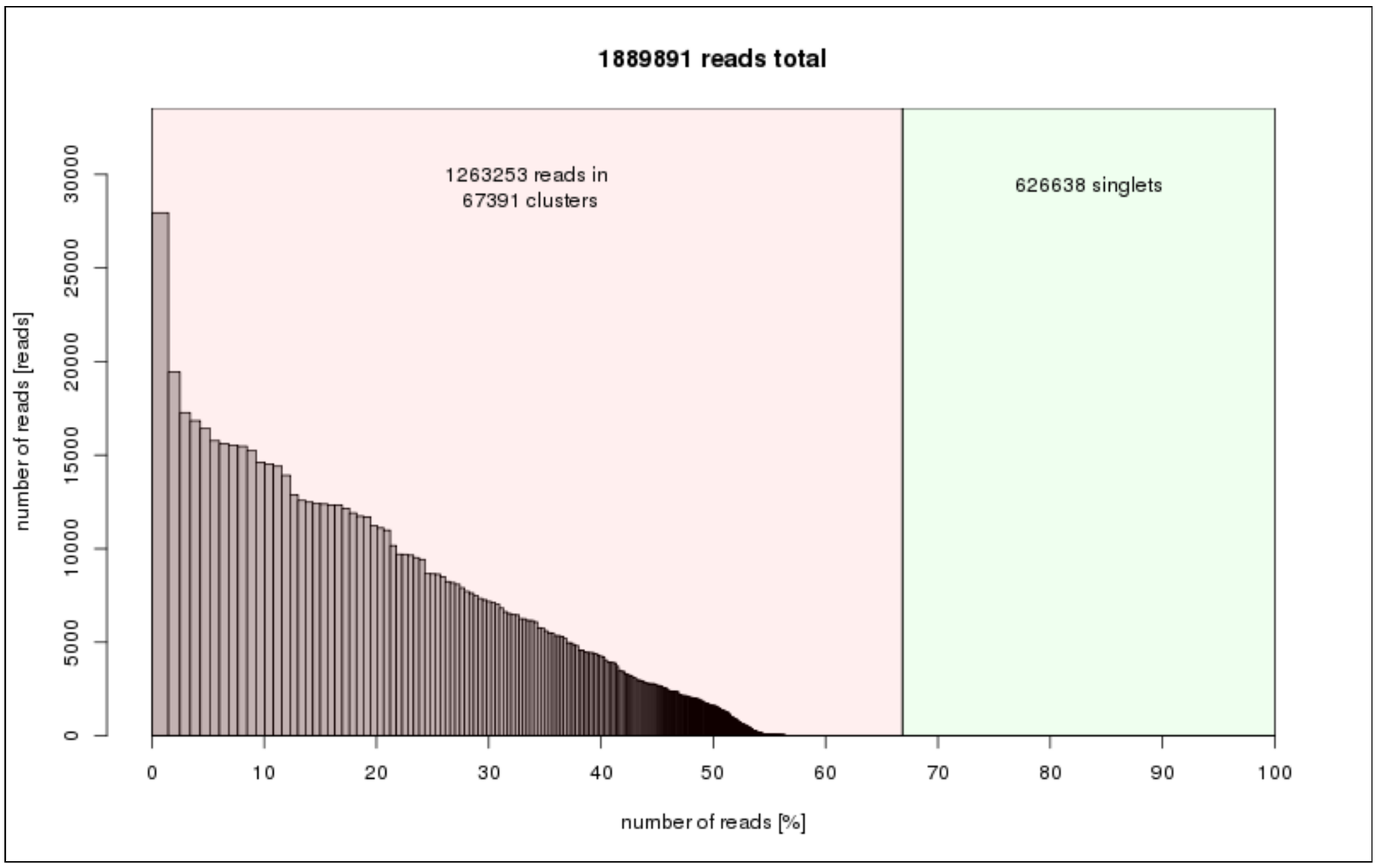
If you use RepeatExplorer in your work please cite:

Novak, P., Neumann, P., Pech, J., Steinhaisl, J., Macas, J. (2013) - RepeatExplorer: a Galaxy-based web server for genome-wide characterization of eukaryotic repetitive elements from next generation sequence reads. *Bioinformatics* 29:792-793.
or
Novak, P., Neumann, P., Macas, J. (2010) - Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data. *BMC Bioinformatics* 11:378.

Sequence clustering results

Number of sequences used for clustering: 1889891

Number of similarity hits: 72978787



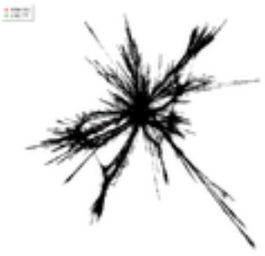
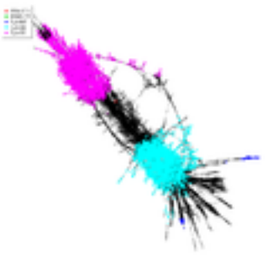
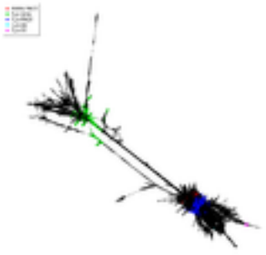
Comparative analysis summary

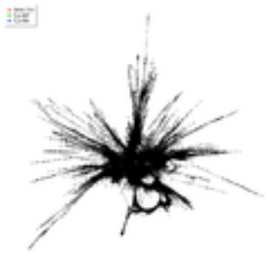
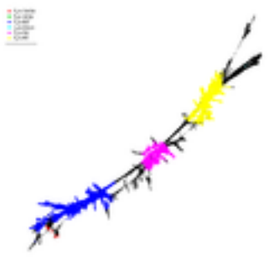
group	reads total	reads in clusters	reads in singlets
A1_155_	175474	123089 (70.1%)	52385 (29.9%)
A1_073_	175473	121860 (69.4%)	53613 (30.6%)
A1_097_	175474	126379 (72%)	49095 (28%)
A2_255_	180063	134153 (74.5%)	45910 (25.5%)
A2_034_	180063	131465 (73%)	48598 (27%)
A2_044_	180063	131191 (72.9%)	48872 (27.1%)
A2_099_	180063	127077 (70.6%)	52986 (29.4%)
D5_002_	92631	48683 (52.6%)	43948 (47.4%)
D5_031_	92631	45357 (49%)	47274 (51%)
D5_004_	92631	48557 (52.4%)	44074 (47.6%)
D5_053_	92631	43564 (47%)	49067 (53%)
A2_101_	180063	137231 (76.2%)	42832 (23.8%)
D5_ggg_	92631	44647 (48.2%)	47984 (51.8%)

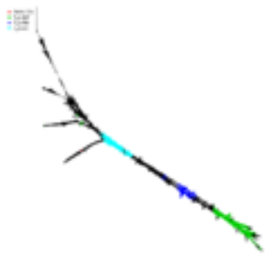
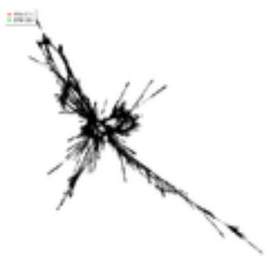
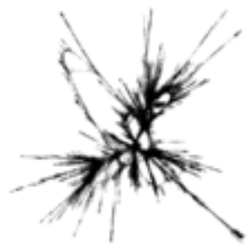
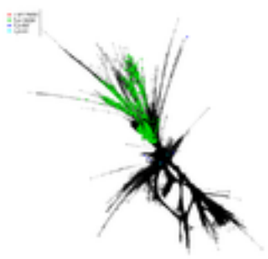
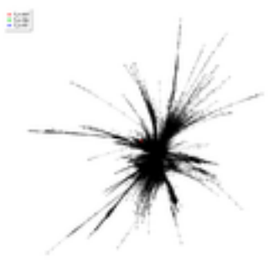
Top clusters

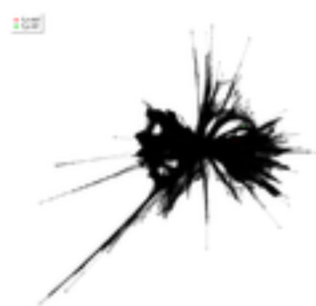
cluster	total length [bp]	number of reads	Genome proportion[%]	cumulative GP [%]	Repeat Masker	Protein domain hits	blastn hits	Repeat Masker custom library	Layout	group - nu
					Simple_repeat (241hits, 0.394%) Low_complexity (17hits, 0.0257%) LTR.ERV1 (3hits,	DTM-CD1 NA NA				

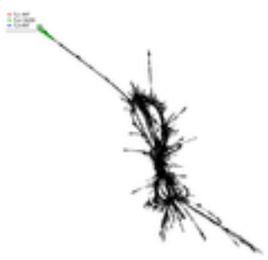
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_

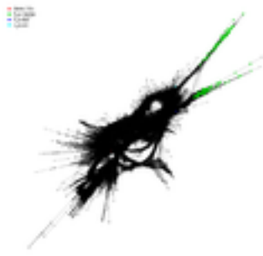
1	CL1	2655440 27952	1.480	1.5	0.00768%) LTR.Copia (4hits, 0.00584%) LTR.Ngaro (2hits, 0.00407%) LTR.Pao (2hits, 0.00346%) LTR.Gypsy (2hits.....	(1 hits 0.00358%) LINE-RT NA NA (1 hits 0.00358%)	Unspecified (**29498hits, 90.2%**)		A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
2	CL2	1847370 19446	1.030	2.5	LTR.Gypsy (212hits, 0.874%) Simple_repeat (400hits, 0.868%) Low_complexity (75hits, 0.177%) LTR.Copia (7hits, 0.0163%) Unknown (5hits, 0.0149%) DNA.CMC.EnSpm (1hits, 0.00374%) LINE.Penelope	Ty3-CHDII Ty3/gypsy chromovirus (45 hits 0.231%) Ty3-INT Ty3/gypsy chromovirus (40 hits 0.206%) Ty3-GAG Ty3/gypsy chromovirus (1 hits 0.00514%)	Unspecified (**20431hits, 99.8%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
3	CL3	1640840 17272	0.914	3.4	LTR.Gypsy (**14575hits, 78.6%**) Simple_repeat (8hits, 0.0196%) Low_complexity (2hits, 0.00542%) LTR.ERV1 (1hits, 0.00402%) LTR.ERVK (1hits, 0.00232%) LTR.Copia (1hits, 0.00219%)	Ty3-RH Ty3/gypsy chromovirus (5225 hits 30.3%) Ty3-RT Ty3/gypsy chromovirus (5218 hits 30.2%) Ty3-INT Ty3/gypsy chromovirus (86 hits 0.498%) DTA-CD1 NA NA (1 hits 0.00579%) PARA-RT NA NA (1 hits 0.00579%)	organelle/mitochondria (24 hits 0.139%) organelle/plastid (1 hits 0.00579%)	Unspecified (**17834hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
4	CL4	1599990 16842	0.891	4.3	LTR.Gypsy (**2969hits, 13.7%**) LTR.Copia (9hits, 0.0284%) Simple_repeat (12hits, 0.0179%) Low_complexity (5hits, 0.0125%) DNA.CMC.EnSpm (2hits, 0.00838%) LTR.ERV1 (2hits, 0.00563%) DNA.M.....	Ty3-PROT Ty3/gypsy chromovirus (663 hits 3.94%) Ty3-GAG Ty3/gypsy chromovirus (571 hits 3.39%) PARA-PROT NA NA (33 hits 0.196%) Ty3-RT Ty3/gypsy chromovirus (5 hits 0.0297%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.00594%)		Unspecified (**18214hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
					Simple_repeat (338hits, 0.74%) Low_complexity (70hits, 0.189%) LTR.Gypsy (47hits, 0.135%) LINE.I (1hits,	DHH-CD2 NA NA (1 hits 0.00609%) Ty3-INT Ty3/gypsy chromovirus (1 hits		Unspecified (**19586hits,**		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_

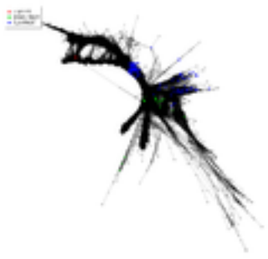
5	CL5	1560090 16422	0.869	5.2	0.00404%) LTR.Copia (1hits, 0.0034%) DNA.TcMar.ISRm11 (1hits, 0.0025%) DNA.CMC.EnSpm	0.00609%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.00609%)		**109%**)		group D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
6	CL6	1498055 15769	0.834	6.0	Simple_repeat (296hits, 0.83%) Low_complexity (27hits, 0.065%) DNA (8hits, 0.0267%) LTR.Gypsy (6hits, 0.0195%) DNA.CMC.Chapaev (4hits, 0.0116%) LTR.Copia (2hits, 0.00768%) LINE.R2.Hero (2hit.....			Unspecified (**17369hits, 91.7%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
7	CL7	1482285 15603	0.826	6.8	Simple_repeat (215hits, 0.573%) Low_complexity (72hits, 0.2%) LTR.Gypsy (45hits, 0.146%) LINE.L1 (3hits, 0.0101%) LINE.R2 (1hits, 0.00425%) LTR.Copia (1hits, 0.00405%) LTR.ERV1 (1hits, 0.00263%)	DTC-CD1 NA NA (1 hits 0.00641%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.00641%)		Unspecified (**14435hits, 74.3%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
8	CL8	1475255 15529	0.822	7.7	LTR.Gypsy (**11596hits, 68.4%**) LTR (4hits, 0.0201%) LTR.ERV1 (2hits, 0.00678%) LINE.Penelope (2hits, 0.0061%) LTR.Copia (2hits, 0.00502%) LINE.Jockey (1hits, 0.00359%) LTR.DIRS (1hits, ...	Ty3-INT Ty3/gypsy chromovirus (4303 hits 27.7%) Ty3-RT Ty3/gypsy chromovirus (3047 hits 19.6%) Ty3-RH Ty3/gypsy chromovirus (2183 hits 14.1%) Ty3-CHDII Ty3/gypsy chromovirus (26 hits 0.167%) Ty3-PROT	organelle/mitochondria (9 hits 0.058%)	Unspecified (**17026hits, 104%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
					LTR.Gypsy (**8525hits, 49.6%**) Simple_repeat (118hits, 0.357%) Low_complexity (16hits, 0.0437%)	Ty3-INT Ty3/gypsy Ogre/Tat (3228 hits 20.9%) Ty3-RT Ty3/gypsy Ogre/Tat (1728 hits 11.2%) Ty3-RH Ty3/gypsy	organelle/mitochondria	Unspecified		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_

