

Supplementary Material

Supplementary Figures Legends:

Fig. S1. Repetitive clusters (n=122) in *D. buzzatii* identified by RepeatExplorer after clusterization of 270366 reads. Together, these clusters represent 14.7% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The pBuM-1 and CDSTR198 satellite DNAs are indicated.

Fig. S2. Repetitive clusters (n=328) in *D. seriema* identified by RepeatExplorer after clusterization of 526010 reads. Together, these clusters represent 26.9% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The pBuM-2, DBC-150 and *CDSTR138* satellite DNAs are indicated.

Fig. S3. Repetitive clusters (n=217) in *D. mojavensis* identified by RepeatExplorer after clusterization of 323342 reads. Together, these clusters represent 14.9% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The *CDSTR130* and pBuM-1 satellite DNAs are indicated.

Fig. S4. SatDNA consensus sequences from *D. buzzatii*, *D. seriema* and *D. mojavensis*.

Fig. S5. FISH on polytene chromosomes: **(A)** *CDSTR130* (green) and *pBuM* (red) satDNAs probes on *D. mojavensis*, and **(B)** *CDSTR138* satDNA probe (red) on *D. seriema*.

Supplementary Tables Legends:

Table S1. List of primers used in the present study.

Table S2. Description of all clusters retrieved from 1834708 reads of *D. buzzatii* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Table S3. Description of all clusters retrieved from 2144275 reads of *D. seriema* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Table S4. Description of all clusters retrieved from 2174346 reads of *D. mojavensis* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Table S5. Description of the ten most abundant clusters of the *D. melanogaster* genome identified by RepeatExplorer. The satDNA families with monomer lengths smaller than 50 bp are highlighted in bold.

Table S6. Main features of 37 *CDSTR198* arrays located on euchromatic regions and their chromosome location according to GenomeBrowser analysis.

Table S7. List of genes associated with *CDSTR198* arrays and their relative positions in relation to *CDSTR198*.

Supplementary Figure 1.

D. buzzatii

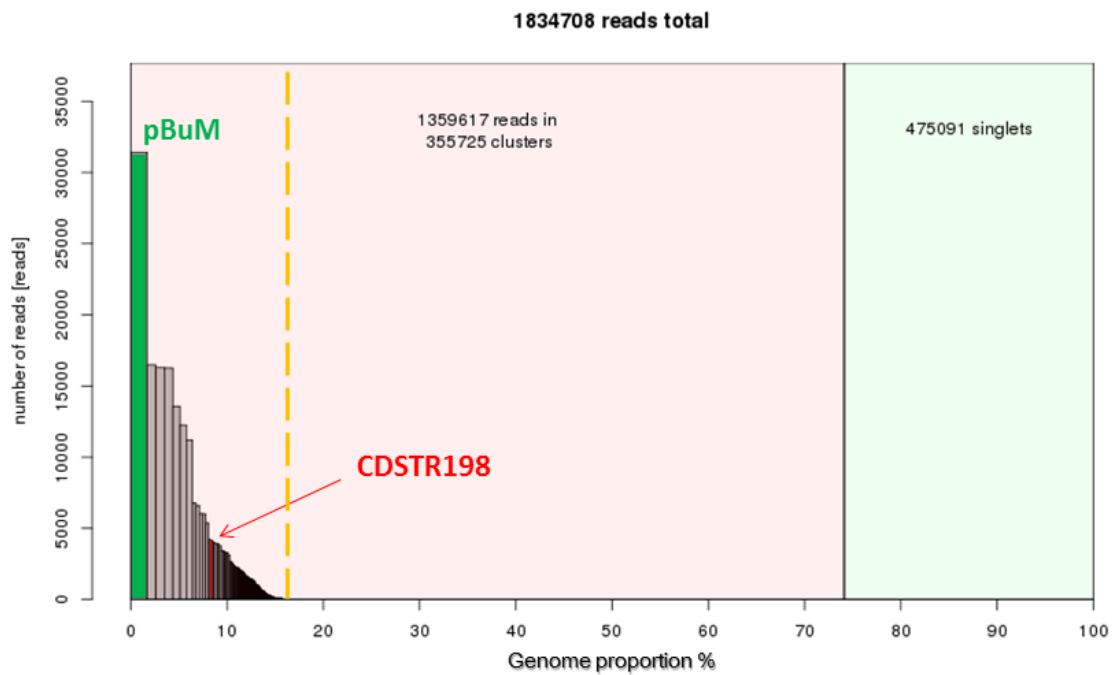


Fig. S1. Repetitive clusters (n=122) in *D. buzzatii* identified by RepeatExplorer after clusterization of 270366 reads. Together, these clusters represent 14.7% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The pBuM-1 and CDSTR198 satellite DNAs are indicated.

Supplementary Figure 2.

D. seriema

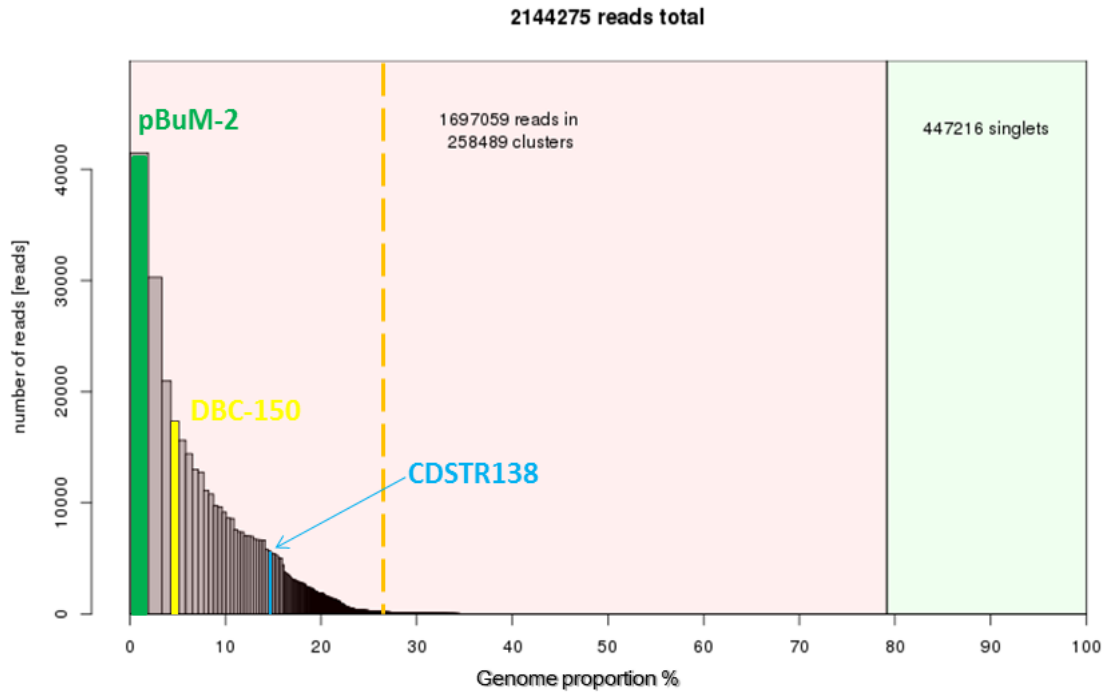


Fig. S2. Repetitive clusters (n=328) in *D. seriema* identified by RepeatExplorer after clusterization of 526010 reads. Together, these clusters represent 26.9% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The pBuM-2, DBC-150 and *CDSTR138* satellite DNAs are indicated.

