

Tandem Repeat Analyzer

Run statistics:

Number of input sequences: 990220
 Number of analyzed sequences: 990220
 Threshold for cluster merging: 0.2
 Proportion of sequences in analyzed clusters : 77 %

Consensus files - fasta format:

[Putative satellites \(high confidence\) - total 13 found](#)
[Putative satellites \(low confidence\) - total 17 found](#)
[Putative LTR elements - total 3 found](#)
[rDNA - total 1 found](#)

Documentation

For the explanation of TAREAN output see [the help section](#)

How to cite:

A paper on TAREAN is in preparation. Publications about graph-based repeat clustering and RepeatExplorer are listed below.

Novak, P., Neumann, P., Pech, J., Steinhals, 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.

Novak, P., Neumann, P., Macas, J. (2010) - [Graph-based clustering and characterization of repetitive sequences in next-generation sequencing data](#). *BMC Bioinformatics* **11**:378.

Putative satellites (high confidence)

Example of TAREAN output

(HTML summary of results)

Input data: 990,220 reads
from *Vicia faba*

Cluster	Genome Proportion(%)	Size real	Satellite probability	Consensus length	Consensus	Kmer analysis	Graph layout	Connected component index C	Pair completeness index C	Kmer coverage	V	E	Pbs score	The longest ORF length	Similarity based annotation
7	CL7	3.200	32038	0.98	59	GTCTGTTGCGAAGATTTTGTACTCAATGGATGGTACCTTGTCTATGGAAGTA	report	1.00	0.99	0.54	13667	2.0e+07	0	78	
11	CL11	1.200	12005	0.98	191	CATCCAAATTTAGGTACTCATCTAGCAAGTAAAGACTAATTAAGTACATATTCATATACA TTGAAATAATCAATATCATGTAGTATATTTACCACATATCATATGATATGATATAAGA TGAAACAATTCATATTTCTCTCTC	report	1.00	0.99	0.56	12005	1.4e+07	0	49	
39	CL39	0.290	2862	0.97	702	TAATACTAAAAGGAGGCAACTAAATGGTGGGTAAAGAAATTTCCGCAAAACAGTAGCTAGGTC GCCTTTGCAACCAAGTATTTTCTGAAATCAACCATTTTCAAAATTTTATAAACAATGCCTG AGGACACCAATTAAGTATATATCTACTGACATATTTTCTCATTGATTTTCAATTTGTCAT AGTATAGGCTAGTCTCTCTATAAAGATTCTAATAAGACAAAGAGAGTGTCTCTGTC CTTGAAGAGGAAATAGAGCAACAGCAATATGCCATAAAGTATTTAATGACCTCTTTGTT GAAAAGCGCTAATACCGTCCCAATGTAAGCATTGTTTAAATAGCACCTTAAAGAGCT TTAATATAAATAAATAAATTAATAAACAATAAATAAAGAGGCAACGAAATTTGTTG TCATAAACAATAGCTGCGCTGACCTGCTGCTAATATAAATAAATAAATAAATTTTAA	report	0.98	0.98	0.45	2862	2.1e+05	0	117	
62	CL62	0.150	1436	0.99	687	GTCATGATAGTAAATGGCTATTTCTAGTAAATGATTAATTTAGTTATAAATAAATAATATAT TTATGCTATTTTCTCAATGCTAGTAAATGGCTAATTTGATTAATAAATAAATGATGAAAGT AGTGTATAGGCTTTTCTTATTAATCGGATTTATGATATATAATTTTATAAATAAATAA GATTTATATTTGAAATTTAAGTAAATGATTTATTTTGGAGAGTATTTAATCATTAAAA TGAGTAACCCCAATTAAGTATATATCTACTGACATATTTTCTCATTGATTTTCAATTT AACATTACTGAAATGATTAATAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA AAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT TTTATGCTCCATCTCAAGTAGGAGTCTCTCACTCTGCAATTTTATCTGATATGAAAGT AGTAAATTTATCATTCTGAAATAAGTCACTCTCTTTAATTTGAAATCTCATAGAC	report	0.99	0.98	0.27	1436	3.3e+04	0	60	
70	CL70	0.120	1175	0.93	38	CTGATGAAATTTGAAGTGAACATAAATCGAAGAAAT	report	0.95	0.96	0.41	1175	1.7e+04	0	195	