9	CL9	1469745 15471	0.819	8.5	LTR.Pao (5hits, 0.0157%) LTR.Copia (3hits, 0.0115%) DNA.CMC.EnSpm (4hits, 0.011%) LTR.DIRS.....	Ogre/Tat (909 hits 5.88%) Ty3-RH Ty3/gypsy Athila (42 hits 0.271%) Ty3-RH Ty3/gypsy chromoviru.....	(74 hits 0.478%)	(**15995hits, 100%**)		D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
10	CL10	1447515 15237	0.806	9.3	Simple_repeat (352hits, 1.11%) Low_complexity (46hits, 0.135%) LTR.Gypsy (4hits, 0.0132%) LTR.Copia (3hits, 0.00912%) LTR.Gypsy. (1hits, 0.00615%) Satellite (2hits, 0.0049%) LTR.Caulimovirus.....	DTA-CD1 NA NA (2 hits 0.0131%) DTM-CD1 NA NA (1 hits 0.00656%)		Unspecified (**16600hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
11	CL11	1388520 14616	0.773	10.1	Simple_repeat (364hits, 1.14%) Low_complexity (26hits, 0.0812%) LINE.L2 (1hits, 0.00547%) DNA.Sola (1hits, 0.00519%) DNA.Academ (1hits, 0.00468%) LINE.L1 (1hits, 0.00382%) LTR.Gypsy (1hits, ...			Unspecified (**14666hits, 87.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
12	CL12	1379495 14521	0.768	10.8	LTR.Gypsy (**2496hits, 13%**) Simple_repeat (83hits, 0.192%) Low_complexity (39hits, 0.124%) LTR.Copia (2hits, 0.00522%) DNA.MULE.MuDR (1hits, 0.00486%) DNA.Sola (1hits, 0.00348%) DNA.PIF.....	Ty3-CHDII Ty3/gypsy chromovirus (1913 hits 13.2%) Ty3-INT Ty3/gypsy chromovirus (6 hits 0.0413%) LINE-ENDO NA NA (2 hits 0.0138%) Ty3-RT Ty3/gypsy chromovirus (2 hits 0.0138%)	45S_rDNA/25S_rDNA (1 hits 0.00689%)	Unspecified (**11340hits, 68.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
13	CL13	1368855 14409	0.762	11.6	LTR.Gypsy (107hits, 0.264%) Simple_repeat (78hits, 0.249%) LTR.Copia (24hits, 0.0598%) LTR (4hits, 0.00796%)	Ty3-INT Ty3/gypsy chromovirus (3 hits 0.0208%) Ty3-RT Ty3/gypsy chromovirus (2 hits	organelle/plastid (1 hits 0.00694%)	Unspecified (**18884hits,**		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_

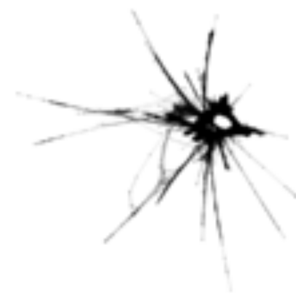
						LINE.L1 (1hits, 0.00365%) DNA.hAT.Charlie (1hits, 0.00234%) Low_complexity (1hits, 0.00226%)	0.0139%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.00694%)		**113%**)		D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
14	CL14	1322400	13920	0.737	12.3	Simple_repeat (384hits, 1.14%) Low_complexity (123hits, 0.407%) DNA.MULE.MuDR (2hits, 0.00817%) LTR.Gypsy (2hits, 0.00575%) DNA.PiggyBac (1hits, 0.00416%) DNA.hAT.Ac (1hits, 0.00378%) LTR.Pa......	Ty3-INT Ty3/gypsy chromovirus (1 hits 0.00718%)		Unspecified (**15593hits, 105%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
15	CL15	1224170	12886	0.682	13.0	Simple_repeat (61hits, 0.15%) LTR.Gypsy (4hits, 0.0172%) Low_complexity (3hits, 0.0089%)			Unspecified (**15044hits, 97.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
16	CL16	1195385	12583	0.666	13.7	Simple_repeat (125hits, 0.286%) Low_complexity (28hits, 0.0794%) LTR.Copia (5hits, 0.0234%) LTR.DIRS (4hits, 0.0157%) LINE.CR1 (3hits, 0.0131%) LTR.Gypsy (2hits, 0.0087%) LTR (2hits, 0.00653......	Ty3-INT Ty3/gypsy chromovirus (6 hits 0.0477%) Ty3-RT Ty3/gypsy chromovirus (1 hits 0.00795%)	45S_rDNA/18S_rDNA (1 hits 0.00795%)	Unspecified (**1845hits, 9.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
17	CL17	1186740	12492	0.661	14.3	LTR.Gypsy (**9879hits, 72.6%**) DNA.Maverick (1hits, 0.00708%) Simple_repeat (2hits,	Ty3-INT Ty3/gypsy chromovirus (8587 hits 68.7%) Ty3-CHDII Ty3/gypsy chromovirus (600 hits 4.8%)	organelle/mitochondria (2 hits 0.016%) organelle/plastid (2 hits 0.016%)	Unspecified (**12932hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_

						0.00573%)	DTC-CD1 NA NA (1 hits 0.00801%)		
18	CL18	1179140	12412	0.657	15.0	Simple_repeat (221hits, 0.504%) LTR.Gypsy (9hits, 0.0334%) DNA.hAT.Tip100 (5hits, 0.0198%) LINE.L2 (6hits, 0.0162%) DNA.CMC.EnSpm (3hits, 0.0151%) RC.Helitron (2hits, 0.00729%) DNA.CMC.Chapa.....		Unspecified (**7184hits, 48.4%**)	
19	CL19	1177145	12391	0.656	15.7	Simple_repeat (**1534hits, 6.47%**) Low_complexity (249hits, 1.13%) LTR.Gypsy (128hits, 0.89%) DNA.Crypton (18hits, 0.12%) LTR.Ngaro (2hits, 0.0101%) LTR.Pao (1hits, 0.00433%) LTR.ERVK (1.....	Ty3-CHDII Ty3/gypsy chromovirus (60 hits 0.484%) Ty1-INT Ty1/copia AleII (1 hits 0.00807%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.00807%)	Unspecified (**12915hits, 95.9%**)	
20	CL20	1171730	12334	0.653	16.3	Simple_repeat (64hits, 0.223%) LTR.Gypsy (22hits, 0.101%) Low_complexity (20hits, 0.072%) Satellite (4hits, 0.0153%) DNA.hAT.hATm (1hits, 0.00401%)	Ty3-INT Ty3/gypsy chromovirus (1 hits 0.00811%)	Unspecified (**13279hits, 103%**)	
						Simple_repeat (42hits, 0.113%) LTR.Gypsy (5hits, 0.0161%)			

21	CL21	1170780	12324	0.652	17.0	Low_complexity (3hits, 0.0108%) Satellite (1hits, 0.00478%) DNA.PIF.ISL2EU (1hits, 0.00427%) DNA.hAT.Tip100 (1hits, 0.00359%) RC.Hel.....			Unspecified (**11902hits, 89.7%**)	
22	CL22	1155010	12158	0.643	17.6	Simple_repeat (118hits, 0.409%) Low_complexity (18hits, 0.0662%) LTR.DIRS (1hits, 0.00606%) LINE.L1 (1hits, 0.00537%) LTR.Gypsy (1hits, 0.00372%) LINE.R1 (1hits, 0.00294%)	Ty1-RH Ty1/copia AleI/Retrofit (1 hits 0.00823%)		Unspecified (**13533hits, 102%**)	
23	CL23	1131070	11906	0.630	18.2	LTR.Gypsy (51hits, 0.163%) LINE.L1.Tx1 (21hits, 0.113%) Simple_repeat (15hits, 0.0387%) Low_complexity (3hits, 0.00955%) LINE.I (2hits, 0.00566%) LTR.ERV1 (1hits, 0.00451%) DNA.MULE.MuDR (1hits, 0.00371%)	Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0084%)		Unspecified (**14116hits, 105%**)	
24	CL24	1115300	11740	0.621	18.8	LTR.Gypsy (439hits, 2.91%) Simple_repeat (176hits, 0.483%) Low_complexity (11hits, 0.0335%) DNA.CMC.EnSpm (3hits, 0.0158%) RC.Helitron (1hits, 0.00726%) DNA.PIF.Harbinger (1hits, 0.00502%) D.....	Ty3-CHDII Ty3/gypsy chromovirus (205 hits 1.75%) DHH-CD1 NA NA (1 hits 0.00852%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.00852%) Ty3-RT Ty3/gypsy chromovirus (1 hits 0.00852%)	organelle/plastid (2 hits 0.017%)	Unspecified (**16379hits, 121%**)	
						Simple_repeat (57hits, 0.243%)			Unspecified	

25	CL25	1111120	11696	0.619	19.5	DNA.CMC.EnSpm (1hits, 0.00441%) DNA.P (1hits, 0.00441%)			Unspecified (**15677hits, 95.5%**)	
26	CL26	1067610	11238	0.595	20.1	Simple_repeat (**703hits, 4.16%**) LTR.Gypsy (**769hits, 3.81%**) Low_complexity (75hits, 0.383%) LTR.Copia (2hits, 0.00806%) LINE.L1 (2hits, 0.00796%) DNA.hAT.Ac. (1hits, 0.00674%) DN.....	DTH-CD1 NA NA (2 hits 0.0178%)		Unspecified (**11428hits, 93.4%**)	
27	CL27	1055640	11112	0.588	20.7	Simple_repeat (243hits, 1.05%) Low_complexity (65hits, 0.283%) LTR.Gypsy (4hits, 0.0158%) DNA.PIF.Harbinger (2hits, 0.0131%) DNA.Maverick (2hits, 0.00957%) DNA.hAT.Ac (1hits, 0.00673%) DNA.G.....	DHH-CD1 NA NA (2 hits 0.018%)	organelle/mitochondria (1 hits 0.009%)	Unspecified (**11917hits, 102%**)	
28	CL28	1043860	10988	0.581	21.2	LTR.Gypsy (**1811hits, 13.3%**) DNA.CMC.EnSpm (3hits, 0.0128%) DNA.hAT.Charlie (2hits, 0.00786%) Low_complexity (1hits, 0.00527%) DNA.Maverick (1hits, 0.0046%) Simple_repeat (1hits, 0.00249%)	Ty3-PROT Ty3/gypsy chromovirus (364 hits 3.31%) PARA-PROT NA NA (27 hits 0.246%) LINE-RT NA NA (1 hits 0.0091%)		Unspecified (**11879hits, 103%**)	
29	CL29	965675	10165	0.538	21.8	Simple_repeat (5hits, 0.0223%) LTR.Gypsy (2hits,			Unspecified (**13365hits,	

						0.0109%) LTR.ERV4 (2hits, 0.00787%)		**119%**)		D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
30	CL30	921975	9705	0.514	22.3	LTR.Gypsy (**8831hits, 83.8%**) Simple_repeat (12hits, 0.0478%) LTR.ERV1 (2hits, 0.00705%) DNA.MULE.MuDR (1hits, 0.00358%)	Ty3-INT Ty3/gypsy chromovirus (9594 hits 98.9%)	Unspecified (**9878hits, 99.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
31	CL31	921120	9696	0.513	22.8	Simple_repeat (84hits, 0.338%) LINE.L1 (1hits, 0.00499%) LINE.I (1hits, 0.00369%)		Unspecified (**475hits, 3.57%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
32	CL32	916940	9652	0.511	23.3	Simple_repeat (206hits, 1.07%) DNA.hAT.hATm (13hits, 0.0725%) LINE.L1 (10hits, 0.0652%) LTR.Gypsy (13hits, 0.0635%) DNA.CMC.EnSpm (11hits, 0.0592%) Low_complexity (13hits, 0.0581%) DNA.MULE.......		Unspecified (**1146hits, 7.76%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (89hits, 0.396%) LTR.Gypsy (2hits, 0.00951%)				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

33	CL33	904685	9523	0.504	23.8	Low_complexity (2hits, 0.00796%) DNA.CMC.EnSpm (1hits, 0.00586%) DNA.TcMar.Fot1 (1hits, 0.00486%) Satellite (1hits, 0.00122%)		Unspecified (**5142hits, 39.7%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
34	CL34	895470	9426	0.499	24.3	Simple_repeat (180hits, 0.839%) Low_complexity (9hits, 0.0389%) DNA.Maverick (3hits, 0.023%) LTR.Gypsy (3hits, 0.0153%) LTR.Pao (1hits, 0.00503%) LINE.L2 (1hits, 0.00447%) LTR.Copia (1hits, 0.00402%)	DTA-CD1 NA NA (1 hits 0.0106%)	Unspecified (**10833hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
35	CL35	823460	8668	0.459	24.8	Simple_repeat (97hits, 0.61%) Low_complexity (7hits, 0.034%) LTR.Gypsy (5hits, 0.0289%) LINE.CR1 (2hits, 0.0109%) LTR.Copia (1hits, 0.00887%) LTR.Pao (1hits, 0.00789%) LTR.ERV1 (1hits, 0.00546%)	Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0115%)	Unspecified (**8755hits, 86.7%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
36	CL36	822130	8654	0.458	25.2	LTR.Gypsy (146hits, 0.992%) Simple_repeat (54hits, 0.376%) LTR.ERVK (14hits, 0.046%) LTR.Copia (5hits, 0.0179%) Low_complexity (3hits, 0.0163%) SINE.MIR (1hits, 0.00851%) DNA.hAT.Tag1 (1hits......	Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0116%)	Unspecified (**10614hits, 104%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (167hits, 0.84%) Low_complexity (12hits, 0.0461%) DNA.hAT.hATm				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

37	CL37	820420	8636	0.457	25.7	(3hits, 0.0165%) LINE.L1 (2hits, 0.0149%) DNA (1hits, 0.0067%) LTR.Copia (1hits, 0.00585%) LTR.Ngaro (1hits, 0.00573%)			Unspecified (**9535hits, 98%**)	
38	CL38	807595	8501	0.450	26.1	Simple_repeat (261hits, 1.34%) Low_complexity (37hits, 0.197%) DNA (4hits, 0.0212%) LTR.Gypsy (2hits, 0.0163%) Satellite (1hits, 0.00644%) LINE.RTE.X (1hits, 0.00545%) DNA.CMC.Transib (1hits, 0.00446%)	LINE-RH NA NA (1 hits 0.0118%)		Unspecified (**9712hits, 106%**)	
39	CL39	783180	8244	0.436	26.6	Simple_repeat (509hits, 2.69%) Low_complexity (50hits, 0.247%) DNA.Maverick (22hits, 0.141%) LTR.Gypsy (8hits, 0.0501%) DNA.CMC.EnSpm (7hits, 0.0432%) LTR.Copia (1hits, 0.00562%)		organelle/plastid (1 hits 0.0121%)	Unspecified (**8679hits, 96.4%**)	
40	CL40	777385	8183	0.433	27.0	LTR.Gypsy (**5680hits, 64.2%**) Simple_repeat (2hits, 0.01%) DNA.Sola (1hits, 0.00527%)	Ty3-INT Ty3/gypsy chromovirus (5618 hits 68.7%)		Unspecified (**8703hits, 102%**)	
						LTR.Gypsy (**7396hits, 85.6%**)	Ty3-RT Ty3/gypsy			

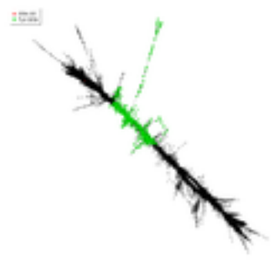
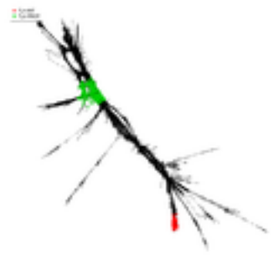
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

