLVERFNQTLKRML
FT                      RRVVAEDGRDWDLMIPYVLFGIREVPQASTGFTPFELLFGRQPRGLLDVAR
FT                      QAWEQEPAPQRSLIEHVQDMRQRIERVMPLVRQHLTEAQHAQRRLYDRPAQ
FT                      AREFQPGDQVLVLVPTATSKFLASWKGPYVVVEKVGPVNYRVRQPGRRREE
FT                      QSYHINLLKRWVSPSSQLVTFAESPHPTVHLGEQLSAIQKTELETLVSQFK
FT                      DVFSEHPGRTTVIQHEIKTTPGVIVQQRPYRVSEARRLAIEEEVQKMLKLG
FT                      VIEPSRSPWSSPIVMVPKPDGTLRFCNDFRKLNEASSFDGYPMPRVDELLD
FT                      RLGSARFISTLDLTKGYWQVPLAPGAKEKTAFTTPSGHWHYRVLPFGLHGA
FT                      PATFQRMMDILLRPHQSYAAAYLDDVVVHLMCWEEHLTPLRRVLLELRRAG
FT                      LTANPKKCHLGLAEAKYLGYHIGRGLIQPQQAKVEALQKTPRPTNKSQVRA
FT                      FLGLAGYYRCFIPNFSSVASPLTDLTKKGQPERVTWNPVAEHAFQTLKKAL
FT                      ASSPILHAPDFNCPFILQTDASDSGLGAVLSQLHEGEEHPVVYVSRKLTTA
FT                      ESKYAAVEKEALAIKWAVLELKYYLLGRSFTLVTDHAPLQWMASAKNTNAR
FT                      VTRWFLALQDFHFKVQHRAGAAHGNADGLSRMWSGWTGLAKHSPSHTPLTA
FT                      PFFHNRMTTQTRKRQRGGG"
XX
SQ      Sequence 4231 BP; 985 A; 1245 C; 1125 G; 876 T; 0 other;