108	CL108	0.049	487	0.97	1482	AATGAGTTTTTTAAATAATGATAAATCTATTTTTTTGATAAATATATATTTTCAACATTTACCTTTA AAATAAATCTAAATCATCATAGTCTTTAGTAGTCTGTTAAGAGGCTTTTAAATAAATAAAGT TAACAAATTAATCTTTTCTGAAATCAACCATTTTCAAAATTTGATGATATAGAAATTTGG ATCGTTACTTATCAATAAATAAACAATAATTTATGCTTACATGACGTCATCATCTGAAATTTCTAC GAAAAGTATAATATATAATCAAAATTTGCGAAAATAAATGTTGATCAATTTAAAAGAGTATAAAGT ACATTAACCATAGTCTAAATGTTTAAACCATGGAAGTAAACCATTTTCTACCGCATATAATATAA AATATGTTAGTTTTAATAGCAATATTTAAATAATTTATGATAATTTTATAGATAAAGGCTAAATATT TTAACAACATATGTAATTTGTTAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TTCACATATATTTAGTCACTTTGGTAAATCATAGTAAAGCTTTTCAATCTCATAGTATTAATCT GTTTTCTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA CTCTCTTAAGTTTTCTTATTTAAAGGAGCACTAAATTTTTTTCTTAAATTTGCTGCACTTTTAT TGGTTTTCTACCTGAGTGTATTTGTTGGTAGGTAAGTAAAGTAAATCTTATGATGAAATATATTT CTTTATATCTTATTAATCTTATAGGTTCTTCACTCGCAAAAGAACTCATAGATTTTATGCAACT AGGTTGAGCAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TGATGATTTAGGTTGAGGAGCTCTTTAGTAAAGTCTTTGATGATTTGATGATGATGATGATG CTGAGCTTGAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TTAAGAAATTAATTTGAGTAAATCAATGATTTGCTGATTTTGTAAACATGAGGCTGATTTGAACT TCTACTTATATCTATTAATTTATTTGATATATAA	report	0.99	1.00	0.61	487	6.7e+03	0	63	
109	CL109	0.047	461	0.76	870	CATTGCTATATCTGCGATCGAGATATATCATTTCAGCTCGAAATAAATAAATAAATAAATAA ATATTTATGTTTTATATATATAGATATATATATTTTGGAAATCAATAAATAAATAAATAAATAA ATATTTAATTTCTTTATATTTCTACCATTTAGTTAGGCTTCTACATGCTTCCGATTCATATTA ACATGGAATACATATGGAAGTCAATATGACAGGTTTATCAATATGGGATTTCTTAAAGGTTATTT TAACTCATGAGATTCACACCTGATGCTACAATATATATGAAAATAATGACATGCTTATCAATAAT TTTTAAGAAATTTTAAATACATGCAAGATATAAACAATTTCCGCAAAATTCATAAAGGATTAAT TTAAGACCTTTTACATAATTTAAAJACTTATGATTTTATTTAGTGTGTTGTTGTTGTTGTTG TATGTTTAAAGGATCTTAAATTTGTTTGTGATATGTTGTTGTTGTTGTTGTTGTTGTTGTTG TTTTGTAATAAATGATTTTGGAGTAAAGGAGGAAATAAATAAATAAATAAATAAATAAATAA CTTTCAGTTATTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA CACATGATGAGTCACTTTTCACTGATTTTCAAAACCGAGAGATAAATAAACAAGTTTCAATCTG	report	0.91	0.95	0.57	461	8.1e+03	0	116	
123	CL123	0.033	326	0.95	878	TCCTTTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA TCCCACTTAAATCATCTAATAAATAAATTTGTAATAAATGATCACTTCTGATGTTCTTAAATA AATTTTCAATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA CACTATGCAATTCATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA ACACTATGCAATTCATCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA ACACTTTTCAAGCTGATGATTAAGTCACTTAAAGGACTTGTGAGGTTAAACCCAGGTTTTAACT TTAAGGCTCTTTGTTGATATCTTTGATGATGATGATGATGATGATGATGATGATGATGATGAT TTAGTAGGAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT TCCATTTTGTGATATTTAGGATTAATAAACAATTTATTTAGCTTTTAAATAAATAAATAAATAA CTCTAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA GATTTGATGATCTATTTATTTGTTGATATATATTTCTTTTAAATGTTTGCATATAGGTTGATGAT TTGGTTGTTGCTTTAGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT	report	0.98	0.99	0.63	326	3.5e+03	0	91	
137	CL137	0.027	263	0.88	603	TGTTGATGCTGATGAAAGGACACATGAGGAGTCACTTTAGTAAATTTTCAAAACAATGAGGAT AAATAAATCAATTAAGAAATAAATAAATTTCAACTTTAGATGGACAAATATGATGCTTAAATA TATCTTCAATTTTAAACAATCAACATTTTATCATTTTCAATCTTAAATAAATAAATAAATAAATAA AGTCTTAAATGGGAAAGAAATATATCTAGTCTTACACATTAAGGCTTATCAATAATGCTGCTG GAATTAATCAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT TAAGTCTTGGACACCTGATGACATTTTGAAGTCACTCTCTTCAATAAATAAATAAATAAATAA TGTGCGGCGACCTTATGTAAGAAATATATAAACCCTTTGCAATGGAGAAATCAATAAATCAAT CAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	report	0.97	0.99	0.47	263	2.4e+03	0	90	
143	CL143	0.023	230	0.96	352	ACGGTATGCAAAAGTCAATAAATTTAGTAAATTTAGAGCACTCACAAGACACAATAAATAAATAA TAATAAATTTGATTAATGATGCTAAATGATTTAAACAACAAAAGAAAGCACTAATGCTGACATA TTAATATACAAACAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT TACCACACAATAAAGGATTAATGCTGACACAATAAATAAATTTAGGATTTACGAGGCTTTAGGAT AAAAGAGCAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	report	1.00	1.00	0.58	230	5.7e+03	0	51	