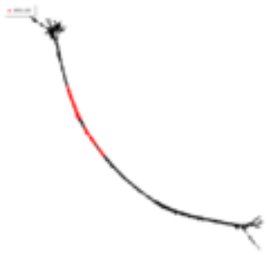
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

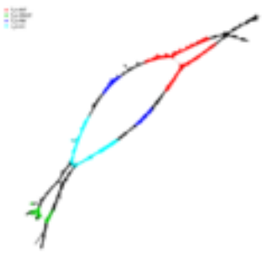
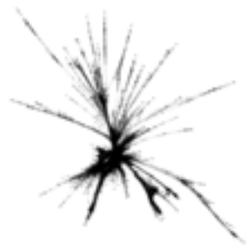
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

41	CL41	769215	8097	0.428	27.4	LTR (14hits, 0.152%) Simple_repeat (4hits, 0.0125%) LTR.ERV1 (1hits, 0.0104%) LTR.Caulimovirus (1hits, 0.00819%)	chromovirus (4570 hits 56.4%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.0124%)	organelle/mitochondria (5 hits 0.0618%)	Unspecified (**8277hits, 99.3%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
42	CL42	750975	7905	0.418	27.8	Simple_repeat (36hits, 0.243%) LINE.CR1 (4hits, 0.0336%) LINE.LOA (1hits, 0.00506%) LINE.I (1hits, 0.00426%)	Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0127%)		Unspecified (**8111hits, 72.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
43	CL43	733400	7720	0.408	28.3	LTR.Gypsy (**7715hits, 95.9%**)	Ty3-RT Ty3/gypsy chromovirus (5880 hits 76.2%)	organelle/mitochondria (130 hits 1.68%)	Unspecified (**7867hits, 99.2%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
44	CL44	724565	7627	0.404	28.7	LTR.Gypsy (**593hits, 5.67%**) LTR.Copia. (85hits, 0.524%) Simple_repeat (34hits, 0.19%) Low_complexity (2hits, 0.0106%) DNA.MULE.NOF (1hits, 0.00704%) LTR (1hits, 0.00511%)	Ty3-RH Ty3/gypsy chromovirus (1 hits 0.0131%) Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0131%)		Unspecified (**8508hits, 97.7%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Gypsy (**1327hits, 14.4%**) Simple_repeat (100hits, 0.547%) LTR.Copia (50hits,	Ty3-GAG Ty3/gypsy				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

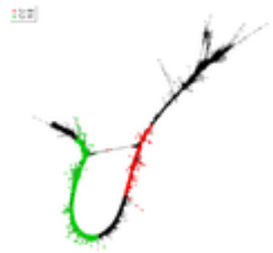
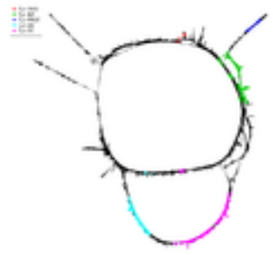
45	CL45	711075	7485	0.396	29.1	0.449%) Low_complexity (47hits, 0.326%) DNA.PiggyBac (1hits, 0.0101%) DNA.Maverick (1hits, 0.0097%) DNA.....	Athila (1745 hits 23.3%) DTH-CD1 NA NA (1 hits 0.0134%)		Unspecified (**7919hits, 101%**)		**group** A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
46	CL46	697585	7343	0.389	29.4	Simple_repeat (229hits, 1.44%) Low_complexity (30hits, 0.198%) LTR.Copia (4hits, 0.0404%) DNA.PIF.ISL2EU (2hits, 0.0142%) LTR.Gypsy (1hits, 0.00559%) DNA.hAT.Ac (1hits, 0.0043%)			Unspecified (**7777hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
47	CL47	690365	7267	0.385	29.8	LTR.Gypsy (**1572hits, 17.4%**) LTR.Copia (205hits, 1.71%) LTR.Copia. (11hits, 0.0895%) Simple_repeat (7hits, 0.0349%) Low_complexity (4hits, 0.0256%) LINE.CR1 (2hits, 0.0155%) LINE.L1.Tx.....	Ty3-PROT Ty3/gypsy Athila (1122 hits 15.4%) Ty3-INT Ty3/gypsy Athila (99 hits 1.36%) Ty3-PROT Ty3/gypsy Ogre/Tat (8 hits 0.11%)		Unspecified (**7633hits, 95.5%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
48	CL48	682005	7179	0.380	30.2	Simple_repeat (63hits, 0.395%) Low_complexity (12hits, 0.076%) LTR.Copia (2hits, 0.0136%) LINE.Rex.Babar (1hits, 0.0103%) LINE.L1 (1hits, 0.0085%) DNA.Zator (1hits, 0.00718%) LTR.ERV4 (1hits.....	Ty3-INT Ty3/gypsy chromovirus (2 hits 0.0279%)	organelle/plastid (2 hits 0.0279%)	Unspecified (**8436hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (99hits, 0.468%) Low_complexity (14hits, 0.0889%)					**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

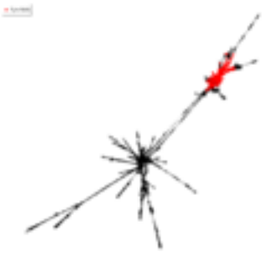
49	CL49	675830	7114	0.376	30.6	DNA.CMC.EnSpm (2hits, 0.0148%) DNA.Academ (2hits, 0.0107%) LINE.RTE.X (1hits, 0.00755%) DNA.hAT.Tip100 (1hits, 0.00681%)			Unspecified (**1229hits, 13.2%**)	
50	CL50	667185	7023	0.372	31.0	LTR.Gypsy (106hits, 0.943%) LTR.Copia (32hits, 0.149%) LTR.ERV1 (19hits, 0.136%) Simple_repeat (2hits, 0.00914%)	Ty3-GAG Ty3/gypsy chromovirus (931 hits 13.3%)		Unspecified (**7836hits, 105%**)	
51	CL51	648375	6825	0.361	31.3	DNA.CMC.EnSpm (**1433hits, 17.7%**) Simple_repeat (310hits, 2.8%) Low_complexity (65hits, 0.575%) LTR.Gypsy (4hits, 0.0355%)	DTC-CD1 NA NA (1121 hits 16.4%)		Unspecified (**7173hits, 101%**)	
52	CL52	629090	6622	0.350	31.7	Simple_repeat (128hits, 0.791%) Low_complexity (10hits, 0.0744%) LTR.Gypsy (5hits, 0.0412%) DNA.TcMar.Sagan (2hits, 0.0194%) LINE.L2 (2hits, 0.0105%)	DTM-CD1 NA NA (1 hits 0.0151%)	organelle/plastid (1 hits 0.0151%)	Unspecified (**4879hits, 61.1%**)	
						LTR.Gypsy (**3899hits, 53.2%**) LTR.Copia (129hits, 1.35%)	Ty3-INT Ty3/gypsy Athila (1409 hits 21.6%) Ty3-RT Ty3/gypsy Athila (872 hits			

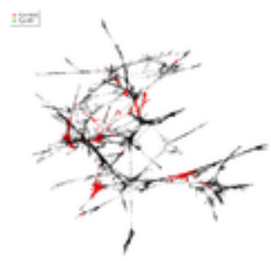
53	CL53	620445	6531	0.346	32.0	Simple_repeat (87hits, 0.673%) Low_complexity (14hits, 0.12%) LTR (2hits, 0.0142%) DNA.MULE.MuDR (1hits, 0.0113%) DNA.Dada (2hit.....	13.4%) Ty3-RH Ty3/gypsy Athila (440 hits 6.74%) Ty3-PROT Ty3/gypsy Athila (299 hits 4.58%) Ty3-RT Ty3/gypsy Ogre/Tat (4 hit.....	Unspecified (**6652hits, 99.6%**)	
54	CL54	615505	6479	0.343	32.4	Simple_repeat (145hits, 0.967%) DNA.CMC.EnSpm (4hits, 0.0336%) Low_complexity (2hits, 0.0146%) LTR.Gypsy (1hits, 0.0122%) LTR.Copia (2hits, 0.011%) Satellite (1hits, 0.00552%)	DTM-CD1 NA NA (1 hits 0.0154%)	Unspecified (**4468hits, 57%**)	
55	CL55	613510	6458	0.342	32.7	LTR.Gypsy (**329hits, 3.22%**) Simple_repeat (179hits, 1.42%) Low_complexity (65hits, 0.548%) DNA.MULE.NOF (1hits, 0.0126%) LINE.R2 (1hits, 0.0075%)		Unspecified (**5921hits, 82.9%**)	
56	CL56	594035	6253	0.331	33.0	Simple_repeat (69hits, 0.532%) LTR.Gypsy (8hits, 0.083%) Low_complexity (6hits, 0.0453%) DNA.CMC.EnSpm (2hits, 0.0131%) DNA.MULE.MuDR (1hits, 0.00471%)		Unspecified (**6941hits, 99.1%**)	
						Simple_repeat (23hits, 0.151%)			

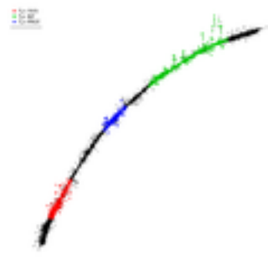
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

57	CL57	593275	6245	0.330	33.4	LINE.L1 (1hits, 0.0086%) LTR.Gypsy (1hits, 0.00843%) Low_complexity (1hits, 0.00725%)		Unspecified (**4738hits, 54.9%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
58	CL58	585675	6165	0.326	33.7	LTR.Gypsy (**4886hits, 72.2%**) LTR (2hits, 0.028%)	Ty3-RH Ty3/gypsy chromovirus (4195 hits 68%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0162%)	Unspecified (**6663hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
59	CL59	585105	6159	0.326	34.0	Simple_repeat (152hits, 0.917%) Low_complexity (10hits, 0.0766%) DNA.CMC.EnSpm (3hits, 0.0294%) LTR.Gypsy (3hits, 0.0258%) LINE.L2 (2hits, 0.0186%) DNA.hAT.Tag1 (1hits, 0.00906%) DNA.P (1hit......		Unspecified (**3808hits, 47.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
60	CL60	577695	6081	0.322	34.3	Simple_repeat (151hits, 0.891%) Low_complexity (38hits, 0.299%) DNA.CMC.EnSpm (2hits, 0.0121%) LINE.L1 (1hits, 0.00796%) LTR.ERV1 (1hits, 0.00623%)		Unspecified (**1294hits, 16.4%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Copia (**4205hits, 68.3%**)	Ty1-RT Ty1/copia Tork (1613 hits 28%) Ty1-RH Ty1/copia Tork (922 hits 16%)			**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

61	CL61	548245	5771	0.305	34.6	Simple_repeat (196hits, 1.28%) Low_complexity (143hits, 0.979%) LTR (1hits, 0.0117%) LTR.Gypsy (1hits, 0.00511%)	Ty1-RT Ty1/copia AleII (6 hits 0.104%) Ty1-RT Ty1/copia AleI/Retrofit (4 hits 0.0693%) Ty1-RT Ty1/copia Angela (1 hits 0.0173%)		Unspecified (**5994hits, 101%**)	
62	CL62	546345	5751	0.304	34.9	LTR.Copia (**2749hits, 43.1%**) Simple_repeat (77hits, 0.695%) Low_complexity (35hits, 0.319%) tRNA (9hits, 0.0835%) DNA.hAT.hATm (1hits, 0.00988%) LTR.Gypsy (1hits, 0.00915%) DNA.PiggyBac (1hits, 0.00732%)	Ty1-RT Ty1/copia Bianca (364 hits 6.33%) Ty1-INT Ty1/copia Bianca (334 hits 5.81%) Ty1-RH Ty1/copia Bianca (192 hits 3.34%) Ty1-PROT Ty1/copia Bianca (40 hits 0.696%) Ty1-GAG Ty1/copia Bianca (13 hits.....	organelle/plastid (10 hits 0.174%)	Unspecified (**5960hits, 101%**)	
63	CL63	533330	5614	0.297	35.2	Simple_repeat (24hits, 0.199%) Low_complexity (15hits, 0.142%) LTR.Gypsy (4hits, 0.0339%) LTR.Copia (1hits, 0.012%) LTR.Caulimovirus (1hits, 0.0118%) LINE.CR1 (1hits, 0.0109%) DNA.hAT.hAT5 (1hits, 0.00825%)			Unspecified (**3660hits, 48.9%**)	
64	CL64	523070	5506	0.291	35.5	Simple_repeat (142hits, 0.907%) Low_complexity (26hits, 0.208%) LTR.Gypsy (5hits, 0.0436%) DNA.Ginger (3hits, 0.0344%) LTR.ERV1 (4hits, 0.0315%) DNA.hAT.Tip100 (3hits, 0.0268%) LINE.L1 (1hit.....			Unspecified (**803hits, 10.6%**)	
						Simple_repeat				

65	CL65	520695	5481	0.290	35.8	(196hits, 1.84%) Low_complexity (12hits, 0.112%) LINE.L1 (1hits, 0.00826%)		Unspecified (**5568hits, 89.4%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
66	CL66	508440	5352	0.283	36.1	DNA.MULE.MuDR (121hits, 1.51%) Simple_repeat (141hits, 1.12%) Low_complexity (94hits, 0.937%) DNA.TcMar.Mariner (1hits, 0.0128%) LTR.Copia (1hits, 0.00649%)	Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0187%)	Unspecified (**3570hits, 55%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
67	CL67	507870	5346	0.283	36.4	LTR.Gypsy (**350hits, 5.05%**) Simple_repeat (222hits, 1.6%) Low_complexity (29hits, 0.237%) LINE.Proto1 (1hits, 0.0165%) LTR.Ngaro (2hits, 0.0163%) DNA.CMC.EnSpm (1hits, 0.00985%) LTR.Co.....	Ty3-GAG Ty3/gypsy Ogre/Tat (713 hits 13.3%)	Unspecified (**5780hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
68	CL68	504450	5310	0.281	36.7	LTR.Gypsy (**4303hits, 72.7%**) LTR.DIRS (4hits, 0.0391%) Simple_repeat (2hits, 0.0127%)	Ty3-INT Ty3/gypsy chromovirus (2670 hits 50.3%) Ty3-CHDII Ty3/gypsy chromovirus (78 hits 1.47%)	Unspecified (**5553hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Gypsy (181hits, 2.32%) Simple_repeat (136hits, 1.24%) LINE.L1 (5hits,				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