Supplementary Figure 3

D. mojavensis

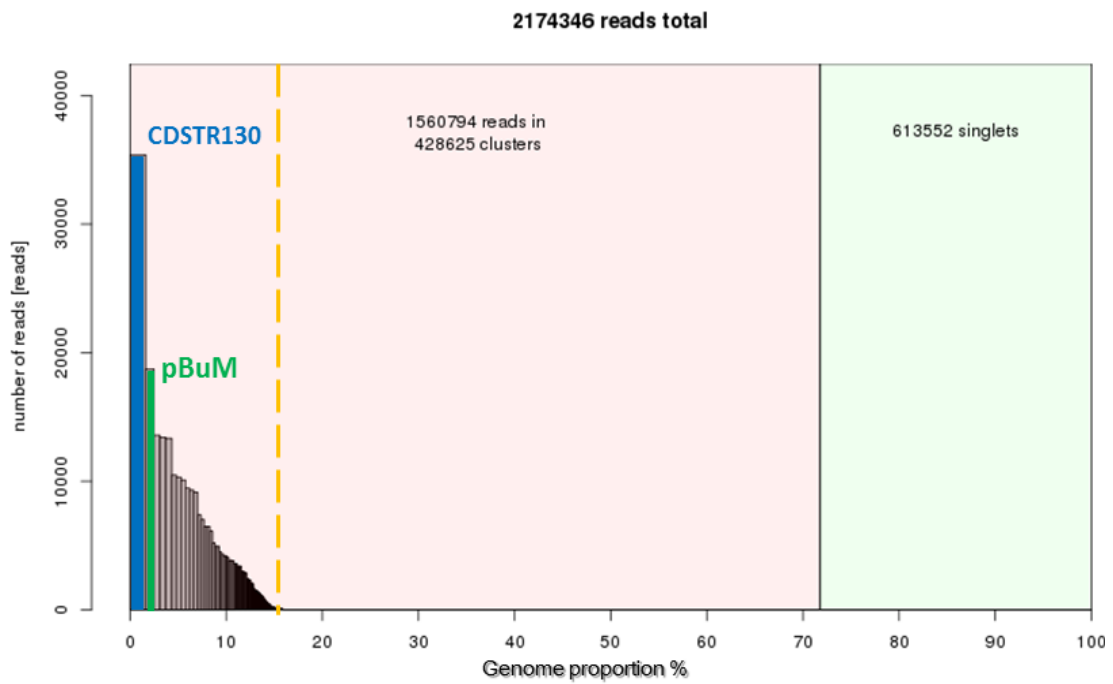


Fig. S3. Repetitive clusters (n=217) in *D. mojavensis* identified by RepeatExplorer after clusterization of 323342 reads. Together, these clusters represent 14.9% of the genome (identified by the yellow traced line). Each bar in the graphic represents a cluster of similar reads. The *CDSTR130* and pBuM-1 satellite DNAs are indicated.

Supplementary Figure 4

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>CDSTR130_SatDNA_D.mojavensis_MF170235
CAATAGAGAAAAATTGCAAAATGTGATGGAAAAATCAAAAAAGCAAAGGGATTTTATATTTTAAAG
CTTTGATAACAAAATATTGAAAGATATTCGGCAATAAACTGGTAAATATTG

>CDSTR138_SatDNA_D.seriema_MF170236
CAACTGTTGATTTTTGTATATAGAATACGAATAAAATCAAATATATGGTGTAGAAGAGTATATTTG
CGCCGATTTACCATGAACATAACACTAGTTTGATTTTTTATTCATTTATAGTGAGTATAGGCATAT
CTGGGC

>CDSTR198_SatDNA_D.buzzatii_MF170237
AAGGTAGAAAGGTAGTTGGTGTAGATAAACCAGAAAAAGAGCTAAAAACGGCTAAAAACGGCTAGAA
AATAGCCAGAAAGGTAGATTGAACATTAATGGGCAAATGGATGGATAAATAAGACTGGTCATCATC
CAATGAACAGAATCATGATTAAGAGATAGAAATATGATTAGAAAAGTAGGATAGAAAAGGTTAGAAAG

>pBuM-1a_SatDNA_D.buzzatii_MF170238
GCAAAAGACTCCGTC AATTAGAAAACAAAAAATGTTATAGTTTTGAGGATTAACCGGCAAAAACCG
TATTATTTGTCATTTGATTTCTTTATGGAATACCGTTTTAGAAAGCGTCTTTTATCGTATTACTCAG
ATATATCTTAAGATTTAGCATAATCTAAGAACTTTTTGAAATATTCACATTTGTCCA

>pBuM-1b_SatDNA_D.buzzatii_Y_MF170239
TAA AATTACTACTTGAAACTAGAAAGAAAAGAAAGTTATAGTTTTGAGGTTTAACCGGCAAAAATC
GTATTATTTATCATTAGATTTCTTTATAGCATGCCGTTTATAAGCGTGTCTTATCGGATTATTCAG
ATATATTGCAAAATTTAACATAGCTCGAGACCTTTTTGAAATATTAACATTAATCCA

>pBuM-1_SatDNA_D.mojavensis_MF170240
CCTGAAATGCGGTATAAGATCAGAAAATTGACTTTTTTCTATGTATAACAGGCAATAACAGGACTA
TTTCGGGGCCGATTTTCAGTACGACTTTCTTTGTTGGAAGCATCTTTTAGAGCCCTATCTATTGACG
TATTCAGATTTTCAATGGGCCAACAACCTTTTTGAAATATTTACATTATTATCCC
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Fig. S4. satDNA consensus sequences from *D. buzzatii*, *D. seriema* and *D. mojavensis*.

Supplementary Figure 5.