154	CL154	0.019	186	0.98	560	TATTTTATTTCAATGATTAATAAATAAGCAATGATCTATAACATAGGATGATCTACTGTAATCTATAA CTCAATATGCTAGGGGGGATAAATCAATATATTGACTAGTCTTATATATCAATATTTGGGTACAAAACTTTG TTTACAAATCAATGACTATCCATGGATGTTCCACCTATACACATATTTTCCATCAAAAATCTGATTTTGACT GTAAACACATTTCAACTGATTTTAAGTATTTTAAAGTAAACACACATTTAGACACAAAGATTAAGGAATATAT ATGATATTAAGTCTTAATTTGACATATCAAAATATTTAAATGAAGGATGATCTACATTTCTCTTTGATT ATGGCAAAAGCTAGGATTTAATATCTGATAAAAACTCTCGAATATGTACCTTAAAGCATCTCCAATGGAG AATTTTTGGTGGTGTGATATTTTGGTGTCCAAATGCAATGCAATTAAGCAGTCTAATCAACCTTAAT	report	0.98	0.96	0.58	186	1.4e+03	0	91	
157	CL157	0.018	182	0.99	781	GGTAATGTATCACACGCTTTATTTTAAATAAATAAAGTAAGTTTTCTACTAATCAATCTTTTAAAGA AGGAAGATACATTTGGTATTTGGCAGATGACGGGATGATATCTTCACTGCAACATTAATATGGATGAT TTGTTTTCTCAATAACTCTATGTTGTAATTTTGAAGTCTTATATAAAGAAATGAGGATATTAAGCTTT TTTTAATCATTGACATGTCACACATGTAGATAGATGAACCAATTAATGGAATGATATTTTCTGAAAC CAAAATCTTTCTATAATATAGGTAGAAATGGTATCTTTTCAATATGATCATTAAAAACACATTAATGAT ATATCTATTTGGTAAACCTTATCTTTTGGTCAAGATCATACTAATATCTAAGAAAACACTAAGAGTGGTG TATCAACAGTTCTTACTGCTCAATGTAAGAAACACATAAAATTTTCTGATGATTTCAACCTCTACTGCG TTATGTTAGTAAGTCTATTTTATACATTAATATTTTAAAGTCTGGGATGGAATGTAAAACTTA CAATTTGACTTAAAAAATGACTAAAAATTAATTTTAAAGCAATGCTTTAATATGATAGATGATGAT CTCTCATTTTGGCTAAAGAAATCAAGAATGAAGGTTACTATATGAATAAATAA	report	0.99	0.96	0.75	182	1.7e+03	0	97	
158	CL158	0.018	182	0.99	313	GTGGATAGCACTGCAGACTTTATTTATGAAGATAAATAACAAATAAAGAACTCTTAATGTGGAATTTATTTG TTTTATGATTTGCCCTAATTTATAGCAAGTAAAGCAAAACATATAGCATCTGCTGCTTTTCTCAAGCATCACTT TATTTCTATAAATCACTCTCAATAAATGCTGGTGTGTTAAGATTTTCACTGATTTTCAACAGAGAGATGTTA GGAACTACAAAAATTTCCCATAGTCGATCTGAAAGCGGTATAAATGGAATTAATAACAATACA	report	0.99	0.98	0.75	182	3.5e+03	0	70	