//
ID      Gypsy20-VV_I repbase;    DNA;    PLN; 9884 BP.
XX
AC      AM483798;
XX
DT      16-AUG-2007 (Rel. 12.08, Created)
DT      16-AUG-2007 (Rel. 16.07, Last updated, Version 2)
XX
DE      LTR retrotransposon from grapevine: internal portion.
XX
KW      Gypsy; LTR Retrotransposon; Transposable Element;
KW      Interspersed repeat; internal portion; LG_I; Gypsy20-VV_I.
XX
NM      Gypsy20-VV_I.
XX
OS      Vitis vinifera
OC      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC      Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC      Pentapetalae; rosids; Vitales; Vitaceae; Vitis.
XX
RN      [1]
RA      Jaillon O., Aury J.M., Noel B., Policriti A., Clepet C.,
RA      Casagrande A., Choisne N., Aubourg S., Vitulo N. et al.;
RT      "The grapevine genome sequence suggests ancestral
RT      hexaploidization in major angiosperm phyla.";
RL      Nature 449(7161), 463-467 (2007).
XX
RN      [2]
RP      1-9884
RA      Xu Z. and Wang H.;
RT      "LTR_FINDER: an efficient tool for the prediction of full-length
```

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RT     LTR retrotransposons.";
RL     Nucleic Acids Res 35(Web Server issue), W265-W268 (2007).
XX
RN     [3]
RP     1-9884
RA     Kohany O. and Jurka J.;
RT     "LTR retrotransposons from grapevine.";
RL     Repbase Reports 7(8), 718-718 (2007).
XX
DR     Genbank; AM483798; Positions    15688     5805.
XX
CC     Positions [4820-5323] - Integrase core
CC     'ACAAG' target site duplication
CC     LTRs are 95% similar to each other.
XX
FH     Key            Location/Qualifiers
FT     CDS            4454..5530
FT                    /product="Gypsy20-VV_I_3p"
FT                    /translation="MLLEKAPWYAHIANYLVTGEVPSEWKAQDRKHFFAKI
FT                    HAYYWEELFLFKYCADQIIRKCVPEEEQQGILNHCHENACGGHFASHKIAM
FT                    KVLQSGFTWPSLFKDSHIMCRICDRCQRLGKLTKRNQMPMNLILIVDLFYV
FT                    WGIDFMGPFPMSFGNSYILVGLDYVSKWVEAIPCKHNDNRVVLKFLKENIF
FT                    SRFGVPKAIISDGGTHFCNKPFKALLSKYGVKHKVATPYHPQTSGQVELEN
FT                    REIKNILMKVVITSRKDWSIKLHDSLWAYRTVYKTILGMSPYRLVYGKACH
FT                    LPVEVEYKAWWAIKRLNMDLIRAGAKRCLDLNEMEELRNDAYINSKVAKQR
FT                    MKRWHDQLISNKEFQK"
FT     CDS            join(340..1224,1228..3960)
FT                    /product="Gypsy20-VV_I_1p"
FT                    /translation="METTPEDQQSHHGHQDNPNEFRSMRDRMHPPRMSAPS
FT                    CIVPPTEQLVIKPHIVPLLPTFHGMESENPYAHIKEFEDVCNTFREGGTSI
FT                    DLMKLKLFPFTLKDKAKIWLNSLRPRSIRTWTDLQVEFLKKFFSTHRTNGL
FT                    KRQISNFSAKENEKFYECWERYMEAINACPHHGFDTWLLVSYFYDGMSSSM
FT                    KQLLETMCGGDFMSKNPEEAMDFLSYVAEVSRGWDEPHRGEVGKMKSQPNA
FT                    FHAKAGMYTLNEDVDMKAKFAAMTRRVEELEPKKMHEVQAVAETPMQVKPC
FT                    SICSYEHLVEECLTIPVAREMFGEQANVIRQFKPNSNVSYDNTYNSSWRNH
FT                    PNFSWKPRAPQYQQPAQPSQPSQQASSLEQAIVNLSKVVGDFVGDQKSINS
FT                    QLSQRIDSVENTLNKRMDGMQNDLSQKIDNLQYSISRLTNLNIVQEKGRFP
FT                    SQPHQNPKGIHEVETHEGESSQVRDVKALITLRSGKKVESPTPKLYVEEKV
FT                    EKETKKREEMKGKKKDISEGKEDHDSTVNANPEKELIKDELMKKRTSPPFP
FT                    QALHGKNGIKNASEILEVLRQVKVNIPLLDMIKQVPTYAKFLKDLCTIKRG
FT                    LNVNKKAFLTEQVSVIIQCKSPLKYKDPGCPTISVMIGGKVVEKALLDLGA
FT                    SVNLLPYSVYKKLGLGELKPTSITLSLADRSVKIPRGIIEDVLVQVDNFYY
FT                    LVDFVVLDTDPLVKEANYVPIILGRPFLATSNAIINCRNGLMQLTFGNMTL
FT                    EFNIFHMSKKLIPPEEEEGPEEVCIIDTLMEEHCNQNMQDRLNESLEGLEE
FT                    GVTEPADVFATLQGWRKKEEILSLINKDEGQDDVKEEFPKLNLKPLPMELK
FT                    YTYLEENNKCPVVISSSLTSHQEISLLEVLKRCKKAIGWQISDLKGINPLV
FT                    CTHHIYMEEKTKPIRQPQRRLNPHLQEVVRTEVLKLLQAGIIYPISDSPWV
FT                    SPTQVVPKKSGITVVQNEKGEEIATRLTSGWRVCIDYRKLNAVTRKYHFPL
FT                    PFIDQVLERVSGHPFYCFLDGYSGYLQIEIDVEDQEKTTFTCPFGTYAYRR
FT                    MPFGLCNALATFQICMLSIFSDMVERIMEVFMDDITIYGGTFEECLVNLEA
FT                    VLKRCIEKDLVLNWEKCHFMVHQGIVLGHIISKKGIEVDKAKVELIAKLPS
FT                    PTTVKGVRQFLGYAGFYKRFIQDFSKLSRPLGELLTKDAKFVWDERC"
XX
SQ     Sequence 9884 BP; 2946 A; 1979 C; 2086 G; 2873 T; 0 other;

//
ID     Gypsy8-I_Dpse repbase;     DNA;      INV; 7193 BP.
XX
AC     Unknown_singleton_95;
XX
DT     14-MAY-2009 (Rel. 14.05, Created)
DT     14-MAY-2009 (Rel. 14.05, Last updated, Version -1)
XX
DE     LTR retrotransposon from fruit fly: internal portion.
XX
KW     Gypsy; LTR Retrotransposon; Transposable Element; Gypsy8_Dpse;
KW     Gypsy8-LTR_Dpse; Gypsy8-I_Dpse.
XX
OS     Drosophila pseudoobscura
OC     Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC     Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
OC     Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
OC     obscura group; pseudoobscura subgroup.
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     XX
     RN   [1]
     RP   1-7193
     RA   Jurka J. and Kohany O.;
     RT   "LTR retrotransposons from fruit fly.";
     RL   Repbase Reports 9(5), 1068-1068 (2009).
     XX
     DR   Genome; Unknown_singleton_95; Positions   38071   30879.
     XX
     CC   Positions [2105-2662] - Reverse transcriptase
     CC   Positions [3704-4204] - Integrase core
     CC   LTRs are 98% similar to each other.
     XX
     FH   Key          Location/Qualifiers
     FT   CDS          81..1409
     FT                /product="Gypsy8-I_Dpse_4p"
     FT                /translation="MGKGQWIHRLRKEELVQCGHAFGVRLEGTVDEMRRTF
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     FT                AALWRSPVDIQRELIASLSVPIPERSHTGTPSRPRHPGRDRSREAERERVE
     FT                PATTRPAHLDYARVAKQVREWSFRFDGTTKPLEFLEQVEWSAETYGLDPDL
     FT                IPRAMPELLKGRALMWFVANNRQWRTWKEFSSSFQAYFLPRGYFEKLLQEV
     FT                RMRKQKWGEPFKEYMVEMQTLMRPLKCPQEEQTELIRENSMPDLRAYMRPH
     FT                RCKDLDTMMELADEFEALERDRLEFQRENPTVKARAANPFHKPADTTACRR
     FT                CKDGPLEEAAREERGAHGRLPTPTNGNIEDGYVKNPAQACRRCGSADHWSR
     FT                ECNGRPLTYCWRCGKVGISAWQCCRKTGNAPRPTPRRAVPGSQETVPQA"
     FT   CDS          1109..4204
     FT                /product="Gypsy8-I_Dpse_2p"
     FT                /translation="MQRRPAGGGSTGGKGSAWPLADTDQRQYRGRICQESG
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     FT                GRARVARNGPSSLVGRLICEEEQLSAVVEVAGVELQATVDTGATSSFVSRE
     FT                LADRLKGEGREVAAKKRVRLADGHSQEITHQIETKVGFGNKEIPMVLLVLP
     FT                GVIDELVLGWDYLRAVGAVVTCAGHRVVIPAQDRERGGQEERLSVAKAEAG
     FT                ETGPEYANKTDTTLRTAAREVAESTNGNEGAREEPVEDFLARELEAFAKIE
     FT                GVSNVAVHTITMSDPQPIKQRYYPKNPKMQAEINQKVDELVEKGCIEPSKS
     FT                PYSSPIVMVKKKNGKWRLCVDFRQVNARSVKDAYPMPRIDYILDQLREAKF
     FT                ISSLDLKDGYWQIPLAESSRPITAFTVPGKGLYQWKVMPFGLHSASATFQR
     FT                ALDQVIGPEMMPHAFAYQDDIVVIGRTEEEHRRNLKEVFRRLRLANLRLNA
     FT                DKCEFFRKELRYLGHKVTGEGICTDPEKVAAIAELKPPTNVKELRQYLGVA
     FT                SWYRRFVPDFATLVQPLTGLLKKKTEWVWTRERQEAFEEVKRRLVADPVLA
     FT                CPDFSKKFILQTDASDYGLGAILTQETERGERVISYASRTLNGPERNYSAT
     FT                EKECLAIVWAIRRLRPYLEGYRFKVVTDHMALKWLNSIESPSGRVARWALE
     FT                LQQYDFEIAYRKGQLNVVADALSRQPVEERGRRIRNVEGTPPVGEPPCKWL
     FT                EGMAEKIRKEAPKYPDYVEKGGNLYRHIPHRAGSEEVASWKLCVPKYARER
     FT                VLKESHDNPEAGHAGGRRTAARVAARYYWPGMYRDVRAYVRKCELCLRFKP
     FT                SQLQAAGEMLTQVPEEPWATVCADFVGPLPRSKHGNSMLLVLVDRFSKWTE
     FT                LVPLRKATAEALIKACRERIIARFGAPKVFITDNGVQFAGRAFKRFLEQLG
     FT                VRHQFTAPYTPQENPTERTNRTIKTMIAQFTRGRSKVLGRKMAGANAGHEF
     FT                GSVGYNGIFTGVRGARKGTPAAQGSI"
     FT   CDS          5669..7192
     FT                /product="Gypsy8-I_Dpse_3p"
     FT                /translation="MQRGYICGWKTERRTLEGNYQQGENTARKKKEKKMET
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     FT                WCDGSQFLQLLASPLVSPAPSGHDSVSPTVSSDEGAGEIEDDVICVDGPRA
     FT                PTAQEKASVRRPRTMRDRGEALKQKFQEATAEEKRRIRRVLEAARTIRRRR
     FT                DERLEARRQQERKATRKEEPGHESDEAPPPPPFRVVRPPMQSPARGERASN
     FT                PEAEWQRRLQQAEEEEDELWQPTPPAEDEEGSERRPPQAKEQQQPHQQYQQ
     FT                QQQPQQQQRQHQHQQPQQQQQPQQQQQQQQQQQQQENGQWQQQPQWRGPEA
     FT                AVIGPYVSQEVRTAVRQGMVWHHQTLHITWASGPAPCETQPETGARVWEES
     FT                PLGSNDRDPRRRNHKSDPAPATAEAATAEAASAETATAEAATAEAATAEAA
     FT                TAEAATAEAATAETATAEAATAEAATAEAATTEVTEHAEVEAWERGPWVWP
     FT                APERSGAVERPT"
     XX
     SQ   Sequence 7193 BP; 1924 A; 1773 C; 2515 G; 981 T; 0 other;

     //
     ID   HARB-9_ALy  repbase;   DNA;    PLN; 3370 BP.
     XX
     AC   .
     XX
     DT   21-JAN-2012 (Rel. 18.02, Created)
     DT   21-JAN-2012 (Rel. 18.02, Last updated, Version -1)
     XX
     DE   Harbinger-type DNA transposon from Arabidopsis lyrata - a
```

```
DE   consensus.
XX
KW   Harbinger; DNA transposon; Transposable Element; HARB-9_ALy.
XX
OS   Arabidopsis lyrata
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC   Camelineae; Arabidopsis.
XX
RN   [1]
RA   Hu T.T., Pattyn P., Bakker E.G., Cao J., Cheng J.F., Clark R.M.,
RA   Fahlgren N., Fawcett J.A., Grimwood J. et al.;
RT   "The Arabidopsis lyrata genome sequence and the basis of rapid
RT   genome size change.";
RL   Nat Genet 43(5), 476-481 (2011).
XX
RN   [2]
RP   1-3370
RA   Jurka J.;
RT   "Harbinger DNA transposons from Arabidopsis lyrata.";
RL   Repbase Reports 13(2), 962-962 (2013).
XX
DR   [2] (Consensus)
XX
CC   >97% identical to consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             join(781..1083,1640..3055)
FT                   /product="HARB-9_ALy_1p"
FT                   /translation="MGRCDEFDPPSSLLKLIENDDIPGDCDVGELAISLSV
FT                   LGVSGIPTLTLSVNFGISFSKXHTWSNLKPFFSFSTCTNNFLAFSICITFR
FT                   TKNLVIYTNIYHIKMYIYKNVYTDVSQTSQHHNLVKMNFNIGEPSSFVNSS
FT                   SSSDSSEFDEWLMNENASTEREEQIAANLYVNNNRLLHQITQESDHVSHRG
FT                   SIHGHAVIQRDXENAHLNLFNDYFSNNHVYGEREFHRRFRMSKRLFLHIVD
FT                   AVKQHDNYFTQHRLVTGKMGLSTLQKVTAAFRILAYGMXADAADEYIKIGE
FT                   STAIECMKRFCRAIVELFSEWYLRSPTSEDVARLLNIGQQRGFPGMLGSLD
FT                   CMHWKWKNCPTAWAGQFAGRSGSPTIILEAVADYDLWIWHAYFGMPGSNND
FT                   INVLNSSNLFSKLAQGIAPPANYIIQGQEYTMGYYLADGIYPKWSTIVQTI
FT                   SDPQGPKKKLFAARQESCRKDVERAFGVLQSKFAIIAGAARYWKKEVLHDI
FT                   MTACIIMHNMIIEDERDITAPIREARSVPEATVEMAINENTRFQQFLSRNL
FT                   QIKNKETHLALRNALIDHIWEHYGNN"
XX
SQ   Sequence 3370 BP; 1073 A; 567 C; 562 G; 1158 T; 10 other;

//
ID   HAT-18_Mad  repbase;    DNA;    PLN; 3889 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 16.12, Created)
DT   22-MAR-2011 (Rel. 16.12, Last updated, Version -1)
XX
DE   Autonomous hAT elements, consensus.
XX
KW   hAT; DNA transposon; Transposable Element; HAT-18_Mad.
XX
OS   Malus domestica
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Rosales; Rosaceae; Maloideae;
OC   Maleae; Malus.
XX
RN   [1]
RP   1-3889
RA   Velasco R., Zharkikh A., Affourtit J., Dhingra A., Cestaro A.,
RA   Kalyanaraman A., Fontana P., Bhatnagar S.K. et al.;
RT   "The genome of the domesticated apple (Malus x domestica
RT   Borkh).";
RL   Nat Genet 42(10), 833-839 (2010).
XX
RN   [2]
RP   1-3889
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RA    Bao W. and Jurka J.;
RT    "hAT-type DNA transposons from the apple genome.";
RL    Repbase Reports 11(12), 2914-2914 (2011).
XX
DR    [2] (Consensus)
XX
CC    TIRs are 9-bp long.
XX
FH    Key             Location/Qualifiers
FT    CDS             join(1441..2565,2511..3350)
FT                    /product="HAT-18_Mad_1p"
FT                    /translation="MKADNNQPVLTNESMGSGLVPHTFNQKRLELKVVMFV
FT                    IKDEQPFKVVEGGGYIDMMKEAQPRFKIPNRRKIAAGVWDLFVLEKSKLFE
FT                    AMHNQRVSITTDTWTSIQNINYMVVTAHFMDSEWKLHKRIINFIKITGHKG
FT                    DDIGKVLEVCLNQWGIEKIFSITVDNASANDVAVDYMKKRLREMNSLLVGG
FT                    KYLHMRCACHILNLVVKSGLKELAKSVEGIRNCVKYIHSSPARLDKFRDFA
FT                    ILFKMDKMSNVPFDVSTRWNATYKMLDVAYKFRKVFLRMAEENVQFRDYFE
FT                    EMEMDSKKNLVKRVGPPXEEDWEKALAFTHFLKKFHDATLKLSATKKVTST
FT                    LLWDQVVALQIEIEKKKRKMLPILHCKGWLLQEKKKKDATNPTLQRVATTM
FT                    MRKFNKYWGSFENVNPLMFLGQVLDPCYKLQMITISLKALGWDDRKVDWML
FT                    KEIKKCLLDLYNEYRRGSSTTIGAPLEDVELNEEFIIQACGGDENKIEMMK
FT                    ELIQERREQRLLEISNEVDKYFAAPYISIVVGGFDLLSWWKSNTKEFPILS
FT                    QIAKDIFAIPTSTVASENAFSLGRRVVDPFRASLTPKMVEALVCTSDWLRA
FT                    DEVNFYKEPTEDMLQFYKEMEEVETSKICFNFFSKFVVKWFSTLILLATNM
FT                    FSLFVM"
XX
SQ    Sequence 3889 BP; 1174 A; 627 C; 867 G; 1220 T; 1 other;

//
ID    HERVK9I     repbase;    DNA;    PRI; 6021 BP.
XX
AC    .
XX
DT    24-OCT-1997 (Rel. 2.09, Created)
DT    09-SEP-2002 (Rel. 7.08, Last updated, Version 2)
XX
DE    HERVK9I/HERV-K(HML-3) endogenous retrovirus, flanked by MER9.
XX
KW    ERV2; Endogenous Retrovirus; Transposable Element; HERV;
KW    HERVK superfamily; HERVK9I; MER9.
XX
OS    Homo sapiens
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC    Catarrhini; Hominidae; Homo.
XX
RN    [1]
RP    1-5947
RA    Kapitonov V.V. and Jurka J.;
RT    "HERVK9I.";
RL    Direct Submission to Repbase Update (17-OCT-1997).
XX
RN    [2]
RP    1-5937
RA    Kapitonov V.V. and Jurka J.;
RT    "HERVK9I.";
RL    Direct Submission to Repbase Update (02-DEC-1998).
XX
RN    [3]
RA    Mayer J. and Meese M.;
RT    "The Human Endogenous Retrovirus Family HERV-K(HML-3).";
RL    Genomics (80), 331-343, 2002.
XX
RN    [4]
RP    1-6021
RA    Mayer J. and Meese M.;
RT    "HERVK9I: The endogenous retrovirus.";
RL    Direct Submission to Repbase Update (26-AUG-2002)Direct
RL    submmission to.
XX
DR    [4] (Consensus)
XX
CC    putative gag gene: nt 123-1559
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CC     putative protease gene: nt 1421-2365
CC     putative polymerase gene: nt 2257-5097
CC     putative envelope gene: nt 4883-5694
CC     nt 5689: 661 bp insert in some loci
CC     nt 5195: 206 bp insert in some loci
CC     consensus sequence derived from 73 proviral loci.
XX
SQ     Sequence 6021 BP; 1869 A; 1224 C; 1308 G; 1620 T; 0 other;

//
ID     Harbinger-1_PGr repbase;      DNA;     PLN; 6862 BP.
XX
AC     .
XX
DT     10-OCT-2012 (Rel. 17.10, Created)
DT     10-OCT-2012 (Rel. 17.10, Last updated, Version -1)
XX
DE     Harbinger-type DNA transposon from Puccinia graminis - a
DE     consensus.
XX
KW     Harbinger; DNA transposon; Transposable Element; Harbinger-1_PGr.
XX
OS     Puccinia graminis
OC     Eukaryota; Fungi; Dikarya; Basidiomycota; Pucciniomycotina;
OC     Pucciniomycetes; Pucciniales; Pucciniaceae; Puccinia.
XX
RN     [1]
RP     1-4696
RG     The Broad Institute Genome Sequencing Platform;
RT     "The Genome Sequence of Puccinia graminis f. sp. tritici Strain
RT     CRL 75-36-700-3.";
RL     Direct Submission to EMBL/GenBank/DDBJ (02-FEB-2007).
XX
RN     [2]
RA     Duplessis S., Cuomo C.A., Lin Y.C., Aerts A., Tisserant E.,
RA     Veneault-Fourrey C., Joly D.L., Hacquard S. et al.;
RT     "From the Cover: Obligate biotrophy features unraveled by the
RT     genomic analysis of rust fungi.";
RL     Proc Natl Acad Sci U S A 108(22), 9166-9171 (2011).
XX
RN     [3]
RP     1-6862
RA     Kojima K.K. and Jurka J.;
RT     "DNA transposons from Puccinia graminis.";
RL     Repbase Reports 11(6), 1799-1799 (2011).
XX
DR     [3] (Consensus)
XX
CC     This consensus is generated from 6 sequences with >92%
CC     identity.
CC     The exon-intron structure is predicted with Softberry FGENESH.
XX
SQ     Sequence 6862 BP; 1681 A; 1770 C; 1447 G; 1964 T; 0 other;

//
ID     Harbinger-38_CCri repbase;      DNA;     PLN; 5307 BP.
XX
AC     .
XX
DT     04-JUN-2013 (Rel. 18.11, Created)
DT     04-JUN-2013 (Rel. 18.11, Last updated, Version 1)
XX
DE     DNA transposon from the red seaweed: consensus.
XX
KW     Harbinger; DNA transposon; Transposable Element;
KW     Harbinger-38_CCri.
XX
OS     Chondrus crispus
OC     Eukaryota; Rhodophyta; Florideophyceae; Gigartinales;
OC     Gigartinaceae; Chondrus.
XX
RN     [1]
RP     1-5307
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RA    Collén J., Porcel B., Carré W., Ball S.G., Chaparro C., Tonon T.,
RA    Barbeyron T., Michel G., Noel B., Valentin K. et al.;
RT    "Genome structure and metabolic features in the red seaweed
RT    Chondrus crispus shed light on evolution of the Archaeplastida.";
RL    Proc Natl Acad Sci U S A 110(13), 5247-5252 (2013).
XX
RN    [2]
RP    1-5307
RA    Bao W. and Jurka J.;
RT    "DNA transposons from the red seaweed.";
RL    Repbase Reports 13(11), 2667-2667 (2013).
XX
DR    [2] (Consensus)
XX
CC    ~97% identical to consensus.
XX
FH    Key            Location/Qualifiers
FT    CDS            232..1413
FT                   /product="Harbinger-38_CCri_1p"
FT                   /translation="MGRGRQKDHCTSLVRRRQLHLQVALRTVSSRRQMIPG
FT                   SALSDTKSILTLAAKFSSATKDYHYHLLRVRRISHQDFSFNFNCLTDRECL
FT                   QNFRFQKRQISQLVSVMSWPETQTRTSRNRYRASPILATCIVLRRLAAPSR
FT                   WGDLEELFGKHAPQLSEIFWEAIEHLLNTRKHLVTEDISELFIAQRAELYA
FT                   QRIHDKGKALPNCVGFIDGTVLGIARPSGSLAQRVAYNGHKRKHAIKYQAV
FT                   NTPDGLIQHLYGPLEGRRHDWTLYVRSKMDDILPRVLLVEGKQYCIYGDSG
FT                   YNQRWFIDVPFQGSNISPAQSAFNKAMSSVRISVEWIFKEVKLQFSAIDFK
FT                   RKMKVREHPVGMIYLASILLSNFRNCLYPNQISRYFDCPPPDLTTYVNHRN
FT                   "
FT    CDS            4729..4178
FT                   /product="Harbinger-38_CCri_2p"
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FT                   RKKKKTKMAYGADDSLDAFGEHMKDADLARISLERERLQFERDMAESGREE
FT                   RLQERLERQKEREEERRERREERVEQQKLEVEKFKALIEAFARKK"
XX
SQ    Sequence 5307 BP; 1105 A; 1454 C; 1447 G; 1227 T; 74 other;

//
ID    Helitron-1_HM repbase;    DNA;    INV; 12703 BP.
XX
AC    .
XX
DT    16-DEC-2008 (Rel. 13.12, Created)
DT    07-OCT-2011 (Rel. 16.10, Last updated, Version 2)
XX
DE    Helitron DNA transposon from hydra - consensus.
XX
KW    Helitron; DNA transposon; Transposable Element; Helitron-1_HM.
XX
NM    Helitron-1_HM.
XX
OS    Hydra vulgaris
OC    Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
OC    Anthoathecata; Aplanulata; Hydridae; Hydra.
XX
RN    [1]
RP    1-12703
RA    Bao W. and Jurka J.;
RT    "Helitron DNA transposons from Hydra magnipapillata.";
RL    Repbase Reports 8(12), 2056-2056 (2008).
XX
DR    [1] (Consensus)
XX
CC    Termini are determined.
CC    This sequence was derived from sequence data generated by TIGR,
CC    J Craig Venter Institute.
XX
FH    Key            Location/Qualifiers
FT    CDS            1791..6281
FT                   /product="Helitron-1_HM_1p"
FT                   /translation="MIFLVIKFFYFIVNFRLVKKKEIISVALINMFNENDD
FT                   IEMDDRLDVVLYLQDDVSAIRRVENNRRRNERNRLRRDEINCLQNERNRLD
FT                   RDNVNRRQNERNRLDRDNVNRRQNERRAVGQGRMYSIARSNAIPDYNYLGE
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FT                    LAFKNMAEVEDEEIRKAAIEGRSASVVKMSLLEGGDRRRYNLPSHDEVAVV
FT                    FVGEDGAPPTSREVVIYPRGHPLKIVSSMSANLDPMVYPLFFPRGDAGWHN
FT                    QLVHNPERATLVRNHVTLSQFYNYRLSVRQFFCSLFYGKKLFQQYAVDAYV
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FT                    GSPRALKENFEDAMAIIKKYGKPDLFITFTCNPKWREITENLYPGQNANDR
FT                    PDLVTRVFKLKLNNLLNDIFKHGVLGKVVTHVQVIEFQKRGLPHAHILLHL
FT                    ANDDKLETSQDIDNLICAEIPDPIVNCELYDIIKTCMIHGPCGILNPNSPC
FT                    MKDGVCSKKYPKDFNANTVAVHNGYPRYRRRDNGLVINIKGNNVDNRWVVP
FT                    YNPWLSKKYQAHINVEACMSVKAVKYLYKYIYKGHDCANVLINEQVNHDEI
FT                    NTFLDCRYVSAPEALWRIFEYPISHMSHSIIRLKVHLPENQIVYFREGEEQ
FT                    VALDRAAQRDTHLTAWFKLNSENEGANRYSYVDIPYHFVFDDKHCKWKVRQ
FT                    RGGNKVIVRMYKVSPTGELFFLRLLLLQAKGAKSWEDLRTVNGIVLETFRE
FT                    ACVFNGLLQDDTEWQNTLSEAVLTRMPKQIRQLFSIILTFCEPDDPLHLWN
FT                    SYKAFMMEDFIHRQVPFILAEQATLLQIEKIINQSGKTLSDYNLPVVDEFI
FT                    DFNLENLNDNVQQSIDEANRMRPLLNVNQLNVSNAVLAALNEQPCVENQHS
FT                    RLFFMDGPAGSGKTFTYNYLIAEMSSRGVKSATAAWTGIAATLLTNGSTLH
FT                    GLFKLPVPILDNSTCNVTPNSIQGQFLRQVSLFMLDETSMIPKHALNAIDR
FT                    LLKDVCNNNFPFGGKVILFGGDFRQILPVVKRGRPAEVVESCIKCSLQWQW
FT                    VQKFTLTENMRVRDGEGDFSEWLLKLGSGTIPGKEEDPFKGCIEIPQQCII
FT                    RENESIVEKIFGDAQQDDYAKRVILTPTNVDSLSINEEVLERLHGEVKTYL
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FT                    AGLCNGTRMKVCALQNNYIDAEVLTGVSEGKRVFVPRIQLAPSDSNLPFVL
FT                    KRRQFPVRLAYSMTINKSQGQTFDRVGVYLKKPCFSHGQLYVACSRTRAFN
FT                    SLFFKIDKHPIQGMVGEKYYTNNVIFSNVLNL"
XX
SQ   Sequence 12703 BP; 4239 A; 1533 C; 2013 G; 4913 T; 5 other;

//
ID   Helitron-2_CRe repbase;    DNA;    PLN; 23720 BP.
XX
AC   .
XX
DT   18-JAN-2012 (Rel. 19.12, Created)
DT   19-JAN-2012 (Rel. 19.12, Last updated, Version 1)
XX
DE   Autonomous Helitron transposable elements - a consensus sequence.
XX
KW   Helitron; DNA transposon; Transposable Element; HELITRON2;
KW   Helitron-2_CRe.
XX
OS   Chlamydomonas reinhardtii
OC   Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae;
OC   Chlamydomonadales; Chlamydomonadaceae; Chlamydomonas.
XX
RN   [1]
RP   1-23720
RA   Bao W. and Jurka J.;
RT   "Helitron2 transposable elements in the Chlamydomonas reinhardtii
RT   genome.";
RL   Direct Submission to Repbase Update (18-JAN-2012).
XX
DR   [1] (Consensus)
XX
CC   Helitron-2_CRe is a familiy of autonomous transposable elements.
CC   Both termini are determined. Its features are same with those of
CC   Helitron-1_CRe, except for that the Tpase is in the oppsite
CC   direction compared to Helitron-1_CRe.
XX
FH   Key              Location/Qualifiers
FT   CDS              join(11491..11281,11088..10978,10788..10526,
FT                    9634..8686,8499..8381,8281..7448,7208..7173,
FT                    6987..4210,3895..2822,2638..1616)
FT                    /product="Helitron-2_CRe_1p"
FT                    /translation="MAAAAAAAVLLASGWMGAGQAQWRALRLDGLPVSGGE
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FT                    AWDALVLGLGAGAAVAGAVAWAGARVELELPWHLAWVRMVAGELLQPSLHT
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FT                    KLRSSSVHGMETWLHHHADEIELALAGVPNPDAVAAAAGVGGAAMPWEVQL
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FT                   GLQRVAEMMGLASDAEKQPAAEAWQERQWHTLTDCISATRAAARVAGDTAG
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FT                   CGRRRRQRDVHWHRVSGLREWLDEQLSVMLPGTAEAPRDGNTLWAPPTSAE
FT                   AVALLAGATGAASMPEITERVMREGPASGRTVYRLQAHPAAGTVQLAADGD
FT                   HQLRLTVMEERLVAVWRPLRNLMVCRPPAAGGGPGHWEMRAHVIAFKAPEP
FT                   QQLAAVFPCSLARVPECITVVFVSPAQTYQQLEALARRVPALMVRGKVVAA
FT                   WARHLAALYPSARLDEAAVQEWERQPPTAVADALARRAVCTQTQGEASALL
FT                   RTLRAEQEGYARARYGTAEEAAARGASTAMAAAVNSDSSSGSDSEAIIVQQ
FT                   SLARPSRKRPRLLSAAHMQRLLCGLDRDASVAVRQLLLAHNFKAAATKLLR
FT                   HHGGAPTKEAVTQMQVQLQTQHCNYEQVLTDHERALTAEANASGSTRPLSR
FT                   PPAGAPLPPGSLFVVHEPQALSPVQREHGARRPQSLPALPAEAAQRAGAAA
FT                   PAAAAAGAEVAAAFSSCGQNVTHMQGIDDVDLSPTPADSPALRAVFQDACA
FT                   DERALQLLLDGWPLASCTEQAPQSDYQPEWPLRVHVNRFPNGTGACPAGMQ
FT                   MLSWIQLQLQRWYPPAPDGTEDCSAQAPHFILDMFDAWQRHTVNQQVAVRF
FT                   KLDPQLIMSLGDMGPDTLVEAADVLAAGLSRTEQAQRLHGSPPEVEQLVRG
FT                   ARITGAHVVGSPGSYAALRSRAYGLWAAYGPPSATVTLNPASVHSDATFTL
FT                   MGRPYTFDVRTGAPQHRPMAAERWDLVAGHPLACAESFEAFMDAFCDVFLG
FT                   WPAGSDVQQRSNCLFGRVDAFFFKFEMNQRGELHVHGCIWQPGLQPARLRK
FT                   ALADPRSCPDVLDFLESVQTQWFASPLLFSGGERPVHAQKLSTEQLQEVAE
FT                   AAGSERLTELQRDVLREVLVEVKARGAMEDAAVSCRPPLQCSSLTEAERLG
FT                   LFAAHAVLETLLHAHRDGTCTTSHSKHATDSNCRMRLPRMLHWLTTYLHEQ
FT                   SVCVHLKRYGRYMVSHMVALLLAVPCNHTVTFACDVGRWLRTRELWDQRHE
FT                   GIPRTDPVWERRPQLPSLEQLAADAADYALKYATKSEAVQGSRALIAAATM
FT                   LRRRMHLMTPEQQAGIESEHLPIQDVLDQLRHPFAAFADASASAWAPRPPT
FT                   AGVSAAGESSTPAQAQFTAEVTARAQQSATVAALRTARPVGAAAVQREGMF
FT                   NLAHAINLLTAQQTFSAPAAALLLMRGTDAHESHQFRAIDYRMFSQHVQSQ
FT                   LKRADPELRPRDTQLRLVRTMGSVGAGGSPRGEGQLPAASTIASDVPDPGP
FT                   SGSVQQLEQPAVAPARYRSSSYLKDYLYRGEALRELSPMMMAMLFYKVLER
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FT                   VAQIPRANAWPAVGRTAAAAVVRSTQEWTHERLAAAQQRMHDYDLGGQYAA
FT                   QALAQAQGAVQQQLLLYNSGTAAVTAKLVLISPLAVTTAAPEVQGVWPDAA
FT                   NPGAEPPYVLCPEDSQPTPEDTARLWNLSDDQQQAFMLYAQLLLAEAAGVR
FT                   QPPVCSVLTGKAGSGKSRVLQALLWFAYQHRCESLIALVSYTWRAALHDST
FT                   PGVLGTSTTSFFATAGTFGPPHRDRVERNLNGVRFIFLDEFSTCGLSHWAR
FT                   ICMHVHAARRHVGIDSTHLYHGPLSDLHGLLVGDLRQLPQPRHVPLYSGAA
FT                   EESLRRLLAPGAGDGGAMERQIRQLEHPEGSMNLMGRELWNMVPFAFVLTH
FT                   QHRQQAGVGDNNEPLFMLAEKFGGVQEISQADLDTACQQLNARVWQPPKPG
FT                   IDPVPQPFAVVQRHVVRVPLALQLVQLHALAQRQQLLLWRSADLSPDGSSL
FT                   PISHVHQLEALGGAEDDSGVPAVCAFFAGIRYVFTSNEHVRLYHINNNSAT
FT                   GTGIVLHPNEPPLPDASIAPVHVLKFVPSAVM"
XX
SQ   Sequence 23720 BP; 4463 A; 8859 C; 6195 G; 4196 T; 7 other;

//
ID   Hitchcock_LTR repbase;      DNA;      VRT; 543 BP.
XX
AC   .
XX
DT   14-SEP-2004 (Rel. 9.08, Created)
DT   01-JUL-2005 (Rel. 10.08, Last updated, Version 2)
XX
DE   Gallus gallus Hitchcock_LTR, putative LTR.
XX
KW   LTR Retrotransposon; Transposable Element; GGLTR5B; Hitchcock_LTR;
KW   putative LTR; retrotransposon.
XX
NM   Hitchcock_LTR.
XX
OS   Gallus gallus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes;
OC   Phasianidae; Phasianinae; Gallus.
XX
RN   [1]
RP   1-543
RA   Smit A.F.;
RT   "GGLTR5B retrotransposon LTR.";
RL   Direct Submission to Repbase Update (SEP-2004).
XX
RN   [2]
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```
RP   1-543
RA   Wicker T., Robertson J.S., Schulze S.R., Feltus F.A., Magrini V.,
RA   Morrison J.A., Mardis E.R., Wilson R.K. et al.;
RT   "The repetitive landscape of the chicken genome.";
RL   Genome Res 15(1), 126-136 (2005).
XX
DR   [2] (Consensus)
XX
CC   No internal component of this putative retrotransposon has been
CC   identified. Wicker et. al. classify it as an LTR due to the
CC   conserved termini TG/CA, and absence of SINE characteristics.
XX
SQ   Sequence 543 BP; 133 A; 104 C; 134 G; 169 T; 3 other;

//
ID   I-66_AAe    repbase;    DNA;    INV; 6707 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 16.04, Created)
DT   22-MAR-2011 (Rel. 16.04, Last updated, Version -1)
XX
DE   An I non-LTR retrotransposon from Aedes aegypti.
XX
KW   I; Non-LTR Retrotransposon; Transposable Element; I-66_AAe.
XX
OS   Aedes aegypti
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
OC   Culicoidea; Culicidae; Culicinae; Aedini; Aedes; Stegomyia.
XX
RN   [1]
RA   Nene V., Wortman J.R., Lawson D., Haas B., Kodira C. and Tu Z.J.
RA   et al.;
RT   "Genome sequence of Aedes aegypti, a major arbovirus vector.";
RL   Science 316(5832), 1718-1723 (2007).
XX
RN   [2]
RP   1-6707
RA   Kojima K.K. and Jurka J.;
RT   "I clade non-LTR retrotransposons from the yellow fever
RT   mosquito.";
RL   Repbase Reports 11(4), 1337-1337 (2011).
XX
DR   [2] (Consensus)
XX
CC   This consensus is generated from 16 sequences with >97%
CC   identity.
XX
FH   Key           Location/Qualifiers
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FT                 /note="endonuclease, reverse transcriptase and
FT                 ribonuclease H."
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XX
SQ    Sequence 6707 BP; 2206 A; 1540 C; 1411 G; 1550 T; 0 other;


//
ID    I-73_AAe    repbase;    DNA;     INV; 6820 BP.
XX
AC    .
XX
DT    22-MAR-2011 (Rel. 16.04, Created)
DT    22-MAR-2011 (Rel. 16.04, Last updated, Version -1)
XX
DE    An I non-LTR retrotransposon from Aedes aegypti.
XX
KW    I; Non-LTR Retrotransposon; Transposable Element; I-73_AAe.
XX
OS    Aedes aegypti
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
OC    Culicoidea; Culicidae; Culicinae; Aedini; Aedes; Stegomyia.
XX
RN    [1]
RA    Nene V., Wortman J.R., Lawson D., Haas B., Kodira C. and Tu Z.J.
RA    et al.;
RT    "Genome sequence of Aedes aegypti, a major arbovirus vector.";
RL    Science 316(5832), 1718-1723 (2007).
XX
RN    [2]
RP    1-6820
RA    Kojima K.K. and Jurka J.;
RT    "I clade non-LTR retrotransposons from the yellow fever
RT    mosquito.";
RL    Repbase Reports 11(4), 1344-1344 (2011).
XX
DR    [2] (Consensus)
XX
CC    This consensus is generated from 10 sequences with >99%
CC    identity.
XX
FH    Key            Location/Qualifiers
FT    CDS            2953..6639
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FT                   ribonuclease H."
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XX
SQ   Sequence 6820 BP; 2143 A; 1686 C; 1476 G; 1514 T; 1 other;

//
ID   Jockey-6_DK repbase;    DNA;     INV; 3710 BP.
XX
AC   .
XX
DT   21-JUN-2012 (Rel. 17.07, Created)
DT   21-JUN-2012 (Rel. 17.07, Last updated, Version 1)
XX
DE   Non-LTR retrotransposon from the Drosophila kikkawai genome:
DE   consensus.
XX
KW   Jockey; Non-LTR Retrotransposon; Transposable Element;
KW   Jockey-6_DK.
XX
OS   Drosophila kikkawai
OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
OC   melanogaster group; montium subgroup.
XX
RN   [1]
RP   1-3710
RA   Kojima K.K. and Jurka J.;
RT   "Non-LTR retrotransposons from the Drosophila kikkawai genome.";
RL   Repbase Reports 12(7), 1343-1343 (2012).
XX
DR   [1] (Consensus)
XX
CC   ~98% identical to consensus. 5'-truncated.
CC   This consensus sequence was derived from the data released in
CC   Genbank by the Baylor College of  Medicine Human Genome
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CC    Sequencing Center, prior to publication.
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FT                    LKQ"
XX
SQ    Sequence 3710 BP; 1053 A; 967 C; 781 G; 906 T; 3 other;

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ID    Juno3_Av_I   repbase;     DNA;     INV; 4920 BP.
XX
AC    .
XX
DT    12-APR-2017 (Rel. 22.04, Created)
DT    12-APR-2017 (Rel. 22.04, Last updated, Version 1)
XX
DE    Juno3_Av_I is an internal portion of Juno3_Av.
XX
KW    LTR Retrotransposon; Transposable Element; Juno3_Av_I.
XX
OS    Adineta vaga
OC    Eukaryota; Metazoa; Lophotrochozoa; Rotifera; Bdelloidea;
OC    Adinetida; Adinetidae; Adineta.
XX
RN    [1]
RP    1-4920
RA    Fernando Rodriguez ., Aubrey W. Kenefick . and Irina R.
RA    Arkhipova .;
RT    "LTR-Retrotransposons from Bdelloid Rotifers Capture Additional
RT    ORFs Shared between Highly Diverse Retroelement Types.";
RL    Viruses 9(4), 1-12 (2017).
XX
DR    [1] (Consensus)
XX
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XX
SQ   Sequence 4920 BP; 1888 A; 878 C; 723 G; 1431 T; 0 other;

//
ID   Keno-5_XT   repbase;    DNA;    VRT; 5525 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 17.10, Created)
DT   22-MAR-2011 (Rel. 17.10, Last updated, Version -1)
XX
DE   A U2 snRNA gene-specific non-LTR Retrotransposon family from
DE   Xenopus tropicalis.
XX
KW   Tx1; Non-LTR Retrotransposon; Transposable Element; Keno-5_XT.
XX
OS   Xenopus tropicalis
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Pipoidea; Pipidae; Xenopodinae;
OC   Xenopus; Silurana.
XX
RN   [1]
RA   Hellsten U., Harland R.M., Gilchrist M.J., Hendrix D., Jurka J.,
RA   Kapitonov V., Ovcharenko I., Putnam N.H. et al.;
RT   "The genome of the Western clawed frog Xenopus tropicalis.";
RL   Science 328(5978), 633-636 (2010).
XX
RN   [2]
RP   1-5525
RA   Kojima K.K. and Jurka J.;
RT   "U2 snRNA gene-specific non-LTR retrotransposons from Xenopus
RT   tropicalis.";
RL   Repbase Reports 12(10), 2269-2269 (2012).
XX
DR   [2] (Consensus)
XX
CC   This family is specifically inserted into U2 small nuclear RNA
CC   genes at the same site. Related families have been reported as
CC   L1-53_XT, L1-54_XT, L1-55_XT, and L1-56_XT. It appears to
CC   generate no target site duplications.
XX
FH   Key             Location/Qualifiers
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FT                      DREILENFLAPITLLNVDYKVMAKLISLRVKPFLNVLIHPDQVCGVPGRTM
FT                      AESLNVIRDAIWYSNDRKQKLAILSLDFEKAFDRVSHEYLFKVLRKMALPD
FT                      FIVNGIKVLYNSCFSQISINGFLTKNVFLKSGVKQGCPLSPFLFICAIEPL
FT                      LILLRNDKIIRGVPVPGGGGRQVKVLSYMDDVTLLCTTAYSLKRALLHISG
FT                      FCGASGFKLNLHKCDCLGIGVFDMSVAPGIKMQHNQIKILGVIFNAENKGD
FT                      LNWDIVLTRLEKKTCMWNLRDLTMEGKVLIIKMVLLPIMLHIALVFPPSSL
FT                      YIKRLTRVCFKFLWGSKMEKLKRDRMYKSKQCGGKDVPNLLLFFYVKFFCF
FT                      CFKLFNTDGIFSCFLKYAAGMVFKPWFRVPLNTPVLLCPPKHYVVLEKAVR
FT                      LFRLKEIEPEVLGDQRKVTKILRHDDVVLTVSNFSEARSKQVWRNVFGKFL
FT                      ANVHKDLAWAIVHQCLPTREFQHRRGLVGRGKCPRETCCIDETILHLFWNC
FT                      PYAQELWKSVGPLFKHIGGFKDFNHFYVLYGLFTCTSVKQHEICWMILNCF
FT                      KNAIWKVRNILLFKHDFISVNDCIKIALSEMYIYYLRDKKLLGKNEAMSMW
FT                      GLASWNILL"
XX
SQ   Sequence 5525 BP; 1451 A; 1051 C; 1343 G; 1667 T; 13 other;

//
ID   L1-30_ACar  repbase;    DNA;    VRT; 6517 BP.
XX
AC   .
XX
DT   20-JUN-2012 (Rel. 17.10, Created)
DT   20-JUN-2012 (Rel. 17.10, Last updated, Version 1)
XX
DE   L1-type non-LTR retrotransposons - a consensus sequence.
XX
KW   L1; Non-LTR Retrotransposon; Transposable Element; L1-30_ACar.
XX
OS   Anolis carolinensis
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata;
OC   Toxicofera; Iguania; Dactyloidae; Anolis.
XX
RN   [1]
RA   Alf??ldi J., Di Palma F., Grabherr M., Williams C., Kong L.,
RA   Mauceli E., Russell P., Lowe C.B., Glor R.E. et al.;
RT   "The genome of the green anole lizard and a comparative analysis
RT   with birds and mammals.";
RL   Nature 477(7366), 587-591 (2011).
XX
RN   [2]
RP   1-6517
RA   Kojima K.K. and Jurka J.;
RT   "Non-LTR retrotransposons from green anole.";
RL   Repbase Reports 12(10), 2133-2133 (2012).
XX
DR   [2] (Consensus)
XX
CC   ~96% identical to consensus.
XX
FH   Key             Location/Qualifiers
FT   CDS             1359..2462
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FT                   /product="L1-30_ACar_1p"
FT                   /translation="MITAKWKMEKDPKDNKSMLRRGSLNDEINLRDLMKEI
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FT                   EIQDIKAETINNTKDIKELKMDNKKTEKIQSKMQKKLESLESKNQKLEKIQ
FT                   EKCEQQESEFQLRFRNIEEDSKENIRTVVSQLIAKILQCSELEADSQIDRV
FT                   YRIQTNYAKKNQSIRDVIVRFIKKNTRDEILKSNLTNPPYYKQRRVAIMKE
FT                   IPASIMNRRRRYYFLTDELKKLNIRFRWEKFEGIMTTYKGEKFWLTSEDKA
FT                   RDFYRKLKRDIDPESVSPNKEKVLNPKNPKKRRFDSPKEIEENLRRKDKTD
FT                   KAAPSSEADDEEDDDSPIDDNPTDE"
FT   CDS           2413..5700
FT                   /product="L1-30_ACar_2p"
FT                   /note="apurinic-like endonuclease and reverse
FT                   transcriptase."
FT                   /translation="MMKRTTTAQSMTTQPMNDFTQTIKCFSNNINGLNSPS
FT                   KRKRLFSKLWKEKYNITALQETHIAKKHVKYLINDPLGQVYYSSDIKKKRG
FT                   VALYIDTKFKPLEKFKDNEGRVIGVMIEIGDEKILLCNIYAPNGPKTKFIK
FT                   FVWENINQIDFDHIMIFGDYNGVLDNKLDKTYNQKRKKEFSTLPKMFIRFK
FT                   EEFDLKDTWRELNPNQKDYTHLSSRHHQWSRIDMIWVTKTLLTKIDKIKIL
FT                   SRDLSDHCPLVMVINHKNHKRKWRLNDNLIKLEKDIDRIKIKSKEFFKLND
FT                   TPEVSPQIIWDAYKAVIRGDLIQLSASKNKRRNQEINXLVKQIDSEEKKLK
FT                   QNPKNQLTKRKLELLKKQKNTWEIERLANRLKWAKQQTFENANKPGRWLAR
FT                   MIRKRKQNKHIAKIKVGDREIIKDEEIKEEFKIFYKNLYSKDPIGQENIVK
FT                   YLGEQKLPKITEDQRLGLNKEITEEEIKKAIKDLKVNKSPGPDGFTGEFYK
FT                   TVQEEIIQYLKKIMNQALNLKKIPESWKEAEIIMIHKEGTEAQEISNYRPI
FT                   SLLNIDYKIYTKVLANRFKEFLNDWISEDQTGFLKNRSTKDNVRIILDIIE
FT                   YYESNPQKELGLVSIDAEKAFDNLNWEFFKLLLQEIDIGWQFQNAINAIYD
FT                   XQKARVSINGLTSEEFRIEKGTRQGCPLSPLLFIFALEILLKAIKKDKNLH
FT                   GTKLDKQEIKIRAFADDIICIVEDPQRELNNWLEKIEEFGKVAGFKLNKRR
FT                   TKILTKNMTKKKQENLHKISGLEIATKIKYLGIWISAKNNQLLELNYLAKW
FT                   KEIKKDLENWQNLNLSLLGRIAVIKMNILPKLLYLFQNVPIIRNTKIFKDW
FT                   NKDISKFIWKNRKPRIKYSIMITPKLKGGFGLPDLRLYYEACSLEWVKEWV
FT                   TLKKEKILTIEGFDLRRGWHGYMWYDMTKVEKKFGNHFIRSALLKVWIKYK
FT                   NYFYTKTPLWLSPLEANQRRLLGWTIWPTYKEILGGLNNRDEEPFVKSMEE
FT                   IQKNYKNVSWFQYIQIKEFYKKDRQVGFNQESGFWDKFLQVKEKSITILYK
FT                   KLLDWVTEREEVTKSMIQWAKNIGRPINIDEWESIWKKK"
XX
SQ   Sequence 6517 BP; 2674 A; 1087 C; 1259 G; 1487 T; 10 other;

//
ID   L1-35_ALy   repbase;   DNA;     PLN; 6092 BP.
XX
AC   .
XX
DT   30-AUG-2018 (Rel. 24.07, Created)
DT   30-AUG-2018 (Rel. 24.07, Last updated, Version 1)
XX
DE   L1 non-LTR retrotransposon from Arabidopsis lyrata - a sampled
DE   insertion.
XX
KW   L1; Non-LTR Retrotransposon; Transposable Element; L1-35_ALy.
XX
OS   Arabidopsis lyrata
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; malvids; Brassicales; Brassicaceae;
OC   Camelineae; Arabidopsis.
XX
RN   [1]
RP   1-6092
RA   Hu T.T., Pattyn P., Bakker E.G., Cao J., Cheng J.F., Clark R.M.,
RA   Fahlgren N., Fawcett J.A. and Grimwood J.;
RG   et al;
RT   "The Arabidopsis lyrata genome sequence and the basis of rapid
RT   genome size change.";
RL   Nat Genet 43(5), 476-481 (2011).
XX
RN   [2]
RP   1-6092
RA   Bao W.;
RT   "Non-LTR retrotransposons from the Arabidopsis lyrata genome.";
RL   Repbase Reports 19(7), 1251-1251 (2019).
XX
DR   [2] (Consensus)
```