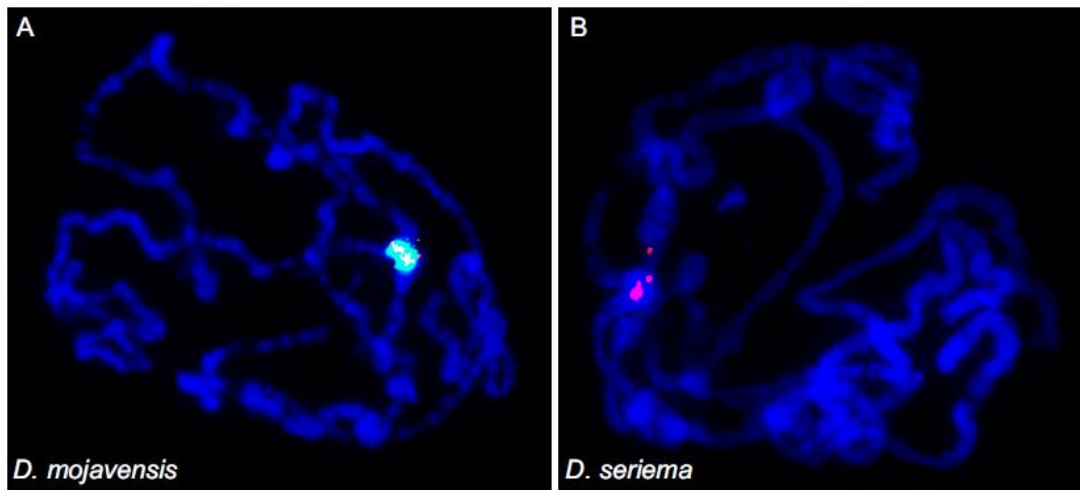


Fig. S5. FISH on polytene chromosomes: (A) *CDSTR130* (green) and *pBuM* (red) satDNAs probes on *D. mojavensis*, and (B) *CDSTR138* satDNA probe (red) on *D. seriema*.

Supplementary Table 1. List of primers used in the present study.

	Primer sets	Primer sequences
<i>D. buzzatii</i>	<i>pBuM-a</i>	Fwd: CAATTAGAAAACAGGAAATTG Rev: GACGGAGTCTTTTGCTGGACAA
	<i>pBuM-1b</i>	Fwd: GAAACTAGAAGGAAATAAACG Rev: CAAGGAGTCCTTTTATGGATTA
	<i>CDSTR198</i>	Fwd: GGTAGATTGAACACTAATGGGC Rev: CCTTTCTGCCTTTTTTCTAGCCG
<i>D. seriema</i>	<i>CDSTR138</i>	Fwd:CCGATTTTCCATGAACATAACC Rev: CGCAAATATACTCTACTACACC
<i>D. mojavensis</i>	<i>CDSTR130</i>	Fwd: CAATAGAGGCAAATGAATTTAG Rev: CATTACTAACCAGTTTATTGCCG
	<i>pBuM-1a</i>	Fwd: GCCGATTTTCAGTACGACTTACTTCG Rev: CCAGAAATAGTCCTGTTATTGCCTG

Table S2. Description of all clusters retrieved from 1834708 reads of *D. buzzatii* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Cluster	Genome Proportion %	RepeatMasker Annotation	Reads number on each cluster	Outside reads with similarity %
CL1	1.710	<i>pBuM-1</i>	31409	0.00038
CL2	0.898	RC.Helitron	16475	0.19870
CL3	0.888	DNA.hAT.Pegasus	16285	2.70400
CL4	0.886	DNA.hAT.hobo	16263	3.69400
CL5	0.739	Helitron	13567	4.80500
CL6	0.668	RC.Helitron	12252	8.96000
CL7	0.611	Non-LTR CR1	11208	0.11510
CL8	0.370	Galileo	6790	0.55450
CL9	0.360	Homo6	6601	6.44000
CL10	0.328	LINE-like	6024	0.03731
CL11	0.327	Galileo	6007	0.49990
CL12	0.294	rRNA	5393	0.05911
CL13	0.229	<i>CDSTR198</i>	4202	0.00650
CL14	0.226	Unclassified	4142	0.08527
CL15	0.217	LTR BEL	3982	0.06588
CL16	0.215	PERI	3940	2.02800
CL17	0.213	LTR BEL	3914	0.30090
CL18	0.205	Galileo/Helitron	3766	6.62800
CL19	0.188	rRNA	3442	0.16500
CL20	0.185	LTRGypsy	3387	0.08860
CL21	0.181	Non-LTR_R1	3317	0.05204
CL22	0.179	LTR Gypsy/Minicopia	3290	0.05014
CL23	0.170	LTR Gypsy	3122	0.03179
CL24	0.145	LTR BEL	2653	0.04116
CL25	0.143	LTR Gypsy	2622	0.42640
CL26	0.136	LTR Osvaldo	2493	0.12570
CL27	0.129	PARISa	2364	0.08243
CL28	0.125	INVADER6_I	2292	0.14160
CL29	0.124	LTR BEL	2279	0.42260
CL30	0.121	Galileo	2214	0.29560
CL31	0.120	LTR Copia	2198	0.28850
CL32	0.113	LTR Gypsy	2070	0.13140
CL33	0.110	RC.Helitron	2025	0.28540
CL34	0.109	LTR Osvaldo	1996	0.06629
CL35	0.104	Unclassified	1917	0.27710
CL36	0.100	Unclassified	1835	0.05137
CL37	0.095	Non-LTR Jockey	1736	0.02687
CL38	0.089	LTR BEL	1640	0.57820
CL39	0.089	Non-LTR R1	1632	0.21130
CL40	0.087	LTORBEL	1592	0.02742
CL41	0.084	Homo9	1537	0.29000
CL42	0.082	LTR Gypsy	1501	0.03540