Putative satellites (low confidence)

Cluster	Genome Proportion[%]	Size real	Satellite probability	Consensus length	Consensus	Kmer analysis	Graph layout	Connected component index C	Pair completeness index C	Kmer coverage	V	E	Pbs score	The longest ORF length	Similarity based annotation
19	CL19	0.680	6755	0.037	130	GATAAAGATCAGAAAATCTTAGGATGATTTAACTGCAACGACAAAAGCTTGGAAATATCTCAACTGGAATAGAAAT CAGGGAGACTTAGGGTGCATCTGACTGAACACAGAAAGGCTTTCGACTG	report	0.95	0.72	0.26	6755	970393	0.000	173	
26	CL26	0.470	4671	0.022	50	CCTGGCTAGATCAGGAATCGAATCTGGAATAGTGTGTCACAGATGTC	report	0.89	0.62	0.29	4671	610423	0.000	132	
34	CL34	0.330	3241	0.085	169	GAAATTCAAAATAAACCCAGGGCTTGTGCAAAAGCTCAAGAACTTTGGGGCACTCTCAATGTGTTATTTGAGATGCTCA TGCAAAATGACGACGAGATTTATTTCTAAGGCGGTTTGGCTCGCTTCCGTTTGGCAAAAAGCAATTCACGCG GTACCGTGG	report	0.85	0.98	0.52	3241	545116	0.000	130	0.52% 45S_rDNA/25S_rDNA%
40	CL40	0.290	2857	0.039	53	AAATCTTTGAGAGTTTATCTGAACGAGTAAATCTCGAGATGAATCAGAAT	report	0.80	0.69	0.26	2857	136812	0.053	124	
47	CL47	0.230	2280	0.421	177	TACGTTGAAGCAGACAGTCTCTAGATCTTGTGAAGATGTTTCCCTAGTGAAGTACTGACCGGTTCTTAAGATCTCA ACTGAATTTCTCGTGAATTCAGATAGGTTCTCAATCTCGCAATTTTCCCTGCGAAGTGGACGAGTCTTA CAATCTCAACGGTATAC	report	0.97	0.81	0.23	2280	198250	0.000	91	
49	CL49	0.200	2004	0.026	64	ATACTATTCAGATTTCTCTAGAGATGTCAGATGTGATCAGATAGGCTGACATCTG	report	0.87	0.63	0.44	2004	128970	0.000	126	
51	CL51	0.200	1984	0.041	58	TACTTGAATGAAGCTCGAATAGTGGGCTGGAAGGAACTGATAGTAGGGT	report	0.83	0.70	0.47	1984	500088	0.000	96	
72	CL72	0.120	1139	0.046	57	TCCATCGGAGTAAACAATCTCAACACGAATCTCCCAATAGCAGGAGTACCA	report	0.80	0.77	0.48	1139	56254	0.000	173	
79	CL79	0.100	1012	0.024	50	AAGTTTAAACAGCAAGGTTTGAATCAATACGACGAGATCAAGA	report	0.73	0.85	0.34	1012	26291	0.000	140	
86	CL86	0.079	787	0.066	1257	TTGATTTTATGTTGCTGGTGAATAAACCAATTCACATACACAGTGTACTGATTTCTAGTTACATATGGAATTT AAATTAAGTGTCAACTTCACTAAGAAAGCAATTTTGTAGAGTGGTCTCTGCTCAATTTTTTAAATGAT TTAAATAGATGAATCAATCATATAGATATTTATGTTGTGTAATTTTATCCATTTAAATTAATTTTGTGAC GAAATTTGGATTTTACTTTTATTTTAAAGGAAAATCTATTTAGTCCCTCAACTATATCTCTGGTTAACTTTGCT CTCTTAATTTTCTTTTCTTTTATATATGATTTTCTTTTAAACCAACTATAAATCTCATATGATATAGACA TCAATGAAATTTGAGCTTAACTCATATAGTTTCTTTTAAATGATTTTCAATTTTGGATGAACATGGTTTATAT CTATGTTTGGATCATTTTACTGATTTTGGCAAAATAGGATTTACACATTTTAAAGTTTAAATTTGCTCT