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      FH   Key           Location/Qualifiers
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      FT                 DDVLEKGLHTYNEWALAVERWFEHPPDNYLMFVPIWVQIWRLPINFYTTPA
      FT                 ITALADLIGQVKVVEFDPDKPQILEYVRALVSFDVSRPLRRAKVVNLPHGE
      FT                 TTKVHFEYERVQKRCYECQRLTHEREACPLFLMKLQEKADARKKGQPVAKE
      FT                 VKAPFLKEADVLFGILEENQVGINPLTGRQRIAPEVLEGMRQYWNVSMEDE
      FT                 RLIRIDRIKKSLKEVESDPILAKSYLQLEPPPLVVKPSVCPKGIVFSYEEG
      FT                 EGSGLPSRLSSGKSVMKVDQRQLGIGDLNLVAREDSGPSYAPMDFLCLAQP
      FT                 SQDISTVYRIGSSGASSSGNIQKKTKQRKRPSKITRKLKEAASKNPREAVN
      FT                 VKEGLSSGVLVKRKSVVESQSSSKGSRPKAIKVIPNEGSPNV"
      FT   CDS           1729..5841
      FT                 /product="L1-35_ALy_2p"
      FT                 /translation="MSIMSWNCQGLGRSQDLAIPRLEEMRKKHFPEMLFLM
      FT                 ETMHGRDVLVDIQEWLGYDRVHTVEPIGKCGGLALFWKSSIKLDFLFFYKN
      FT                 LLDVQVQFGASNFFLSCVYGDPDSSKRSNIWERISRFGVGRRERWCMIGDF
      FT                 NAILHNGEKIGGPRRSDSCFKTFSEMLSACDMMELPSSGNKFTWAGRRGDH
      FT                 WIQCRLDRAFGNKAWFDQFPVSNQAFLDMRGSDHRPVFVNLLASQDSYRGQ
      FT                 FRFDKRFLHKPGVKEAILKAWSSDGGCQSFKVSHRLRCCRKSLSAWKRNNN
      FT                 LNSHDKIKRLEEALEKLQSERWPDRNWLFRLKKDLAEAYREEESFWKQRSR
      FT                 QKWLRSGNRNSKYFHASVKGNRSRKRIEKLKDANGDLQFSEAAKGEVASIY
      FT                 FENLFKSSNPPSFNDWFEGFSPKVTDEMNVRLIARVSKEEIREAAFSLKAS
      FT                 SAPGADGMSAFFFQQYWYIVGDQVIKEIQAFFVNGSFPPEWNYTHLCLIPK
      FT                 IHHPTEMSDLRPISLCSVLYKIVFKILVRRLKPILPQIVSVNQSAFVSERQ
      FT                 ITDNILVAHELVHSLRTNPTISSDFMAVKSDMSKAYDRVEWSYLRSLLLAL
      FT                 GFHRVWIDWIMVCVSSVTYSVLINDHLYGMITPQRGIRQGDLLSPFLFVLC
      FT                 TEGLTHMLNAAQRRGSLHGIKFSEDGPEIHHLLFADDSLFMCKASKDQGQV
      FT                 LQKILNEYGAVTGQSVNLSKSAITFGSRVDPVTKLELQNILGILTEGGTGS
      FT                 YLGLPECFSGSKVELLGYIKDRLKEKLAGWSSRFLSQGGKKVLLKSVALAM
      FT                 PVFAMSCFKLPKTTCDNLASAMADFWWSVGNKSGKIHWQSWEKLCLPKDLG
      FT                 GLGFRDIQGFNQALLAKQAWRILHEPSCLFAQLMKSRYFESSEFLDASLGT
      FT                 RPSFAWRSILHGRDLLNQGILKKVGNGKSLRVWIDLWIEDDGWRAPLRRNN
      FT                 FFNPDLRVSELLNRQARSWDLQILQEHFLPDDIERILKIKPAMRYEDFFAS
      FT                 RYNKGGNFSVKSAYWLASQSINIQGRFEAAVAPSTNGLKNQVWDLPTDPKL
      FT                 KIFLWKALSAALPVAVALAKRGLNLNSKCQICGMDEEETTNHILFSCSLSR
      FT                 QIWALSDYPGPEFGFQNGSIFSNIHHLIDNRSNLKWPALLRTSFPWILWRI
      FT                 WTNRNLTLFEGKSYSALETVEKIREEVNEWMEAQKVESEGEEPAVVVVARD
      FT                 GPQVNVLAAGVWRPPDVGWLKCNIGVAWSRRNRIAGGAWVVRDENGVVLLH
      FT                 SRKGFLNVCSNLDAQLEILMWCIESMRSHNLGRVMFVLQADELVGAVNRPM
      FT                 AWPSFYFHSSEVRELLKGIIEWKLSKESVLANRGASLIAQSVTSDLRLHSY
      FT                 VASGILVG"
      XX
      SQ   Sequence 6092 BP; 1632 A; 1018 C; 1518 G; 1924 T; 0 other;

      //
      ID   L1-4B_LA-5end repbase;    DNA;    MAM; 2556 BP.
      XX
      AC   .
      XX
      DT   26-APR-2010 (Rel. 15.05, Created)
      DT   26-APR-2010 (Rel. 15.07, Last updated, Version 2)
      XX
      DE   Autonomous L1-type non-LTR retrotransposon - consensus.
      XX
      KW   L1; Non-LTR Retrotransposon; Transposable Element; L1-4B_LA-5end.
      XX
      NM   L1-4B_LA-5end.
      XX
      OS   Loxodonta africana
      OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
      OC   Mammalia; Eutheria; Afrotheria; Proboscidea; Elephantidae;
      OC   Loxodonta.
      XX
      RN   [1]
      RP   1-2556
      RA   Bao W. and Jurka J.;
      RT   "Non-LTR retrotransposons from African elephants.";
      RL   Repbase Reports 10(5), 762-762 (2010).
      XX
      DR   [1] (Consensus)
```

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XX
CC    The 5-end of L1 retrotransposons.
CC    We thank the Broad Institute Genome Sequencing Platform and
CC    Genome Sequencing and Analysis Program, Federica Di Palma, and
CC    Kerstin Lindblad-Toh for making the data for Loxodonta africana
CC    available.
XX
SQ    Sequence 2556 BP; 905 A; 719 C; 543 G; 389 T; 0 other;

//
ID    L1MCA_5      repbase;    DNA;     PRI; 2647 BP.
XX
AC    .
XX
DT    31-MAY-2001 (Rel. 6.04, Created)
DT    31-MAY-2001 (Rel. 6.04, Last updated, Version 5)
XX
DE    Primate L1MCA_5 LINE1 repetitive element - a consensus.
XX
KW    L1; Non-LTR Retrotransposon; Transposable Element; L186; L1MCA_5;
KW    LINE1 repeat.
XX
OS    Homo sapiens
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
OC    Catarrhini; Hominidae; Homo.
XX
RN    [1]
RA    Smit A.F.;
RT    "L1MCA_5.";
RL    Direct Submission to Repbase Update (1997).
XX
RN    [2]
RP    1-1858
RA    Jurka J.;
RT    "L1MCA_5.";
RL    Direct Submission to Repbase Update (MAR-2000).
XX
DR    [2] (Consensus)
XX
CC    5' end of LINE elements with L1MC1-3 subfamily 3' ends,
CC    comprising the
CC    5' UTR and part of ORF1.
XX
SQ    Sequence 2647 BP; 1102 A; 458 C; 512 G; 562 T; 13 other;

//
ID    L2-21_CTe    repbase;    DNA;     INV; 2606 BP.
XX
AC    .
XX
DT    22-MAR-2011 (Rel. 19.07, Created)
DT    07-JUL-2014 (Rel. 19.07, Last updated, Version 1)
XX
DE    An L2 non-LTR retrotransposon from Capitella teleta: consensus.
XX
KW    L2; Non-LTR Retrotransposon; Transposable Element; L2-21_CTe.
XX
OS    Capitella teleta
OC    Eukaryota; Metazoa; Lophotrochozoa; Annelida; Polychaeta;
OC    Scolecida; Capitellida; Capitellidae; Capitella.
XX
RN    [1]
RA    Simakov O., Marletaz F., Cho S.J., Edsinger-Gonzales E.,
RA    Havlak P., Hellsten U., Kuo D.H., Larsson T. et al.;
RT    "Insights into bilaterian evolution from three spiralian
RT    genomes.";
RL    Nature 493(7433), 526-531 (2013).
XX
RN    [2]
RP    1-2606
RA    Kojima K.K. and Jurka J.;
RT    "Non-LTR retrotransposons from Capitella teleta (a polychaete
```

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 RT    worm).";
 RL    Repbase Reports 14(7), 2040-2040 (2014).
 XX
 DR    [2] (Consensus)
 XX
 CC    This consensus is generated from 30 sequences with 93-98%
 CC    identity.
 XX
 FH    Key             Location/Qualifiers
 FT    CDS             106..2457
 FT                    /product="L2-21_CTe_1p"
 FT                    /note="reverse transcriptase."
 FT                    /translation="TYKRDQHVKTPTHRXGHTLDLAMTLRIDPHPHVTALD
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 FT                    DLITHNTDPQLYVDLYDDVLSGLLVKHAPIKTGILPSRTKSPWYTDELRLL
 FT                    KQERRLCERRWMKTDLQVHREALVEKRRILNAMLKKTKSQYYNNLIGEHSQ
 FT                    DPKKMFDVVSGLLGKQKTPTLPVHTNSQAMASEFSKFFLNKIETIKASIKS
 FT                    SSTSQPPLSPAVPPTCSLSSWSQVTTEAIRKIITQSPTKHCALDPVPTWLL
 FT                    KRCLEPTLPCICAIINSSLASGVVPTAFKVAHVTPLLKKPSLDASDISNYR
 FT                    PVSNLPFVSKVLERVVNVQLTQYLVENGLQEKFQSAYRQYHSTETALIRVQ
 FT                    NDILLALGERKVCLLLLLDLSAAFDTVEHSVLIDSLSELGVAGTPLDWFRS
 FT                    YLQGRTQQIKVSDSLSTPQPLTSGVPQGSVLGPVLFTLYTAPLGRLIQSFE
 FT                    MNYHLYADDSSLYLTFEANQMNQSVDRMQQCAEAVRQWLGEKQLKMNPNKT
 FT                    ELLLVATKNIAEQVPPGTPAIQIGDTQVTASEAVRYIGVMFDKRLNMERYI
 FT                    ISVCKSARYHLYNIGRIRHLLTRKACEQLIHAFISSRLDYGNALLYGLPQR
 FT                    LLMKLQRIQNIAARILTRTKTRQHISPVLMDLHWLPVAQRIKFKIALLTFK
 FT                    CVHDMAPSYLCELLHSASPTRALRSSDQHHLLRVQRSTNSVQSRAFERHAP
 FT                    EIWNALPDWLRLVDSISVFKKQLKTLLFMEYFI"
 XX
 SQ    Sequence 2606 BP; 729 A; 693 C; 518 G; 663 T; 3 other;

 //
 ID    L2_AC_9      repbase;    DNA;     VRT; 5778 BP.
 XX
 AC    .
 XX
 DT    06-DEC-2011 (Rel. 17.01, Created)
 DT    06-DEC-2011 (Rel. 17.01, Last updated, Version 1)
 XX
 DE    L2 non-LTR retrotransposons - a consensus sequence.
 XX
 KW    L2; Non-LTR Retrotransposon; Transposable Element; L2_AC_9.
 XX
 OS    Anolis carolinensis
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Lepidosauria; Squamata; Bifurcata; Unidentata; Episquamata;
 OC    Toxicofera; Iguania; Dactyloidae; Anolis.
 XX
 RN    [1]
 RA    Novick P.A., Basta H., Floumanhaft M., McClure M.A.
 RA    and Boissinot S.;
 RT    "The evolutionary dynamics of autonomous non-LTR retrotransposons
 RT    in the lizard Anolis carolinensis shows more similarity to fish
 RT    than mammals.";
 RL    Mol Biol Evol 26(8), 1811-1822 (2009).
 XX
 DR    [1] (Consensus)
 XX
 FH    Key             Location/Qualifiers
 FT    CDS             1448..2395
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 FT                    /translation="MSWQEFPKENELLHLCDLLGKSFSTVLYQLETLNKKI
 FT                    DHLFKGISLIATNPSPIDIITTVPTSSTNINEELNALEDHGKIKLEEQKVV
 FT                    NRSDLEVAKDGDGLVSGKEGQGRVAWKEINRVSQRTNNTLSPELFGQSRDT
 FT                    SCNLLRTNKVAVEVSDSLLNRGRWSSKRAVHISLSQILSMSRSEVKIKTID
 FT                    WLRRDYQSWNRSLCLLIGLEDRMLLEELFLYGPKLQQWGIILKRVLVDPVI
 FT                    RPLDIGLTREIQESLISSHVCSTPQPCHQSLAVPSPPPSLDDVIILDDSSS
 FT                    LIPAEISLSFKQSNTLGGLSSQDS"
 FT    CDS             2399..5413
 FT                    /product="L2_AC_9_2p"
 FT                    /translation="LSPSIGNLNKPISQEEEGSHVGGPIEVVWGRRKNGHQ
 FT                    QPREKRNRVIATLERNRCGSLQDRPLNLKVLLLNARSVNGKTAIIQDLILD
 FT                    EGADLACITETWLDEPGGVNLTQLCPPGFGVHQQARVEGRGGGVAVIFRQS
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FT                    IALIRCTVPQSMGFECVLLKVGARDSLGILLVYRPPRDPAVSLRELAEVVS
FT                    NAALVSQQLIVLGDFNIHAETTLTGAAQDFMVAMTTMGLTQVISGPTHQAG
FT                    HTLDLVFIVDSGTVRVEEQNILPLSWSDHHLICLSFAVASNLRRGGGPIKM
FT                    VRPRRLMDPDGLLRSLGDLPVLETGDPVDVLADRYNSELARALDTIAPERP
FT                    LSLRRVTSTPWFTEELAVMKRTRRGLECIWRKSQDVSDQARAKAAIKAYSV
FT                    ALRAARKAFTTARIASAANRPSELFRVVGELLRPPEAQELPDDLATRCSDF
FT                    AHHFAGKVAQIRHELDSSLTVVSAEVTEAPVGSILWDSFRLVLPDDVEGIL
FT                    GSVRATTCALDPCPSWLVKLAKDGLLEWFVAIINASLGQGSFPSCFKQAVV
FT                    KPLLKKTSLDPLVCDNYRPISNLPFLGKVLERVVATQLQEFLDDTDFLDRS
FT                    QSGFRPGHSTETALVALVDDLRRELDRGSVTLLVLLDISAAFDTIDHGILL
FT                    GRLSGMGLGGTVLLWLQSFLEGRSQMVKLGDTCSDPWPLTCGVPQGSILSP
FT                    MLFNIYMKPLGEVIRSFGGRCHLYADDTQIHYSFPPDSKEAPRMLNQCLAA
FT                    VADWMRRNKLRINPDKTEALLVNRASDRGIGWQPVLDGVALPLKSQVRSLG
FT                    VLLDSALTLEAQVSAVAGRAFAQLKLVRQLRPYLVKSDLTTVVHALVTSRL
FT                    DYCNALYVGLPLKTARKLQLVQRSAARLITGANYRERSTPLFKELHWLPFI
FT                    FRSQFKVQTIIYKALNGLGPTYLRDRISFHKPARSLRSSGEALLSPLPISQ
FT                    ARLVSTRERAFSAVAPRLWNSLPTEIRQAPTLLAFRRELKTWLFHCAFGE"
XX
SQ    Sequence 5778 BP; 1242 A; 1435 C; 1544 G; 1557 T; 0 other;


//
ID    LINE1-32_SBi repbase;    DNA;    PLN; 4455 BP.
XX
AC    .
XX
DT    01-FEB-2010 (Rel. 15.06, Created)
DT    01-FEB-2010 (Rel. 15.06, Last updated, Version 1)
XX
DE    L1-type non-LTR retrotransposons from Sorghum bicolor.
XX
KW    L1; Non-LTR Retrotransposon; Transposable Element; LINE1-32_SBi.
XX
OS    Sorghum bicolor
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    PACMAD clade; Panicoideae; Andropogonodae; Andropogoneae;
OC    Sorghinae; Sorghum.
XX
RN    [1]
RP    1-4455
RA    Bao W. and Jurka J.;
RT    "Non-LTR retrotransposons from Sorghum bicolor.";
RL    Repbase Reports 10(6), 894-894 (2010).
XX
DR    [1] (Consensus)
XX
CC    the 5-end is not determined.
XX
FH    Key          Location/Qualifiers
FT    CDS          190..660
FT                    /product="LINE1-32_SBi_1p"
FT                    /translation="AREDSVEKATKLKARKNLESKSDKGNNTQPCSFLSRD
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FT                    SDVDILDQKSLNLICSEISKGLGDGGCDPKCLQTPVSQKMLEEVSVINIRK
FT                    ITGFFLDERHFLELQRVC"
FT    CDS          807..4295
FT                    /product="LINE1-32_SBi_2p"
FT                    /translation="MAPRGRSGGMILGIHLLSFDIGEIEEGDFFIRFKVRH
FT                    READFKFNLISVYGPAQLDQKSHFLSEIVRVCSNETLPIVIGGDFNIIRRP
FT                    DEKNNDIYNDRWPFLFNAVIDSLNLREIEMSGRKFTWANHLQNQTFEKLDR
FT                    VLVCTDFETKYPLTTVIALTREISDHTPLLFSTNNPSSSYQYQFKFELGWL
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FT                    NIMEGAVILHEMIHELHSKKKDGVIFKIDFEKAYDKVKWSFLQQTLRMKGF
FT                    SQKWCEWVESFTQGGNVNIKVNDQLGSYFQTRKGLRQGDPMSPILFNIVVD
FT                    MLAILITRAKEAGQVEGVIPNLIHDGLSILQYADDTVIFMSHDAEKAVNMK
FT                    LLLSTFEQLSGLKINFHKSEIFCFGKAKEHEMFYSQTFGCVIGNYPFRYLG
FT                    LPMNTRKLNNKDWKTIEDRIEKRLSGWKGKMLSVGGRLVLLNSVLSSLPMF
FT                    MMSFFEMPKGVLEKIDYFRSRFYWQSDQHKRKYRLAKWEVLCQPKEQGGLG
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FT                   IKNLEIQNKCLLSKWLFKLLNEEGMWQELLRNKYIKDKTLGSCVKKPTDSH
FT                   FWKSLMNVKDSFMDFGSFKVRDGSQTRFWIDTWLGNKPLKDKFPALFNIVR
FT                   RKQDSVAQVISSSPLNISFRRNLVGANLTNWYRIVASLQNINLLEEKDVFV
FT                   WSLNVSGSFTVKSMYAVLINNGVRVSQDLWEIKIPLKIKIFMWYLKKGVIL
FT                   TKDNLVRRNWNGDRKCCFCHSPESIQHLFLDCVYSKFLWRAVHILFGISPP
FT                   RDINDLFIRWSKVATKKYNTLLLTAASALCWAIWITRNEVVFDKCRPKSFL
FT                   QVLFRGTHWLRQWARLQRHDDLRDQLITAGQHLETSALQFFSSNGWLSTRH
FT                   IGHA"
XX
SQ   Sequence 4455 BP; 1457 A; 734 C; 943 G; 1321 T; 0 other;