CL43	0.079	Non-LTR Jockey	1451	0.06051
CL44	0.078	LTR Copia	1437	0.00347
CL45	0.078	Non-LTR Jockey	1428	0.02450
CL46	0.077	LTR Copia	1411	0.11840
CL47	0.074	Non-LTR_I	1351	0.07546
CL48	0.073	DNA.TcMar.Tc1	1340	0.52960
CL49	0.069	Non-LTR Jockey	1260	0.38600
CL50	0.061	Unclassified	1126	0.12680
CL51	0.059	Non-LTR Jockey	1076	0.23030
CL52	0.058	LTR BEL	1066	0.03978
CL53	0.056	LTR Copia	1019	0.15520
CL54	0.055	DNA.CMC.Transib	1015	0.49800
CL55	0.054	LTR Gypsy	987	0.00000
CL56	0.053	Non-LTR RTE.BovB	982	0.00000
CL57	0.050	LTR Gypsy	909	0.12640
CL58	0.049	DNA.TcMar.Tc1	891	0.20170
CL59	0.045	Non-LTR Jockey	828	0.03882
CL60	0.043	DNA.hAT-9	795	0.06751
CL61	0.038	Unclassified	705	0.68000
CL62	0.038	RNA	699	0.00454
CL63	0.037	RC.Helitron	687	0.09555
CL64	0.035	LTR Copia	644	0.00000
CL65	0.035	DNA.hAT.hobo	639	0.30280
CL66	0.035	LTR Copia	636	0.07575
CL67	0.034	LTR Gypsy	627	0.10790
CL68	0.034	Unclassified	625	0.19720
CL69	0.033	Galileo	604	0.25630
CL70	0.030	DNA.TcMar.Tc1	560	0.07143
CL71	0.030	RC.Helitron	543	0.03627
CL72	0.029	Unclassified	530	0.00000
CL73	0.028	DNA.TcMar.Tc1	509	0.22400
CL74	0.026	Non-LTR Jockey	480	0.47450
CL75	0.026	Unclassified	477	0.19390
CL76	0.025	LTR Gypsy	450	0.00000
CL77	0.023	LTR Copia	430	0.00000
CL78	0.023	LTR Gypsy	429	0.36040
CL79	0.022	DNA.hAT.Pegasus	412	0.08403
CL80	0.022	Rep2-DF	396	0.13160
CL81	0.021	LINE jockey	383	0.00000
CL82	0.021	Unclassified	382	0.00000
CL83	0.021	DNA.TcMar.Tc1	376	0.27770
CL84	0.020	DNA.hAT.Ac	375	0.05963
CL85	0.020	LTR Copia	368	0.04246
CL86	0.019	LTR Gypsy	344	0.28300
CL87	0.018	DNA.TcMar.Tc1	335	0.38710
CL88	0.018	LTRGypsy	333	0.05133
CL89	0.018	LTR Copia	332	0.07948
CL90	0.017	LTR Gypsy	314	0.33650

CL91	0.017	LTR Gypsy	314	1.91400
CL92	0.017	DNA.PiggyBac	312	0.00000
CL93	0.017	LTR BEL	309	0.00000
CL94	0.017	DNA.hAT.hobo	309	0.05537
CL95	0.017	LTR Copia	307	0.20480
CL96	0.016	Non-LTR Jockey	299	0.32750
CL97	0.016	LTR Gypsy	298	0.15710
CL98	0.016	DNA.CMC.Transib	297	1.41100
CL99	0.016	Non-LTR Jockey	293	0.00000
CL100	0.016	DNA.TcMar.Tc1	291	0.47050
CL101	0.016	LTR Gypsy	289	0.00000
CL102	0.015	Unclassified	268	0.00000
CL103	0.015	Unclassified	267	0.25610
CL104	0.014	Unclassified	259	0.00000
CL105	0.014	LTR Gypsy	249	0.07072
CL106	0.013	LTR Gypsy	245	0.09872
CL107	0.013	Unclassified	244	0.23550
CL108	0.013	Unclassified	241	0.11280
CL109	0.013	LTR Gypsy	235	0.41250
CL110	0.013	LTR BEL	231	0.00000
CL111	0.012	LTR Gypsy	223	0.16910
CL112	0.012	DNA.TcMar.	221	0.20410
CL113	0.012	DNA.TcMar.	220	0.81220
CL114	0.012	DNA.TcMar.Tc1	213	0.72610
CL115	0.011	LTR Gypsy	205	0.18590
CL116	0.011	Unclassified	204	0.00000
CL117	0.011	DNA Sola1-type	199	0.21910
CL118	0.011	Unclassified	195	0.00000
CL119	0.011	DNA.CMC.Transib	194	2.55300
CL120	0.010	LTR Gypsy	190	0.26460
CL121	0.010	DNA.CMC.Transib	189	0.10960
CL122	0.010	LTR Gypsy	186	0.00000

Table S3. Description of all clusters retrieved from 2144275 reads of *D. seriema* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Cluster	Genome Proportion%	RepeatMasker Annotation	Reads number on each cluster	Outside reads with similarities %
CL1	1.930	pBuM-2	41472	0.176
CL2	1.410	RC.Helitron	30287	24.010
CL3	0.978	Homo6	20966	32.230
CL4	0.809	DBC-150	17349	0.784
CL5	0.730	RC.Helitron	15646	26.060
CL6	0.673	Non-LTR CR1	14427	5.296
CL7	0.607	PERI	13026	24.800
CL8	0.595	RC.Helitron	12761	42.540
CL9	0.519	LTR Gypsy	11132	2.677
CL10	0.504	SSS139	10798	19.010
CL11	0.455	Non-LTR R1	9753	0.749
CL12	0.450	Non-LTR R1	9650	1.907
CL13	0.428	LTR BEL	9170	2.345
CL14	0.403	rRNA	8643	0.104
CL15	0.401	Galileo	8605	6.392
CL16	0.355	LTR Gypsy	7615	2.232
CL17	0.345	Unclassified	7408	0.310
CL18	0.344	Unclassified	7385	0.163
CL19	0.329	RC.Helitron	7044	31.960
CL20	0.328	Galileo	7041	9.260
CL21	0.326	Non-LTR Jockey	6993	2.331
CL22	0.314	Non-LTR Jockey	6743	4.968
CL23	0.313	LTR BEL	6705	1.253
CL24	0.311	Unclassified	6674	1.049
CL25	0.311	LTR BEL	6658	6.008
CL26	0.272	LTR Gypsy	5826	1.442
CL27	0.266	CDSTR138	5709	0.893
CL28	0.257	Non-LTR R1	5502	3.017
CL29	0.253	LTR Gypsy	5433	4.013
CL30	0.249	LTR Gypsy	5343	1.029
CL31	0.238	rRNA	5094	1.924
CL32	0.234	LTR Copia	5022	3.146
CL33	0.206	rRNA	4421	3.936
CL34	0.176	LTR Gypsy	3781	1.878
CL35	0.171	LTR BEL	3663	2.266
CL36	0.167	LTR Gypsy	3583	5.610
CL37	0.160	Unclassified	3438	2.967
CL38	0.152	LTR Gypsy	3257	2.395
CL39	0.147	LTR Gypsy	3143	6.713
CL40	0.144	Unclassified	3082	4.121