TCAGTGTAAAGTAAACAGTAAAGTTTGTGTAATAAATAAATTAATTAACATTTTACACAATATCATAA TTAGATCATATGTTTCTACATATCATAAATTAATCATGTTAAATTTGCTCTTTTATGATGTAATGATTAAT ATCTATATAGATGACTTCAAAATATAAATTAAGATTTAACTTATTTGATTAAGAAATATAGAAATTA TTATGTTGCAAAATTTTCTGCTAACTATCATATCTCTGCTGCAACAGAGTAAATATGAGGAAAGGAAACA ACACATTTTGTGTTAATCTAGAAATAGAGTTTCAATGCAAAATAACACATTTAATTAATGTTGACATCA AACATATATGATTTTAAAGTGTGTAATAAATAAAGTCAATTTGATGATGCTGTTAGTTGTTACTAGGAAA TGATATAGAGGATGTTTAAACACATTTAGTCAAAATTTACTTTTATGATGATTTGATTAATGATGATTTG TAAACAACTCTCACTTTAAAGGTTTAAAGTCACTTTTAAAGTGTCAATTAAGAGGCTATACAAAATAA TAAATTAATGAGAAATTAATTAATTAATCAATTTCACTCCGATATCAAT	report	0.83	0.85	0.49	787	13558	0.000	90	
117	CL117	0.037	369	0.063	687	ATACCAACATGTTGATCTATATGATTTTAAATTAATACTAATATAGATATGGAATTAATCAAGG TGGCCCATTAACAATATGCTCATTCAAGATAGATAAATCAATGATGTTTAAATTTTTTAAAGGAAATA AABAAATTAATTTGATTAATACAAAGGAAATTAATCAATAAAGCAACTTGAAGAAACTTAAACAAAT AAGATATAGTAAATAGGATTTAAACAATCTTACTTGGACATTTATCTACTGAAACAGTTTCTTCA AATAAACAATTTAATGCTTTGACTAGAACATGTTTACAGATTTGAAATAGAAATTTAGCTGAAAGATAAA AACATATCAAGATTAATTTTTTATAATCAAGCTCTGACTTGTCAACCAATTTGAGTTGAATGGAAGGATACA TGCAGCCCAATTAAGTAAAGTGTCTATTTGATGCTGTTAGGATTTGGTCAAAATAGATTTGATGATTTT AGTTTCTGATGTTTGGAGTTTGGTCTCTCTTTGTTGATTTCTCTATCTTTTCTCAATATATTTTGGAA TTATAAATAAATAAATTTCTATGTTTAAATTTTTTATGTT	report	0.75	0.98	0.55	369	5745	0.000	71	
121	CL121	0.033	327	0.086	44	ATGATCATGATGATGAACCTTTACACTAGTCAAGTATGTA	report	0.85	0.97	0.52	327	4746	0.000	51	
124	CL124	0.033	326	0.088	867	ATATTCATATATGTTTTTTTTGTTGATGTTTAAATGTTTAAATTTTTCTATATCAATAAAGACATTTA TAATCTAAATTCATATAGCTTAATATAAGTCAATATGAAATAGAAATCAATCTGACAGGATGGAACAAAT TTCACTCTAGCAAGTGGTTTTTATCTAATAAAGGAAATAAATGCTACAGTGTACATGTTGTTGTTGATAA AGATGAAGATGATCAATAACTTTGTAATATCCGATACACTGATGCTCACTTGGCGAAATTTATGTTCAACATAT GGATCAATGATATATCGGACATCTAGGAGTCTGCTCTTATATTTTAAACAGAAACAAATATATCTCAGG TGTTTTCTTATGCTCTACTACAGATTTAAATTAAGTCTCCCAAAATTTATAGGTTTCAAGACTTGAACATA CTTCTCTAAATTAATAACAATTTCTAGTTTATTTGAAATAGATAGTGGTTACCCCTTACTTGAAGTTGAG TTTTGAAAGGTTGACGGTGAATCAATTTAAATCATGCTTGAATTTAGAGTTTTTCTCAAGGCTCACTCGA GATTAATAGCTCAAAATCGATATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT CACAATTTACAGTGTGAT AACTTTTACATGAT	report	0.80	0.99	0.61	326	3636	0.000	74	7.06% organelle/plastid%