69	CL69	493430	5194	0.275	36.9	0.0726%) Low_complexity (5hits, 0.0521%) DNA (1hits, 0.0152%) LINE.L2 (1hits, 0.0146%) DNA.TcMar.Tc2 (1hits, 0.0142%.....		Unspecified (**4338hits, 63.2%**)		group A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
70	CL70	472910	4978	0.263	37.2	LTR.Gypsy (**927hits, 15%**) Simple_repeat (37hits, 0.366%) Low_complexity (25hits, 0.269%) LINE.Penelope (1hits, 0.0125%)	Ty3-CHDII Ty3/gypsy chromovirus (441 hits 8.86%) Ty3-CHDCR Ty3/gypsy chromovirus (1 hits 0.0201%)	Unspecified (**1826hits, 31.5%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
71	CL71	471675	4965	0.263	37.5	Simple_repeat (5hits, 0.0248%) LTR.Copia (1hits, 0.0104%) LTR (1hits, 0.00848%) LINE.L1.Tx1 (1hits, 0.00657%)		Unspecified (88hits, 0.931%)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
72	CL72	463030	4874	0.258	37.7	LTR.Gypsy (64hits, 0.791%) LTR.Copia (9hits, 0.102%) Simple_repeat (9hits, 0.0665%) LTR.ERV1 (3hits, 0.0337%) Low_complexity (3hits, 0.0222%) LTR.Pao (3hits, 0.0205%) LTR.ERVK (1hits, 0.013%.....	Ty3-GAG Ty3/gypsy chromovirus (434 hits 8.9%) Ty3-RT Ty3/gypsy chromovirus (2 hits 0.041%)	Unspecified (**5413hits, 103%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Copia (**4035hits, 79.3%**)	Ty1-INT Ty1/copia Tork (1122 hits 23.3%) Ty1-GAG Ty1/copia Tork (670 hits			group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

73	CL73	457425	4815	0.255	38.0	Simple_repeat (26hits, 0.172%) LTR.Gypsy (1hits, 0.0164%) Low_complexity (1hits, 0.0094%)	13.9%) Ty1-PROT Ty1/copia Tork (509 hits 10.6%) Ty1-INT Ty1/copia AleII (8 hits 0.166%) Ty1-INT Ty1/copia Ivana/Oryco (6 hits 0.125%)	organelle/mitochondria (2 hits 0.0415%)	Unspecified (**4892hits, 99.7%**)	
74	CL74	435860	4588	0.243	38.2	LTR.Gypsy (30hits, 0.412%) Simple_repeat (35hits, 0.318%) LTR.Pao (19hits, 0.156%) LTR.Copia (2hits, 0.0184%) DNA.hAT.hobo (1hits, 0.0142%)	Ty3-GAG Ty3/gypsy chromovirus (188 hits 4.1%)		Unspecified (**4722hits, 89%**)	
75	CL75	434340	4572	0.242	38.5	LTR.Gypsy (22hits, 0.247%) Simple_repeat (11hits, 0.0677%) LTR.ERVK (1hits, 0.012%)			Unspecified (**604hits, 8.18%**)	
76	CL76	426265	4487	0.237	38.7	LTR.Gypsy (**348hits, 6.13%**) Simple_repeat (134hits, 1.33%) Low_complexity (9hits, 0.088%) LTR.ERVK (2hits, 0.0251%) DNA.MULE.MuDR (1hits, 0.0106%)	Ty3-GAG Ty3/gypsy Ogre/Tat (253 hits 5.64%) Ty3-PROT Ty3/gypsy Ogre/Tat (155 hits 3.45%)		Unspecified (**4685hits, 99.2%**)	
						Simple_repeat (**277hits, 4.19%**) LTR.ERVK (124hits, 1.01%) LTR.Gypsy (5hits,			

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

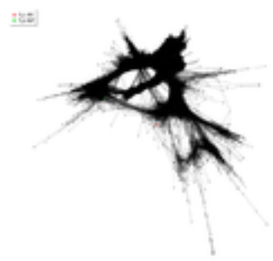
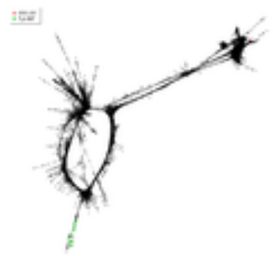
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

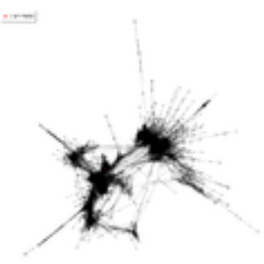
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

77	CL77	423035	4453	0.236	38.9	0.0392%) Unknown (2hits, 0.0156%) Low_complexity (1hits, 0.0125%) LTR.Copia (1hits, 0.0118%) DNA.PiggyBac (1hits, 0.00851%)		Unspecified (**6677hits, 118%**)		**group** A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
78	CL78	422655	4449	0.235	39.2	Simple_repeat (263hits, 2.4%) LTR.Gypsy (159hits, 1.95%) Low_complexity (55hits, 0.549%) LTR (10hits, 0.115%) LTR.Copia (1hits, 0.00828%) DNA (1hits, 0.00757%)		Unspecified (**4611hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
79	CL79	420755	4429	0.234	39.4	Simple_repeat (109hits, 1.2%) Low_complexity (6hits, 0.0675%) DNA (2hits, 0.0333%)		Unspecified (**4993hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
80	CL80	416385	4383	0.232	39.6	Simple_repeat (181hits, 2.09%) LTR.Gypsy (20hits, 0.364%) Low_complexity (6hits, 0.062%) DNA.hAT.Tag1 (4hits, 0.0394%) LTR.Copia (1hits, 0.0142%) DNA.CMC.EnSpm (1hits, 0.0113%) DNA.hAT.Charlie (1hits, 0.00985%)	Ty3-CHDCR Ty3/gypsy chromovirus (23 hits 0.525%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0228%)	Unspecified (**4421hits, 85%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

81	CL81	410020	4316	0.228	39.9	Simple_repeat (6hits, 0.0549%) LTR.Copia (1hits, 0.019%)		Unspecified (**5129hits, 98.9%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
82	CL82	404700	4260	0.225	40.1	Simple_repeat (270hits, 2.56%) LTR.Gypsy (258hits, 2.28%) Low_complexity (96hits, 1.19%) RC.Helitron (1hits, 0.0163%) DNA (1hits, 0.0119%) LTR.Copia (1hits, 0.00741%)	Ty1-RT Ty1/copia Ivana/Oryco (1 hits 0.0235%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0235%)	Unspecified (**5518hits, 108%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
83	CL83	401090	4222	0.223	40.3	Simple_repeat (37hits, 0.412%) LTR.Gypsy (7hits, 0.128%) LTR.ERV1 (2hits, 0.0254%) LTR.Pao (1hits, 0.00798%)	Ty3-GAG Ty3/gypsy chromovirus (416 hits 9.85%)	Unspecified (**4804hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
84	CL84	385225	4055	0.215	40.5	LTR.Gypsy (69hits, 1.25%) Simple_repeat (44hits, 0.492%) Low_complexity (16hits, 0.194%) LINE.L1 (3hits, 0.0395%) DNA.hAT.hATm (1hits, 0.0195%) DNA.TcMar.Fot1 (1hits, 0.0169%) LTR.Copia (1hi.....	Ty3-INT Ty3/gypsy Ogre/Tat (14 hits 0.345%) DTC-CD1 NA NA (1 hits 0.0247%)	Unspecified (**4160hits, 94.2%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Copia (**1000hits, 21.2%**)				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

85	CL85	374965	3947	0.209	40.7	Simple_repeat (146hits, 1.78%) Low_complexity (8hits, 0.0744%) LTR.Gypsy (3hits, 0.0347%)	Ty1-RH Ty1/copia Angela (107 hits 2.71%)		Unspecified (**4061hits, 100%**)	
86	CL86	373160	3928	0.208	41.0	Simple_repeat (14hits, 0.126%) LTR.Gypsy (1hits, 0.015%) Low_complexity (1hits, 0.0107%)			Unspecified (**3222hits, 61.2%**)	
87	CL87	371735	3913	0.207	41.2	Simple_repeat (**214hits, 3.15%**) Low_complexity (45hits, 0.759%) LTR.Gypsy (2hits, 0.0288%) LTR.Caulimovirus (1hits, 0.0161%) DNA.MULE.MuDR (1hits, 0.0153%) LTR.Copia (1hits, 0.0145%) D.....	organelle/mitochondria (2 hits 0.0511%)		Unspecified (**4073hits, 101%**)	
88	CL88	368695	3881	0.205	41.4	Simple_repeat (3hits, 0.0404%) LTR.Copia (1hits, 0.0171%) LTR.Gypsy (1hits, 0.0146%) DNA.CMC.EnSpm (1hits, 0.00976%) LINE.L1 (1hits, 0.00976%)	LINE-ENDO NA NA (1 hits 0.0258%)		Unspecified (**4253hits, 105%**)	
						Simple_repeat (15hits, 0.109%) LINE.RTE.X (1hits,				

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

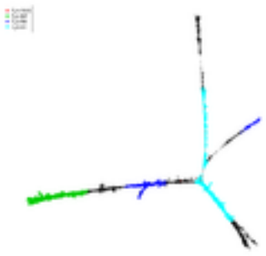
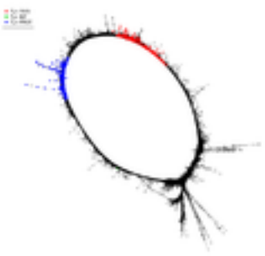
89	CL89	353305	3719	0.197	41.6	0.0147%) LTR.ERV1 (1hits, 0.0108%) Low_complexity (1hits, 0.0105%) LINE.CR1 (1hits, 0.0105%)		Unspecified (**3808hits, 90.7%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

90	CL90	333355	3509	0.186	41.7	Simple_repeat (30hits, 0.31%) Low_complexity (5hits, 0.0594%) LTR.Gypsy (1hits, 0.0138%)	organelle/plastid (7094 hits 202%) organelle/mitochondria (1 hits 0.0285%)	Unspecified (**3526hits, 99%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

91	CL91	328225	3455	0.183	41.9	Simple_repeat (144hits, 1.79%) LTR.Copia (61hits, 1.44%) Low_complexity (62hits, 0.841%) LTR.Pao (1hits, 0.0253%) RC.Helitron (1hits, 0.0149%) DNA.P (1hits, 0.0107%)	Ty1-RH Ty1/copia Angela (47 hits 1.36%) Ty1-RH Ty1/copia Tork (11 hits 0.318%) Ty1-RH Ty1/copia Ivana/Oryco (3 hits 0.0868%)	Unspecified (**3610hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

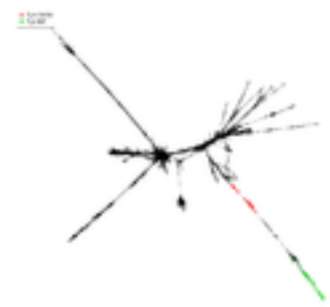
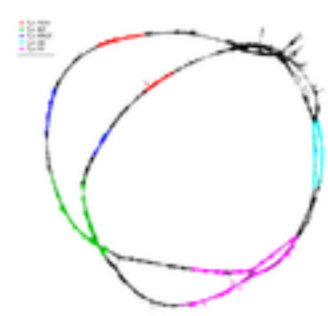
92	CL92	326515	3437	0.182	42.1	Simple_repeat (64hits, 0.912%) Low_complexity (40hits, 0.664%) DNA.PIF.ISL2EU (1hits, 0.0168%) LTR.Copia (1hits, 0.0138%) DNA.hAT.Charlie (1hits, 0.00949%)		Unspecified (**2185hits, 50.4%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

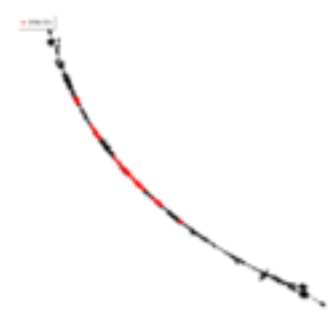
						Simple_repeat (99hits, 1.39%)				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

93	CL93	315115	3317	0.176	42.3	Low_complexity (9hits, 0.112%) LTR.Gypsy (2hits, 0.0333%) DNA.TcMar.Tc1 (1hits, 0.0216%)	Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0301%)		Unspecified (**3457hits, 101%**)	
94	CL94	311980	3284	0.174	42.5	Simple_repeat (110hits, 1.2%) Low_complexity (49hits, 0.646%) LTR.Gypsy (13hits, 0.168%)			Unspecified (**842hits, 17.3%**)	
95	CL95	307610	3238	0.171	42.6	LTR.Gypsy (**2497hits, 70.8%**) Simple_repeat (1hits, 0.0218%) LINE.L2 (1hits, 0.0205%)	Ty3-INT Ty3/gypsy Athila (776 hits 24%) Ty3-RT Ty3/gypsy Athila (741 hits 22.9%) Ty3-RH Ty3/gypsy Athila (333 hits 10.3%) Ty3-GAG Ty3/gypsy chromovirus (1 hits 0.0309%)	organelle/mitochondria (1 hits 0.0309%)	Unspecified (**3324hits, 99.1%**)	
96	CL96	305805	3219	0.170	42.8	LTR.Copia (**447hits, 9.88%**) Simple_repeat (29hits, 0.355%) Low_complexity (22hits, 0.341%) LTR.ERV1 (3hits, 0.0497%) DNA.MULE.MuDR (1hits, 0.00948%)	Ty1-GAG Ty1/copia Tork (298 hits 9.26%) Ty1-PROT Ty1/copia Tork (274 hits 8.51%) Ty1-INT Ty1/copia Tork (1 hits 0.0311%) Ty1-PROT Ty1/copia Ivana/Oryco (1 hits 0.0311%) Ty1-PROT Ty1/copia TAR (1 hits 0.0311%)		Unspecified (**3371hits, 101%**)	
						LTR.Copia (**210hits,**				

97	CL97	295260	3108	0.164	43.0	**5.18%**) LTR.Gypsy (46hits, 0.894%) Simple_repeat (1hits, 0.00813%)		organelle/plastid (6338 hits 204%)	Unspecified (**3123hits, 98.9%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
98	CL98	294025	3095	0.164	43.1	LTR.Copia (102hits, 2.63%) Simple_repeat (12hits, 0.179%)		organelle/plastid (3077 hits 99.4%)	Unspecified (**224hits, 4%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
99	CL99	284240	2992	0.158	43.3	Simple_repeat (129hits, 1.94%) Low_complexity (7hits, 0.14%)		organelle/plastid (3015 hits 101%)	Unspecified (**837hits, 22.8%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
100	CL100	282720	2976	0.157	43.4	LTR.Gypsy (9hits, 0.243%) Simple_repeat (10hits, 0.152%) Low_complexity (4hits, 0.0612%) DNA.MULE.MuDR (1hits, 0.018%)			Unspecified (**3108hits, 98.5%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Copia (**1772hits, 54%**) Simple_repeat	Ty1-RT Ty1/copia Angela (147 hits 4.96%) Ty1-RH Ty1/copia Angela (67 hits				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

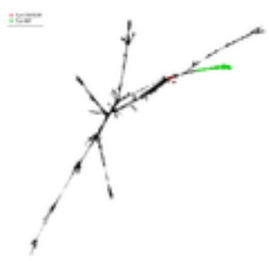
101	CL101	281295	2961	0.157	43.6	(38hits, 0.496%) Low_complexity (21hits, 0.289%) LTR.Gypsy (2hits, 0.0324%) DNA.Dada (1hits, 0.0167%)	2.26%) Ty1-INT Ty1/copia Angela (18 hits 0.608%) Ty1-GAG Ty1/copia Angela (17 hits 0.574%) Ty1-RT Ty1/copia AleII (17 hits 0.5.....	Unspecified (**3089hits, 101%**)	
102	CL102	278255	2929	0.155	43.8	Simple_repeat (17hits, 0.19%)	organelle/plastid (2992 hits 102%)	Unspecified (**1329hits, 38.4%**)	
103	CL103	273980	2884	0.153	43.9	LTR.Copia (**215hits, 6.67%**) rRNA (**137hits, 3.48%**) Simple_repeat (18hits, 0.204%) Low_complexity (17hits, 0.192%)	organelle/plastid (5753 hits 199%) organelle/mitochondria (3 hits 0.104%)	Unspecified (**2236hits, 65%**)	
104	CL104	270085	2843	0.150	44.1	LTR.Gypsy (58hits, 1.26%) Simple_repeat (44hits, 0.693%) Low_complexity (18hits, 0.273%) LTR.ERV4 (1hits, 0.0167%) LTR (1hits, 0.0118%)		Unspecified (**2948hits, 100%**)	
						Simple_repeat (158hits, 2.63%) Low_complexity			