CL41	0.143	LTR Copia	3076	2.503
CL42	0.140	LTR BEL	3011	1.328
CL43	0.137	LTR Gypsy	2933	0.852
CL44	0.136	RC.Helitron	2910	0.687
CL45	0.133	LTR Gypsy	2856	2.066
CL46	0.132	Unclassified	2830	0.177
CL47	0.129	LTR Gypsy	2766	3.868
CL48	0.129	Unclassified	2759	8.191
CL49	0.123	LTR Gypsy	2647	2.909
CL50	0.115	RC.Helitron/DNA.hAT.P egasus	2474	0.000
CL51	0.115	Non-LTR I	2473	3.275
CL52	0.114	LTR BEL	2440	3.238
CL53	0.111	LTR Gypsy	2378	0.925
CL54	0.111	DNA.Ginger	2373	6.153
CL55	0.109	Unclassified	2343	0.427
CL56	0.107	LTR Gypsy	2289	3.102
CL57	0.100	LTR Gypsy	2152	2.138
CL58	0.098	Non-LTR Jockey	2100	0.048
CL59	0.096	Galileo	2061	2.232
CL60	0.094	LTR BEL	2023	3.114
CL61	0.091	LTR Gypsy	1960	2.092
CL62	0.090	LTR Gypsy	1922	1.769
CL63	0.089	RC.Helitron	1919	1.928
CL64	0.089	LTR Gypsy	1910	1.571
CL65	0.089	LTR Gypsy	1899	2.791
CL66	0.088	LTR Gypsy	1895	3.219
CL67	0.088	Non-LTR Jockey	1883	1.009
CL68	0.085	LTR Gypsy	1832	4.039
CL69	0.082	Non-LTR Jockey	1758	2.446
CL70	0.079	Non-LTR Jockey	1698	4.005
CL71	0.078	DNA.TcMar.Tc1	1665	3.363
CL72	0.075	LTR Gypsy	1612	1.365
CL73	0.074	Unclassified	1596	0.125
CL74	0.074	Unclassified	1586	0.568
CL75	0.072	Unclassified	1555	0.000
CL76	0.072	DNA.CMC.Transib	1545	24.140
CL77	0.071	LTR BEL	1530	1.046
CL78	0.069	LTR Gypsy	1486	2.826
CL79	0.067	DNA.hAT.Tip100	1435	3.902
CL80	0.067	DNA.TcMar.Tc1	1429	2.799
CL81	0.066	LTR ERVL	1411	0.071
CL82	0.066	Unclassified	1406	0.854
CL83	0.065	Non-LTR Jockey	1400	0.643
CL84	0.064	DNA.TcMar.Tc1	1366	2.928
CL85	0.062	LTR Copia	1340	0.298

CL86	0.061	Galileo	1311	3.051
CL87	0.061	LTR Copia	1306	2.374
CL88	0.059	Non-LTR Jockey	1263	3.959
CL89	0.059	Non-LTR Jockey	1261	1.983
CL90	0.057	LTR Gypsy	1215	2.881
CL91	0.056	DNA.hAT.Ac	1200	5.917
CL92	0.054	Unclassified	1165	0.000
CL93	0.054	DNA.TcMar.Tc1	1163	4.729
CL94	0.049	Non-LTR RTE	1043	1.534
CL95	0.048	LTR Gypsy	1019	0.687
CL96	0.045	LTR Gypsy	969	0.516
CL97	0.044	LTR Gypsy	953	3.043
CL98	0.044	Unclassified	940	0.319
CL99	0.044	LTR Gypsy	934	0.107
CL100	0.043	Unclassified	932	0.000
CL101	0.042	LTR Gypsy	903	0.111
CL102	0.042	DNA.Maverick	895	0.335
CL103	0.041	Unclassified	869	0.115
CL104	0.038	LTR Gypsy	810	2.469
CL105	0.037	DNA.hAT.Pegasus	800	4.625
CL106	0.037	Unclassified	785	0.255
CL107	0.035	Unclassified	749	0.000
CL108	0.033	LTR Gypsy	715	2.378
CL109	0.033	Unclassified	709	0.000
CL110	0.033	Non-LTR R1	709	1.975
CL111	0.033	LTR Copia	701	0.856
CL112	0.032	Unclassified	688	0.000
CL113	0.030	Unclassified	639	0.157
CL114	0.029	Unclassified	631	0.000
CL115	0.029	LTR Gypsy	625	3.520
CL116	0.029	LTR Copia	624	3.526
CL117	0.029	LTR Gypsy	623	3.371
CL118	0.029	Unclassified	620	0.000
CL119	0.028	Unclassified	605	0.000
CL120	0.028	LTR Gypsy	600	1.167
CL121	0.028	Non-LTR I	595	0.840
CL122	0.027	Unclassified	585	0.000
CL123	0.027	Unclassified	579	0.000
CL124	0.027	DNA.PIF	575	0.000
CL125	0.026	Unclassified	550	0.000
CL126	0.026	Unclassified	549	0.000
CL127	0.025	LTR Gypsy	541	0.000
CL128	0.025	Galileo	532	4.511
CL129	0.025	DNA.TcMar.Tc1	531	4.520
CL130	0.025	LTR Copia	528	0.379
CL131	0.024	RC.Helitron	521	0.000

CL132	0.024	LTR Gypsy	518	1.158
CL133	0.024	CDSTR198	513	0.195
CL134	0.024	LTR Gypsy	503	0.000
CL135	0.023	LTR Copia	499	1.804
CL136	0.023	Unclassified	493	0.000
CL137	0.022	Unclassified	483	0.207
CL138	0.022	Unclassified	480	0.000
CL139	0.022	Unclassified	479	0.000
CL140	0.022	Galileo	476	4.202
CL141	0.022	Unclassified	470	0.000
CL142	0.022	Unclassified	467	0.214
CL143	0.021	DNA.TcMar.Tc1	449	3.786
CL144	0.020	Unclassified	438	0.000
CL145	0.020	Unclassified	436	0.000
CL146	0.020	Unclassified	436	0.000
CL147	0.020	LTR Gypsy	434	1.152
CL148	0.020	Unclassified	432	0.232
CL149	0.020	RC.Helitron	430	3.953
CL150	0.020	Non-LTR L1	429	0.000
CL151	0.020	LTR Gypsy	426	0.000
CL152	0.020	Unclassified	426	0.000
CL153	0.020	Unclassified	424	0.236
CL154	0.020	Unclassified	423	0.000
CL155	0.020	Unclassified	420	0.000
CL156	0.020	Unclassified	420	0.000
CL157	0.020	Unclassified	420	0.000
CL158	0.019	Unclassified	419	0.000
CL159	0.019	Non-LTR Jockey	412	1.456
CL160	0.019	RC.Helitron	410	2.439
CL161	0.019	DNA.hAT.hATm	410	0.000
CL162	0.019	DNA.hAT.hobo	409	1.711
CL163	0.019	Unclassified	407	0.000
CL164	0.019	Unclassified	405	0.000
CL165	0.019	Unclassified	404	0.000
CL166	0.019	Unclassified	399	0.000
CL167	0.018	LTR BEL	397	0.000
CL168	0.018	LTR Gypsy	396	0.505
CL169	0.018	Unclassified	394	0.000
CL170	0.018	LTR BEL	394	1.523
CL171	0.018	Unclassified	392	0.000
CL172	0.018	Unclassified	389	0.000
CL173	0.018	Unclassified	387	0.000
CL174	0.018	DNA.CMC.Transib	387	8.010
CL175	0.018	Unclassified	383	0.000
CL176	0.018	Unclassified	381	0.000
CL177	0.018	Unclassified	380	0.000