rDNA

Cluster	Genome Proportion[%]	Size real	Satellite probability	Consensus length	Consensus	Kmer analysis	Graph layout	Connected component index C	Pair completeness index C	Kmer coverage	V	E	Pbs score	The longest ORF length	Similarity based annotation	
98	CL98	0.06	596	0.99	362	GGGTAAATATTATCGTTAGCAAGGATAAAACATAAATCTGGTGTAAATTTTATTTGGTGTAAATATTATCGTTA ATAAGGAGAAAACGAATAATTCGGTTAAATTTAATTTGTTGTCGGGAGACTAAAATGCCGGTAATAAGGAAA GACCCGAATATGTATACAATAAAGAGCATTACATACAGGTGCGATCACCAGCAGCAATGACCCGGATCCCATCAGA ACTCCGACGTTAAGCGTCTTGGGCGAGAGTAGTACTAGGATGGTGACCTCCCTGGGAAGTCTTGTGTGCACCTCTTT TTGCGTATTTTGAAGGAGTCTTTTATTTTATTAATCG	report	0.99	0.99	0.83	596	41572	0	86	43.29%	5S_rDNA/5S_rDNA%



Other clusters

Cluster	Genome Proportion[%]	Size real	Satellite probability	Consensus length	Consensus	Kmer analysis	Graph layout	Connected component index C	Pair completeness index C	Kmer coverage	V	E	Pbs score	The longest ORF length	Similarity based annotation
1	CL1	16.000	162199	7.8e-22		N/A		0.02174	0.89		37857	980689			0.00% organelle/plastid%
2	CL2	12.000	116614	1.3e-21		N/A		0.01780	0.86		38536	814583			4.99% organelle/mitochondria%
3	CL3	3.600	35486	2.2e-23		N/A		0.00132	0.81		35479	3961892			
3	CL3	3.600	35486	2.2e-23		N/A		0.00132	0.81		35479	3961892			
4	CL4	3.600	35313	1.7e-08		N/A		0.36770	0.84		35069	1558025			
5	CL5	3.400	34106	9.5e-06		N/A		0.46569	0.63		34104	3713198			
8	CL8	2.000	19997	3.8e-22		N/A		0.00690	0.80		19997	1489306			0.02% organelle/mitochondria%
9	CL9	1.600	15824	3.3e-22		N/A		0.00531	0.81		15824	6796896			
12	CL12	0.850	8459	1.5e-21		N/A		0.00012	0.55		8459	28788			
13	CL13	0.850	8459	4.7e-23		N/A		0.00059	0.77		8459	131061			
14	CL14	0.840	8338	1.4e-23		N/A		0.00084	0.83		8338	219419			6.82% organelle/mitochondria%
15	CL15	0.840	8314	2.7e-22		N/A		0.00036	0.67		8314	93163			
16	CL16	0.760	7536	3.1e-24		N/A		0.00013	0.90		7536	136175			1.51% organelle/mitochondria%
17	CL17	0.710	7021	2.1e-06		N/A		0.43769	0.65		7021	322212			
20	CL20	0.650	6480	3.9e-23		N/A		0.00185	0.78		6480	79344			1.85% organelle/mitochondria%
21	CL21	0.650	6479	4.6e-05		N/A		0.52307	0.71		6479	27305			

Detailed report for cluster CL7

	kmer	variant	total_score	monomer_length	score_bn	consensus	graph_image	logo_image
1	11	2	0.538	59	5.0e-03	GTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
2	15	2	0.505	59	5.5e-03	TCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
3	19	2	0.484	59	5.4e-03	TCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
4	23	3	0.463	59	5.6e-03	TCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
5	27	3	0.421	59	5.2e-03	AGTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGT		
6	11	1	0.323	58	1.2e-03	TTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTAGTTTGTGTTGAGATTTTG		
7	27	6	0.279	118	1.1e-03	AGGTAGTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTAGTCTGTTGTCGAGATT TTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGA		
8	15	1	0.275	58	1.2e-03	GAAGGTAGTCTGTTGTTGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATG		
9	23	2	0.248	58	1.4e-03	TCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
10	19	1	0.245	58	1.2e-03	TAGTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGG		
11	27	2	0.215	58	1.3e-03	GTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTA		
12	27	5	0.190	117	7.4e-04	ATTATGGAAGGTAGTCTGTTGTCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTCATTATGGAAGGTAGTCTGTTG TCGAGATTTTGTACTCCAATGGATGGTAGCCTTGTC		