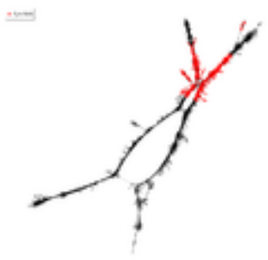
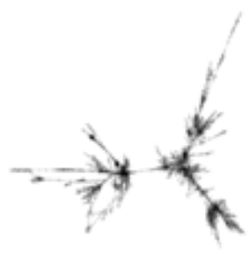
105	CL105	266950	2810	0.149	44.2	(9hits, 0.142%) LTR.Gypsy (8hits, 0.139%) LTR.Copia (9hits, 0.131%) LTR.Pao (7hits, 0.111%)	Ty3-RT Ty3/gypsy chromovirus (1 hits 0.0356%)		Unspecified (**3389hits, 105%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
106	CL106	265335	2793	0.148	44.4	Simple_repeat (**206hits, 4.3%**) Low_complexity (108hits, 2.23%) LTR.Gypsy (62hits, 1.84%) LTR.Copia (2hits, 0.0411%) rRNA (2hits, 0.0268%) DNA.PIF.Harbinger (1hits, 0.0132%)	Ty3-INT Ty3/gypsy chromovirus (28 hits 1%) Ty3-CHDII Ty3/gypsy chromovirus (14 hits 0.501%)	45S_rDNA/25S_rDNA (1 hits 0.0358%)	Unspecified (**2795hits, 91.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
107	CL107	264385	2783	0.147	44.5	Simple_repeat (44hits, 0.421%) DNA.PIF.ISL2EU (3hits, 0.042%) DNA.CMC.EnSpm (2hits, 0.0314%) LTR.Gypsy (1hits, 0.0238%) DNA (1hits, 0.0212%) Low_complexity (1hits, 0.0151%) DNA.Ginger (1hits, 0.0144%)			Unspecified (**181hits, 4.11%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
108	CL108	264195	2781	0.147	44.7	LTR.Copia (**1882hits, 61.4%**) LINE.L1 (7hits, 0.116%) Simple_repeat (8hits, 0.106%) LTR.ERV1 (1hits, 0.0257%) LTR.Pao (1hits, 0.0132%)	Ty1-RT Ty1/copia Tork (379 hits 13.6%) Ty1-INT Ty1/copia Tork (258 hits 9.28%) Ty1-RH Ty1/copia Tork (211 hits 7.59%) Ty1-GAG Ty1/copia Tork (157 hits 5.65%) Ty1-PROT Ty1/copia Tork (110 hits 3.96%)		Unspecified (**2958hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
								45S_rDNA/18S_rDNA			**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

109	CL109	264100	2780	0.147	44.8	rRNA (**2224hits, 75.8%**)	DTM-CD1 NA NA (15 hits 0.54%)	(1750 hits 62.9%) 45S_rDNA/25S_rDNA (323 hits 11.6%) 45S_rDNA/5.8S_rDNA (209 hits 7.52%)	Unspecified (**2794hits, 99.1%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
110	CL110	260585	2743	0.145	44.9	DNA.MULE.MuDR (36hits, 1.07%) LTR.Copia (16hits, 0.407%) Simple_repeat (19hits, 0.281%)		organelle/plastid (2735 hits 99.7%)	Unspecified (**721hits, 19.5%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
111	CL111	256215	2697	0.143	45.1	DNA.MULE.MuDR (65hits, 1.52%) Simple_repeat (23hits, 0.441%) Low_complexity (7hits, 0.144%) DNA (1hits, 0.0293%) DNA.CMC.Transib (1hits, 0.0141%) LTR.Gypsy (1hits, 0.0121%) LINE.L1 (1hits, 0.0113%)	DTM-CD1 NA NA (464 hits 17.2%)		Unspecified (**2755hits, 99.9%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
112	CL112	254505	2679	0.142	45.2	Simple_repeat (59hits, 1.05%) Low_complexity (3hits, 0.0519%) LTR.Gypsy (1hits, 0.0157%)			Unspecified (**1897hits, 59%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						rRNA (98hits, 2.63%)					**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

113	CL113	253935	2673	0.141	45.4	Simple_repeat (84hits, 1.48%) Low_complexity (4hits, 0.0894%) SINE.tRNA.Deu.L2 (1hits, 0.0264%)	organelle/plastid (4754 hits 178%) organelle/mitochondria (57 hits 2.13%)	Unspecified (**1742hits, 50.7%**)	
114	CL114	250420	2636	0.139	45.5	LTR.Gypsy (86hits, 1.21%) Simple_repeat (2hits, 0.0343%)	organelle/plastid (5009 hits 190%) organelle/mitochondria (1 hits 0.0379%)	Unspecified (**2200hits, 73.8%**)	
115	CL115	244340	2572	0.136	45.6	Simple_repeat (**177hits, 5.11%**) Low_complexity (3hits, 0.0536%) LTR.Copia (1hits, 0.034%)		Unspecified (54hits, 1.54%)	
116	CL116	243770	2566	0.136	45.8	Satellite (**1168hits, 34.9%**) Low_complexity (6hits, 0.122%) Simple_repeat (6hits, 0.064%) LTR (2hits, 0.041%)	5S_rDNA/5S_rDNA (1162 hits 45.3%)	Unspecified (**2849hits, 106%**)	
						rRNA (**1299hits,**			

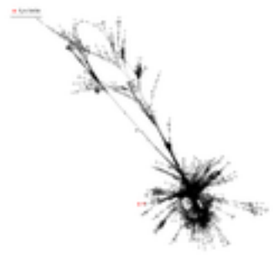
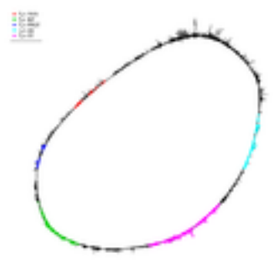
						48.5%)				
117	CL117	240635	2533	0.134	45.9	Low_complexity (35hits, 0.495%) Simple_repeat (33hits, 0.466%)		45S_rDNA/18S_rDNA (1224 hits 48.3%) organelle/mitochondria (66 hits 2.61%)	Unspecified (**2539hits, 98.8%**)	
118	CL118	232370	2446	0.129	46.0	LTR.Gypsy (**131hits, 4.04%**) Simple_repeat (94hits, 1.91%) Low_complexity (40hits, 0.905%)	Ty3-GAG Ty3/gypsy Athila (109 hits 4.46%) Ty3-GAG Ty3/gypsy Ogre/Tat (1 hits 0.0409%)		Unspecified (**2600hits, 101%**)	
119	CL119	228760	2408	0.127	46.2	rRNA (93hits, 2.93%) Simple_repeat (26hits, 0.323%)	Ty1-RT Ty1/copia Ivana/Oryco (1 hits 0.0415%)	45S_rDNA/25S_rDNA (83 hits 3.45%)	Unspecified (**2437hits, 88.4%**)	
120	CL120	226575	2385	0.126	46.3	DNA.hAT.Ac (57hits, 2.27%) Simple_repeat (13hits, 0.145%) Low_complexity (10hits, 0.12%)		organelle/plastid (2340 hits 98.1%)	Unspecified (**525hits, 17.8%**)	

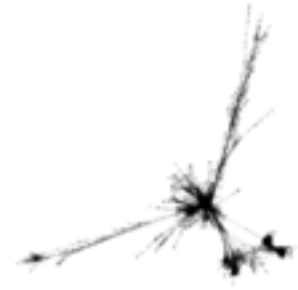
121	CL121	225720	2376	0.126	46.4	Simple_repeat (34hits, 0.679%) Low_complexity (11hits, 0.214%)		Unspecified (**999hits, 34.1%**)	
122	CL122	225625	2375	0.126	46.5	Simple_repeat (72hits, 1.28%)	organelle/plastid (2291 hits 96.5%)	Unspecified (**751hits, 24.6%**)	
123	CL123	225625	2375	0.126	46.7	Simple_repeat (32hits, 0.501%) Low_complexity (21hits, 0.323%) LTR.Gypsy (7hits, 0.225%) DNA.CMC.Transib (2hits, 0.0293%)	DTA-CD1 NA NA (1 hits 0.0421%)	Unspecified (**2888hits, 110%**)	
124	CL124	224960	2368	0.125	46.8	LTR.Gypsy (**183hits, 6.69%**) Simple_repeat (78hits, 1.68%) Low_complexity (26hits, 0.583%) LINE.LOA (1hits, 0.0333%) DNA.Maverick (1hits, 0.0249%) DNA.hAT.Tip100 (1hits, 0.0156%) LINE.R.....	Ty3-INT Ty3/gypsy chromovirus (134 hits 5.66%) Ty3-CHDCR Ty3/gypsy chromovirus (12 hits 0.507%)	Unspecified (**2472hits, 101%**)	
						LTR.Copia (24hits,			

125	CL125	223060	2348	0.124	46.9	0.517%) Simple_repeat (22hits, 0.504%) Low_complexity (7hits, 0.221%)		organelle/plastid (2255 hits 96%) organelle/mitochondria (14 hits 0.596%)	Unspecified (**740hits, 25%**)	
126	CL126	210900	2220	0.117	47.0	LTR.Gypsy (**235hits, 8.43%**) LTR.Copia (4hits, 0.138%) LINE.I (2hits, 0.0431%) DNA.PIF.Harbinger (1hits, 0.0213%) Simple_repeat (1hits, 0.0199%) LINE.L2 (1hits, 0.019%)	Ty3-GAG Ty3/gypsy Athila (534 hits 24.1%) Ty3-GAG Ty3/gypsy Ogre/Tat (1 hits 0.045%)		Unspecified (**2246hits, 99.2%**)	
127	CL127	209665	2207	0.117	47.2	Simple_repeat (**200hits, 4.35%**) LTR.Copia (50hits, 1.79%) Low_complexity (38hits, 0.768%) LTR.Gypsy (7hits, 0.205%) LTR.Copia. (2hits, 0.0525%)			Unspecified (**2327hits, 102%**)	
128	CL128	205580	2164	0.115	47.3	Simple_repeat (41hits, 0.944%) Low_complexity (5hits, 0.105%) LTR.Gypsy (2hits, 0.0457%) LINE.Tad1 (1hits, 0.0316%) DNA.hAT.hATx (1hits, 0.0224%)			Unspecified (**2363hits, 104%**)	
						Simple_repeat (**154hits, 4.18%**)				

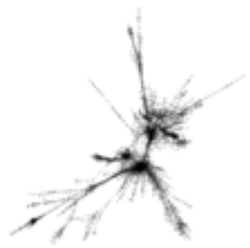
129	CL129	204345	2151	0.114	47.4	Low_complexity (2hits, 0.0548%) LINE.L2 (1hits, 0.045%) DNA.Ginger (2hits, 0.0391%)		Unspecified (**116hits, 3.35%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
130	CL130	204155	2149	0.114	47.5		organelle/plastid (4295 hits 200%) organelle/mitochondria (1 hits 0.0465%)	Unspecified (**1494hits, 59%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
131	CL131	203110	2138	0.113	47.6	Simple_repeat (85hits, 1.17%) LTR.Gypsy (14hits, 0.42%) Low_complexity (1hits, 0.0177%)	organelle/plastid (2106 hits 98.5%) organelle/mitochondria (5 hits 0.234%)	Unspecified (**810hits, 27.8%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
132	CL132	202065	2127	0.113	47.7	Simple_repeat (60hits, 1.2%) Low_complexity (55hits, 1.04%) LTR.Gypsy (1hits, 0.0247%) LTR.ERV1 (1hits, 0.0247%)	organelle/plastid (2041 hits 96%)	Unspecified (**748hits, 29.4%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						DNA.PIF.Harbinger (**193hits, 7.66%**) Simple_repeat				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

133	CL133	201305	2119	0.112	47.8	(**193hits, 5.21%**) Low_complexity (7hits, 0.138%) LTR.Pao (1hits, 0.0313%) DNA.CMC.EnSpm (1hits, 0.0184%)	DTH-CD1 NA NA (322 hits 15.2%)	Unspecified (**2228hits, 101%**)		group A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
134	CL134	196460	2068	0.109	47.9	DNA.CMC.EnSpm (66hits, 1.7%) Simple_repeat (1hits, 0.0107%)	organelle/plastid (4133 hits 200%)	Unspecified (**1720hits, 73.4%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
135	CL135	194845	2051	0.109	48.1	Simple_repeat (28hits, 0.504%) Low_complexity (5hits, 0.135%) DNA.hAT.hAT1 (3hits, 0.077%) DNA.CMC.EnSpm (1hits, 0.0298%) LTR.Gypsy (1hits, 0.0257%)	organelle/plastid (2 hits 0.0975%)	Unspecified (**422hits, 15.4%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
136	CL136	194465	2047	0.108	48.2	DNA.CMC.EnSpm (48hits, 2.05%) Simple_repeat (34hits, 0.454%) SINE.tRNA (5hits, 0.197%)	organelle/plastid (2025 hits 98.9%)	Unspecified (**259hits, 7.94%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (**376hits, 9.23%**) Low_complexity				group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

137	CL137	191900	2020	0.107	48.3	(38hits, 1.01%) LTR.Gypsy (8hits, 0.315%) Satellite (3hits, 0.0829%) LTR.Copia (1hits, 0.0266%)	Ty3-CHDII Ty3/gypsy chromovirus (2 hits 0.099%)		Unspecified (**2336hits, 107%**)	
138	CL138	191615	2017	0.107	48.4	LTR.Copia (**994hits, 44.2%**) Simple_repeat (11hits, 0.182%) LTR.ERV1 (6hits, 0.152%) LTR.ERVK (4hits, 0.0626%) Low_complexity (1hits, 0.0292%) LTR.Gypsy (1hits, 0.0177%)	Ty1-RT Ty1/copia TAR (218 hits 10.8%) Ty1-INT Ty1/copia TAR (121 hits 6%) Ty1-RH Ty1/copia TAR (68 hits 3.37%) Ty1-GAG Ty1/copia TAR (34 hits 1.69%) Ty1-PROT Ty1/copia TAR (25 hits 1.24%) Ty1-RH	organelle/mitochondria (10 hits 0.496%)	Unspecified (**2075hits, 100%**)	
139	CL139	191140	2012	0.106	48.5	Simple_repeat (12hits, 0.207%) Low_complexity (1hits, 0.0173%)		contamination (2023 hits 101%)		
140	CL140	188955	1989	0.105	48.6	DNA.MULE.MuDR (37hits, 0.587%) Simple_repeat (21hits, 0.555%) Low_complexity (5hits, 0.156%)		organelle/plastid (1969 hits 99%)	Unspecified (**752hits, 29.2%**)	
						Simple_repeat (5hits, 0.071%)				