//
ID   LTR-12B_Crp repbase;    DNA;    VRT; 2482 BP.
XX
AC   .
XX
DT   25-SEP-2012 (Rel. 18.04, Created)
DT   24-APR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE   LTR retrotransposon from the saltwater crocodile: long terminal
DE   repeat.
XX
KW   LTR Retrotransposon; Transposable Element; LTR-12B_Crp.
XX
OS   Crocodylus porosus
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Crocodylia; Longirostres;
OC   Crocodylidae; Crocodylus.
XX
RN   [1]
RP   1-2482
RG   International Crocodilian Genomes Working Group;
RT   "LTR retrotransposons from the saltwater crocodile.";
RL   Direct Submission to Repbase Update (08-OCT-2012).
XX
DR   [1] (Consensus)
XX
CC   >89% identical to consensus. 4bp TSD.
XX
SQ   Sequence 2482 BP; 512 A; 698 C; 486 G; 785 T; 1 other;

//
ID   LTR11_MEu   repbase;    DNA;    MAM; 372 BP.
XX
AC   .
XX
DT   03-FEB-2010 (Rel. 16.02, Created)
DT   03-FEB-2010 (Rel. 16.02, Last updated, Version 2)
XX
DE   Long terminal repeat of an ERV1-type endogenous retrovirus -
DE   consensus.
XX
KW   ERV1; Endogenous Retrovirus; Transposable Element; LTR11_MEu.
XX
OS   Notamacropus eugenii
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Metatheria; Diprotodontia; Macropodidae; Notamacropus.
XX
RN   [1]
RP   1-372
RA   Jurka J. and Walichiewicz K.;
RT   "Long terminal repeats from Tammar wallaby.";
RL   Repbase Reports 11(2), 784-784 (2011).
XX
DR   [1] (Consensus)
XX
CC   We thank the Tammar Wallaby Genome Sequencing Consortium for
CC   making their data publicly available, and the BCM-HGSC for
CC   providing the genome assembly.
XX
SQ   Sequence 372 BP; 105 A; 65 C; 119 G; 82 T; 1 other;

//
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```
 ID    LTR3B_Ami    repbase;    DNA;     VRT; 1082 BP.
 XX
 AC    .
 XX
 DT    07-OCT-2012 (Rel. 18.04, Created)
 DT    24-APR-2013 (Rel. 18.04, Last updated, Version 1)
 XX
 DE    LTR retrotransposon from the American alligator: long terminal
 DE    repeat.
 XX
 KW    Gypsy; LTR Retrotransposon; Transposable Element; LTR3B_Ami.
 XX
 OS    Alligator mississippiensis
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Crocodylia; Alligatoridae;
 OC    Alligatorinae; Alligator.
 XX
 RN    [1]
 RP    1-1082
 RG    International Crocodilian Genomes Working Group;
 RT    "LTR retrotransposons from the American alligator.";
 RL    Direct Submission to Repbase Update (09-OCT-2012).
 XX
 DR    [1] (Consensus)
 XX
 CC    >94% identical to consensus. 5bp TSD.
 XX
 SQ    Sequence 1082 BP; 260 A; 263 C; 399 G; 157 T; 3 other;

 //
 ID    MERMITEJ     repbase;    DNA;     PLN; 1498 BP.
 XX
 AC    .
 XX
 DT    06-NOV-2002 (Rel. 7.10, Created)
 DT    23-JUN-2016 (Rel. 21.06, Last updated, Version 2)
 XX
 DE    Rice non-autonomous DNA transposon MERMITEJ - a consensus.
 XX
 KW    MuDR; DNA transposon; Transposable Element; Nonautonomous;
 KW    target site duplication; MERMITEJ.
 XX
 NM    MERMITEJ.
 XX
 OS    Oryza sativa
 OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC    BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
 XX
 RN    [1]
 RA    Tarchini R., Biddle P., Wineland R., Tingey S. and Rafalski A.;
 RT    "The complete sequence of 340 kb of DNA around the rice Adh1-adh2
 RT    region reveals interrupted colinearity with maize chromosome 4.";
 RL    Plant Cell 12(3), 381-391 (2000).
 XX
 RN    [2]
 RP    1-1498
 RA    Jurka J. and Drazkiewicz A.;
 RT    "MERMITEJ: a non-autonomous DNA transposon from Oryza sativa.";
 RL    Direct Submission to Repbase Update (25-JUL-2002).
 XX
 DR    [2] (Consensus)
 XX
 CC    9-bp target site duplications.
 XX
 SQ    Sequence 1498 BP; 222 A; 528 C; 515 G; 233 T; 0 other;

 //
 ID    MacERV4_int repbase;    DNA;     PRI; 7442 BP.
 XX
 AC    .
 XX
 DT    24-SEP-2007 (Rel. 13.02, Created)
```

```
 DT   27-FEB-2008 (Rel. 13.02, Last updated, Version 1)
 XX
 DE   ERV2 Endogenous Retrovirus from Cercopithecidae.
 XX
 KW   ERV2; Endogenous Retrovirus; Transposable Element; ERVK; LTR;
 KW   MacERV4_int.
 XX
 OS   Cercopithecidae
 OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC   Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 OC   Catarrhini.
 XX
 RN   [1]
 RP   1-7442
 RA   Smit A.F.;
 RT   "MacERV4_int - ERV2 Endogenous Retrovirus from Cercopithecidae.";
 RL   Direct Submission to Repbase Update (21-FEB-2008).
 XX
 DR   [1] (Consensus)
 XX
 CC   1-3%  ORFs: gag 154-2130, pro 1944-2891 (probably ca 2094-2891),
 CC   pol 2870-5485, env 5476-7236.
 XX
 FH   Key            Location/Qualifiers
 FT   CDS            154..2130
 FT                  /product="MacERV4_int_1p"
 FT                  /note="gag."
 FT                  /translation="MGQELSQHQIYVGQLKEALKIRGVKVKGNDLFKFFDF
 FT                  VKDTCPWFPQEGTIDIKRWRRVGDCFQDYYNTFGPEKIPVTAFSYWNLIRD
 FT                  LIDKKEADPQVMAAVAQTEHILKVSSRSNLAKPPQDTEEDLISLESDHEEI
 FT                  KSPSVTDKEMPHENKPKKYPILQMLQKEEEINKPNQSDINWDDLEEEAAKY
 FT                  HNPDLPPFTSYPPPYNKTHNEASAPIVMAAIDPKEELKQKIAQLEEQIKLE
 FT                  ELHQSLIIRLQKLKTGNEKIPNSDAMEGSLRPLQRPGQHVPRGGLVASRHR
 FT                  EDSSPKDVFPVTETIDEQGQAWRHHTGFDFTIIKELKTAASQYGATAPYTL
 FT                  AIVESVAENWLTPTDWNTLVRAVLSGGDHLIWKSEFFENCRDTAKRNQQAG
 FT                  NGWDFDMLTGSGNYADTQAQMQYDPGLFSQIQAAATKAWRKLPVKGDPGAS
 FT                  LTAVKQGPDEPFSDFVHRLMTTAGRIFGNAETGVDYVKQLAYENANPACQA
 FT                  AIRPYRKKTDLTGYIRLCSDIGPSYQQGLAMAAAFSGQTVRDFLINKGKDK
 FT                  GGCFRCGKRGHFAKDCRENQNKSPEAKIPGLCPRCKRGRHWANECKSKTDS
 FT                  QGNPLPPRQGNGMRGQPQAPKQAYGAVSFVPASNSNPFQNLVEQPQEVQDW
 FT                  TSVPPPTQY*"
 FT   CDS            1944..2891
 FT                  /product="MacERV4_int_2p"
 FT                  /note="pro (probably ca 2094-2891)."
 FT                  /translation="QSRKSFTPQAGKRDEGPASGPETSIWGSQLCSSQQQQ
 FT                  SISKLSRATPGSAGLDLSSTSHTILTPEMGPQTLNTGIYGPLPPNTFGLLL
 FT                  GRSSVTMRGLQVLPGVIDNDYEGEIKIMARAIDSIITVPQGVRIAQLLLLP
 FT                  LVKTDNNIQYSNRNIKGFGSSDIYWVQPITNQKPSLTLWLDGKAFTGLIDT
 FT                  GADVTIIKQEDWPSHWPTTETLTHLRGIGQSSNPKQSSKYLTWTDKENNSG
 FT                  LIKPFVIPYLPVNLWGRDLLSQMKIIMCSPNDIVTAQMLTQGYTPGKGLGK
 FT                  GENGIPQPILVSGQLDKKGFGNF*"
 FT   CDS            2870..5485
 FT                  /product="MacERV4_int_3p"
 FT                  /note="pol."
 FT                  /translation="KGVWKFLAQATDIPAPQRCADPITWKSDEPVWVDQWP
 FT                  LLNDKLSAAQQLVQEQLAAGHIEESNSPWNTPIFVIKKKSGKWRLLQDLRA
 FT                  VNITMILMGALQPGLPSPVAIPQKYFKIIIDLKDCFFTIPLHPADQKRFAF
 FT                  SLPSTNFKQPMKRYQWKVLPQGMANSPTLCQKYVAAAIEPVRKTWAQMYII
 FT                  HYMDDILIAGEIGEQVLQCFAQLKQELTAAGLQIAPEKVQLQDPYTYLGFQ
 FT                  INGPKIIINQKAVIRRDHLKTLNDFQKLLGDINWLRPYLKLTTGELKPLFDI
 FT                  LKGDSNPKSPRSITKEALMALQQVEHAIATQFVTGIDYSQPLIFLIFNTTI
 FT                  TPTGLFWQNNPIMWVHLPSSPKKVLLPYYDAIADLIILGRENSRKYFGIEP
 FT                  STIIQPYTQSRIHWLLQNTEAWPIACASYTGAIDNHYPPNKLIQFCKLHAF
 FT                  VFPHITSKEPLNDALLIFTDGSSTGLAAYTYNNVVVKFQTTYTSAQLVELQ
 FT                  AIIAALSAFPCQPLNIYTDSAYLAHSIPLLETVPQIKHISDTANLFLQCQQ
 FT                  LIRKRTTPFFLGHIRAHSGLPGPLTQGNATADAATKTIATVTTDNLQQAQK
 FT                  AHALHHLNAQTLRLMFKLTREQARQIVKQCANCITYLPVPHLGVNPRGLIP
 FT                  NEIWQMDVTHHLEFGQLKYIHVCIDTYSGFISATLQTGEATKHVIAHLLHC
 FT                  FSILGIPKQIKTDNGPGYIAKTFLQFCNTLQIKHTTGIPYNPQGQGIVERA
 FT                  HLSLKTVITKLKGGSWYPVKGTPRNILNHALFILNFLNLDSHGKSAADRFW
 FT                  HPESQKQFAMVKWKDPLDSSWHGPDPVLIWGRGSVCIFSQKNDAARWLPER
 FT                  LVRQINHNHCQSREDKSP*"
 FT   CDS            5476..7236
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FT                     /product="MacERV4_int_4p"
FT                     /note="env."
FT                     /translation="ISLRSSFLLVFQKMKPNMRFLWRIIALYNIVTVYAGF
FT                     GDPRKARELLRKQYGQPCDCRGGQVSEPPSDRITQVTCXGKTAYLMPNQLW
FT                     KCKSTPRDTSPSGPLLECPCSSFQSSVHSSCYTSYQQCKSGNRTYYTATLL
FT                     KTQTGGTNDVQVLGSTNKLVQSPCNGQKGKPVCWSTTAPIHISDGGGPLDT
FT                     ARIKTVQKKLEEIHKALYPELQYHPLALPELRDNFRLDAQTFDILNATYNL
FT                     LQMSNTSLAHDCWLCLKMGPPIPLAIPNLSLPYVNYSNESLVNNSCPITPP
FT                     LLVQPMTFSNSSCLFSPSYNNTKEIDLGYVVFGNCTSIINATNPLCAVNGS
FT                     VFVCGNNMAYTYLPTNWTGLCVLATLLPDIDIIPGDEPIPIPAIEHFIYRP
FT                     KRAIQFIPLLAGLGITTAFTTGATGLGVSLTQYTKLSNQLISDVQTLSSTI
FT                     QDLQDQVDSLAEVVLQNRRGLDLLTAEQGGICLALQEKCCFYANKSGIVRD
FT                     KIKTLQEELEKRRKGLAANPLWTGLDGLLPYLLPFLGPLLTLLLFLTLGPI
FT                     ILNKLMAFVRQQIEAFQAKPIQVHYHRLEMTENGESYLP*"
XX
SQ     Sequence 7442 BP; 2389 A; 1712 C; 1426 G; 1914 T; 1 other;

//
ID     Mariner-1_Crp repbase;      DNA;      VRT; 2881 BP.
XX
AC     .
XX
DT     16-SEP-2012 (Rel. 18.04, Created)
DT     24-APR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE     DNA transposon.
XX
KW     Mariner/Tc1; DNA transposon; Transposable Element; Mariner-1_Crp.
XX
OS     Crocodylus porosus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Crocodylia; Longirostres;
OC     Crocodylidae; Crocodylus.
XX
RN     [1]
RP     1-2881
RG     International Crocodilian Genomes Working Group;
RT     "DNA transposons from the saltwater crocodile.";
RL     Direct Submission to Repbase Update (16-SEP-2012).
XX
DR     [1] (Consensus)
XX
CC     >90% identical to consensus.
XX
FH     Key            Location/Qualifiers
FT     CDS            823..2610
FT                     /product="Mariner-1_Crp_1p"
FT                     /translation="MAEKHKSGGSDVSSSKKRRTITMETKMEIIKRSEKGE
FT                     TPTEMGRALDIPRTTIVTILKDKARIQEHVKDSAPMHSTVITKQRVGLIAQ
FT                     VEKLLIIWLEDQNKRRAPVSLGIIQEKARSLYDDLKKQQGESSNAEPFTAS
FT                     KGWFMRFKARANLHNIKVSGEAASADEEAARAFPETLAEIIEESGYCAQQV
FT                     FNVDETGLFWKKMPSRTYIAKEEKSMPGYKAAKDRLTLLLGANAAGDFKLK
FT                     PLLVYRSENPRAFKGHSKAFLPVIWKSNPKAWVNKNIFEDWFNHHFVPSVR
FT                     DYCSKNNLAFKALLILDNAPGHPTILDDMHPDIKVVFLPPNTTSLLQPTDQ
FT                     GVIASFKAYYLRRTFAQAIRAIEKEGGPTLKEFWKGFNIYHAVKNIGEAWN
FT                     EVKQSNLNGVWRKLCPKFVSDFQGFTDTVEEVTKNVVEMGKELNLDVAPED
FT                     VDELLASHSEELTNEDLIELEQQKVAEEEDAPTVEETPPRKVLTTKVLAEA
FT                     FQHLEAAMSLFEEHDPDIERSASVNRGISSMYSCYREIYKQKKRTSVQTSL
FT                     RTFFKKADKTPGKPAAKTPEKTPAKXPSKSPAKNPSKSPAKSPQRSPSK"
XX
SQ     Sequence 2881 BP; 783 A; 658 C; 768 G; 670 T; 2 other;

//
ID     Mariner-2_NV repbase;      DNA;      INV; 2441 BP.
XX
AC     .
XX
DT     06-JUL-2007 (Rel. 12.07, Created)
DT     06-JUL-2007 (Rel. 12.07, Last updated, Version 1)
XX
DE     Starlet sea anemone Mariner-2_NV autonomous DNA transposon -
DE     consensus.
XX
```

```
KW    Mariner/Tc1; DNA transposon; Transposable Element; mariner;
KW    Pogo group; TA TSDs; Mariner-2_NV.
XX
OS    Nematostella vectensis
OC    Eukaryota; Metazoa; Cnidaria; Anthozoa; Hexacorallia; Actiniaria;
OC    Edwardsiidae; Nematostella.
XX
RN    [1]
RP    1-2441
RA    Putnam N.H., Srivastava M., Hellsten U., Dirks B., Chapman J.,
RA    Salamov A., Terry A., Shapiro H., Lindquist E. et al.;
RT    "Sea anemone genome reveals ancestral eumetazoan gene repertoire
RT    and genomic organization.";
RL    Science 317(5834), 86-94 (2007).
XX
RN    [2]
RP    1-2441
RA    Kapitonov V.V. and Jurka J.;
RT    "Mariner-2_NV - a family of autonomous DNA transposons from the
RT    starlet sea anemone genome.";
RL    Repbase Reports 7(7), 610-610 (2007).
XX
DR    [2] (Consensus)
XX
CC    This transposon belongs to the Pogo group of the Mariner
CC    superfamily. The genome contains only 3 copies of Mariner-2_NV.
CC    The transposon encodes a 444-aa transposase (2 exons).
XX
FH    Key             Location/Qualifiers
FT    CDS             join(384..957,1157..1914)
FT                    /product="Mariner-2_NVp"
FT                    /translation="MASKQARIELSLKKNVLKLAAGGSSQRKLADQCKVSK
FT                    TQISNIIKKKHAIEVAFEQNSNSEKRRFVSAPNDRINDAIWEWFTRCRAMN
FT                    IPITGPMIQAQALKYAETFGIGDFKASNGWLESFKCRKNIHCSILSGESSS
FT                    VPTETVDECQSRLEALCEGYRAEDIFNMDETGMYYRALPDRSLVVRGADCH
FT                    GDRQMRLQNRKILLFEDNAPSHGMEDIELTNIKVVFYPPNTTSRLQPLDQG
FT                    IIKNLKAFYRKKLLEKVVSAINEAEFSDACSVARKVDVLDCCMWIPWAVRQ
FT                    IKPETVTNCFTHAGYPRSLLTDDRLVQGAQNAAEPDLQHLIETVATGLNIT
FT                    EPLTDDDFVHHDDQVPTEDDDNENWVPEVIQEHVLGKDSVPETADDDEECD
FT                    ETSDGSGSLEPMSVIKDAKTALYWAQQLKLFSLEKNMTGIFPISSELEDN"
XX
SQ    Sequence 2441 BP; 758 A; 510 C; 514 G; 659 T; 0 other;

//
ID    Mariner-N1743_AMi repbase;    DNA;    VRT; 582 BP.
XX
AC    .
XX
DT    28-JAN-2013 (Rel. 18.04, Created)
DT    24-APR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE    DNA transposon from the alligator: consensus.
XX
KW    Mariner/Tc1; DNA transposon; Transposable Element; Nonautonomous;
KW    Mariner-N1743_AMi.
XX
OS    Alligator mississippiensis
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Crocodylia; Alligatoridae;
OC    Alligatorinae; Alligator.
XX
RN    [1]
RP    1-582
RG    International Crocodilian Genomes Working Group;
RT    "Transposable elements from the crocodilian genomes.";
RL    Direct Submission to Repbase Update (28-JAN-2013).
XX
DR    [1] (Consensus)
XX
CC    Mariner.1743_Amis#DNA/TcMar-Tigger.
XX
SQ    Sequence 582 BP; 123 A; 135 C; 222 G; 102 T; 0 other;
```

```
   //
   ID    MuDR-1_GAr   repbase;     DNA;      PLN; 8481 BP.
   XX
   AC    .
   XX
   DT    01-JUN-2014 (Rel. 23.07, Created)
   DT    01-JUN-2014 (Rel. 23.07, Last updated, Version 1)
   XX
   DE    DNA transposon from the Gossypium arboreum genome: consensus.
   XX
   KW    MuDR; DNA transposon; Transposable Element; MuDR-1_GAr.
   XX
   OS    Gossypium arboreum
   OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
   OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
   OC    Pentapetalae; rosids; malvids; Malvales; Malvaceae; Malvoideae;
   OC    Gossypium.
   XX
   RN    [1]
   RP    1-8481
   RA    Jurka J.;
   RT    "DNA transposons from the Gossypium arboreum genome.";
   RL    Repbase Reports 18(7), 737-737 (2018).
   XX
   DR    [1] (Consensus)
   XX
   CC    >93% identical to consensus.
   XX
   FH    Key            Location/Qualifiers
   FT    CDS            join(1364..3097,3101..4042)
   FT                   /product="MuDR-1_GAr_1p"
   FT                   /translation="MDNQFFVCVYFDGIILTTTVGCIFECRQQIAMRFNRN
   FT                   VSLDDMKGRINAKIVRRCGRRISKLFYKFPVSTDPIKFTEMELVDDEDVET
   FT                   MIALYCGNGSDKNAPIHLFAELAGMEQNEDLTAYGEEHAAQEPCVVAPISY
   FT                   VDSESTIRGIDIDLNVTPDIDVVGDDGYDSSDPCDEEVDSDSDPDVDDVPD
   FT                   DIDDEDVNDDGNINASSVGNQMRRIVIHNNPGPHMSLIDPDAAHXAEFPEY
   FT                   PEILPAHRLAVNSDHEELLVGQRFESKEECVFAIKRYSMNISVDYKVAVSK
   FT                   PTLYIGECWKSAEGCNWRVRAAFIQKSQMWEIRKFVGPHTCTSTRMTEDHG
   FT                   KLDSKTICTFIMPMVKDMPTIKVSVLIAEMQARFQYRVSYRKAWIAKQMAM
   FT                   EQLYGDFDASYNELQGWIAAMREYVPGTIIELQTRPYYGPDDQLQPGKRIF
   FT                   HRMFWTFDPCVRAFPHCKPFVQVDGTWLYGKYTQILLLAVAQDGNRNVLPI
   FT                   AFAIVDKENMESWEFFLTNLRRYVISNDNICIISDRGKGLIAAIRRSGVPW
   FT                   RSVYCIRHIAANFHRDYKNADWKRQVVKMGKLPYLFNICFNALGQYCNLSF
   FT                   LNTYTAHELEPHIFRQRMARLESDMEGQTNTSFRQWLGTMEPWQWAQSFDE
   FT                   GFRYGQMTTNLVEGVNAVLLKTRHLPISSVFSATFYRLATLMPRMGQQQVN
   FT                   QIEAGHVFVEDVRDAMVANRRMARSMNVEIYSRRHETFRVTETIGRRPGIP
   FT                   PRSYGVDLRNRRCDCRRFQTLHYPCAHVVAACAKVNLNVEQFVDDVYTLER
   FT                   TLRVWENEFPVLPDLSTWEVPPTTFELVPDRGLRRNPRGRPQSSRIRNEMD
   FT                   IREKSDGKRCGLCRLAGHNRSKCPQRNYHVGQSSRSGRN"
   XX
   SQ    Sequence 8481 BP; 2580 A; 1495 C; 1670 G; 2701 T; 35 other;


   //
   ID    MuDRx-4_PI   repbase;     DNA;      PLN; 2842 BP.
   XX
   AC    .
   XX
   DT    14-DEC-2011 (Rel. 19.08, Created)
   DT    14-DEC-2011 (Rel. 19.08, Last updated, Version 1)
   XX
   DE    MuDRx-type DNA transposon-consensus.
   XX
   KW    MuDR; DNA transposon; Transposable Element; MuDRx-4_PI.
   XX
   OS    Phytophthora infestans
   OC    Eukaryota; Stramenopiles; Oomycetes; Peronosporales;
   OC    Phytophthora.
   XX
   RN    [1]
   RP    1-2842
   RA    Kojima K.K. and Jurka J.;
   RT    "DNA transposons from oomycetes.";
   RL    Repbase Reports 14(8), 2202-2202 (2014).
```

```
     XX
     DR    [1] (Consensus)
     XX
     CC    ~98% identical to consensus. ~80-bp TIRs.
     XX
     FH    Key             Location/Qualifiers
     FT    CDS             235..2190
     FT                    /product="MuDRx-4_PI_1p"
     FT                    /note="DDE-transposase."
     FT                    /translation="MTRRRPPRGANSPSPLNTSLVESSRRRGRTRFSPTSR
     FT                    PSRPYRGTSTSDVAVTDTSMHSSDVASTLPATSIRGEAQESPSPSLTIESM
     FT                    STQPPTSSSANPTSSQHTQSPRSLSPTTTELPQSTASSVRSQVVSKPRDGR
     FT                    TKVYYQGYAFTRANATVVKITYRCSSYRKNCRAQFAYYADSASFDFGNMEP
     FT                    HTCRAILGLVGSETGSGDHCIDVSEAVMDEVDKLAAETTMTQKEIWTGIVQ
     FT                    KFYMLDGPPVRGVSKQVVENRVQNARGTRAGGPTSLIEKPPLSKVKGSHQG
     FT                    FFQFQYSWHDAIKAQKDPVGIDRIIGWGHPALLSLLCFENLSWYIDGTFRC
     FT                    APNHYKQCVTIMVYDQSSKLYVPVVHVLTTSMTKKSYLKLLQCVQDSVGSK
     FT                    LVPKDVVCDFEGALIGAMCAFFPDIRIIGCLFHFKQACSRKLKRYGIPKLE
     FT                    AKVAMSPSVFDVLTVIDPSKIAVQGIAWVKAKIRKTCETKQLVYSRQKWRI
     FT                    FWAYFQRTWMDTFPPTFWNVYGINRDIVSRTNNPLERFHRELNKRFRPHPS
     FT                    MKQFATTLEILAREYVLQRNAIISGIAVPPVRVRFVLPRAPRLPSVAAIED
     FT                    SASSSDSEGQVDDVDVNSDPYSTDVSSTSEENAVLEEADADYEQDNSFEYE
     FT                    GVV"
     XX
     SQ    Sequence 2842 BP; 779 A; 707 C; 661 G; 695 T; 0 other;


