

“High evolutionary turnover of satellite families in *Caenorhabditis*”

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Table S1. Location of satellites in deletions found in natural isolates of *C. elegans*

Maydan et al. [28] have provided a catalogue of several indels in twelve natural isolates of *C. elegans*, which add up to about 3.2 Mb of the genome (excluding duplications). We have determined the position of satellites in all those indels. We would expect 56.6 satellites distributed throughout these regions, since there are 17.7 satellites/Mb in *C. elegans* (Table 2). Satellites were found only in some of them, with a total number of 58 satellites of different sizes and repeats. Therefore we can conclude that satellites are randomly distributed in the deletions found in the different strains studied by Maydan et al. In order to avoid redundancies, we do not show small indels present as a fraction of longer indels.

Chr.	Indel			Satellite			
	start	end	size	start	end	length	Repeat
1	11364959	11370480	5521	11363099	11366734	3635	22
1	13111296	13153623	42327	13149264	13151975	2711	13
1	15016450	15028313	11863	15025303	15028836	3533	21
2	885958	894076	8118	891132	892028	896	59
2	899953	912358	12405	898795	901439	2644	22
2	899953	912358	12405	902801	903323	522	17
2	1535351	1593891	58540	1578533	1579326	793	23
2	1750664	1822745	72081	1796659	1797045	386	34
2	1750664	1822745	72081	1812740	1812972	232	18
2	1750664	1822745	72081	1815685	1815917	232	26
2	1825029	1934453	109424	1892812	1893498	686	26
2	1995557	2022712	27155	2000886	2001208	322	12
2	1995557	2022712	27155	2002111	2002471	360	32
2	1995557	2022712	27155	2008284	2009472	1188	31
2	2063759	2138338	74579	2115413	2116408	995	11
2	2265489	2338778	73289	2329985	2330860	875	40
2	2344994	2353289	8295	2348338	2348687	349	33
2	2521667	2546368	24701	2525627	2526075	448	18
2	2521667	2546368	24701	2526938	2527351	413	12
2	2521667	2546368	24701	2529568	2530452	884	35
2	3196064	3249275	53211	3246628	3247181	553	20
2	3335696	3363341	27645	3361867	3363047	1180	43
2	3672299	3693900	21601	3691106	3692335	1229	31
2	13610426	13617819	7393	13612519	13612876	357	14
2	14982543	14985471	2928	14984063	14985128	1065	20
3	949229	973819	24590	951024	953927	2903	12
3	1295561	1307017	11456	1299749	1303117	3368	25
3	1311955	1316567	4612	1312378	1312777	399	21
3	1311955	1316567	4612	1314691	1315015	324	21
3	1346343	1409647	63304	1362848	1369996	7148	10
3	1893285	1895451	2166	1890358	1894009	3651	19
3	12320776	12322654	1878	12320572	12322233	1661	35
4	2563486	2594976	31490	2572290	2575957	3667	164

4	4124569	4166385	41816	4142135	4142511	376	12
4	17134566	17145165	10599	17138350	17140071	1721	184
4	17134566	17145165	10599	17140409	17141319	910	15
5	1274592	1274909	317	1273381	1274666	1285	35
5	3247858	3433564	185706	3373169	3373914	745	21
5	4783636	4788086	4450	4784583	4784785	202	16
5	15282820	15399718	116898	15295228	15296185	957	35
5	15282820	15399718	116898	15320755	15321325	570	40
5	15282820	15399718	116898	15321461	15322267	806	15
5	17238425	17347568	109143	17265086	17267237	2151	156
5	17238425	17347568	109143	17308688	17311507	2819	11
5	17371630	17489726	118096	17384209	17394484	10275	59
5	17371630	17489726	118096	17412041	17412354	313	19
5	17491246	17588401	97155	17587172	17587321	149	12
5	17801810	17820902	19092	17817696	17818236	540	34
5	18186552	18247813	61261	18190373	18190779	406	11
5	18678249	18684222	5973	18679671	18683869	4198	18
5	18770400	18776232	5832	18774110	18774554	444	11
5	19230781	19237263	6482	19229066	19231343	2277	12
5	19230781	19237263	6482	19232563	19232783	220	12
5	19390251	19469469	79218	19402218	19402465	247	17
5	19480251	19492283	12032	19488470	19489504	1034	17
5	19833649	19846181	12532	19836950	19837768	818	33
5	20435644	20439262	3618	20432075	20438121	6046	180
6	1752189	1778099	25910	1752274	1755174	2900	27

Table S2.**Satellite family members in the chromosomes of *C. elegans***

In this table the families are ordered by increasing length of the repeat.. Only families with more than 9 members are shown. The consensus sequence of each family is given in Additional file 2. Members with one asterisk are shared with other species. All other families are species specific in *C. elegans*.