CL178	0.018	Unclassified	379	0.000
CL179	0.018	Unclassified	379	0.000
CL180	0.017	DNA.TcMar.Tc1	374	1.337
CL181	0.017	Unclassified	373	0.000
CL182	0.017	Unclassified	371	0.000
CL183	0.017	Unclassified	370	0.000
CL184	0.017	Unclassified	369	0.000
CL185	0.017	DNA.TcMar.Tc1	365	1.370
CL186	0.017	Unclassified	365	0.000
CL187	0.017	Unclassified	365	0.000
CL188	0.017	Unclassified	365	0.000
CL189	0.017	DNA.hAT	365	0.000
CL190	0.017	DNA.CMC.Transib	364	0.000
CL191	0.017	Unclassified	364	0.000
CL192	0.017	Unclassified	364	0.000
CL193	0.017	Unclassified	363	0.000
CL194	0.017	Unclassified	358	0.000
CL195	0.017	LTR Copia	356	0.281
CL196	0.017	Unclassified	356	0.000
CL197	0.017	Unclassified	354	0.000
CL198	0.017	Unclassified	353	0.000
CL199	0.017	Unclassified	353	0.000
CL200	0.016	Unclassified	349	0.286
CL201	0.016	rDNA	349	0.000
CL202	0.016	tRNA	349	0.000
CL203	0.016	Unclassified	349	0.000
CL204	0.016	Unclassified	348	0.000
CL205	0.016	Unclassified	347	0.000
CL206	0.016	Unclassified	346	0.000
CL207	0.016	Unclassified	344	0.000
CL208	0.016	LTR BEL	343	0.000
CL209	0.016	Unclassified	339	0.000
CL210	0.016	Unclassified	337	0.000
CL211	0.016	Unclassified	335	0.000
CL212	0.015	Unclassified	332	0.000
CL213	0.015	Unclassified	331	0.000
CL214	0.015	Unclassified	328	0.000
CL215	0.015	Unclassified	328	0.000
CL216	0.015	Unclassified	326	0.000
CL217	0.015	LTR ERVK	326	0.000
CL218	0.015	Unclassified	324	0.000
CL219	0.015	Unclassified	323	0.000
CL220	0.015	Unclassified	323	0.000
CL221	0.015	Unclassified	319	0.000
CL222	0.015	Unclassified	313	0.000
CL223	0.015	Unclassified	312	0.000

CL224	0.015	Unclassified	311	0.000
CL225	0.015	Unclassified	311	0.000
CL226	0.015	Unclassified	311	0.000
CL227	0.014	Unclassified	308	0.000
CL228	0.014	Unclassified	304	0.000
CL229	0.014	DNA.CMC.Chapaev	304	0.000
CL230	0.014	Unclassified	302	0.000
CL231	0.014	Unclassified	300	0.000
CL232	0.014	Unclassified	300	0.000
CL233	0.014	Unclassified	299	0.000
CL234	0.014	LTR Gypsy	299	0.000
CL235	0.014	Unclassified	299	0.000
CL236	0.014	Unclassified	298	0.000
CL237	0.014	Unclassified	296	0.000
CL238	0.014	Non-LTR CR1	296	0.000
CL239	0.014	DNA.CMC.EnSpm	295	0.000
CL240	0.014	Unclassified	295	0.000
CL241	0.014	Unclassified	292	0.000
CL242	0.014	Unclassified	291	0.000
CL243	0.013	Unclassified	289	0.000
CL244	0.013	Non-LTR I	287	0.000
CL245	0.013	Unclassified	287	0.000
CL246	0.013	Unclassified	286	0.000
CL247	0.013	Unclassified	286	0.000
CL248	0.013	Unclassified	283	0.000
CL249	0.013	DNA.TcMar.Tc	282	2.482
CL250	0.013	Unclassified	279	0.000
CL251	0.013	LTR Copia	277	0.000
CL252	0.013	Unclassified	276	0.000
CL253	0.013	Unclassified	274	0.000
CL254	0.013	Unclassified	274	0.000
CL255	0.013	Unclassified	273	0.000
CL256	0.013	Unclassified	273	0.000
CL257	0.013	Unclassified	273	0.000
CL258	0.013	Unclassified	273	0.000
CL259	0.013	DNA.Maverick	271	1.107
CL260	0.013	Unclassified	268	0.000
CL261	0.013	DNA.PiggyBac	268	0.746
CL262	0.013	Unclassified	267	0.000
CL263	0.012	Unclassified	265	0.000
CL264	0.012	Unclassified	264	0.000
CL265	0.012	Unclassified	263	0.000
CL266	0.012	Unclassified	263	0.000
CL267	0.012	Unclassified	262	0.000
CL268	0.012	Unclassified	261	0.000
CL269	0.012	Unclassified	259	0.000

CL270	0.012	Unclassified	259	0.000
CL271	0.012	Unclassified	257	0.000
CL272	0.012	LTR Gypsy	257	0.000
CL273	0.012	Unclassified	255	0.000
CL274	0.012	Unclassified	254	0.000
CL275	0.012	LTR ERVK	254	0.000
CL276	0.012	Unclassified	253	0.000
CL277	0.012	Unclassified	251	0.000
CL278	0.012	Unclassified	251	0.000
CL279	0.012	Unclassified	250	0.000
CL280	0.012	Unclassified	250	0.000
CL281	0.012	Unclassified	248	0.000
CL282	0.011	Unclassified	247	0.000
CL283	0.011	Unclassified	246	0.000
CL284	0.011	Unclassified	245	0.000
CL285	0.011	Unclassified	245	0.000
CL286	0.011	Unclassified	244	0.000
CL287	0.011	Unclassified	243	0.000
CL288	0.011	Unclassified	243	0.411
CL289	0.011	Unclassified	241	0.000
CL290	0.011	Unclassified	240	0.000
CL291	0.011	Unclassified	238	0.000
CL292	0.011	Unclassified	238	0.000
CL293	0.011	LTR Copia	238	0.840
CL294	0.011	Unclassified	237	0.000
CL295	0.011	Unclassified	237	0.000
CL296	0.011	Unclassified	236	0.000
CL297	0.011	Unclassified	235	0.000
CL298	0.011	Unclassified	235	0.000
CL299	0.011	Unclassified	234	0.000
CL300	0.011	Unclassified	234	0.000
CL301	0.011	Unclassified	234	0.000
CL302	0.011	Unclassified	233	0.000
CL303	0.011	Unclassified	233	0.000
CL304	0.011	Unclassified	231	0.000
CL305	0.011	Unclassified	230	0.000
CL306	0.011	Unclassified	229	0.000
CL307	0.011	Unclassified	227	0.000
CL308	0.011	DNA.PIF.ISL2EU	226	0.000
CL309	0.011	Unclassified	226	0.000
CL310	0.011	Unclassified	225	0.000
CL311	0.011	Unclassified	225	0.000
CL312	0.010	Unclassified	224	0.000
CL313	0.010	Unclassified	224	0.000
CL314	0.010	Non-LTR Penelope	224	0.000
CL315	0.010	Unclassified	223	0.000