     //
     ID    Nimb-1_PH    repbase;    DNA;    INV; 6864 BP.
     XX
     AC    .
     XX
     DT    05-MAY-2017 (Rel. 22.05, Created)
     DT    05-MAY-2017 (Rel. 22.05, Last updated, Version 1)
     XX
     DE    Non-LTR Retrotransposon, consensus.
     XX
     KW    Nimb; Non-LTR Retrotransposon; Transposable Element; Nimb-1_PH.
     XX
     OS    Parhyale hawaiensis
     OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Crustacea;
     OC    Malacostraca; Eumalacostraca; Peracarida; Amphipoda; Senticaudata;
     OC    Talitrida; Talitroidea; Hyalidae; Parhyale.
     XX
     RN    [1]
     RP    1-6864
     RA    Bao W.;
     RT    "Non-LTR retrotransposons from Parhyale hawaiensis.";
     RL    Repbase Reports 17(5), 603-603 (2017).
     XX
     DR    [1] (Consensus)
     XX
     CC    >93% identical to the consensus.
     XX
     FH    Key             Location/Qualifiers
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     FT                    GDLLQALSESGVKSVYRVKKKENGRDIDTPIYILTFDAHTLPPAVEIGWVK
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XX
SQ      Sequence 6864 BP; 1672 A; 2005 C; 1734 G; 1453 T; 0 other;


//
ID      NonLTR-2_LVa repbase;      DNA;      INV; 4991 BP.
XX
AC      .
XX
DT      17-APR-2015 (Rel. 14.07, Created)
DT      22-OCT-2019 (Rel. 24.10, Last updated, Version 2)
XX
DE      Non-LTR Retrotransposon, consensus.
XX
KW      Non-LTR Retrotransposon; Transposable Element; NonLTR-2_LVa.
XX
NM      NonLTR-2_LVa.
XX
OS      Litopenaeus vannamei
OC      Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Crustacea;
OC      Malacostraca; Eumalacostraca; Eucarida; Decapoda;
OC      Dendrobranchiata; Penaeoidea; Penaeidae; Litopenaeus.
XX
RN      [1]
RP      1-4991
RA      Alcivar-Warren A., Bogden R., Tao Q., Iyer S., Mikhaylenko G.,
RA      Wittendorp J., Mraz A., Hart E., Hatas E. et al.;
RT      "The shrimp epigenome (shrimpENCODE) project: efforts to sequence
RT      the genome of specific pathogen-free (SPF) Litopenaeus vannamei
RT      from the United States.";
RL       unpublished.
XX
RN      [2]
RP      1-4991
RA      Bao W.;
RT      "Non-LTR retrotransposons from the shrimp genome.";
RL      Repbase Reports 15(4), 1580-1580 (2015).
XX
DR      [2] (Consensus)
XX
CC      ~99% identical to the consensus.
CC      The Shrimp Epigenome (shrimpENCODE) Project' is funded by the
CC      FUCOBI Foundation of Ecuador, Environmental Genomics Inc., MA,
CC      USA, and USDA-NRSP-8.
XX
FH      Key             Location/Qualifiers
FT      CDS             347..1909
FT                      /product="NonLTR-2_LVa_1p"
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FT   CDS             1913..4714
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FT                     NPHGRDHSWWRRIAPYLENGPPDPDYAAAL"
XX
SQ   Sequence 4991 BP; 1903 A; 1175 C; 970 G; 943 T; 0 other;

//
ID   Penelope-11_HM repbase;    DNA;    INV; 6338 BP.
XX
AC   .
XX
DT   26-JAN-2009 (Rel. 14.02, Created)
DT   26-JAN-2009 (Rel. 14.02, Last updated, Version 1)
XX
DE   Penelope-like element.
XX
KW   Penelope; Non-LTR Retrotransposon; Transposable Element;
KW   Penelope-11_HM.
XX
OS   Hydra vulgaris
OC   Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroidolina;
OC   Anthoathecata; Aplanulata; Hydridae; Hydra.
XX
RN   [1]
RP   1-6338
RA   Bao W. and Jurka J.;
RT   "Penelope-like elements from Hydra magnipapillata.";
RL   Repbase Reports 9(2), 449-449 (2009).
XX
DR   [1] (Consensus)
XX
CC   This sequence was derived from sequence data generated by TIGR,
CC   J Craig Venter Institute.
XX
FH   Key             Location/Qualifiers
FT   CDS             598..2505
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FT                     /translation="MPQWAGKLNANYNKQLKEKINITRTNMQNKTITNISG
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XX
SQ     Sequence 6338 BP; 2438 A; 1340 C; 847 G; 1703 T; 10 other;

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ID     Penelope-73N1_LMi repbase;    DNA;     INV; 590 BP.
XX
AC     .
XX
DT     21-JUL-2014 (Rel. 20.01, Created)
DT     21-JUL-2014 (Rel. 20.01, Last updated, Version 1)
XX
DE     Non-LTR retrotransposon, consensus.
XX
KW     Penelope; Non-LTR Retrotransposon; Transposable Element;
KW     Nonautonomous; Penelope-73N1_LMi; non-autonomous.
XX
OS     Locusta migratoria
OC     Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC     Pterygota; Neoptera; Polyneoptera; Orthoptera; Caelifera;
OC     Acrididea; Acridomorpha; Acridoidea; Acrididae; Oedipodinae;
OC     Locusta.
XX
RN     [1]
RP     1-590
RA     Bao W. and Jurka J.;
RT     "Non-LTR retrotransposons from the migratory locust.";
RL     Repbase Reports 15(1), 132-132 (2015).
XX
DR     [1] (Consensus)
XX
CC     >90% identical to consensus.
XX
SQ     Sequence 590 BP; 198 A; 98 C; 98 G; 196 T; 0 other;

//
ID     PtConagree_I repbase;    DNA;     PLN; 13428 BP.
XX
AC     .
XX
DT     18-MAR-2013 (Rel. 18.04, Created)
DT     18-MAR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE     Internal portion of a novel LTR retrotransposon discovered in
DE     Loblolly pine fosmid (accession no. APFE01000000) and BAC
DE     (accession nos. AC241263-AC241362) sequences.
XX
KW     LTR Retrotransposon; Transposable Element; PtConagree_I.
XX
OS     Pinus taeda
OC     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC     Spermatophyta; Pinidae; Pinales; Pinaceae; Pinus; Pinus.
XX
RN     [1]
RP     1-13428
RA     Wegrzyn J.L., Lin B., Zieve J., Dougherty W.M.,
RA     Martinez-Garcia P.J., Neale D.B. and Stevens K.A.;
RT     "Insights into the loblolly pine genome: characterization of BAC
RT     and fosmid sequences.";
RL     PLoS ONE 8(9),  (2013).
XX
RN     [2]
RP     1-13428
RA     Kovach A., Wegrzyn J.L., Parra G., Holt C., Bruening G.E.,
RA     Loopstra C.A., Hartigan J., Yandell M., Langley C.H. et al.;
RT     "The Pinus taeda genome is characterized by diverse and highly
RT     diverged repetitive sequences.";
RL     BMC Genomics 11, 420-434 (2010).
XX
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DR    [1] (Consensus)
XX
CC    32 copies across BAC and fosmid sequences.
XX
FH    Key            Location/Qualifiers
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XX
SQ    Sequence 13428 BP; 3575 A; 2956 C; 2846 G; 4051 T; 0 other;

//
ID    RETROFIT2_I repbase;     DNA;     PLN; 4356 BP.
XX
AC    AC135598;
XX
DT    28-MAY-2005 (Rel. 10.05, Created)
DT    03-JUN-2005 (Rel. 10.05, Last updated, Version 1)
XX
DE    Rice copia-type LTR retrotransposon RETROFIT2_I, internal region.
XX
KW    Copia; LTR Retrotransposon; Transposable Element; RETROFIT;
KW    internal portion; RETROFIT2_I.
XX
OS    Oryza sativa
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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OC     BOP clade; Oryzoideae; Oryzeae; Oryzinae; Oryza.
XX
RN     [1]
RP     1-4356
RA     Jurka J.;
RT     "Copia-type RETROFIT2 LTR retrotransposon.";
RL     Repbase Reports 5(5), 126-126 (2005).
XX
DR     Genbank; AC135598; Positions  117963  122318.
XX
CC     RETROFIT2 is ~69% identical to RETROFIT and appears to have
CC     intact protein-coding ORF and LTRs.
XX
FH     Key            Location/Qualifiers
FT     CDS            1..4353
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FT                    YVSTNDQVADGFTKALPVKQLENFKYNLNLGKVVIEG"
XX
SQ     Sequence 4356 BP; 1245 A; 894 C; 1012 G; 1205 T; 0 other;

//
ID     RNERVK23     repbase;     DNA;     ROD; 8217 BP.
XX
AC     .
XX
DT     29-AUG-2008 (Rel. 13.08, Created)
DT     29-AUG-2008 (Rel. 13.08, Last updated, Version -1)
XX
DE     ERV2 Endogenous Retrovirus from Muridae.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element; LTR; ERVK;
KW     RNERVK23.
XX
OS     Muridae
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha;
OC     Muroidea.
XX
RN     [1]
RP     1-8217
RA     Smit A.F.;
RT     "RNERVK23 - ERV2 Endogenous Retrovirus from Muridae.";
RL     Direct Submission to Repbase Update (05-AUG-2008).
XX
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 DR   [1] (Consensus)
 XX
 CC   RNLTR23 LTRs 9% subst ORFs: gag 190-2370, pro 2378-3052, pol
 CC   3075-6545, env 6598-7893 closest to RNERVK and SMRVH (pol) and
 CC   Gibbon ape leukemia virus (env) (maybe rat specific).
 XX
 SQ   Sequence 8217 BP; 1984 A; 2157 C; 1782 G; 2264 T; 30 other;

 //
 ID   RTAg4        repbase;   DNA;    INV; 7072 BP.
 XX
 AC   AB090813;
 XX
 DT   14-SEP-2005 (Rel. 10.09, Created)
 DT   24-SEP-2010 (Rel. 15.10, Last updated, Version 2)
 XX
 DE   Anopheles gambiae retrotransposon RTAg4 DNA, complete sequence.
 XX
 KW   R1; Non-LTR Retrotransposon; Transposable Element; RTAg4.
 XX
 NM   RTAg4.
 XX
 OS   Anopheles gambiae
 OC   Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
 OC   Pterygota; Neoptera; Holometabola; Diptera; Nematocera;
 OC   Culicoidea; Culicidae; Anophelinae; Anopheles.
 XX
 RN   [1]
 RP   1-7072
 RA   Kojima K.K. and Fujiwara H.;
 RT   "Evolution of target specificity in R1 clade non-LTR
 RT   retrotransposons.";
 RL   Mol Biol Evol 20(3), 351-361 (2003).
 XX
 DR   EMBL/GenBank/DDBJ; AB090813; Positions          1    7072.
 XX
 FH   Key          Location/Qualifiers
 FT   CDS          1147..3318
 FT                /product="RTAg4_1p"
 FT                /translation="MSDEAQPQQVSAPYQLWPRKGSVVVMQPQPIERPATP
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 FT                LLLTGTRSVLELQTAANATLQQSSGQGGNRETARKRQQRLRRRERERQQQQ
 FT                QQQQQQQQQQQQQQQQQQRQQQQCQQQRQQQPQQQQLQQPQQQLWTTVVRG
 FT                RPSQRHRQPQQQQQQQQQQGERYVPPQLRQQRQQQQRPRQQQQQQQQQQQQ
 FT                QGERYVPPQLRQQRQQQHQQQQQQQQQQRQQQQRQQQRQQQQRQQQQQQQ
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 FT                GRTPPETERDRLEHIVSDLFPQHPPLVWPEAADIEGEEQPGAVADVSDDEL
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XX
SQ    Sequence 7072 BP; 1751 A; 2015 C; 2113 G; 1193 T; 0 other;

//
ID    RTE-1B_DAn    repbase;    DNA;    INV; 3251 BP.
XX
AC    .
XX
DT    04-JAN-2012 (Rel. 17.03, Created)
DT    04-JAN-2012 (Rel. 17.03, Last updated, Version 1)
XX
DE    Non-LTR retrotransposon from fruit flies.
XX
KW    RTE; Non-LTR Retrotransposon; Transposable Element; RTE-1B_DAn.
XX
OS    Drosophila ananassae
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Holometabola; Diptera; Brachycera;
OC    Muscomorpha; Ephydroidea; Drosophilidae; Drosophila; Sophophora;
OC    melanogaster group; ananassae subgroup.
XX
RN    [1]
RG    Drosophila 12 Genomes Consortium;
RT    "Evolution of genes and genomes on the Drosophila phylogeny.";
RL    Nature 450(7167), 203-218 (2007).
XX
RN    [2]
RP    1-3251
RA    Kojima K.K. and Jurka J.;
RT    "Non-LTR retrotransposons from Drosophila ananassae.";
RL    Repbase Reports 12(3), 403-403 (2012).
XX
DR    [2] (Consensus)
XX
CC    ~94% identical to consensus. ~78% identical to RTE-1_DAn.
XX
FH    Key           Location/Qualifiers
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FT                  /note="apurinic-like endonuclease and reverse
FT                  transcriptase."
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FT                  DADLAVLHNGKISAPFQTNTGVKQGCPLSPLLFNLVIDEIMSEVCSSNRGI
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FT                  AFGRLQRIWRNQQISRKTKLRIFNACIKSVLLYGSETWLTSQRMVLKLQAF
FT                  VNKCLRIICGIFWPNRITNDDLWRCTNEAPIQQQIKRKKWKWIGHALRKGR
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FT                  RWNALVDALSSQAE"
XX
SQ    Sequence 3251 BP; 1045 A; 809 C; 800 G; 597 T; 0 other;

//
ID    R_Av          repbase;    DNA;    INV; 24273 BP.
XX
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AC    .
XX
DT    07-SEP-2017 (Rel. 22.09, Created)
DT    07-SEP-2017 (Rel. 22.09, Last updated, Version 1)
XX
DE    R_Av is a Penelope-like retroelement.
XX
KW    Penelope; Non-LTR Retrotransposon; Transposable Element; R_Av.
XX
OS    Adineta vaga
OC    Eukaryota; Metazoa; Lophotrochozoa; Rotifera; Bdelloidea;
OC    Adinetida; Adinetidae; Adineta.
XX
RN    [1]
RP    1-24273
RA    Irina R. Arkhipova ., Irina A. Yushenova .
RA    and Fernando Rodriguez .;
RT    "Giant Reverse Transcriptase-Encoding Transposable Elements at
RT    Telomeres.";
RL    Molecular Biology and Evolution 34(9), 2245-2257
RL    (2017)10.1093/molbev/msx159.
XX
DR    [1] (Consensus)
XX
CC    repeat_region   10126..10153
CC    repeat_region   10153..10178
CC    repeat_region   10181..10222
CC    repeat_region   10224..10271
CC    repeat_region   10272..10297
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XX
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FT                   SYIRLNQSAIRPRKQQEVEIKNEHKDISTKVQDYLIEHHHIPRTIPIFKQY
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FT                   NEFDNIV*"
XX
SQ   Sequence 24273 BP; 8398 A; 4259 C; 3508 G; 8070 T; 38 other;

//
ID   Rex1-1_HRo  repbase;    DNA;    INV; 3884 BP.
XX
AC   .
XX
DT   22-MAR-2011 (Rel. 21.07, Created)
DT   22-MAR-2011 (Rel. 21.07, Last updated, Version -1)
XX
DE   Rex1-like non-LTR retrotransposon: consensus sequence.
XX
KW   Rex1; Non-LTR Retrotransposon; Transposable Element; Rex1-1_HRo.
XX
OS   Helobdella robusta
OC   Eukaryota; Metazoa; Lophotrochozoa; Annelida; Clitellata;
OC   Hirudinea; Rhynchobdellida; Glossiphoniidae; Helobdella.
XX
RN   [1]
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RA    Simakov O., Marletaz F., Cho S.J., Edsinger-Gonzales E.,
RA    Havlak P., Hellsten U., Kuo D.H., Larsson T. et al.;
RT    "Insights into bilaterian evolution from three spiralian
RT    genomes.";
RL    Nature 493(7433), 526-531 (2013).
XX
RN    [2]
RP    1-3884
RA    Kojima K.K. and Jurka J.;
RT    "Non-LTR retrotransposons from the Californian leech genome.";
RL    Repbase Reports 16(7), 1485-1485 (2016).
XX
DR    [2] (Consensus)
XX
CC    This consensus is generated from 30 sequences with >88%
CC    identity.
CC    This sequence was derived from sequence data generated by DOE
CC    Joint Genome Institute.
XX
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FT                    IVSPHAVNDALETLCLKCIIDSEPYFICAIYHPPNHPSYEVSTLMGYIDEL
FT                    SNTALGSDSKLIIGGDFNQLDHHSILQTGLHPIFWGPTHQGHNLDRIYGIN
FT                    VNLDITHTYRSHVSTHHLGVVAAPPPPPTNSTSRNNTTRKVISFRRRHPSQ
FT                    SSACLQHLNNIDFNNIFDFNITTTNNTLPAIFNNNTINFDNIKNNNDNNSP
FT                    TNSNNNCNNKNNINNGANDNNNNNNNINDNTFITNSIDNFLQHCFDKFYKI
FT                    INSTYNTYYPTSNITIRSSDPPFISPFIKYLLRQKNKFMRSGSILKAAAIT
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FT                    SPIDYRPISITPILSRILEKFIVRSFIYPCFNHPSIKPLLQDQFAFRPTGS
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FT                    GFQTFHALKTLRSHGLRGIKLFDITESLIISRIKYAAPSWSGFATQQQLQQ
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XX
SQ    Sequence 3884 BP; 1266 A; 1078 C; 401 G; 1139 T; 0 other;

//
ID    SINE2-1_PMaj repbase;    DNA;    VRT; 135 BP.
XX
AC    .
XX
DT    17-OCT-2018 (Rel. 24.09, Created)
DT    17-OCT-2018 (Rel. 24.09, Last updated, Version 2)
XX
DE    SINE from the great tit genome, consensus.
XX
KW    SINE2/tRNA; SINE; Non-LTR Retrotransposon; Transposable Element;
KW    SINE2-1_PMaj.
XX
OS    Parus major
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Paridae; Parus.
XX
RN    [1]
RP    1-135
RA    Kojima K.K.;
RT    "SINEs from the great tit genome.";
RL    Repbase Reports 19(9), 1808-1808 (2019).
XX
DR    [1] (Consensus)
```

```
 XX
 CC    ~90% identical to consensus. tRNA-Ile-derived. Mobilized by
 CC    CR1-X-type non-LTR retrotransposons. The consensus is ~96%
 CC    identical to that of TguSINE1 from zebrafinch.
 XX
 SQ    Sequence 135 BP; 31 A; 28 C; 35 G; 41 T; 0 other;

 //
 ID    SMAR18      repbase;    DNA;    INV; 2677 BP.
 XX
 AC    .
 XX
 DT    04-OCT-2007 (Rel. 12.10, Created)
 DT    23-OCT-2007 (Rel. 12.10, Last updated, Version 1)
 XX
 DE    Consensus sequence of Mariner-type family of repeats.
 XX
 KW    Mariner/Tc1; DNA transposon; Transposable Element; SMAR18.
 XX
 OS    Schmidtea mediterranea
 OC    Eukaryota; Metazoa; Platyhelminthes; Rhabditophora; Seriata;
 OC    Tricladida; Continenticola; Geoplanoidea; Dugesiidae; Schmidtea.
 XX
 RN    [1]
 RP    1-2677
 RA    Jurka J.;
 RT    "Mariner-type element from freshwater planarian (Schmidtea
 RT    mediterranea).";
 RL    Repbase Reports 7(10), 1076-1076 (2007).
 XX
 DR    [1] (Consensus)
 XX
 CC    Youngest copies are 99% identical with consensus.
 XX
 FH    Key           Location/Qualifiers
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 FT                  EQIFNADETGLNWKKMPHRTYISKNEKVAPGFKAAKDRITLLLCSNASGDY
 FT                  ITKPLFINRSLNPRALKNVDKSKLPVYWRANSKAWVTSSIFRDWFLNCFVP
 FT                  EVENYLKIKNIDFKVLLILDNAPGHPKDLNHPNVEIAFLPPNTTSIIQPLD
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 FT                  TLKCIREGLSLVEKMKSFFTTNDPSLERSSKLMREIDINLAPYYEIEKQLK
 FT                  KTPTKN"
 XX
 SQ    Sequence 2677 BP; 970 A; 427 C; 448 G; 832 T; 0 other;

 //
 ID    StubV_scSl1 repbase;    DNA;    PLN; 7698 BP.
 XX
 AC    .
 XX
 DT    07-MAR-2017 (Rel. 22.11, Created)
 DT    07-MAR-2017 (Rel. 22.11, Last updated, Version 1)
 XX
 DE    Solanum tuberosum virus: a member of endogenous Florendovirus, a
 DE    genus of Caulimovirus - consensus.
 XX
 KW    Caulimoviridae; Integrated Virus; Caulimovirus; StubV_scSl1.
 XX
 OS    Solanum lycopersicum
 OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC    Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
 OC    Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
 OC    Solanoideae; Solaneae; Solanum; Lycopersicon.
 XX
 RN    [1]
 RP    1-7698
 RA    Geering A.D., Maumus F., Copetti D., Choisne N., Zwickl D.J.,
 RA    Zytnicki M., McTaggart A.R., Scalabrin S. et al.;
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RT    "Endogenous florendoviruses are major components of plant genomes
RT    and hallmarks of virus evolution.";
RL    Nat Commun 5, 5269-5269 (2014).
XX
DR    [1] (Consensus)
XX
CC    Complete genome.
XX
FH    Key             Location/Qualifiers
FT    CDS             496..5979
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FT                    /translation="MDKNQNILNKINISSQSTKIAKIENDLQNWSIPEEPF
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FT                    QLAPKACLESVRGETMLMEANHSHSSIFVPRTLQWKDILSNNEWHFENITQ
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FT                    SSKSERKKTRSKRSTQKKQDVCWNCGKRGHRANECRSKTKKKKINLLDMDK
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FT                    CTCGKEPQIRVLSDNSKEALFDVIQHINDDEARNRFLLELKNLILNTDKPK
FT                    SRPIVEPFSMKQIMNRSENHSEPTIADLRHEVSLLKNEIREIKSRLSMIET
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FT                    CKDADNQIMYSRITIKRILEPTEWFADHLHTPIALTMTHRPQTYNWYDYKA
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XX
SQ    Sequence 7698 BP; 2683 A; 1506 C; 1255 G; 2254 T; 0 other;

//
ID    TE-X-12_DR   repbase;     DNA;     VRT; 1351 BP.
XX
AC    .
XX
DT    17-JAN-2014 (Rel. 19.06, Created)
DT    11-JUN-2018 (Rel. 23.06, Last updated, Version 2)
XX
DE    repeats from zebrafish - a consensus.
XX
KW    Multicopy gene; Nonautonomous; TE-X-12_DR.
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```
XX
NM    TE-X-12_DR.
XX
OS    Danio rerio
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
OC    Cypriniformes; Cyprinidae; Danio.
XX
RN    [1]
RA    Howe K., Clark M.D., Torroja C.F., Torrance J., Berthelot C.,
RA    Muffato M., Collins J.E., Humphray S., McLaren K. et al.;
RT    "The zebrafish reference genome sequence and its relationship to
RT    the human genome.";
RL    Nature 496(7446), 498-503 (2013).
XX
RN    [2]
RP    1-1351
RA    Bao W. and Jurka J.;
RT    "Transposable elements from zebrafish.";
RL    Repbase Reports 14(6), 1867-1867 (2014).
XX
RN    [3]
RP    1-1351
RA    Bao W.;
RT    "Reclassified.";
RL    Direct Submission to Repbase Update (11-JUN-2018).
XX
DR    [3] (Consensus)
XX
CC    Termini are not determined, ~85% identical to the consensus.
CC    [3]: reclassified into multiple copy gene.
XX
SQ    Sequence 1351 BP; 471 A; 262 C; 303 G; 311 T; 4 other;