141	CL141	187340	1972	0.104	48.7	LTR.Copia (3hits, 0.0587%) DNA.CMC.EnSpm (1hits, 0.0422%) LTR.Gypsy (1hits, 0.0208%)		Unspecified (**2100hits, 103%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
142	CL142	185250	1950	0.103	48.8	Simple_repeat (**304hits, 7.83%**) Low_complexity (45hits, 1.09%) LTR.Copia (10hits, 0.332%) DNA (2hits, 0.0691%) DNA.hAT.hATx (1hits, 0.0302%)	organelle/plastid (1 hits 0.0513%)	Unspecified (**2138hits, 104%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
143	CL143	184395	1941	0.103	48.9	Simple_repeat (77hits, 2.22%) Low_complexity (30hits, 0.975%)	organelle/plastid (1828 hits 94.2%)	Unspecified (**688hits, 28.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
144	CL144	177745	1871	0.099	49.0	Simple_repeat (64hits, 1.26%) DNA.Maverick (12hits, 0.519%) Low_complexity (10hits, 0.275%)	organelle/plastid (1825 hits 97.5%)	Unspecified (**182hits, 5.02%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

145	CL145	176890	1862	0.099	49.1	Simple_repeat (1hits, 0.00961%)	organelle/plastid (1864 hits 100%)	Unspecified (**442hits, 18%**)	
146	CL146	175655	1849	0.098	49.2	Simple_repeat (77hits, 1.73%) Low_complexity (27hits, 0.682%)	organelle/plastid (1780 hits 96.3%) organelle/mitochondria (11 hits 0.595%)	Unspecified (**868hits, 30.4%**)	
147	CL147	167200	1760	0.093	49.3	rRNA (**1001hits, 55.5%**) Simple_repeat (2hits, 0.0449%) DNA.CMC.EnSpm (2hits, 0.0383%) LTR.ERV1 (1hits, 0.0275%) Low_complexity (1hits, 0.0209%)	45S_rDNA/25S_rDNA (978 hits 55.6%)	Unspecified (**1827hits, 101%**)	
148	CL148	165870	1746	0.092	49.4	Simple_repeat (76hits, 2.2%) Low_complexity (1hits, 0.0163%)	organelle/plastid (3484 hits 200%)	Unspecified (**1752hits, 98.8%**)	

149	CL149	164255	1729	0.091	49.5	Simple_repeat (33hits, 0.897%) Low_complexity (20hits, 0.626%)	organelle/plastid (1679 hits 97.1%) organelle/mitochondria (20 hits 1.16%)	Unspecified (**273hits, 11%**)		group A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
150	CL150	163780	1724	0.091	49.6	LTR.Gypsy (5hits, 0.149%) Simple_repeat (5hits, 0.0959%) Low_complexity (3hits, 0.0733%) SINE.tRNA (1hits, 0.0348%) LINE.L2 (1hits, 0.0232%)		Unspecified (**2078hits, 111%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
151	CL151	161405	1699	0.090	49.7	Simple_repeat (101hits, 2.99%) Low_complexity (5hits, 0.126%)	organelle/plastid (1633 hits 96.1%)	Unspecified (**231hits, 8.12%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
152	CL152	158270	1666	0.088	49.7	rRNA (**1649hits, 97.4%**) Simple_repeat (42hits, 1.61%)	45S_rDNA/25S_rDNA (1621 hits 97.3%)	Unspecified (**1667hits, 98.9%**)		group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_

153	CL153	157510	1658	0.088	49.8	tRNA (13hits, 0.583%) Low_complexity (16hits, 0.514%) LTR.Gypsy (9hits, 0.2%)	organelle/plastid (1601 hits 96.6%)	Unspecified (**474hits, 17.5%**)		**group** A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
154	CL154	154755	1629	0.086	49.9	Simple_repeat (**156hits, 5%**) LTR.Copia (22hits, 1.11%) Low_complexity (24hits, 0.657%) LTR.Gypsy (7hits, 0.292%) DNA.MULE.MuDR (1hits, 0.0582%) LTR.ERV1 (1hits, 0.0362%)		Unspecified (**1690hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
155	CL155	154090	1622	0.086	50.0	Simple_repeat (44hits, 1.11%) Low_complexity (4hits, 0.123%) LTR.Gypsy (2hits, 0.0649%)		Unspecified (**1971hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
156	CL156	153900	1620	0.086	50.1	Simple_repeat (55hits, 1.44%) LTR.Gypsy (2hits, 0.0507%) Low_complexity (1hits, 0.026%)	Ty3-INT Ty3/gypsy chromovirus (1 hits 0.0617%)	Unspecified (**1898hits, 92.2%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						DNA.PIF.Harbinger (**86hits, 4.1%**) Simple_repeat (89hits, 2.6%)				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

157	CL157	153235	1613	0.085	50.2	Low_complexity (17hits, 0.573%) RC.Helitron (8hits, 0.328%) DNA (3hits, 0.146%) DNA.PIF.Harbinger. (1hits, 0.0385%) LTR.G.....	DTH-CD1 NA NA (177 hits 11%)		Unspecified (**1702hits, 99.1%**)	

group
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

158	CL158	151335	1593	0.084	50.3	rRNA (68hits, 2.81%) Simple_repeat (72hits, 2.16%) Low_complexity (1hits, 0.0205%)		organelle/plastid (3094 hits 194%) organelle/mitochondria (35 hits 2.2%)	Unspecified (**1606hits, 98.8%**)	

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

159	CL159	149910	1578	0.084	50.3	Simple_repeat (68hits, 1.73%) LTR.Gypsy (23hits, 0.833%) Low_complexity (7hits, 0.235%)			Unspecified (**1684hits, 102%**)	

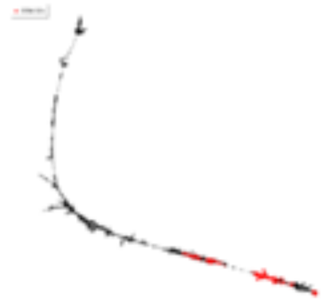
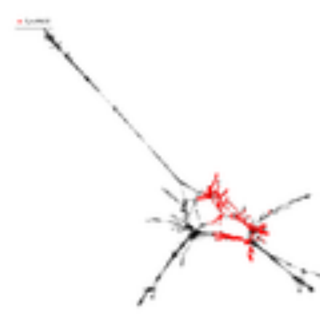
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

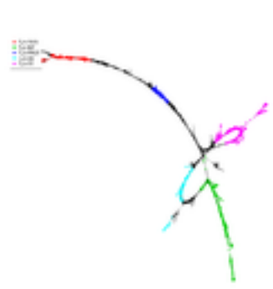
160	CL160	145920	1536	0.081	50.4	Simple_repeat (41hits, 0.994%) Low_complexity (7hits, 0.131%)		organelle/plastid (1453 hits 94.6%) organelle/mitochondria (13 hits 0.846%)	Unspecified (**424hits, 16.8%**)	

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

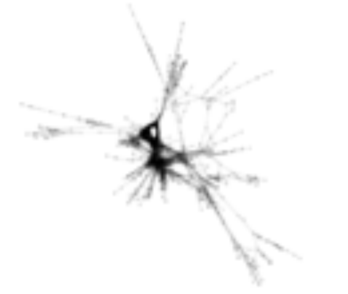
						Simple_repeat (42hits, 1.51%)				

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

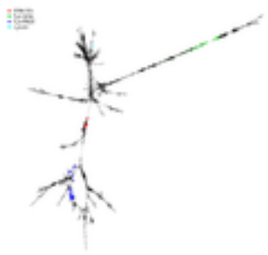
161	CL161	144115	1517	0.080	50.5	DNA.MULE.MuDR (29hits, 1.33%) Low_complexity (14hits, 0.543%) LTR.Gypsy (1hits, 0.0291%)	DTM-CD1 NA NA (271 hits 17.9%)	Unspecified (**1491hits, 94.1%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
162	CL162	141645	1491	0.079	50.6	Simple_repeat (7hits, 0.246%) LTR.Gypsy (1hits, 0.0233%)		Unspecified (**1448hits, 82.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
163	CL163	140125	1475	0.078	50.7	LTR.Gypsy (**310hits, 17.1%**) Low_complexity (1hits, 0.0293%) Simple_repeat (1hits, 0.0278%)	Ty3-PROT Ty3/gypsy Ogre/Tat (331 hits 22.4%)	Unspecified (**1589hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
164	CL164	133095	1401	0.074	50.7	Simple_repeat (78hits, 2.62%) Low_complexity (46hits, 1.84%) DNA.MULE.MuDR (1hits, 0.0308%)		Unspecified (**1623hits, 106%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						LTR.Gypsy (**876hits, 59.1%**) LTR.Copia (8hits,	Ty3-INT Ty3/gypsy chromovirus (243 hits 17.7%) Ty3-RT Ty3/gypsy chromovirus (206			**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

165	CL165	130150	1370	0.072	50.8	0.37%) DNA.CMC.EnSpm (5hits, 0.214%) Low_complexity (3hits, 0.101%) Simple_repeat (3hits, 0.0884%)	hits 15%) Ty3-RH Ty3/gypsy chromovirus (104 hits 7.59%) Ty3-GAG Ty3/gypsy chromovirus (101 hits 7.37%) Ty3-PROT Ty3/gyp.....	organelle/mitochondria (5 hits 0.365%)	Unspecified (**1373hits, 98.9%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
166	CL166	129960	1368	0.072	50.9	LTR.Copia (**78hits, 4.18%**) LTR.Gypsy (**67hits, 3.45%**) Simple_repeat (16hits, 0.486%) Low_complexity (13hits, 0.454%) LTR.Caulimovirus (2hits, 0.112%) LTR.Pao (1hits, 0.0431%)			Unspecified (**1388hits, 99.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
167	CL167	128630	1354	0.072	51.0	LTR.Copia (**204hits, 10.5%**) Simple_repeat (**114hits, 3.9%**) Low_complexity (84hits, 2.84%) tRNA (21hits, 1.02%)		organelle/plastid (1252 hits 92.5%)	Unspecified (**297hits, 11%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
168	CL168	127965	1347	0.071	51.0	Simple_repeat (**108hits, 3.97%**) Low_complexity (65hits, 2.38%)		organelle/plastid (1267 hits 94.1%)	Unspecified (**227hits, 12.7%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
											group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

169	CL169	125400	1320	0.070	51.1	Simple_repeat (110hits, 2.95%) Low_complexity (74hits, 2.37%)			Unspecified (**111hits, 5.11%**)	
170	CL170	123405	1299	0.069	51.2	Simple_repeat (19hits, 0.759%) LTR.Gypsy (9hits, 0.485%) DNA.TcMar.Pogo (1hits, 0.0446%) Low_complexity (1hits, 0.0365%) snRNA (1hits, 0.0284%)	Ty3-INT Ty3/gypsy chromovirus (5 hits 0.385%) Ty3-RH Ty3/gypsy chromovirus (1 hits 0.077%)		Unspecified (**1505hits, 106%**)	
171	CL171	122170	1286	0.068	51.2	LTR.Copia (**560hits, 38.9%**) Simple_repeat (16hits, 0.484%) LTR.Caulimovirus (4hits, 0.123%) Low_complexity (3hits, 0.103%) LTR.ERV1 (1hits, 0.0401%)	Ty1-INT Ty1/copia Angela (248 hits 19.3%) Ty1-PROT Ty1/copia Angela (98 hits 7.62%) Ty1-GAG Ty1/copia Angela (75 hits 5.83%) Ty1-GAG Ty1/copia Tork (1 hits 0.0778%)		Unspecified (**1306hits, 99.6%**)	
172	CL172	119225	1255	0.066	51.3	Low_complexity (56hits, 2.37%) Simple_repeat (55hits, 1.9%)		organelle/plastid (1160 hits 92.4%)	Unspecified (**276hits, 11.3%**)	
						Simple_repeat				

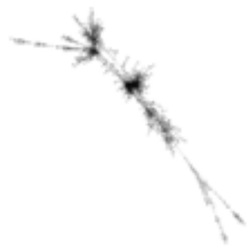
173	CL173	118845	1251	0.066	51.4	(50hits, 1.95%) Low_complexity (3hits, 0.123%) LTR.Gypsy (1hits, 0.0362%)			Unspecified (**1275hits, 99.9%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
174	CL174	115615	1217	0.064	51.4	Simple_repeat (31hits, 0.951%) Low_complexity (1hits, 0.0268%)		organelle/plastid (1223 hits 100%)	Unspecified (**309hits, 16%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
175	CL175	110295	1161	0.061	51.5	Simple_repeat (**155hits, 8.52%**) Low_complexity (26hits, 1.23%) DNA.hAT (4hits, 0.234%)			Unspecified (**1258hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
176	CL176	107445	1131	0.060	51.5	Simple_repeat (38hits, 1.63%) LTR.Gypsy (17hits, 0.891%) Low_complexity (3hits, 0.128%) DNA.hAT.Ac (1hits, 0.0512%) DNA.MULE.MuDR (1hits, 0.0428%) LTR.Pao (1hits, 0.0279%)	Ty3-CHDCR Ty3/gypsy chromovirus (8 hits 0.707%)		Unspecified (**1240hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (**199hits, 9.98%**) Low_complexity					**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

177	CL177	100510	1058	0.056	51.6	(**106hits, 6.07%**) LINE.L1 (**63hits, 5%**) Satellite (18hits, 1.47%) DNA (14hits, 1.09%) DNA.CMC.EnSpm (3hits, 0.203%) DNA.MULE.....	Unspecified (**1202hits, 105%**)	
178	CL178	97185	1023	0.054	51.7	DNA.MULE.MuDR (**95hits, 6.59%**) Simple_repeat (49hits, 2.14%) Low_complexity (7hits, 0.353%) LTR.DIRS (1hits, 0.0669%)	Unspecified (**1035hits, 99.3%**)	
179	CL179	96710	1018	0.054	51.7	LTR.Gypsy (**66hits, 3.72%**) Simple_repeat (17hits, 0.669%) LTR.Copia (1hits, 0.0496%) Low_complexity (1hits, 0.0486%)	Unspecified (**1065hits, 101%**)	
180	CL180	93575	985	0.052	51.8	Simple_repeat (46hits, 1.46%) DNA.CMC.EnSpm (5hits, 0.297%) LINE.L2 (2hits, 0.093%) LTR.Gypsy (1hits, 0.078%) DNA.hAT.Tip100 (1hits, 0.0716%) DNA.hAT.Ac (1hits, 0.0705%)	Unspecified (**253hits, 19.8%**)	