CL316	0.010	Unclassified	222	0.000
CL317	0.010	LTR Gypsy	221	0.000
CL318	0.010	Unclassified	221	0.000
CL319	0.010	Unclassified	220	0.000
CL320	0.010	Unclassified	219	0.000
CL321	0.010	Non-LTR CR1	219	0.000
CL322	0.010	Unclassified	219	0.000
CL323	0.010	Unclassified	218	0.000
CL324	0.010	Unclassified	218	0.000
CL325	0.010	Unclassified	218	0.459
CL326	0.010	Unclassified	218	0.000
CL327	0.010	Unclassified	216	0.000
CL328	0.010	Unclassified	214	0.000

Table S4. Description of all clusters retrieved from 2174346 reads of *D. mojavensis* by RepeatExplorer. The satDNA families analyzed in this study are highlighted in bold red.

Cluster	Genome Proportion %	RepeatMasker Annotation	Reads number on each cluster	Outside reads with similarity %
CL1	1.630	<i>CDSTR130</i>	35395	0.494
CL2	0.861	<i>pBuM</i>	18724	0.417
CL3	0.625	RC.Helitron	13585	41.430
CL4	0.616	Homo6	13402	45.750
CL5	0.614	RC.Helitron	13345	42.750
CL6	0.482	Homo6	10483	33.900
CL7	0.475	RC.Helitron	10323	42.020
CL8	0.464	Non-LTR Jockey	10096	0.366
CL9	0.435	RC.Helitron	9461	21.380
CL10	0.429	Galileo	9320	2.157
CL11	0.420	Non-LTR R1	9132	1.818
CL12	0.340	RC.Helitron	7382	31.140
CL13	0.323	Unclassified	7027	0.896
CL14	0.299	RC.Helitron	6496	3.079
CL15	0.298	Non-LTR R1	6480	0.972
CL16	0.281	LTR BEL	6119	0.082
CL17	0.239	Unclassified	5196	0.019
CL18	0.227	Non-LTR R1	4944	3.621
CL19	0.227	Non-LTR CR1	4935	2.411
CL20	0.208	Non-LTR Jockey	4515	0.975
CL21	0.200	rRNA	4355	0.987
CL22	0.194	LTR BEL	4216	0.427
CL23	0.194	Non-LTR R1	4208	0.048
CL24	0.188	PERI	4096	29.050
CL25	0.178	Non-LTR Jockey	3860	0.130
CL26	0.177	LTR Gypsy	3856	0.778
CL27	0.175	Non-LTR Jockey	3814	0.000
CL28	0.166	Non-LTR Jockey /TART	3605	3.523
CL29	0.166	rRNA	3601	1.000
CL30	0.157	LTR Gypsy	3420	1.637
CL31	0.157	LTR Gypsy	3409	0.264
CL32	0.156	LTR BEL	3392	0.884
CL33	0.138	LTR Gypsy	3007	0.200
CL34	0.137	LTR Gypsy	2978	0.000
CL35	0.135	RC.Helitron	2925	9.983
CL36	0.132	LTR Gypsy	2867	1.604
CL37	0.111	RC.Helitron	2413	2.445
CL38	0.110	DNA.hAT.Ac	2399	0.125
CL39	0.107	Rep2-DF	2337	2.696

CL40	0.106	LTR Copia	2302	0.174
CL41	0.097	DNA.TcMar.Tc1	2103	3.281
CL42	0.094	LTR BEL	2045	1.125
CL43	0.093	DNA.TcMar.Tc1	2032	1.280
CL44	0.077	DNA.TcMar.Tc1	1681	0.833
CL45	0.072	LTR BEL	1570	3.694
CL46	0.072	Unclassified	1559	1.668
CL47	0.071	DNA.CMC.Transib	1540	0.779
CL48	0.069	LTR Gypsy	1492	0.335
CL49	0.067	LTR Gypsy	1448	0.691
CL50	0.063	Unclassified	1379	2.321
CL51	0.062	DNA.hAT.Tip100	1360	2.426
CL52	0.062	Unclassified	1358	0.074
CL53	0.059	Unclassified	1284	0.000
CL54	0.054	LTR Gypsy	1177	1.359
CL55	0.053	Non-LTR R1	1164	0.172
CL56	0.052	Non-LTR Jockey	1126	0.178
CL57	0.051	Unclassified	1105	0.000
CL58	0.050	LTR BEL	1093	0.366
CL59	0.049	Galileo	1066	1.876
CL60	0.048	LTR BEL	1045	0.766
CL61	0.041	Non-LTR Jockey	883	1.133
CL62	0.040	LTR Gypsy	870	0.575
CL63	0.040	LTR Gypsy	869	0.000
CL64	0.037	DNA.TcMar.Mariner	804	0.746
CL65	0.036	DNA.TcMar.Tc1	780	0.000
CL66	0.034	DNA.TA-1	731	1.231
CL67	0.033	DNA-1_RPr	724	0.000
CL68	0.030	LTR Gypsy	661	1.210
CL69	0.030	RC.Helitron	657	0.457
CL70	0.029	Non-LTR Jockey	627	0.478
CL71	0.026	LTR BEL	565	1.593
CL72	0.026	LTR Gypsy	562	0.000
CL73	0.025	Unclassified	537	0.000
CL74	0.024	LTR Gypsy	527	0.000
CL75	0.024	Non-LTR Jockey	518	1.158
CL76	0.023	DNA.TcMar.Tc1	502	0.398
CL77	0.023	LTR ERV1	496	0.202
CL78	0.022	DNA.TcMar.Tc1	482	5.394
CL79	0.022	DNA.TcMar.Tc1	472	0.424
CL80	0.021	rDNA	454	0.000
CL81	0.020	LTR BEL	442	0.226
CL82	0.020	DNA.piggyBac	441	1.134
CL83	0.020	DNA.TcMar.	438	1.598
CL84	0.019	Non-LTR Jockey	417	0.000
CL85	0.018	Non-LTR CR1	381	7.612