//
ID    TREP_CE      repbase;     DNA;      INV; 232 BP.
XX
AC    X97533;
XX
DT    09-JUL-2004 (Rel. 9.06, Created)
DT    09-JUL-2004 (Rel. 9.06, Last updated, Version 1)
XX
DE    C.elegans DNA for telomeric repeat.
XX
KW    TREP_CE; Telomeric repeat.
XX
OS    Caenorhabditis elegans
OC    Eukaryota; Metazoa; Ecdysozoa; Nematoda; Chromadorea; Rhabditida;
OC    Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
XX
RN    [1]
RA    Wicky C., Villeneuve M.A., Lauper N., Codourey L., Tobler H.
RA    and Muller F.;
RT    "Telomeric repeats (TTAGGC)n are sufficient for chromosome
RT    capping function in Caenorhabditis elegans.";
RL    Proc. Natl. Acad. Sci. U.S.A 93(17), 8983-8988 (1996).
XX
DR    Genbank; X97533; Positions       1     232.
XX
SQ    Sequence 232 BP; 43 A; 38 C; 71 G; 80 T; 0 other;

//
ID    TguERV1_I    repbase;     DNA;      VRT; 9723 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    29-NOV-2012 (Rel. 17.12, Last updated, Version 2)
XX
DE    Internal portion of ERV1 Endogenous Retrovirus from Estrildidae.
XX
KW    ERV1; Endogenous Retrovirus; Transposable Element; LTR;
KW    TguERV1_I.
```

```
XX
NM    TguERV1_I.
XX
OS    Estrildidae
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
XX
RN    [1]
RP    1-9723
RA    Smit A.F.;
RT    "TguERV1_I - ERV1 Endogenous Retrovirus from Estrildidae.";
RL    Repbase Reports 9(1), 82-82 (2009).
XX
DR    [1] (Consensus)
XX
CC    ORFs gag 2331-4049, pol 4050-7610, env 7571-9685
CC    rnd-5_family-722.
XX
FH    Key           Location/Qualifiers
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FT                  SHPSKVYATEILEQGTAEALLPPPRNQEGRGVEERVGERVKSEPSPTSASP
FT                  NLSSGSSTLEKTVIKARVSPPTPRSGEPSRFYPPLPSSDSEWDESEPSPKP
FT                  SPQGPIASRTRRQTRMNPPPQTTRKQTKGVIQAPLRQAIASDGEPRIIKVP
FT                  FFSMDLEAWEKTAKGYRNDPIGVAKRLKFMVKQHLPDWADMQLLLDALTET
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FT                  FIVKGLERAIPKTINWSALYAVKQGPSQTPSDFLDHLRDAMRRYTTLDPGS
FT                  EEGIQQLINLFLGQSTGDIRRKLQKIRGPNSRDLETLLDEAWRVFSNREEG
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FT                  ERRRGDEQRKSDRGGERVVAHAKED"
FT    CDS           4050..7607
FT                  /product="TguERV1_I_2p"
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FT                  KNFRKIMDQVFPGVWASNIPGRAKNAVPIQIKLKEGERAVRVKQYPLKKED
FT                  REGISPIIENFLQIGLLKECQSDFNTPILPVKKPDGSYRLVQDLRAVNRVT
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FT                  NPKTGRRNQLTWCVLPQGYKNSPTIFGEQLAKDLESWEPPPGEGQLLQYVD
FT                  DLLIATQTQETCVDWTVSLLNFLGLQGYRVSQKKAQMVRQTVIYLGYEVSA
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FT                  IFPAELRKIVWDSASDIERELQAWWTLVNFTYNPMTSKVTAFVLTIHNASV
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XX
SQ    Sequence 9723 BP; 3038 A; 1805 C; 2383 G; 2495 T; 2 other;

//
ID    TguERV2_I    repbase;    DNA;    VRT; 7001 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    29-NOV-2012 (Rel. 17.12, Last updated, Version 2)
XX
DE    Internal portion of ERV1 Endogenous Retrovirus from Estrildidae.
XX
KW    ERV1; Endogenous Retrovirus; Transposable Element; LTR;
KW    TguERV2_I.
XX
NM    TguERV2_I.
XX
OS    Estrildidae
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
XX
RN    [1]
RP    1-7001
RA    Smit A.F.;
RT    "TguERV2_I - ERV1 Endogenous Retrovirus from Estrildidae.";
RL    Repbase Reports 9(1), 85-85 (2009).
XX
DR    [1] (Consensus)
XX
FH    Key           Location/Qualifiers
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FT                    KFLKYQILEECESEYNTPIFPVRKPNGEYRLVQDLRAINEITKDIYPVVAN
FT                    PYTLLTSVKETYKWFTVIDLKDAFFCIPLDKESRNLFAFEWENPGNGRKTQ
FT                    LTWTRLPQGFKNSPTLFGNQLAKELETWTARGQVPREQYLLLQYVDDILIA
FT                    TEEKATCIKVTIEILNSLGMAGYKVSKEKAQIAQQTVIYLGCEISQGQRKL
FT                    GTNRIQAICAIPEPQNLHELRVFLGMTGWCRLWIMDYGLIAKPLYEAQKTQ
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FT                  PFTWGKPQKEAFLKLKEALTTAPALGLPDLSKDFQLFVHERMRLALGVLTQ
FT                  RLGSWKRPVGYFSKQLDNVSAGWPSCLRAVAATVILIQEARKLTMGRHIDV
FT                  YVPHMVTTVLEQKGGHWLSPSRMMKFQVILTEQDDVTLKTTNLLNPALFLG
FT                  TTSEESPLEHDCVEVIEHTCAARADLKDVPLEQPDWELFTDGSSFMENGIR
FT                  HAGYAVTTISTVVEAKALPPNTSAQKAELVALTRALELSEGKKVNIWTDSK
FT                  YAFGVVHVHGALWKERGLFSSQGMHIKHQDAVLQLIRAVQKPEQVAIMHCK
FT                  AHQSGNSKICEGNRKADWTARQAARKVQTTMALVPLKLNVSQFNLPPQPKY
FT                  SAEDEKLGHLLNAQKNPEGWYVTAHGQIVVPPLVMREVLQIKHNECHWGAE
FT                  ALVKFLKRYLVSVRMLTMAKSIMSKCEICLKNNPVARRQAQLGRVRVGIEP
FT                  GDYWQVDFVELPRTRGYKYLLVGVDTFSGWPEALPCRTNQAKETVKWLLQE
FT                  IIPRFGVPLGISSDRGPHFIATVVKEVSRLLGITWDLHTPWRPQSSGQVER
FT                  MNQTLKRQISKICQEAKLQWPQALPIALLRIRIKPRSGMSVSPYEILYGKP
FT                  YESPGPNPNIHVTGKQEVYNYVLSLGKTLARLRSALVWNRPLTLENPVHDI
FT                  HPGDEVYIKNWNEEPLKEKWTGPHQVLLTTFTAVKVAGVDSWIHYTRVKKA
FT                  HPGLRTV"
XX
SQ       Sequence 7001 BP; 2315 A; 1366 C; 1693 G; 1620 T; 7 other;

//
ID       TguERVK3a_I repbase;      DNA;      VRT; 7747 BP.
XX
AC       .
XX
DT       08-JAN-2009 (Rel. 14.01, Created)
DT       29-NOV-2012 (Rel. 17.12, Last updated, Version 2)
XX
DE       Internal portion of ERV2 Endogenous Retrovirus from Taeniopygia.
XX
KW       ERV2; Endogenous Retrovirus; Transposable Element; LTR; ERVK;
KW       TguERVK3a_I.
XX
NM       TguERVK3a_I.
XX
OS       Taeniopygia
OC       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC       Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC       Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC       Estrildidae; Estrildinae.
XX
RN       [1]
RP       1-7747
RA       Smit A.F.;
RT       "TguERVK3a_I - ERV2 Endogenous Retrovirus from Taeniopygia.";
RL       Repbase Reports 9(1), 301-301 (2009).
XX
DR       [1] (Consensus)
XX
CC       <5% gag 560-2431, pro-pol 2413-6213 , env 6214-7695 Closest to
CC       TguERVK2; low copy number.
XX
FH       Key             Location/Qualifiers
FT       CDS             560..2428
FT                       /product="TguERVK3a_I_1p"
FT                       /translation="MGAKLSVPDRKLYLQVVGLLEGGNVKYKKSEVKKFVR
FT                       WLSLTFQEISAEKLYQVPFWDQVGREILRQGDPSLSPFTHLALQIRLLVKN
FT                       KFEGLPQPARDKSKPSSTPGPLSSPSTPAPSTSSARAPLQGSANGASATLP
FT                       CPQTPVSPQCTAPSLRKSVSFKNPPESPSPSDPQNGRQSLSRQTPQDGGDR
FT                       MEFPATCAPSSQNSLPFPAPSNPFHSAANPFRSSDSSLSPPTVVSPPPDVT
FT                       SPPPYSAQGGARPSAPPPSPGHAPPMTSSGSQGPSSGSHGLGSGGGERGNC
FT                       GLPHSPPTFSAAPVTFTTRRGGRLLAQWSPIPQQTIRELCKAQKEFGRDSE
FT                       YFRGLLRATLDSNEYVPSDMRILFSCLITPAEFMAWESAWRREVRDALPDL
FT                       WAIAEASLDADGGIISIDHLCGIGEWDSAAKQADKIPREALAISAKAAKQA
FT                       FFKLRPAGMVTNYLSIKQDPQEAFVTFIDRLCRAXEVQVPDSNLRQGILTE
FT                       VAKQNANSACKAAILSLPLDPEPTIQDMLEVCARKVTIVPPEQRETPRPPP
FT                       KRVSFAEVATPPPSTPSTPSETRRPAPRGNTXDRTCHLCKKPGHWMPQCPL
FT                       REQFYEFRRQQEGRGNPPTKGASKN"
FT       CDS             2413..6210
FT                       /product="TguERVK3a_I_2p"
FT                       /translation="RGFKKLRSERSSPLRSDKNRVGRKTSSAGEEEGNTIS
FT                       PECSPPPDTSTGHDXKRPAKPWRVEPQYFKEDVDTIPREWLGRSPDQPRPI
FT                       LNTHCNFPPYRLALTESIHLADSDWRFVTIDTESPGTWRKLRCKYIVLGDT
FT                       KFTPLNIHIAPCTTSTNPEKLLLWLYCAEPPMFLPKGQVIAQAIPVTGSPV
FT                       FPEHLWKKSAAQAHKVCAAHIMGSDKPRMGCNIWHGDQHRWLNGLLDTGAD
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FT                         VTVIPSKDWPSRWELQDVAGQIQGVGGSQLAKQSKNIVQFVGPDGQSAYIR
FT                         PFVLDYTEPLWGRDLMAQWGAKLEIPTPQVFRLAVTEERPTKKLNWLSDTP
FT                         VVWVEQWPLNKQKLKALQELVDEQLAKGNIQETTSPWNSPVFVLKKPGRDEW
FT                         RLLHDLRAINNVIEPMGSLQPGMPSPTMLPENWNLAVIDVKNCFFQIPLHP
FT                         DDAPRFAFSVPTINREAPMKRYHWRVLPQGMKNSPTICQWYVSLVLDPIRK
FT                         AVRDAIILHYMDDILICAPTDDLLAHALRLTTDLLVDAGFELRNDKIQKMP
FT                         PWKYLGLEIRKRTIVPQKLAIKNQIRTLADVQQLCGSLNWVRPWLGIPTED
FT                         LAPLFNLLKGGEEPCSPRELTPEAQAALEKVQELMSARQAHRYIPDLPFKF
FT                         IILGRLPHLHGVIFQWRETPKGDKDQGRRDPLSIIEWVFLSHNRSKRMTRP
FT                         QELVAELIRKARARIRELAGVDFECIHLPIKLNSGQFTKAMLEHLLQENEA
FT                         LQFALDSYTGQISVLRPAHKIFDSDIQFTLTTKQIQSKQPLNALTIFTDAS
FT                         GGSHKSVMTWKDPQTQRWEADVAEVEGSPQIAELAAVVRAFERFSEPFNLV
FT                         TDSAYVAGVVSRAQDAILQGVSNESLHRLLSKLIKLVSHREQPFYVMHIRS
FT                         HTNLPGFLAEGNRRADSLAAAPAQMAPLPDVFQQAKLSHQLHHQNAPGLVR
FT                         QFHLTRDQAKAIVATCPSCKSLPLPSVSAGANPRGLQACEVWQMDVTHINS
FT                         FGRFKYVHVSVDTFSGAVYASAHTGEKAADVKKHLMLAFSTLGIPKLLKTD
FT                         NAPGYKSREFAAFLQQWGIEHRTGIAYSPSGQAVVERTHQSLKRMLQQQTP
FT                         TMKVESPQVRLARALFTINFLNCSYXNPNPPIARHFGQCEHAKVKERPPVM
FT                         IKDPETWRLEGPYDLVTWGRGYACVSTPSGLRWVPSKFVRPYTAKVSPGSE
FT                         KPQVAMAAFRRRRKPXLNNPDSFLLLAESPPIPEYPEDSLDPFSLDLSLDL
FT                         PLLFE"
FT   CDS             6271..7692
FT                         /product="TguERVK3a_I_3p"
FT                         /translation="MSSASPILLALTIGLFIGASRAWIVPQPAANVWNTLA
FT                         NSIGQDHLCLSTSSASNPFLSCLVGIPYPLDHLPFNFPKTVPAPRNRSTKF
FT                         QNIQLKPPHEWRVWYRSLPVLDDEPQELSLLGSALAYTCVQFFMTREPHPI
FT                         AKSRSYLXIKQTMNDYTARKWCLKVIQIDAATNYEDQPRKLPKGTFFLCGN
FT                         RAWAGIPSRLLGGPCTFGQLTLFTPNKTQIAHWKEVNSTTNLARRKRDATF
FT                         QNLDENCKXEIFHWAKAKSALITTFVPWWAIAQSLNELQSLECWVAKQANL
FT                         TSAALSGLLEDEKVTRQATLQNRAAIDYLLLLHNHRCEEFAGLCCFNLSSR
FT                         AEDVQVSIDKMKGMXTKIKQETSGWLDHLFEEWGLSSWAQSIAKTALMLLL
FT                         TVCIFVIGFSVVKNLVLKTVLSSSASNHRATSSQSQSIQVCVAEIAPLTGP
FT                         DTTEDDPEYEXMKDXWFXDQNQKDCSPPV"
XX
SQ   Sequence 7747 BP; 1817 A; 2324 C; 1882 G; 1688 T; 36 other;

//
ID   TguERVK5_I  repbase;     DNA;     VRT; 8294 BP.
XX
AC   .
XX
DT   08-JAN-2009 (Rel. 14.01, Created)
DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE   Internal portion of ERV2 Endogenous Retrovirus from Estrildidae.
XX
KW   ERV2; Endogenous Retrovirus; Transposable Element; ERVK; LTR;
KW   TguERVK5_I.
XX
OS   Estrildidae
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
XX
RN   [1]
RP   1-8294
RA   Smit A.F.;
RT   "TguERVK5_I - ERV2 Endogenous Retrovirus from Estrildidae.";
RL   Repbase Reports 9(1), 134-134 (2009).
XX
DR   [1] (Consensus)
XX
CC   ORFs: gag 180-3179, pro >2972-3838, pol 3838-6465, env
CC   <6647-8074.
XX
SQ   Sequence 8294 BP; 2370 A; 1691 C; 1857 G; 2370 T; 6 other;

//
ID   TguERVL2_I-b_fAlb repbase;     DNA;     VRT; 2072 BP.
XX
AC   .
XX
DT   03-SEP-2019 (Rel. 24.09, Created)
```

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DT    03-SEP-2019 (Rel. 24.09, Last updated, Version 1)
XX
DE    Internal region from a long terminal repeat (LTR) retrotransposon
DE    of an ERV3 endogenous retrovirus from Ficedula albicollis.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element;
KW    Endogenous Retrovirus-like; ERVL; LTR; TguERVL2_I-b_fAlb.
XX
OS    Ficedula albicollis
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
OC    Ficedula.
XX
RN    [1]
RP    1-2072
RA    Suh A., Smeds L. and Ellegren H.;
RT    "Abundant recent activity of retrovirus-like retrotransposons
RT    within and among flycatcher species implies a rich source of
RT    structural variation in songbird genomes.";
RL    Molecular Ecology 27(1), 99-111 (2018).
XX
DR    [1] (Consensus)
XX
CC    Internal region
CC    Consensus status: Incomplete 3' end
CC    Similarity to Repbase repeats: TguERVL2_I (88% similarity)
CC    Comment: Internal portion of TguERVL2a4_LTRLb_fAlb.
XX
SQ    Sequence 2072 BP; 554 A; 457 C; 569 G; 464 T; 28 other;

//
ID    TguERVL2b1_LTR-La_fAlb repbase;     DNA;     VRT; 567 BP.
XX
AC    .
XX
DT    18-AUG-2019 (Rel. 24.08, Created)
DT    18-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE    Long terminal repeat of an ERV3 endogenous retrovirus from
DE    Ficedula albicollis.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element; LTR; ERVL;
KW    Endogenous Retrovirus-like; TguERVL2b1_LTR-La_fAlb.
XX
OS    Ficedula albicollis
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
OC    Ficedula.
XX
RN    [1]
RP    1-567
RA    Suh A., Smeds L. and Ellegren H.;
RT    "Abundant recent activity of retroviruslike retrotransposons
RT    within and among flycatcher species implies a rich source of
RT    structural variation in songbird genomes.";
RL    Molecular Ecology 27(1), 99-111 (2019).
XX
DR    [1] (Consensus)
XX
CC    LTR region
CC    TSD: 5 bp
CC    Consensus status: Complete
CC    Similarity to Repbase repeats: Partially TguERVL2a2-LTR +
CC    TguERVL2b1_LTR (73% + 85% similarity).
XX
SQ    Sequence 567 BP; 140 A; 135 C; 109 G; 179 T; 4 other;

//
ID    TguERVL2b5_LTR repbase;     DNA;     VRT; 512 BP.
XX
AC    .
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   XX
   DT   08-JAN-2009 (Rel. 14.01, Created)
   DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
   XX
   DE   Long terminal repeat of ERV3 Endogenous Retrovirus from
   DE   Estrildidae.
   XX
   KW   ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
   KW   TguERVL2b5_LTR.
   XX
   OS   Estrildidae
   OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
   OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
   XX
   RN   [1]
   RP   1-512
   RA   Smit A.F.;
   RT   "TguERVL2b5_LTR - ERV3 Endogenous Retrovirus from Estrildidae.";
   RL   Repbase Reports 9(1), 185-185 (2009).
   XX
   DR   [1] (Consensus)
   XX
   CC   8% 64.
   XX
   SQ   Sequence 512 BP; 123 A; 133 C; 110 G; 146 T; 0 other;

   //
   ID   TguLTR5b    repbase;    DNA;    VRT; 596 BP.
   XX
   AC   .
   XX
   DT   08-JAN-2009 (Rel. 14.01, Created)
   DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
   XX
   DE   ERV3 Endogenous Retrovirus from Passeriformes.
   XX
   KW   ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
   KW   TguLTR5b.
   XX
   OS   Passeriformes
   OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
   OC   Coelurosauria; Aves; Neognathae.
   XX
   RN   [1]
   RP   1-596
   RA   Smit A.F.;
   RT   "TguLTR5b - ERV3 Endogenous Retrovirus from Passeriformes.";
   RL   Repbase Reports 9(1), 75-75 (2009).
   XX
   DR   [1] (Consensus)
   XX
   CC   18% Not represented in chicken.
   XX
   SQ   Sequence 596 BP; 113 A; 128 C; 188 G; 167 T; 0 other;

   //
   ID   TguLTR5c    repbase;    DNA;    VRT; 586 BP.
   XX
   AC   .
   XX
   DT   08-JAN-2009 (Rel. 14.01, Created)
   DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
   XX
   DE   ERV3 Endogenous Retrovirus from Passeriformes.
   XX
   KW   ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
   KW   TguLTR5c.
   XX
   OS   Passeriformes
   OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
   OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
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OC     Coelurosauria; Aves; Neognathae.
XX
RN     [1]
RP     1-586
RA     Smit A.F.;
RT     "TguLTR5c - ERV3 Endogenous Retrovirus from Passeriformes.";
RL     Repbase Reports 9(1), 76-76 (2009).
XX
DR     [1] (Consensus)
XX
CC     23% Not represented in chicken.
XX
SQ     Sequence 586 BP; 123 A; 148 C; 166 G; 148 T; 1 other;

//
ID     TguLTR5d     repbase;     DNA;     VRT; 595 BP.
XX
AC     .
XX
DT     08-JAN-2009 (Rel. 14.01, Created)
DT     21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE     ERV3 Endogenous Retrovirus from Aves.
XX
KW     ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
KW     TguLTR5d.
XX
OS     Aves
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria.
XX
RN     [1]
RP     1-595
RA     Smit A.F.;
RT     "TguLTR5d - ERV3 Endogenous Retrovirus from Aves.";
RL     Repbase Reports 9(1), 43-43 (2009).
XX
DR     [1] (Consensus)
XX
CC     24% Shared with chicken.
XX
SQ     Sequence 595 BP; 117 A; 141 C; 178 G; 158 T; 1 other;

//
ID     TguLTRK2d_I repbase;     DNA;     VRT; 5263 BP.
XX
AC     .
XX
DT     08-JAN-2009 (Rel. 14.01, Created)
DT     21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE     Internal portion of ERV2 Endogenous Retrovirus from Taeniopygia.
XX
KW     ERV2; Endogenous Retrovirus; Transposable Element; ERVK; LTR;
KW     TguLTRK2d_I.
XX
OS     Taeniopygia
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC     Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC     Estrildidae; Estrildinae.
XX
RN     [1]
RP     1-5263
RA     Smit A.F.;
RT     "TguLTRK2d_I - ERV2 Endogenous Retrovirus from Taeniopygia.";
RL     Repbase Reports 9(1), 322-322 (2009).
XX
DR     [1] (Consensus)
XX
CC     Non-autonomous element. Partial gag (434-1521), full env
CC     (3968-5261), but no trace of pol. Many variants of internal
```

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CC    splice products. Pos 1522-2064 unique with respect to
CC    TguLTRK2e_I.
XX
SQ    Sequence 5263 BP; 1403 A; 1050 C; 1403 G; 1399 T; 8 other;

//
ID    TguLTRK2e_I repbase;     DNA;     VRT; 5610 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    Internal portion of ERV2 Endogenous Retrovirus from Taeniopygia.
XX
KW    ERV2; Endogenous Retrovirus; Transposable Element; ERVK; LTR;
KW    TguLTRK2e_I.
XX
OS    Taeniopygia
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC    Estrildidae; Estrildinae.
XX
RN    [1]
RP    1-5610
RA    Smit A.F.;
RT    "TguLTRK2e_I - ERV2 Endogenous Retrovirus from Taeniopygia.";
RL    Repbase Reports 9(1), 324-324 (2009).
XX
DR    [1] (Consensus)
XX
CC    Non-autonomous element. Full gag (434-2461), full env
CC    (4315-5608), but no trace of pol. Many variants of internal
CC    splice products. Pos 1522-2443 unique with respect to
CC    TguLTRK2d_I.
XX
SQ    Sequence 5610 BP; 1563 A; 1116 C; 1386 G; 1533 T; 12 other;

//
ID    TguLTRL2b5  repbase;     DNA;     VRT; 1406 BP.
XX
AC    .
XX
DT    08-JAN-2009 (Rel. 14.01, Created)
DT    21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
XX
DE    ERV3 Endogenous Retrovirus from Estrildidae.
XX
KW    ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
KW    TguLTRL2b5.
XX
OS    Estrildidae
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
OC    Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea.
XX
RN    [1]
RP    1-1406
RA    Smit A.F.;
RT    "TguLTRL2b5 - ERV3 Endogenous Retrovirus from Estrildidae.";
RL    Repbase Reports 9(1), 262-262 (2009).
XX
DR    [1] (Consensus)
XX
CC    mixed subfamilies; << 11%, 54 copies.
XX
SQ    Sequence 1406 BP; 318 A; 275 C; 467 G; 341 T; 5 other;