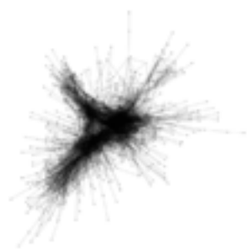
181	CL181	93480	984	0.052	51.8	Simple_repeat (50hits, 2.5%) Low_complexity (28hits, 1.35%)	organelle/plastid (982 hits 99.8%)	Unspecified (**421hits, 29.1%**)	
182	CL182	90820	956	0.051	51.9	Simple_repeat (72hits, 2.75%) Low_complexity (13hits, 0.665%)	organelle/plastid (969 hits 101%)	Unspecified (**520hits, 40%**)	
183	CL183	88825	935	0.050	51.9	LTR.Gypsy (**77hits, 5.65%**) Simple_repeat (23hits, 1.04%)	Ty3-PROT Ty3/gypsy chromovirus (18 hits 1.93%) Ty3-GAG Ty3/gypsy chromovirus (17 hits 1.82%) DTM-CD1 NA NA (7 hits 0.749%) Ty3-RT Ty3/gypsy Ogre/Tat (1 hits 0.107%)	Unspecified (**1055hits, 105%**)	
184	CL184	88635	933	0.049	52.0	Simple_repeat (23hits, 0.908%) Low_complexity (8hits, 0.303%) LTR.Gypsy (4hits, 0.126%) LTR.Pao (1hits, 0.0609%) LTR.Copia (1hits, 0.0417%)	Ty3-INT Ty3/gypsy Athila (1 hits 0.107%)	Unspecified (**978hits, 101%**)	

185	CL185	85595	901	0.048	52.0	Simple_repeat (13hits, 0.647%) Low_complexity (1hits, 0.0386%)	Unspecified (**812hits, 75.6%**)	

group
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

186	CL186	85310	898	0.048	52.1	Simple_repeat (17hits, 0.918%) Low_complexity (6hits, 0.314%)	Unspecified (**929hits, 100%**)	

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

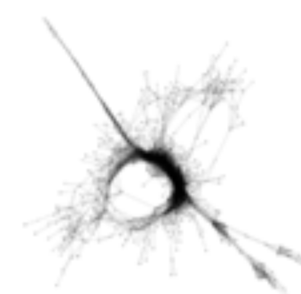
187	CL187	83220	876	0.046	52.1	Low_complexity (**52hits, 3.02%**) Simple_repeat (44hits, 2.69%) DNA.hAT.Tip100 (3hits, 0.18%)	Unspecified (**998hits, 107%**)	

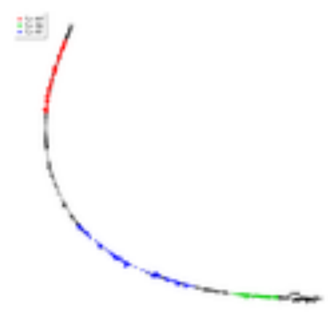
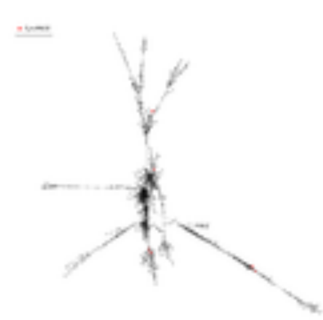
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

188	CL188	82745	871	0.046	52.2	Low_complexity (3hits, 0.168%) Simple_repeat (2hits, 0.106%) LTR.Copia (1hits, 0.0459%) LTR.Gypsy (1hits, 0.0363%)	Unspecified (**893hits, 100%**)	

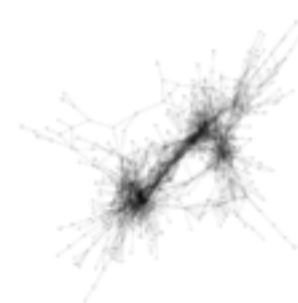
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

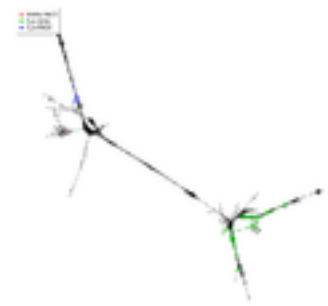
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_

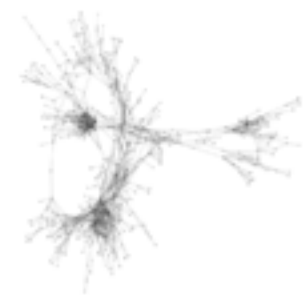
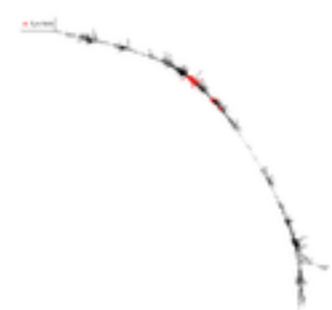
189	CL189	80085	843	0.045	52.2	Simple_repeat (48hits, 2.37%) Low_complexity (1hits, 0.04%)	organelle/plastid (796 hits 94.4%) organelle/mitochondria (29 hits 3.44%)	Unspecified (**179hits, 14.7%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
190	CL190	77520	816	0.043	52.2	Simple_repeat (21hits, 1.35%) Low_complexity (3hits, 0.249%) LTR.Gypsy (1hits, 0.0748%)	organelle/plastid (798 hits 97.8%) organelle/mitochondria (5 hits 0.613%)	Unspecified (**287hits, 29.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
191	CL191	71915	757	0.040	52.3	Simple_repeat (**116hits, 7.67%**) Low_complexity (41hits, 2.91%)		Unspecified (**891hits, 107%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
192	CL192	71155	749	0.040	52.3	Simple_repeat (32hits, 1.48%) Low_complexity (30hits, 1.19%)	organelle/plastid (745 hits 99.5%)	Unspecified (**205hits, 20.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

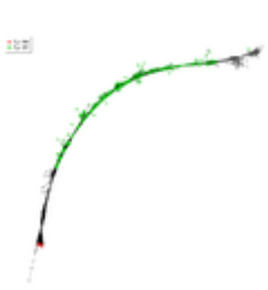
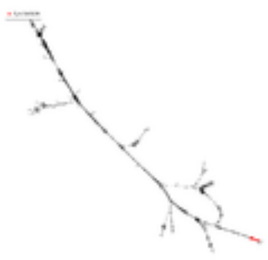
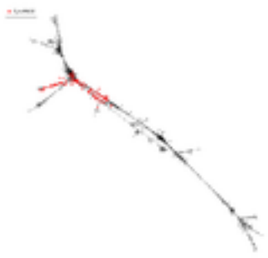
193 CL193	71060	748	0.040	52.4	Simple_repeat (9hits, 0.583%) Low_complexity (4hits, 0.214%)		Unspecified (**774hits, 101%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
194 CL194	70870	746	0.040	52.4	LTR.Copia (**532hits, 65.6%**) Simple_repeat (8hits, 0.399%)	Ty1-INT Ty1/copia AleII (126 hits 16.9%) Ty1-RT Ty1/copia AleII (121 hits 16.2%) Ty1-RH Ty1/copia AleII (66 hits 8.85%) Ty1-RT Ty1/copia unclass(AleI/Retrofit) (3 hits 0.402%) Ty1-INT Ty1/copia TAR (2......	Unspecified (**783hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
195 CL195	68590	722	0.038	52.4	Simple_repeat (28hits, 1.65%) Low_complexity (1hits, 0.0758%)		Unspecified (**724hits, 99%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
196 CL196	66215	697	0.037	52.5	LTR.Gypsy (19hits, 1.81%)	Ty3-PROT Ty3/gypsy chromovirus (6 hits 0.861%)	Unspecified (**756hits, 104%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
					Low_complexity				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

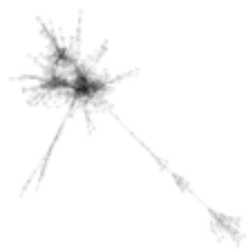
197	CL197	66120	696	0.037	52.5	(12hits, 0.802%) LTR.Gypsy (8hits, 0.759%) Simple_repeat (11hits, 0.634%)	Unspecified (**715hits, 100%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
198	CL198	61560	648	0.034	52.5	Simple_repeat (**377hits, 39.9%**) Low_complexity (16hits, 1.25%)	Unspecified (**39hits, 4.18%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
199	CL199	61085	643	0.034	52.6	LTR.Gypsy (34hits, 2.85%) Simple_repeat (10hits, 0.869%) Low_complexity (6hits, 0.352%)	Unspecified (**678hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
200	CL200	60990	642	0.034	52.6	Simple_repeat (**60hits, 5.81%**) Low_complexity (22hits, 2.3%) DNA.Maverick (2hits, 0.146%) DNA.hAT.Tag1 (1hits, 0.111%) DNA.PIF.Harbinger (1hits, 0.107%) DNA.MULE.MuDR (1hits, 0.0935%)	Unspecified (**684hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
									group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

201	CL201	60610	638	0.034	52.6	DNA.hAT.hATx (1hits, 0.099%) Simple_repeat (2hits, 0.0792%)	Ty1-INT Ty1/copia Ivana/Oryco (1 hits 0.157%)	organelle/plastid (623 hits 97.6%)	Unspecified (**354hits, 49.6%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
202	CL202	58710	618	0.033	52.7	Simple_repeat (**36hits, 3.13%**) Low_complexity (12hits, 1.03%)			Unspecified (**207hits, 24.2%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
203	CL203	58140	612	0.032	52.7	Low_complexity (4hits, 0.267%) Simple_repeat (3hits, 0.191%)			Unspecified (**170hits, 18.4%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
204	CL204	57760	608	0.032	52.7	LTR.Gypsy (**45hits, 4.34%**) Simple_repeat (8hits, 0.523%) Low_complexity (7hits, 0.407%)			Unspecified (**661hits, 104%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
											group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

205	CL205	57665	607	0.032	52.8	LTR.Gypsy (6hits, 0.513%) DNA.Academ (1hits, 0.0694%)		Unspecified (**284hits, 37.6%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
206	CL206	57095	601	0.032	52.8	LTR.Gypsy (**76hits, 9.78%**) Low_complexity (1hits, 0.0788%)	Ty3-GAG Ty3/gypsy chromovirus (71 hits 11.8%) Ty3-PROT Ty3/gypsy chromovirus (9 hits 1.5%) PARA-PROT NA NA (1 hits 0.166%)	Unspecified (**617hits, 99.8%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
207	CL207	56050	590	0.031	52.8	DNA.CMC.Chapaev (1hits, 0.164%) Simple_repeat (1hits, 0.0963%) Low_complexity (1hits, 0.0892%)		Unspecified (**243hits, 29.5%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
208	CL208	55100	580	0.031	52.9	Simple_repeat (20hits, 1.74%) LINE.L1 (1hits, 0.116%) Low_complexity (2hits, 0.113%)		Unspecified (**585hits, 99.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Simple_repeat (5hits, 0.303%)				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

209	CL209	54435	573	0.030	52.9	LTR.Gypsy (2hits, 0.129%) DNA.Ginger (1hits, 0.105%) Low_complexity (1hits, 0.079%)		Unspecified (**583hits, 99.4%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
210	CL210	54150	570	0.030	52.9	Simple_repeat (4hits, 0.36%) Low_complexity (1hits, 0.122%)		Unspecified (**598hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
211	CL211	51110	538	0.029	53.0	LTR.Gypsy (5hits, 0.612%)	Ty3-GAG Ty3/gypsy chromovirus (33 hits 6.13%)	Unspecified (**639hits, 107%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
212	CL212	50540	532	0.028	53.0	Simple_repeat (14hits, 1.3%) RC.Helitron (3hits, 0.235%) Low_complexity (1hits, 0.117%)		Unspecified (**609hits, 106%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
							Ty1-RT Ty1/copia Angela (322 hits 61.5%)			**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

213	CL213	49780	524	0.028	53.0	LTR.Copia (**455hits, 81.9%**)	Ty1-RH Ty1/copia Angela (9 hits 1.72%) Ty1-RT Ty1/copia Tork (2 hits 0.382%) Ty1-RT Ty1/copia Ivana/Oryco (1 hits 0.191%)	Unspecified (**526hits, 99%**)	
214	CL214	48640	512	0.027	53.0	Simple_repeat (**29hits, 3.33%**) LTR.Gypsy (2hits, 0.204%) LINE.L2 (1hits, 0.136%) DNA.hAT.Ac (1hits, 0.0925%) Low_complexity (1hits, 0.0535%) DNA.CMC.EnSpm (1hits, 0.0535%)		Unspecified (**523hits, 99.8%**)	
215	CL215	48545	511	0.027	53.1	LTR.Gypsy (14hits, 1.79%) Simple_repeat (8hits, 0.721%) Low_complexity (6hits, 0.538%)	Ty3-CHDCR Ty3/gypsy chromovirus (8 hits 1.57%)	Unspecified (**534hits, 101%**)	
216	CL216	48260	508	0.027	53.1	LTR.Gypsy (**135hits, 20.3%**) LTR.Copia. (**38hits, 4.19%**) LTR (10hits, 0.568%) Simple_repeat (4hits, 0.269%) Low_complexity (1hits, 0.087%) DNA.MULE.MuDR (1hits, 0.0663%)	Ty3-PROT Ty3/gypsy Athila (81 hits 15.9%)	Unspecified (**521hits, 100%**)	

217	CL217	48165	507	0.027	53.1	Simple_repeat (31hits, 2.65%) Low_complexity (6hits, 0.492%)		Unspecified (**528hits, 101%**)	

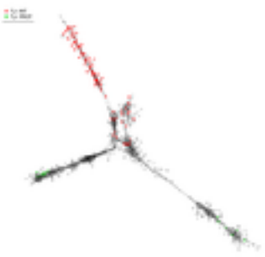
group
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

218	CL218	46740	492	0.026	53.1	Simple_repeat (**41hits, 5.4%**) Low_complexity (13hits, 1.62%)	organelle/plastid (447 hits 90.9%)	Unspecified (**160hits, 23%**)	

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

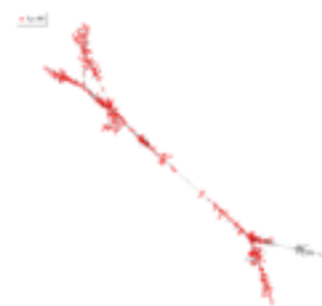
219	CL219	46170	486	0.026	53.2	Simple_repeat (**76hits, 9.02%**) Low_complexity (6hits, 0.492%)	organelle/plastid (838 hits 172%)	Unspecified (**494hits, 99%**)	

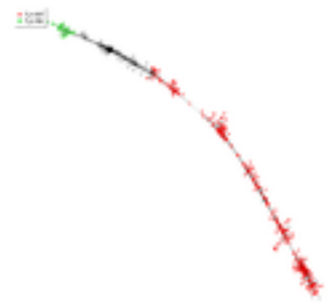
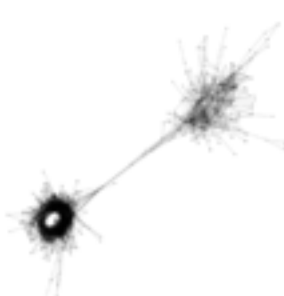
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

220	CL220	44460	468	0.025	53.2	LTR.Copia (**130hits, 19.9%**) Low_complexity (1hits, 0.099%)	Ty1-INT Ty1/copia Angela (68 hits 14.5%) Ty1-INT Ty1/copia Ivana/Oryco (11 hits 2.35%) Ty1-PROT Ty1/copia Angela (6 hits 1.28%) Ty1-INT Ty1/copia TAR (5 hits 1.07%) Ty1-PROT Ty1/copia AleI/Retrofit (5.....	Unspecified (**495hits, 102%**)	