CL86	0.017	Non-LTR Jockey	367	0.273
CL87	0.017	Non-LTR Jockey	362	0.276
CL88	0.016	LTR Gypsy	354	1.412
CL89	0.014	Unclassifeid	310	18.710
CL90	0.014	LINE	298	0.000
CL91	0.013	DNA.hAT.Ac	293	0.341
CL92	0.013	DNA.hAT.Pegasus	289	2.422
CL93	0.013	DNA.hAT.hobo	288	3.819
CL94	0.013	LTR Gypsy	282	0.000
CL95	0.013	DNA.TcMar.Tc1	278	2.158
CL96	0.013	LTR Gypsy	273	0.000
CL97	0.012	Unclassifeid	256	0.000
CL98	0.012	Unclassifeid	255	0.000
CL99	0.011	Unclassifeid	248	0.000
CL100	0.011	Non-LTR Jockey	244	0.410
CL101	0.011	LTR BEL	243	0.000
CL102	0.011	DNA.PIF.Harbinger	242	1.653
CL103	0.011	DNA.TcMar.Tc1	237	1.266
CL104	0.011	LTR Gypsy	235	0.425
CL105	0.010	DNA.CMC.Transib	226	0.443
CL106	0.010	DNA.hAT.hobo	224	3.125
CL107	0.010	DNA.hAT.Pegasus	217	3.687
CL108	0.010	Unclassified	217	0.000
CL109	0.010	DNA.TcMar.Tc1	217	0.461

Table S5. Description of the ten most abundant clusters of the *D. melanogaster* genome identified by RepeatExplorer. The satDNA families with monomer lengths smaller than 50 bp are highlighted in bold.

Cluster	Sequence Annotation	Monomer size (bp)	Genome proportion %	Number of reads on each cluster
1	TGTTATTCTA	10	1.750	86909
2	AGAGA	5	0.715	35548
3	<i>1.688</i>	360	0.551	27393
4	AGACA	5	0.484	24099
5	<i>1.688</i>	360	0.453	22558
6	<i>1.688</i>	360	0.437	21759
7	<i>dodeca</i>	11-12	0.380	18912
8	<i>1.688</i>	360	0.340	16906
9	<i>Responder</i>	240	0.323	16044
10	LTR-Gypsy	-	0.293	14577

Table S6. Main features of 37 *CDSTR198* arrays located on euchromatic regions and their chromosome location according to GenomeBrowser analysis.

Contig	Array Size (bp)	Copy number	Scaffold	Chromosome
<i>713</i>	300	1,51	1	2
<i>714</i>	521	2,63	1	2
<i>834</i>	643	3,24	1	2
<i>894</i>	563	2,84	1_2	2
<i>1013</i>	585	2,95	1_2	2
<i>1263</i>	908	4,58	2	2
<i>1281</i>	462	2,33	2	2
<i>1732</i>	557	2,81	1_2	2
<i>2138</i>	348	1,75	6	3
<i>2239</i>	912	4,6	6	3
<i>2290</i>	814	4,1	6	3
<i>3200</i>	1044	5,27	11	4
<i>4011</i>	884	4,46	13	5
<i>4217</i>	627	3,16	14	5
<i>4994</i>	243	1,22	22	4
<i>5012</i>	530	2,67	22	4
<i>5199</i>	608	3,07	18_1	3
<i>5294</i>	450	2,27	18_1	3
<i>5693</i>	741	3,74	18_2	3
<i>6645</i>	233	1,17	28	X
<i>6973</i>	804	4,06	22	4
<i>8355</i>	287	1,45	40	4
<i>8688</i>	625	3,15	41	5
<i>8952</i>	405	2,04	31	4
<i>9897</i>	499	2,52	52	2
<i>12072</i>	243	1,22	6	3
<i>12476</i>	659	3,33	83	3
<i>13070</i>	678	3,42	24	3
<i>13095</i>	680	3,43	24	3
<i>13237</i>	652	3,29	68	5
<i>14801</i>	521	2,63	121	5
<i>15065</i>	692	3,49	123	4
<i>16146</i>	616	3,11	174	Unmapped
<i>18240</i>	404	2,04	111	5
<i>20000</i>	607	3,06	18	3
<i>27251</i>	322	1,62	2	2
<i>31812</i>	196	0,99	2	2

Table S7. List of genes associated with *CDSTR198* arrays and their relative positions in relation to *CDSTR198*.

Contig	Array Size (bp)	Position of <i>CDSTR198</i> relative to gene	Distance of <i>CDSTR198</i> array to gene	Gene annotation		<i>D. melanogaster</i> orthologous	Scaffold/ chromosome
714	521	Intron	-	EVM prediction scaffold1.763		FBpp0082178	1/2
894	563	Intron	-	EVM prediction scaffold1.1077		FBpp0111784	1/2
1013	585	Intron	-	EVM prediction scaffold1.1420		FBpp0303067	1/2
2138	348	Intron	-	EVM prediction scaffold6.61		FBpp0080953	6/3
4011	884	5'	1.4 kb	EVM prediction scaffold13.141		FBpp0167799	13/5
4217	627	5'	750 bp	FBpp0170282		-	14/5
5012	530	5'	500 bp	EVM prediction scaffold22.170		-	22/4
5199	608	5'	4 kb	Gene.g4503.tl		-	18/3
6645	233	5'	3 kb	EVM prediction scaffold28.31		FBpp0073879	28/X
6973	804	5'	800 bp	EVM prediction scaffold22.28		FBpp0072761	22/4
8355	287	5'	1.9 kb	EVM prediction scaffold40.3		FBpp0072462	40/4
8688	625	Intron	-	EVM prediction scaffold41.61		FBpp0112268	41/5
8952	405	5'	500 bp	EVM prediction scaffold31.206		FBpp0079016	31/4
13070	678	5'	800 bp	EVM prediction scaffold24_1.4		-	24/3
13095	680	5'	300 bp	SNAPPosition:scaffold24_prediction gene_268763..270446		-*	24/3
14801	521	5'	3,9 kb	EVM prediction scaffold121.6		FBpp0074830	121/5

*This predicted gene has no orthologous on *D. melanogaster* or *D. mojavensis* according to *Drosophila buzzatii* Genome Project (<http://dbuz.uab.cat>; Guillen et al. 2015)