//
ID    TguLTRL4b  repbase;     DNA;     VRT; 1064 BP.
XX
AC    .
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     XX
     DT   08-JAN-2009 (Rel. 14.01, Created)
     DT   21-JAN-2009 (Rel. 14.01, Last updated, Version 1)
     XX
     DE   ERV3 Endogenous Retrovirus from Passeriformes.
     XX
     KW   ERV3; Endogenous Retrovirus; Transposable Element; ERVL; LTR;
     KW   TguLTRL4b.
     XX
     OS   Passeriformes
     OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
     OC   Coelurosauria; Aves; Neognathae.
     XX
     RN   [1]
     RP   1-1064
     RA   Smit A.F.;
     RT   "TguLTRL4b - ERV3 Endogenous Retrovirus from Passeriformes.";
     RL   Repbase Reports 9(1), 78-78 (2009).
     XX
     DR   [1] (Consensus)
     XX
     CC   5 bp TSDs 22%.
     XX
     SQ   Sequence 1064 BP; 225 A; 265 C; 354 G; 215 T; 5 other;


     //
     ID   Tgu_rep3-L_Ucy repbase;    DNA;    VRT; 996 BP.
     XX
     AC   .
     XX
     DT   11-JUL-2019 (Rel. 24.08, Created)
     DT   11-JUL-2019 (Rel. 24.08, Last updated, Version 1)
     XX
     DE   Long terminal repeat of an ERV3 endogenous retrovirus from
     DE   Uraeginthus cyanocephalus.
     XX
     KW   ERV3; Endogenous Retrovirus; Transposable Element;
     KW   Endogenous Retrovirus-like; ERVL; LTR; Tgu_rep3-L_Ucy.
     XX
     OS   Uraeginthus cyanocephalus
     OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
     OC   Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
     OC   Coelurosauria; Aves; Neognathae; Passeriformes; Passeroidea;
     OC   Estrildidae; Uraeginthus.
     XX
     RN   [1]
     RP   1-996
     RA   Boman J., Frankl-Vilches C., da Silva dos Santos M.,
     RA   de Oliveira E.H.C., Gahr M. and Suh A.;
     RT   "The Genome of Blue-Capped Cordon-Bleu Uncovers Hidden Diversity
     RT   of LTR Retrotransposons in Zebra Finch.";
     RL   Genes 10(4), 301-301 (2019).
     XX
     DR   [1] (Consensus)
     XX
     CC   LTR region
     CC   TSD: 5 bp
     CC   Consensus status: Complete
     CC   Similarity to Repbase repeats: Partially (ca first 800bp) to
     CC   (Tgu_rep3 (87.94%; Taeniopygia guttata) and last ca 180 bp to
     CC   TguLTR11 (86.23%; Taeniopygia guttata) Both are ERV3s.
     XX
     SQ   Sequence 996 BP; 259 A; 262 C; 233 G; 239 T; 3 other;


     //
     ID   Tx1-15_BF    repbase;    DNA;    INV; 5843 BP.
     XX
     AC   .
     XX
     DT   29-APR-2009 (Rel. 14.04, Created)
     DT   29-APR-2009 (Rel. 14.04, Last updated, Version 1)
     XX
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DE    Amphioxus Tx1-15_BF autonomous Non-LTR Retrotransposon -
DE    consensus.
XX
KW    Tx1; Non-LTR Retrotransposon; Transposable Element; L1-15_BF;
KW    Tx1-15_BF.
XX
OS    Branchiostoma floridae
OC    Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC    Branchiostoma.
XX
RN    [1]
RP    1-5843
RA    Putnam N.H., Butts T., Ferrier D.E., Furlong R.F., Hellsten U.,
RA    Kawashima T., Robinson-Rechavi M., Shoguchi E. et al.;
RT    "The amphioxus genome and the evolution of the chordate
RT    karyotype.";
RL    Nature 453(7198), 1064-1071 (2008).
XX
RN    [2]
RP    1-5843
RA    Kapitonov V. and Jurka J.;
RT    "Young families of Tx1 non-LTR retrotransposons from the
RT    amphioxus genome.";
RL    Repbase Reports 9(4), 852-852 (2009).
XX
DR    [2] (Consensus)
XX
CC    ORF1 is corrupted by mutations.
XX
FH    Key             Location/Qualifiers
FT    CDS             1826..5593
FT                    /product="Tx1-15_BF_2p"
FT                    /note="endonuclease and RT."
FT                    /translation="MTQVEVHISSFNCNGIGNSIKRREVFTWLRDKQHHII
FT                    CLQETHSTLSVEKRWQNEWGGSMIFSHGTSNQRGTAILFQNSIKPCIHQTK
FT                    TDKDGRWLIVDLSLDEYRFCLVNIYAPNEDSPEFFFNISEELDDFSESNEH
FT                    LIITGDFNTVQNPLVDRLATNTTYHPKAFESISELKCKFDLQDIWRFRHPD
FT                    TVRYTWRRRRQASRIDYFLVSFSLINRINNCKIADSFRSDHRLISLSFVTA
FT                    DFPRGRGYWKFNTSLLEDKSFHTKTVEIMKEFFSINSGTANPHVVWEAAKC
FT                    FFRGHCIKFSSFKNKQYLSREKTLIDDINALQTELDSTPSSPDSVLDALDQ
FT                    KQKELELLYSQRVQGVMTRSRAKWMELGDRCSKYFLNLVHRNYTRKNIQKL
FT                    QISENSFTCNPTEILERQTEFYSSLYSFKDPPVPLTPENCKDFFPEDYCRV
FT                    LSENQRQSCEGLITEDELLDAINSFSSGKSPGLDGIPVEVYKQFYSVFKAL
FT                    MLECFNFSLTQGFLTNTQRHGAISLLLKQGGNGQDKDPTLLDNWRPLTLLC
FT                    CDTRILSKCLALRVKSVISHIIDKDQSGFIQGRFIGENIRRILDIIDHYEK
FT                    EQKPGLIFISDYKKAFDSIRWDFIIKSLNFFNFGPQFSAWVKVLYNDITSS
FT                    VLNNGYISQPFCLHRGVRQGCPLSPYLFIIAVEMLAIKVRSNEDLTGLSIL
FT                    GKSTKISQFADDTDFPFTPTLASFYALLKDLESFSCISALTLNFEKCRILR
FT                    IGTLKNTNFKLPTHLPFQWVDGNVEVLGVHIPQDLDTIVDLNFEPRLAKLD
FT                    RLLYPWRIKGISLFGKVTIINSLITSQFTHLFQVLQTPDKSFFQQYERKFF
FT                    SFIWNGGPERISRKTIYNSIENGGLNLTHLYAFACTIKASWVPRLYFNQDW
FT                    STTWVIRLHPSLGSSLFPFFQIRSTKHLKLSPFLLDVLDAWFKYQYKPPTC
FT                    AAEVKQQLLFMNDSILIDSVPIFMNTFINRNIIFVNDILNDMGTISTYEEF
FT                    SRKYDAICDYFKYKQLISAIPQKWKSMLCGNVFESVCKPVQRNSCWLKQVK
FT                    INKDMYQFFLSYYNLIDISHNVQLKWLYLFDTPIPWKQVYSSIIFCTIDSS
FT                    TRFFQYKIVHKFLPTNKLLYIWKCIDTPLCSFCHEEEETYLHVFWECPHLT
FT                    PFWDKIKNWYHSKTTINLKLNGFNIIFGNLHFGTPPIENLITLLAKIYIYR
FT                    CRKPSTLNFDSFLRYVNFFNKVEYYVALKKGKLDKHLGKWGSLCS*"
XX
SQ    Sequence 5843 BP; 1777 A; 1090 C; 1093 G; 1883 T; 0 other;

//
ID    Tx1-1_CPB    repbase;    DNA;    VRT; 8238 BP.
XX
AC    .
XX
DT    02-SEP-2012 (Rel. 18.09, Created)
DT    02-SEP-2012 (Rel. 18.09, Last updated, Version 1)
XX
DE    Non-LTR retrotransposon: consensus.
XX
KW    Tx1; Non-LTR Retrotransposon; Transposable Element; Tx1-1_CPB.
XX
```

```
 OS    Chrysemys picta bellii
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Testudines; Cryptodira; Durocryptodira;
 OC    Testudinoidea; Emydidae; Chrysemys; Chrysemys picta.
 XX
 RN    [1]
 RA    Shaffer H.B., Minx P., Warren D.E., Shedlock A.M., Thomson R.C.,
 RA    Valenzuela N., Abramyan J., Amemiya C.T. et al.;
 RT    "The western painted turtle genome, a model for the evolution of
 RT    extreme physiological adaptations in a slowly evolving lineage.";
 RL    Genome Biol 14(3), R28-R28 (2013).
 XX
 RN    [2]
 RP    1-8238
 RA    Jurka J.;
 RT    "Non-LTR retrotransposons from the western painted turtle.";
 RL    Repbase Reports 13(9), 2252-2252 (2013).
 XX
 DR    [2] (Consensus)
 XX
 CC    ~94% identical to consensus. This family is specifically inserted
 CC    into Gypsy-10_CPB-LTR.
 XX
 FH    Key            Location/Qualifiers
 FT    CDS            1302..4199
 FT                   /product="Tx1-1_CPB_1p"
 FT                   /translation="MAGDEASETPRADPAAPPPPAPPSSPLASTSTAAAEP
 FT                   PATAPAGAPAAAGNEVTSAAATSLAPSDSGGAPPAGRKGQGTKKGKGPAKK
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 FT                   GPTAIVAASKMYGKVVVFFLASEAAAQEAVEKGLAVGGVFVPLEPLEDLGAR
 FT                   LVLTSVPPFLPNAALLPALSTLGRPISVVSPLPLGCKDPALRHVLSFRRQV
 FT                   QLQLPPAARDGEALEGSFLVPYQGARYRVHYSTGEARCYLCRAMGHVRRDC
 FT                   PLARHGGASGTPEPRQGAGPVIAGAPSCPAPEAAPPPFRPTNAPARAQGVS
 FT                   PPARPDEREGPASAACDLAGPVEEGEVGISPGIEEGMPQGESSLLHAAPPL
 FT                   PPRVPEPSPLLPDPTPVSQPPDDAMEGWSLVQGKRGKRKARAPLLPSDAVA
 FT                   PRKTRKGGTDAEPSALPPGGFRPPLPAGEDVAAPEDSTAPPPESLPMEAPD
 FT                   GAPLAPLQSEAPARTKASVASGAGGESPGVVEGDLPSIYEEIEALGLTPVT
 FT                   QGEDDPLPAGLDLSDLASAPLSPCSVPLPTASAPASEEPLDSSTNPAADGT
 FT                   PLAAAEPLEATASATQPGPESPGDSLVAEGQPTSFPGGGPIVDSPPTDAVA
 FT                   LPSALEHEPGIAEGPPPSPQIPEPICGVPPPPPSGPAAGAPDPTIAPSPVP
 FT                   IPDSGPAPDTDPVPVPSTSHDAIAAPGAVSFHIPEDDPQGAAFVFPCPDPP
 FT                   GAAIFPPPPPIEPGSEAGHVAPAHRTPRRGSAPCLPVSVGHGAVTGAPLGD
 FT                   SRRSVTPPPHTLREELREFLEDVRGSRNKVQLALQRWGDFHQILRAARALM
 FT                   GEGKRTGRQAAAAYQRVRLFRDSLIAYGVGHGLLRGPTEAVGVSASEDPPQ
 FT                   PSSWHRSSSQH"
 FT    CDS            4175..8095
 FT                   /product="Tx1-1_CPB_2p"
 FT                   /note="apurinic-like endonuclease and reverse
 FT                   transcriptase."
 FT                   /translation="MAPIIFATLNTRGCRMGLRRSQVLSFLREGGYSVIFL
 FT                   QETHTDPAAEASWRLEWGDRVYFSHLTVRTAGVATLFSPDLRPEVLGVAEA
 FT                   VPGRLLHLRVRMEGLVVNLVNVYAPTSGPERLRFYQQASAFLGTLDPRECL
 FT                   VLGGDFNATLEERDRSGTEQRPAAADVLREIVEHHSLVDVWRDHHPDDVST
 FT                   FTFVRVEVHRSCHSRLDRIYLSRFHLSRAHSSSVRPAPFSDHHLATVTASL
 FT                   CAERPGPAYWHFNNSLLEDVGFVASFREFWLAWRGQRRAFPSARRWWDLGK
 FT                   VRARLFCRDYTRGASRRRDAAIGQLEREVLELERRLAASPGDPSLCGACRE
 FT                   KREELRTLEDHRARGAFVRSRIRLLREMDRGSRFFYALEKKRGAKKHVTCL
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 FT                   DRLELPLTLAEFSEALRRMPTNKSPGMDGLTVEFYRVFWDVLGPDLVTVWA
 FT                   ESLQGGVLPLSCRRAVLALLPKKGDLRDLRNWRPISLLSTDYKIVAKAISL
 FT                   RLGSVLADVIHPDQTYTVPGRTIFDNLYLVRDLLELGCRDGLSFALLSLDQ
 FT                   EKAFDRVDHGYLLGTLRAFGFGPQFVGFLQVLYASAECLVRLNWTLTEPVS
 FT                   FGRGVRQGCPLSGQLYALAIEPFLCLLRRRLTGLVLREPELRLVLSAYADD
 FT                   VLLVVQDPGDLVRVEACQTIYSAASSARVNWVKSSGLVVGDGWQASSLPPA
 FT                   LQAIRWSAGPLLYLGVYLSATHPSPPENWLGLEGRVSERLRKWTGLLRCLS
 FT                   LRGRALVLNQLVLSMLWYRLNTLVPAPGFLANLRTLILEFFWPGLHWVSAG
 FT                   VLHLPLEEGGQGLKCLHAQVHVFRLQALQRLLYGAGSPAWSVLAHAFLRRF
 FT                   RGLRYDRQLLCLHPRGLPRDLSGLPVFYQDLLRTWKLFSVTRSVAATVGAD
 FT                   LLAEPLLHNPQLRVQVAESPMVRQRLVLAEVTKVGDLLDYDRGDWLDPLTL
 FT                   AQRMGLSRPRTPRRVLQEVRAALPPAARDYLDRVLREGTPRPPSTPSPPDL
 FT                   FIGPLPRGPNRPPPRPFAMSRLHDLQPVLFRTAPRKHLYTLVLHVLHVLTL
 FT                   ASRPDTKWRDLLPPLEGEEPRWASLYSALIPKPTGDISWRLLHGAVSTGVY
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FT                     LARFTPIPDTCPFCGVRETLAHVYLECARLQPLFRLLTDVLLRFWLHFSPH
FT                     LFIYALPIRRPTKSRDLLVNLLLALAKLAIYKTRXRRLADGVSCDCGAYFR
FT                     SSVRSRIRAEFLWAASTGSLDAFEEQWALSGVLCSVSPSGSLLLTL"
XX
SQ     Sequence 8238 BP; 1142 A; 2990 C; 2471 G; 1634 T; 1 other;


//
ID     Tx1-5_FR      repbase;    DNA;     VRT; 4503 BP.
XX
AC     .
XX
DT     22-MAR-2011 (Rel. 17.01, Created)
DT     22-MAR-2011 (Rel. 17.01, Last updated, Version -1)
XX
DE     A Tx1 non-LTR Retrotransposon - consensus.
XX
KW     Tx1; Non-LTR Retrotransposon; Transposable Element; Tx1-5_FR.
XX
OS     Takifugu rubripes
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC     Actinopterygii; Neopterygii; Teleostei; Neoteleostei;
OC     Acanthomorphata; Eupercaria; Tetraodontiformes; Tetradontoidea;
OC     Tetraodontidae; Takifugu.
XX
RN     [1]
RP     1-4503
RA     Kojima K.K. and Jurka J.;
RT     "Non-LTR retrotransposons from the pufferfish Fugu rubripes.";
RL     Repbase Reports 12(1), 108-108 (2012).
XX
DR     [1] (Consensus)
XX
CC     This consensus is generated from 10 sequences with >92%
CC     identity. All 3' termini are flanked with (TC)n
CC     microsatellites.
CC     Thus it is likely a Kibi element.
XX
FH     Key           Location/Qualifiers
FT     CDS           join(477..1046,958..4413)
FT                     /product="Tx1-5_FR_1p"
FT                     /note="apurinic-like endonuclease and reverse
FT                     transcriptase."
FT                     /translation="MCCITFLFFAAPSTASPLQASMNKLRVASLNINGGRD
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FT                     AGVATLFSPRLDVRVTSTTEIAAGRALAVRAEVQGFVFCLINIYAPSQGSD
FT                     RLDLFQKVSSFVEQCGQDECVVMGGGLELHHRRHTGQDWTGASSPVSCCAV
FT                     SWGGDWNCTTDVTLDRIGQEPHLQSAAVLSRLGAELGMVDVWRVKHPTIRQ
FT                     YTWVKVVDGVISAARLDRFYLSQGFSNRLVNSHIYPVGFTDHHLATFDFLI
FT                     SQTHKCXSYWHFNVKLLRDTEFXRXFEAFWGTXRGRKGDFECLGQRWEVGK
FT                     AHIRVFCXQYSSHSTTRVKHTIEHLEREIRDLEGSFSTHTSTEGHTLRQKR
FT                     QELSSFLQERVKGALVRSRFTSIKEMDAPTSFFFNLERSVSRAKQMLCLRL
FT                     PDGTMTADQGEMRRHAVDFYGALYRAEDCSREDELLQGLPRLSQRDRSTLD
FT                     ADITLDELTAAVGQMASGRAPGLDGLPADFYKHFWRCLGADLWEVLQECAH
FT                     TGRLPTSCQTAVLSLIPKKGDLALLKNWRPVALLCTDYKLLSKVLANRLKN
FT                     HLDLLVHRDQSYCVPDRSIMDNLFLMRDLFHLCKLYDIDVGISLDQEKAF
FT                     DRVDHKFLFSTLRAFGFGDVFLSLLSLLYRDACCLVKVGGGLSCPVSVQRG
FT                     IRQGCPISGQLYSLAIEPLLNNLRTRLSGLLLPGLPERPQLVVSAYADDIN
FT                     VFVRDQGDVDNLIDSLDLYQEASSAKVNWEKSEALQVGPWAGRDRPRLPGN
FT                     LSWGRQGLKVLGVFLGTENFEKKNWEGAVEQVCTRLSKWKWLLPQLSYRGR
FT                     VLIVNNLVASTLWHRLTVLPSPAGLIEGVQKMIVDFFWSGQHWLRSAVLYL
FT                     PVQEGGQGLVDIASRVTAFRLQAAQRLLYSFGVPWTDMACLLLRKAGRLGY
FT                     DKHLFLLQPQSVDLTGLTPFYQSVLKAWQVLSFKHKAVTIPGMWIFEEPLF
FT                     GNSIITSRVLSSATLRSRLRDAGVVKLGHLLKTSVPDLSDRLNMRSSRLLL
FT                     QLVGEVCASLPEALRVFVLDPSVSELWDDKCEYVFPSLAVCPAVGQWQPEE
FT                     DDLLSLKSSVSVDFEGVGRKDLYILAVKVRNLRPLEGLKASGWTSFFGAGS
FT                     SPGGCWRSLYKPPVDKRTGDLQWRIVHGAIATNRYLVHLDPSTGDGCPFCS
FT                     QSETIYHLFVQCPRLEGLFGQLQRWFLGLGEGFSFRXFIFGPHYRARRKAV
FT                     HQLVNVLSGTAKLAIWKTRKNRVRGQGSEDVVAMMTGLLAARLRVEFNFYK
FT                     LTGQISTFGDIWGVRDVLXSVRENCLILNF"
XX
SQ     Sequence 4503 BP; 1029 A; 1021 C; 1328 G; 1113 T; 12 other;

//
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ID   Tx1-8_AMi   repbase;    DNA;    VRT; 7009 BP.
XX
AC   .
XX
DT   03-OCT-2012 (Rel. 18.04, Created)
DT   24-APR-2013 (Rel. 18.04, Last updated, Version 1)
XX
DE   Non-LTR retrotransposon.
XX
KW   Tx1; Non-LTR Retrotransposon; Transposable Element; Tx1-8_AMi.
XX
OS   Alligator mississippiensis
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Archosauria; Crocodylia; Alligatoridae;
OC   Alligatorinae; Alligator.
XX
RN   [1]
RP   1-7009
RG   International Crocodilian Genomes Working Group;
RT   "Non-LTR retrotransposons from the American alligator genome.";
RL   Direct Submission to Repbase Update (16-OCT-2012).
XX
DR   [1] (Consensus)
XX
CC   >92% identical to consensus. This family is inserted into
CC   (TTCC)n microsatellites.
XX
FH   Key             Location/Qualifiers
FT   CDS             711..2402
FT                   /product="Tx1-8_AMi_1p"
FT                   /translation="MAAPTPGSWHEDVSRDLPLTHGLRVHAPLHVGLEVCV
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FT                   LSFRRQVFMLLKEGPQSLPRSLSLTRSRVGGFIIYLSVGETTCFKCGGSSH
FT                   LAAQCPQGQGGWTIAACGSAEDGASTSGARGRPSEAGSSSSQPPSTPIPSQ
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FT                   AAIPPAPLRCSHQRGRLGGGEGAAGVPPPSPVPQPPESGGSRDSGECLSSG
FT                   GLAPGVAGESATPLVTPQPSGSDGEVSEMEIQLSESRKRRRERDGLSPPKK
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FT                   LAEPPWVPPDYGGSCPC"
FT   CDS             2715..6680
FT                   /product="Tx1-8_AMi_2p"
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FT                   VPGRLLTVRVTLAQHRLLLVNVYAPSDGQERVVFFETLAALLRDASEDDDL
FT                   LLLGGDFNCTTAPRLDRTGPEPHLPSARKLQSALEGADLVDVWRALHPDAR
FT                   QYTWARMGAGGLTMARLDRLYVTRHHLPLLRSSRIAPSGLSDHGLAFCELS
FT                   LPGRACARAPYWCFNVSLLQDSYFRDCFAHFWRRWEAARPSHSSWKLWWDV
FT                   GKVQIRAFCQQYTQLAANETRRRIRELEEDVAELEAALLAAGSDAALSESL
FT                   RFRRKCLRDLAESAARGARIRARCQELVETDAPTRFFFNLERRRAASKVLD
FT                   HLKTPEGRVITEPGEIREHAVAFYRDLFAAEPSCPEATRELHEGLPRLDAL
FT                   EAGELERDLSLEELAAATAGLASGKAPGLDGLPAEFYKTFWPLLGPSLLRV
FT                   FQESLADKVLPISCRRAVLTLLPKKGDLGYIKNWRPVSLLCADYKILAKAL
FT                   ATRLRAVMASLTGPEQSYCVPGRTIQDNLFLLRDLLTASELFGLDVGLISL
FT                   DQEKAFDRVGHAYLFRTLEAFGFGPLFTGALRVLYQDISSLLKVNGVLCAP
FT                   FPARRGIRQGCPLSGMLYALAIEPLLHALRRRLSGVALPLATGPSVGPPLR
FT                   LSAYADDVTVFLNTQEDVRALADCQRAYERASSARINWAKSDTLLLGAWTG
FT                   TPPPDLPGGLTWRREGLKVLGVFLGPPTFMARNWDGLEEGVEARLQRWRWR
FT                   LPSLSYRGRVLVINNLAAATLWHRCAVLDPPPDLLERLQRILVDFFWDGRH
FT                   WLPRAVLHLPVAEGGQGLVDLASRVAAFRLQALQRLLYSEEHLPWQQLACR
FT                   FLQRVGALGFDRELFLLTPTLLNWAVLPAFYRSVVRAWQAAFRLQPRARTL
FT                   CFPQLLREPLVHNSALXCSVPSLASASLTATLIQARVLRLHHLLDPARSAW
FT                   LLPEALAARLGVRSVRTMGHLLRDIRAALPPAAAAALDEHLRARQIPRATD
FT                   AASEAFPPLPVTPAVAAELAGGPGTLLRLPMPPDSDTGCPFASLSRRSLYA
FT                   WVVCVRHAQVLAGRPDTPWRRRLGPPASPPAHPAWRTLYKPPTAKKTGDLQ
FT                   WRLLHGILATGTFASHLDPAASTACPFCPGGVEEDLFHAFLDCPRLRPLFA
FT                   TLEPPLRALGRSLSETTYVCSYPYRAAERGAICLANFLLGQAKMAVLKSRR
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FT                   VEDGRLKYAL"
XX
SQ   Sequence 7009 BP; 992 A; 2376 C; 2115 G; 1523 T; 3 other;
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 //
 ID    fAlbLTR2    repbase;    DNA;    VRT; 479 BP.
 XX
 AC    .
 XX
 DT    03-SEP-2019 (Rel. 24.09, Created)
 DT    03-SEP-2019 (Rel. 24.09, Last updated, Version 1)
 XX
 DE    Long terminal repeat of an ERV1 endogenous retrovirus from
 DE    Ficedula albicollis.
 XX
 KW    ERV1; Endogenous Retrovirus; Transposable Element;
 KW    Endogenous Retrovirus-like; LTR; fAlbLTR2.
 XX
 OS    Ficedula albicollis
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
 OC    Ficedula.
 XX
 RN    [1]
 RP    1-479
 RA    Suh A., Smeds L. and Ellegren H.;
 RT    "Abundant recent activity of retrovirus-like retrotransposons
 RT    within and among flycatcher species implies a rich source of
 RT    structural variation in songbird genomes.";
 RL    Molecular Ecology 27(1), 99-111 (2018).
 XX
 DR    [1] (Consensus)
 XX
 CC    LTR region
 CC    TSD: 4 bp
 CC    Consensus status: Complete
 CC    Similarity to Repbase repeats: None.
 XX
 SQ    Sequence 479 BP; 163 A; 79 C; 89 G; 132 T; 16 other;