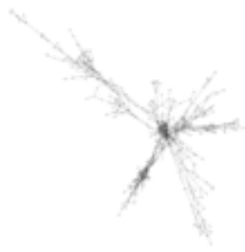
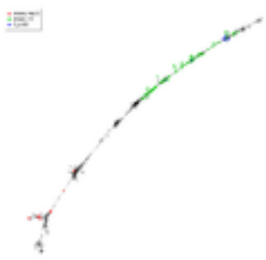
group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

Low_complexity

221	CL221	44365	467	0.025	53.2	(3hits, 0.401%) Simple_repeat (2hits, 0.27%) LTR.Gypsy (1hits, 0.0992%)		Unspecified (**343hits, 57.8%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
222	CL222	42940	452	0.024	53.2	LTR.Copia (**311hits, 60.6%**) Simple_repeat (1hits, 0.0745%)	Ty1-RT Ty1/copia Angela (247 hits 54.6%) Ty1-RT Ty1/copia TAR (49 hits 10.8%) Ty1-RT Ty1/copia AleII (31 hits 6.86%) Ty1-RT Ty1/copia Ivana/Oryco (29 hits 6.42%) Ty1-RT Ty1/copia Tork (7 hits 1.55%)	Unspecified (**468hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
223	CL223	41800	440	0.023	53.3	Simple_repeat (6hits, 0.701%) LTR.Gypsy (1hits, 0.105%)		Unspecified (**482hits, 76.6%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
224	CL224	41515	437	0.023	53.3	LTR.Gypsy (**21hits, 3.96%**) Simple_repeat (18hits, 1.38%) Low_complexity (10hits, 0.812%) LINE.L1 (1hits, 0.113%)	Ty3-INT Ty3/gypsy Ogre/Tat (14 hits 3.2%)	Unspecified (**379hits, 60.2%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

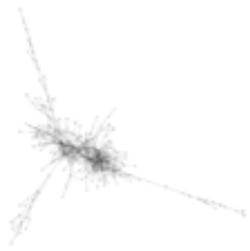
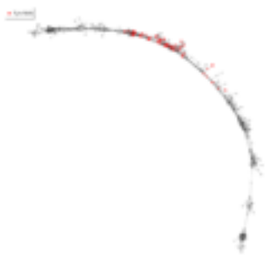
225	CL225	39900	420	0.022	53.3	LTR.Gypsy (**237hits, 49.9%**)	Ty3-INT Ty3/gypsy Athila (263 hits 62.6%) Ty3-RH Ty3/gypsy Athila (25 hits 5.95%)	Unspecified (**427hits, 99.6%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
226	CL226	39235	413	0.022	53.3	Simple_repeat (15hits, 1.65%) LTR.Gypsy (8hits, 1.35%) Low_complexity (8hits, 0.882%)		Unspecified (**452hits, 104%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
227	CL227	38000	400	0.021	53.4	LTR.Copia (**91hits, 19.5%**) Simple_repeat (1hits, 0.0553%)		Unspecified (**428hits, 102%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
228	CL228	37525	395	0.021	53.4			Unspecified (**398hits, 99.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
						Low_complexity				**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

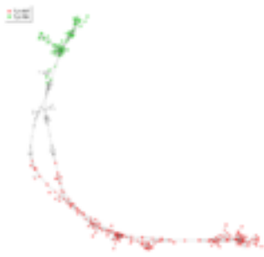
229	CL229	37145	391	0.021	53.4	(2hits, 0.199%) LTR.Gypsy (1hits, 0.14%) Simple_repeat (1hits, 0.0969%)		Unspecified (**399hits, 99.7%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
230	CL230	36575	385	0.020	53.4	LTR.Gypsy (**29hits, 4.07%**) Simple_repeat (12hits, 1.15%) Low_complexity (5hits, 0.498%)	LINE-ENDO NA NA (1 hits 0.26%)	Unspecified (**435hits, 105%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
231	CL231	34865	367	0.019	53.4	Simple_repeat (**66hits, 8.81%**) DNA.hAT.Ac (19hits, 2.76%) Low_complexity (15hits, 1.62%) LTR.Gypsy (1hits, 0.181%)		Unspecified (**428hits, 109%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
232	CL232	34865	367	0.019	53.5	Simple_repeat (14hits, 1.57%) LTR.Copia (1hits, 0.143%)		Unspecified (**404hits, 105%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

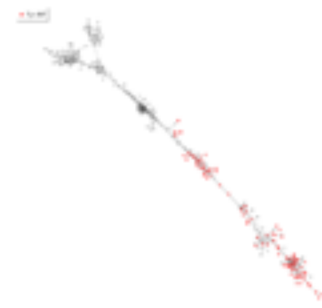
233	CL233	34105	359	0.019	53.5	DNA.MULE.MuDR (1hits, 0.226%) Low_complexity (1hits, 0.114%)		Unspecified (**455hits, 117%**)	
234	CL234	31920	336	0.018	53.5	Low_complexity (1hits, 0.128%)		Unspecified (**387hits, 109%**)	
235	CL235	31825	335	0.018	53.5	Simple_repeat (17hits, 2.4%) LTR.ERVK (1hits, 0.107%)		Unspecified (**392hits, 102%**)	
236	CL236	30305	319	0.017	53.5	LTR.Caulimovirus (**40hits, 10.1%**) LTR.Gypsy (**39hits, 9.24%**) Simple_repeat (1hits, 0.0957%)	PARA-RT NA NA (81 hits 25.4%) Ty3-RT Ty3/gypsy chromovirus (9 hits 2.82%) PARA-PROT NA NA (8 hits 2.51%)	Unspecified (**303hits, 84.4%**)	
						Simple_repeat (**231hits, 49.5%**) Low_complexity (7hits, 1.33%) DNA.Ginger (4hits,			

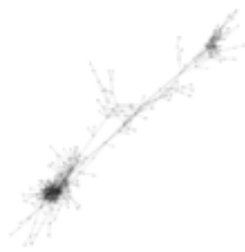
237	CL237	30115	317	0.017	53.5	0.867%) DNA.CMC.EnSpm (3hits, 0.727%) DNA.MULE.MuDR (1hits, 0.252%) DNA.hAT.Charlie (1hits, 0.246%) LINE.L1 (1hits, 0.196%)	Unspecified (**153hits, 35.8%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
238	CL238	28785	303	0.016	53.6	Simple_repeat (1hits, 0.0625%)	Unspecified (**324hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
239	CL239	25935	273	0.014	53.6	Simple_repeat (8hits, 1.23%)	Unspecified (**316hits, 105%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
240	CL240	25840	272	0.014	53.6		Unspecified (**304hits, 105%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
									group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

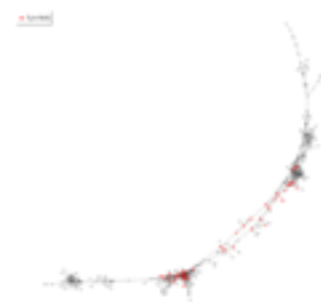
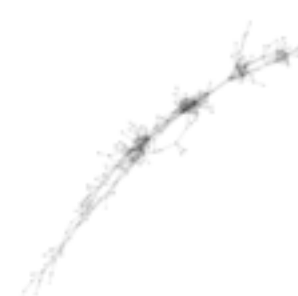
241	CL241	25650	270	0.014	53.6			Unspecified (**271hits, 99.1%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
242	CL242	25460	268	0.014	53.6	Simple_repeat (2hits, 0.628%)		Unspecified (**339hits, 114%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
243	CL243	25460	268	0.014	53.6	Simple_repeat (**100hits, 18.1%**) Low_complexity (2hits, 0.346%)	organelle/plastid (221 hits 82.5%)	Unspecified (**87hits, 19.5%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
244	CL244	25365	267	0.014	53.6	Low_complexity (3hits, 0.473%) Simple_repeat (3hits, 0.292%) LTR.Gypsy (1hits, 0.134%)		Unspecified (**278hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

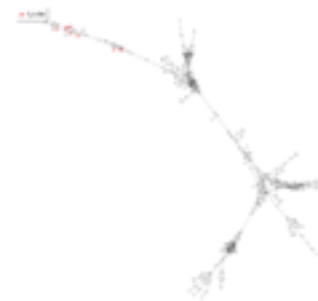
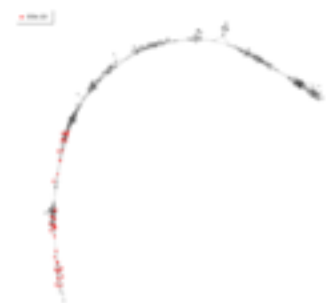
245	CL245	25175	265	0.014	53.7	Simple_repeat (**37hits, 7.77%**) Low_complexity (**23hits, 5.72%**)		Unspecified (**302hits, 109%**)	
246	CL246	24700	260	0.014	53.7		Ty3-GAG Ty3/gypsy chromovirus (54 hits 20.8%) Ty3-GAG Ty3/gypsy Ogre/Tat (1 hits 0.385%)	Unspecified (**265hits, 99.7%**)	
247	CL247	24510	258	0.014	53.7			Unspecified (**233hits, 76%**)	
248	CL248	24415	257	0.014	53.7	Simple_repeat (12hits, 2.43%)		Unspecified (**139hits, 43.1%**)	

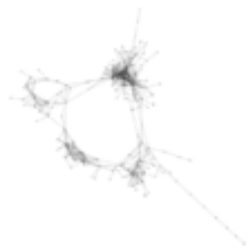
249	CL249	24415	257	0.014	53.7	DNA.MULE.MuDR (1hits, 0.258%) Simple_repeat (2hits, 0.217%)		Unspecified (**261hits, 99.7%**)	
250	CL250	23940	252	0.013	53.7	LTR.Gypsy (**17hits, 6.16%**) Simple_repeat (**20hits, 3.67%**)	Ty3-CHDCR Ty3/gypsy chromovirus (16 hits 6.35%) Ty3-INT Ty3/gypsy chromovirus (1 hits 0.397%)	Unspecified (**306hits, 111%**)	
251	CL251	23845	251	0.013	53.7			Unspecified (**259hits, 100%**)	
252	CL252	23845	251	0.013	53.8	LTR.Gypsy (**213hits, 77%**)	Ty3-INT Ty3/gypsy chromovirus (148 hits 59%) Ty3-RH Ty3/gypsy chromovirus (61 hits 24.3%)	Unspecified (**251hits, 98.6%**)	
							Ty1-INT Ty1/copia Angela (69 hits 28.2%) Ty1-INT Ty1/copia Ivana/Oryco (11 hits		

253	CL253	23275	245	0.013	53.8	LTR.Copia (**104hits, 34.7%**) LINE.Jockey (1hits, 0.223%)	4.49%) Ty1-INT Ty1/copia AleI/Retrofit (2 hits 0.816%) Ty1-INT Ty1/copia Tork (2 hits 0.816%) Ty1-INT Ty1/copia AleII (1......	Unspecified (**252hits, 100%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
254	CL254	23275	245	0.013	53.8	LTR.Gypsy (**10hits, 3.35%**) Simple_repeat (**18hits, 3.18%**) Low_complexity (7hits, 1.67%) LINE.CR1 (1hits, 0.249%)		Unspecified (**239hits, 79.1%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
255	CL255	22990	242	0.013	53.8	Simple_repeat (**21hits, 3.92%**) Low_complexity (9hits, 1.71%) DNA.CMC.EnSpm (1hits, 0.274%)		Unspecified (**250hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
256	CL256	22705	239	0.013	53.8	Simple_repeat (5hits, 0.934%)	Ty3-CHDCR Ty3/gypsy chromovirus (6 hits 2.51%)	Unspecified (**244hits, 98.9%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

257	CL257	22610	238	0.013	53.8	Simple_repeat (**45hits, 12%**) Low_complexity (**11hits, 3.37%**)		Unspecified (**15hits, 3.6%**)	
258	CL258	22610	238	0.013	53.8	Low_complexity (1hits, 0.234%) LTR.Pao (1hits, 0.177%) Simple_repeat (1hits, 0.128%)	organelle/plastid (1 hits 0.42%)	Unspecified (**239hits, 97.8%**)	
259	CL259	22515	237	0.013	53.8	LTR.Gypsy (10hits, 2.18%) Simple_repeat (1hits, 0.258%)		Unspecified (**262hits, 88.2%**)	
260	CL260	22420	236	0.013	53.9	LTR.Copia (**37hits, 12.8%**) Simple_repeat (4hits, 0.504%) Low_complexity (1hits, 0.183%)		Unspecified (**241hits, 99.5%**)	

261	CL261	22040	232	0.012	53.9	Simple_repeat (2hits, 0.318%)		Unspecified (**243hits, 101%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
262	CL262	21470	226	0.012	53.9	DNA.MULE.MuDR (1hits, 0.205%)	Ty3-GAG Ty3/gypsy Athila (41 hits 18.1%) Ty3-GAG Ty3/gypsy Ogre/Tat (2 hits 0.885%)	Unspecified (**229hits, 98.9%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
263	CL263	21280	224	0.012	53.9			Unspecified (**280hits, 116%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
264	CL264	20425	215	0.011	53.9	Simple_repeat (1hits, 0.118%)		Unspecified (**234hits, 103%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

265	CL265	20330	214	0.011	53.9	LTR.Gypsy (6hits, 2.42%)	Ty3-RH Ty3/gypsy chromovirus (7 hits 3.27%)	Unspecified (**229hits, 102%**)		A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
266	CL266	20045	211	0.011	53.9	DNA.PIF.Harbinger (**37hits, 11.2%**) Low_complexity (1hits, 0.269%)	DTH-CD1 NA NA (43 hits 20.4%)	Unspecified (**223hits, 101%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
267	CL267	19665	207	0.011	53.9	Low_complexity (3hits, 0.849%) Simple_repeat (1hits, 0.275%)		Unspecified (**211hits, 100%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
268	CL268	19095	201	0.011	54.0	Simple_repeat (12hits, 2.66%)		Unspecified (**27hits, 8.3%**)		**group** A1_155_ A1_073_ A1_097_ A2_255_ A2_034_ A2_044_ A2_099_ D5_002_ D5_031_ D5_004_ D5_053_ A2_101_ D5_ggg_
										group A1_155_ A1_073_ A1_097_ A2_255_ A2_034_

269	CL269	18525	195	0.010	54.0	Simple_repeat (2hits, 0.416%)	Unspecified (**208hits, 103%**)	
270	CL270	18240	192	0.010	54.0	Simple_repeat (10hits, 2.47%) Low_complexity (1hits, 0.428%)	Unspecified (**233hits, 112%**)	
271	CL271	18240	192	0.010	54.0	Simple_repeat (6hits, 1.74%)	Unspecified (**206hits, 103%**)	
272	CL272	18145	191	0.010	54.0	Simple_repeat (**27hits, 5.73%**) Low_complexity (10hits, 2.41%) LTR.Gypsy (1hits, 0.347%)	Unspecified (**202hits, 95%**)	

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_

group
A1_155_
A1_073_
A1_097_
A2_255_
A2_034_
A2_044_
A2_099_
D5_002_
D5_031_
D5_004_
D5_053_
A2_101_
D5_ggg_