 //
 ID    fAlbLTRL2    repbase;    DNA;    VRT; 483 BP.
 XX
 AC    .
 XX
 DT    01-SEP-2019 (Rel. 24.09, Created)
 DT    01-SEP-2019 (Rel. 24.09, Last updated, Version 1)
 XX
 DE    Long terminal repeat of an ERV3 endogenous retrovirus from
 DE    Ficedula albicollis.
 XX
 KW    ERV3; Endogenous Retrovirus; Transposable Element;
 KW    Endogenous Retrovirus-like; ERVL; LTR; fAlbLTRL2.
 XX
 OS    Ficedula albicollis
 OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC    Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda;
 OC    Coelurosauria; Aves; Neognathae; Passeriformes; Muscicapidae;
 OC    Ficedula.
 XX
 RN    [1]
 RP    1-483
 RA    Suh A., Smeds L. and Ellegren H.;
 RT    "Abundant recent activity of retrovirus-like retrotransposons
 RT    within and among flycatcher species implies a rich source of
 RT    structural variation in songbird genomes.";
 RL    Molecular Ecology 27(1), 99-111 (2018).
 XX
 DR    [1] (Consensus)
 XX
 CC    LTR region
 CC    TSD: 5 bp
 CC    Consensus status: Complete
 CC    Similarity to Repbase repeats: Partially Tgu_rep2 + TguLTRL4a +
 CC    TguLTRL2a8 (66% + 69% + 70% similarity).
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XX
SQ    Sequence 483 BP; 175 A; 81 C; 88 G; 133 T; 6 other;

//
ID    hAT-1_MAc   repbase;    DNA;     PLN; 3441 BP.
XX
AC    .
XX
DT    07-JAN-2013 (Rel. 23.09, Created)
DT    07-JAN-2013 (Rel. 23.09, Last updated, Version 1)
XX
DE    DNA transposon from the wild banana Musa acuminata: consensus.
XX
KW    hAT; DNA transposon; Transposable Element; hAT-1_MAc.
XX
OS    Musa acuminata
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Zingiberales; Musaceae;
OC    Musa.
XX
RN    [1]
RP    1-3441
RA    Jurka J.;
RT    "DNA transposons from the wild banana Musa acuminata.";
RL    Repbase Reports 18(9), 970-970 (2018).
XX
DR    [1] (Consensus)
XX
CC    >94% identical to consensus.
XX
FH    Key          Location/Qualifiers
FT    CDS          583..1647
FT                 /product="hAT-1_MAc_1p"
FT                 /translation="MASVQSNSIESPMASKKDPAWKYNYLKDPKDPNAVTC
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FT                 ESYGNLPEDNVEHLRDEEEDYSMSINPSGKRVYDKKGKEVMSTKKGKKGPM
FT                 DLYMFQGSQKQQGQAGGSKFRQTNISDACDKEIRGRTIQHIARFFYQAGLP
FT                 LSTTRLDSFKDMIEAIGRYGAGLKPPSYYEMRVPLLQKELNYTNDLLKGHK
FT                 ESWATHGCSIMSDVWTDRRRRSIINFMVNCSLGTMFVKSIDASSFVKSGDK
FT                 IYDLLDNFVEEIGEQNVVQIITDNGSNYVLAGNIHLLNLLIILSSIKCVKL
FT                 LSLIIFVILCLR"
FT    CDS          1616..2473
FT                 /product="hAT-1_MAc_2p"
FT                 /translation="VLSFLLSFVSGKLLEXKRQHLYWTPCAAHCIDLMLED
FT                 IGKILEIKKTLERAIFVVGFLYNHIGALNMMREFTGNKELVRHGVTRFATS
FT                 FLTLQSVHRQKHNLRNMFTSEKWVTSKWAKEAKGKRAADIILMSSFWNHVV
FT                 YILKVMGPLVRVLRLVDNENKPAMGYIYEAMDRAKETIKRSFNENEEKYEK
FT                 IFTIIDERWNCQLHRPLHAAGYYLNPEFFYKIKSVGFDAEVLGGLYQCVAR
FT                 LVPSLEVQDKIIRELSLYKNAEGLFGIPIVVRSRTTTSPGINNLI"
XX
SQ    Sequence 3441 BP; 1064 A; 573 C; 740 G; 1058 T; 6 other;

//
ID    hAT-1_SIt   repbase;    DNA;     PLN; 5661 BP.
XX
AC    .
XX
DT    05-JUN-2012 (Rel. 21.05, Created)
DT    05-JUN-2012 (Rel. 21.05, Last updated, Version -1)
XX
DE    DNA transposon from the foxtail millet genome:consensus.
XX
KW    hAT; DNA transposon; Transposable Element; hAT-1_SIt.
XX
OS    Setaria italica
OC    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC    Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC    PACMAD clade; Panicoideae; Panicodae; Paniceae; Cenchrinae;
OC    Setaria.
XX
RN    [1]
RA    Zhang G., Liu X., Quan Z., Cheng S., Xu X., Pan S., Xie M.,
RA    Zeng P., Yue Z., Wang W., Tao Y., Bian C. et al.;
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```
RT    "Genome sequence of foxtail millet (Setaria italica) provides
RT    insights into grass evolution and biofuel potential.";
RL    Nat Biotechnol 30(6), 549-554 (2012).
XX
RN    [2]
RP    1-5661
RA    Jurka J.;
RT    "DNA transposons from the foxtail millet genome.";
RL    Repbase Reports 16(5), 953-953 (2016).
XX
DR    [2] (Consensus)
XX
CC    >91% identical to consensus.
XX
FH    Key            Location/Qualifiers
FT    CDS            4145..5659
FT                   /product="hAT-1_SIt_1p"
FT                   /translation="MKRKGSAATDLRIFMARAAAKKRQPEPENVNQSCNES
FT                   QMQVVLFQGQSGSETSTVPPEPVRSNQPPEXGTTEIGESIPVEENDSSDED
FT                   KNDYGIEHDPGLRAPISSYDVNDQDSVRRAYIALGPCQPKMKRDAFPQHDC
FT                   GGMRRFQHKWFAEFKWIEYSVDKDAAFCFVCYLFKDSCKFPGGDAFVVEGF
FT                   RNWNMKRRIHRHVGAIDSAHSEAEEKYRLFTRPKASIRESVASNTAQFKAK
FT                   YLARLTWSLKCIRFLLRQGLAFRGHDETKDSLNKGNFRELLAWLAGNFEEV
FT                   NLVVLENAPQNCQMIDHKIQKQLIDACAHETTKFIIDELGDECFAILADES
FT                   SDAYLLEQLALCLRFVNKKGEPVERFLGLVQVEDTTSLTLKEAIQSLLMKY
FT                   QLPLSKVRGQGYDGASNMKGHVNGLKKLIMDESPSAYYVHCFAHQLQLTLV
FT                   AVAKENTDCDWFFGQLAYLLNVLGMSCKKIRMLRIAQAEYMIEALKLGEIE
FT                   TGQGLNQEM"
XX
SQ    Sequence 5661 BP; 1347 A; 1429 C; 1442 G; 1426 T; 17 other;


//
ID    hAT-2_PBa    repbase;    DNA;    INV; 4706 BP.
XX
AC    .
XX
DT    15-MAY-2012 (Rel. 19.03, Created)
DT    15-MAY-2012 (Rel. 19.03, Last updated, Version 1)
XX
DE    hAT-type DNA transposon from the Pogonomyrmex barbatus genome:
DE    consensus.
XX
KW    hAT; DNA transposon; Transposable Element; hAT-2_PBa.
XX
OS    Pogonomyrmex barbatus
OC    Eukaryota; Metazoa; Ecdysozoa; Arthropoda; Hexapoda; Insecta;
OC    Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita;
OC    Aculeata; Vespoidea; Formicidae; Myrmicinae; Pogonomyrmex.
XX
RN    [1]
RA    Smith C.R., Smith C.D., Robertson H.M., Helmkampf M., Zimin A.,
RA    Yandell M., Holt C., Hu H., Abouheif E. et al.;
RT    "Draft genome of the red harvester ant Pogonomyrmex barbatus.";
RL    Proc Natl Acad Sci U S A 108(14), 5667-5672 (2011).
XX
RN    [2]
RP    1-4706
RA    Bao W. and Jurka J.;
RT    "DNA transposons from the Pogonomyrmex barbatus genome.";
RL    Repbase Reports 14(3), 650-650 (2014).
XX
DR    [2] (Consensus)
XX
CC    >95% identical to consensus.
XX
FH    Key            Location/Qualifiers
FT    CDS            join(825..1193,1656..3119,3011..4018)
FT                   /product="hAT-2_PBa_1p"
FT                   /translation="MFKAVSFLAFNVDFNTQMAFTVVDDNLFRFFVLTSVK
FT                   RENILSGAAFEFGSALVEFKRALKLGYLVSLFKYCLCKISFHILSKFNFNK
FT                   SCFSVTEKSEFKTNHSFFKSFSSKPPILAAIKERSSVSFTFLVLLYFHFDM
FT                   ESCDALKKKVKRSFSEAWLNDERFKFWIRKVPFDDSLFHCIVCAKNFSCGP
FT                   ISNIIRHAESAQHKRNIDKDVSSSDNDNVTFEQKPLHPNVFKQQWLEIEQF
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FT                      KPWLREVQCDANSFASCTICEKTIAGGLSQIYRHAESKIHKNNCEKFDEIT
FT                      SKSNEDCNIEISELFSSFEERKKFAEIRFAALIAEKNISHENAKIILDFFK
FT                      DVGKDPNVLKSMTMSRQKCTNIITNVLCPVETDRVIENIQNTKFSIFIDES
FT                      TDISSEKWMTFHVRYVHIETLEVHSQLVKLIDIDATDCSAEKLFNAFKYEM
FT                      WKLQIPFSNIVALSCDNASVMVGKHLSFKKKLEEMCNNVLTLSCPCHSASL
FT                      ASHAACAKIPQACEEFLKRITSYITCSPKRWSIFTELSECFEERTHKIVKL
FT                      CNTRWLSHHACIDRLLQSWNTIQHFLNEMIVSEKGTSAENLLRVMQNVDTK
FT                      AYLLFLKYTLHFFNDRERERYICRKFVACHAECRYKSIFAILKIYITFFLN
FT                      VFNAFFQAEETRIHLLQSKSIDFLKEICTNFIKPEILKHLPNITFCKTENH
FT                      KSLNDIFLGSECEEYLHQLIEDGHANMVATVRENCLRFYITAAEEIFKRLP
FT                      VSDTFLSKLQILLPHIALLSTDRETSFHDLSFIAARMGGFDENDLKKEWFA
FT                      LNSDFSVTEKQDLLKLNFDNMWKEILQRQYLNNETKYPNLRSLLNSIRALP
FT                      NSNAAPERIFSLLTDVKTKKRNRLSSTTVNAICVLKSALKARNETALNMKL
FT                      DEKHLSFMSADKLYVTSSVKQKKSFQLHAADDIAGPSSSNMQQ"
XX
SQ     Sequence 4706 BP; 1621 A; 726 C; 778 G; 1580 T; 1 other;

//
ID     hAT-7_PM     repbase;     DNA;     VRT; 2499 BP.
XX
AC     .
XX
DT     01-APR-2013 (Rel. 18.06, Created)
DT     01-APR-2013 (Rel. 18.06, Last updated, Version 1)
XX
DE     DNA transposon family: consensus.
XX
KW     hAT; DNA transposon; Transposable Element; hAT-7_PM.
XX
OS     Petromyzon marinus
OC     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Cyclostomata;
OC     Hyperoartia; Petromyzontiformes; Petromyzontidae; Petromyzon.
XX
RN     [1]
RA     Smith J.J., Kuraku S., Holt C., Sauka-Spengler T., Jiang N.,
RA     Campbell M.S., Yandell M.D., Manousaki T. et al.;
RT     "Sequencing of the sea lamprey (Petromyzon marinus) genome
RT     provides insights into vertebrate evolution.";
RL     Nat Genet 45(4), 415-421 (2013).
XX
RN     [2]
RP     1-2499
RA     Bao W. and Jurka J.;
RT     "DNA transposons from the sea lamprey.";
RL     Repbase Reports 13(6), 1777-1777 (2013).
XX
DR     [2] (Consensus)
XX
FH     Key           Location/Qualifiers
FT     CDS           302..2107
FT                   /product="hAT-7_PM_1p"
FT                   /translation="MSGSRKRKVDNECRVFNTEWTTKYFFTEVQSKAVCLI
FT                   CRETVAVFKEYNISRHFATKHANYASKQSTQERAATAQRLAANLQTQQHFF
FT                   HRQTAIQESTTKASFLVAFEIAKASKPFSEGEFVKECMVQTADILCPEIKS
FT                   KFEKVSLSRRTVTRRVELIDENIASQLNKKSDSFELYSLALDESTDVKDTA
FT                   QLLIFIRGIDDSFAITEEFLTMESLKGTTRGEDLYNQVSAVIERMKLPWSK
FT                   LVNVTTDGSPNLTGKNVGLLKRIQNKVKEENPDQDLIFLHCIIHQESLCKS
FT                   VLQLNHVVNPAVKLVNFIRARGLQHRQFITFLEETDADHQDLLYHSRVRWL
FT                   SLGKVLQRVWELKEDIIAFLELMGKSDEFPELSDKNWLSDFAFAVDIFSHM
FT                   NELNVKLQGKDQFVHDMYKHVKAFKSKLTLFSRQIANKSFAHFPTLAMQEE
FT                   APRNAKKYSKSLEDLHGEFCRRFSDFENIEQSLQLVSCPLSQDSETAPQEL
FT                   QLELIDLQSDSVLKEKFNSVKLNDFYASLNRATFPNLRRTAQKMLTLFGST
FT                   YVCEQTFSVMNANKARHRSKLTDQHLRSILRIATTKITPDLDALAKMGDQQ
FT                   HCSH"
XX
SQ     Sequence 2499 BP; 712 A; 559 C; 567 G; 660 T; 1 other;

//
ID     hAT-N126_CPB repbase;     DNA;     VRT; 863 BP.
XX
AC     .
XX
DT     03-JUN-2017 (Rel. 22.10, Created)
```

```
  DT   31-JUL-2017 (Rel. 22.10, Last updated, Version 1)
  XX
  DE   DNA transposon: consensus.
  XX
  KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
  KW   hAT-N126_CPB.
  XX
  OS   Chrysemys picta bellii
  OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  OC   Archelosauria; Testudines; Cryptodira; Durocryptodira;
  OC   Testudinoidea; Emydidae; Chrysemys; Chrysemys picta.
  XX
  RN   [1]
  RP   1-863
  RA   Shaffer H.B., Minx P., Warren D.E., Shedlock A.M., Thomson R.C.,
  RA   Valenzuela N., Abramyan J. and Amemiya C.T.;
  RG   et al;
  RT   "The western painted turtle genome, a model for the evolution of
  RT   extreme physiological adaptations in a slowly evolving lineage.";
  RL    Genome Biol 14(3), - (2013).
  XX
  RN   [2]
  RP   1-863
  RA   Bao W.;
  RT   "DNA transposons from the western painted turtle.";
  RL   Repbase Reports 17(10), 1120-1120 (2017).
  XX
  DR   [2] (Consensus)
  XX
  CC   ~91% identical to consensus.
  XX
  SQ   Sequence 863 BP; 105 A; 325 C; 327 G; 105 T; 1 other;

  //
  ID   hAT-N17_NS  repbase;    DNA;    PLN; 1086 BP.
  XX
  AC   .
  XX
  DT   11-OCT-2017 (Rel. 22.10, Created)
  DT   11-OCT-2017 (Rel. 22.10, Last updated, Version 1)
  XX
  DE   DNA transposons from the wood tobacco, consensus.
  XX
  KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
  KW   hAT-N17_NS.
  XX
  OS   Nicotiana sylvestris
  OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
  OC   Pentapetalae; asterids; lamiids; Solanales; Solanaceae;
  OC   Nicotianoideae; Nicotianeae; Nicotiana.
  XX
  RN   [1]
  RP   1-1086
  RA   Sierro N., Battey J.N., Ouadi S., Bovet L., Goepfert S.,
  RA   Bakaher N., Peitsch M.C. and Ivanov N.V.;
  RT   "Reference genomes and transcriptomes of Nicotiana sylvestris and
  RT   Nicotiana tomentosiformis.";
  RL    Genome Biol 14(6), - (2013).
  XX
  RN   [2]
  RP   1-1086
  RA   Bao W.;
  RT   "DNA transposons from the wood tobacco.";
  RL   Repbase Reports 17(10), 1167-1167 (2017).
  XX
  DR   [2] (Consensus)
  XX
  CC   ~96% identical to the consensus.
  XX
  SQ   Sequence 1086 BP; 321 A; 183 C; 232 G; 350 T; 0 other;

  //
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```
ID   hAT-N20_TrPr repbase;      DNA;      PLN; 465 BP.
XX
AC   .
XX
DT   05-AUG-2019 (Rel. 24.08, Created)
DT   05-AUG-2019 (Rel. 24.08, Last updated, Version 1)
XX
DE   DNA transposon from the red clover genome, consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   hAT-N20_TrPr.
XX
OS   Trifolium pratense
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; Gunneridae;
OC   Pentapetalae; rosids; fabids; Fabales; Fabaceae; Papilionoideae;
OC   Trifolieae; Trifolium.
XX
RN   [1]
RP   1-465
RA   Kojima K.K.;
RT   "DNA transposons from the red clover genome.";
RL   Repbase Reports 19(8), 1370-1370 (2019).
XX
DR   [1] (Consensus)
XX
CC   ~85% identical to consensus. 8-bp TSDs. 9-bp TIRs.
XX
SQ   Sequence 465 BP; 144 A; 72 C; 79 G; 170 T; 0 other;

//
ID   hAT-N56B_CPB repbase;      DNA;      VRT; 545 BP.
XX
AC   .
XX
DT   03-JUN-2017 (Rel. 22.07, Created)
DT   10-JUL-2017 (Rel. 22.07, Last updated, Version 1)
XX
DE   DNA transposon: consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   hAT-N56B_CPB.
XX
OS   Chrysemys picta bellii
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archelosauria; Testudines; Cryptodira; Durocryptodira;
OC   Testudinoidea; Emydidae; Chrysemys; Chrysemys picta.
XX
RN   [1]
RP   1-545
RA   Shaffer H.B., Minx P., Warren D.E., Shedlock A.M., Thomson R.C.,
RA   Valenzuela N., Abramyan J. and Amemiya C.T.;
RG   et al;
RT   "The western painted turtle genome, a model for the evolution of
RT   extreme physiological adaptations in a slowly evolving lineage.";
RL    Genome Biol 14(3), - (2013).
XX
RN   [2]
RP   1-545
RA   Bao W.;
RT   "DNA transposons from the western painted turtle.";
RL   Repbase Reports 17(7), 774-774 (2017).
XX
DR   [2] (Consensus)
XX
CC   >78% identical to consensus.
XX
SQ   Sequence 545 BP; 43 A; 207 C; 238 G; 57 T; 0 other;

//
ID   hAT-N6_OD    repbase;      DNA;      INV; 1372 BP.
XX
AC   .
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XX
DT   23-SEP-2011 (Rel. 22.03, Created)
DT   23-SEP-2011 (Rel. 22.03, Last updated, Version 1)
XX
DE   DNA transposon from the Oikopleura dioica genome: consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   hAT-N6_OD.
XX
OS   Oikopleura dioica
OC   Eukaryota; Metazoa; Chordata; Tunicata; Appendicularia;
OC   Oikopleuridae; Oikopleura.
XX
RN   [1]
RP   1-1372
RA   Kojima K.K. and Jurka J.;
RT   "DNA transposons from the Oikopleura dioica genome.";
RL   Repbase Reports 17(3), 253-253 (2017).
XX
DR   [1] (Consensus)
XX
CC   ~95% identical to consensus. 8-bp TSDs. ~90bp TIRs. The sequence
CC   596-1207 is an ancient insertion of DNA-TTAA-3_OD-like transposon
CC   with TTAA/TCAA target site duplications.
XX
SQ   Sequence 1372 BP; 425 A; 308 C; 271 G; 368 T; 0 other;

//
ID   hAT-N9_LCh  repbase;    DNA;    VRT; 1628 BP.
XX
AC   .
XX
DT   26-OCT-2012 (Rel. 18.12, Created)
DT   26-OCT-2012 (Rel. 18.12, Last updated, Version 1)
XX
DE   DNA transposon from the coelacanth genome:consensus.
XX
KW   hAT; DNA transposon; Transposable Element; Nonautonomous;
KW   hAT-N9_LCh.
XX
OS   Latimeria chalumnae
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Coelacanthiformes; Coelacanthidae; Latimeria.
XX
RN   [1]
RA   Amemiya C.T., Alföldi J., Lee A.P., Fan S., Philippe H.,
RA   Maccallum I., Braasch I., Manousaki T., Schneider I. et al.;
RT   "The African coelacanth genome provides insights into tetrapod
RT   evolution.";
RL   Nature 496(7445), 311-316 (2013).
XX
RN   [2]
RP   1-1628
RA   Bao W. and Jurka J.;
RT   "DNA transposons from the coelacanth genome.";
RL   Repbase Reports 13(12), 3128-3128 (2013).
XX
DR   [2] (Consensus)
XX
CC   LFSINE element sequence is masked out.
XX
SQ   Sequence 1628 BP; 202 A; 312 C; 202 G; 433 T; 479 other;

//
ID   tRNA-Ala-GCY_ repbase;    DNA;    VRT; 75 BP.
XX
AC   .
XX
DT   05-MAR-2004 (Rel. 14.08, Created)
DT   02-SEP-2009 (Rel. 14.08, Last updated, Version 1)
XX
DE   tRNA from Vertebrata.
XX
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KW    tRNA; Multicopy gene; tRNA-Ala-GCY_.
XX
OS    Vertebrata
OC    Eukaryota; Metazoa; Chordata; Craniata.
XX
RN    [1]
RP    1-75
RA    Smit A.F.;
RT    "tRNA-Ala-GCY_ - tRNA from Vertebrata.";
RL    Direct Submission to Repbase Update (02-SEP-2009).
XX
DR    [1] (Consensus)
XX
SQ    Sequence 75 BP; 14 A; 24 C; 24 G; 13 T; 0 other;

//
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Summary Table

Repeat Class	Fragments	Length
Integrated Virus	1	46
Caulimoviridae	1	46
Interspersed Repeat	1	104
DNA transposon	34	2900
EnSpm/CACTA	8	859
Harbinger	3	186
Helitron	2	111
Mariner/Tc1	6	307
MuDR	3	377
hAT	12	1060
Endogenous Retrovirus	101	42022
ERV1	16	6431
ERV2	31	12259
ERV3	52	23119
LTR Retrotransposon	73	5319
BEL	5	356
Copia	22	1288
DIRS	1	35
Gypsy	40	3244
Non-LTR Retrotransposon	61	25050
CR1	26	17695
I	3	131
Jockey	2	398
L1	5	339
L2	2	156
Nimb	1	86
Penelope	6	496
R1	2	394
RTE	2	4021
Rex1	1	177
SINE	4	761
SINE2/tRNA	2	190
SINE3/5S	2	571
Tx1	6	359
Multicopy gene	2	292
tRNA	1	30
Transposable Element	269	75291
Total	**273**	**75733**

* alignment score for local alignment may not always be equal to alignment score in map of hits because of use of heuristics for stitching fragments reported in map section, and use of different wu-blast parameters on stage of search and stage of producing local alignments.