Family	I	II	III	IV	V	X	Total number	Special features
4_11	16	19	13	12	17	5	82	Related to <i>Helitron 2_CE</i>
18_11*	3	1	8	1	1	0	14	
2_12*	50	48	40	14	47	4	203	Telomeric
23_12*	5	4	2	1	0	1	13	Hexamer dimer
11_14*	11	12	0	2	8	0	33	Heptamer dimer
5_15	8	8	8	24	11	6	65	Related to <i>Helitron Y4_CE</i>
12_16	1	9	5	9	5	0	29	Octamer dimer
14_17*	6	2	0	6	4	0	18	
15_17*	3	3	2	3	2	4	17	
25_18	0	0	0	0	10	1	11	
6_19	10	2	19	5	13	2	51	
10_19	5	2	10	5	9	5	36	
16_19*	0	1	0	0	14	0	15	
24_19	1	3	0	3	0	5	12	Mixed with 23-mer
17_20*	1	4	3	0	5	1	14	Found in <i>Helitrons</i>
22_22*	1	5	3	4	0	0	13	
8_25	5	7	5	5	7	9	38	
21_26	3	1	1	1	2	5	13	
26_31	0	0	10	0	0	0	10	Pairing centers
13_32	0	0	0	0	20	2	22	Pairing centers
1_35	44	36	72	20	40	1	213	Most abundant
3_34	14	15	18	26	39	12	124	Found in <i>Helitrons</i>
20_37	2	1	7	2	0	1	13	Related to 3_34
7_40	9	5	6	7	8	12	47	Related to <i>Helitron Y4_CE</i>
9_43	9	10	9	2	6	0	36	Related to 1_35
19_59	1	3	4	1	4	0	13	Centromere-like
Total in families	208	201	245	153	272	76	1155	Families with more than 9 members
Total in genome	321	354	332	241	396	135	1779	

Table S3 . CENP-A score of satellites with long repeats (>150 bases) in *C. elegans*.

Satellites with a repeat of 59 bases and a high CENP-A score are also included in the Table.

Position	Satellite length	Number of repeats	Repeat length	CENP-A score
Chr I				
338563	2587	14	184	1.544
1026802	2177	12	182 (60)	1.073
9816009	3628	14	200 (26)	1.154
10851619	3760	23	163	0.976
13149264	2712	14	224 (13)	1.539
Chr II				
776994	1966	12	163	1.226
1094273	2358	11	161	0.809
2949871	2395	10	155	0.811
3159311	9176	55	162	1.070
6073584	3812	21	181	2.186
9807896	17344	292	59	1.503
11190043	2046	12	202 (90)	0.999
13428517	4784	24	165	1.076
14322264	9454	43	185	1.339
14333333	4159	25	166	1.142
Chr III				
99472	6101	35	178	2.302
448145	5086	21	164	2.201
1017321	3256	55	59	1.114
1362848	7149	44	162 (11)	1.182
2077622	4889	29	168	1.781
11593322	8828	48	184	1.705
11639888	7523	35	163	1.192
13074654	11986	206	59	1.297
13414618	2540	13	198 (64)	1.398
Chr IV				
2572290	3668	16	164	1.156
4822586	2633	16	163 (36)	1.011
6668156	8287	46	182	1.113
6682649	21927	125	172	1.114
6708756	22979	130	174	1.118
12169268	1954	24	59	1.021
15225055	2294	12	168	1.225
15510686	2554	12	168	1.119
17138350	1722	11	184	1.330
Chr V				
265076	2070	12	172	1.127
1201997	2418	13	185	1.326
1704637	1954	13	163	1.090
4244047	3476	18	200	0.972
9428478	6646	31	214 (32)	0.976
14584093	6934	32	162	0.999
16330572	2637	16	164	1.052
17265086	2152	12	156	1.431
17384209	10276	173	59	0.928
18512827	1516	10	151	0.749
20106050	1857	10	185	0.692
20432075	6047	28	180	1.736
Chr X				
2991962	3370	27	167	1.352
5048783	5263	24	226	0.846
10749197	1878	10	214	0.991
16931765	8401	47	151 (57)	1.150

The repeat length of some satellites has been corrected, since they have an internal repeat of the seed motif. In such cases the value given in parenthesis corresponds to the uncorrected value reported by SATFIND.

Table S4. Chromosome positions of Cele_Fam_24_19_12: (AT3)₃₋₄AATTAAT

Chromosome	Length (bases)	Position	Properties
I	165	4281275	Intergenic
I	840	12782330-r	Intergenic
II	842	4308301	Intergenic
II	604	9719108	Intergenic
II	353	9719725-r	Intergenic. Neighbor of previous satellite
IV	139	1639370	Intron
IV	180	2124726	Intron
IV	616	13461609	Intergenic. Contains inserted <i>Helitron</i>
V	229	4554501	Intergenic. Contains inverted satellite
X	560	2004045	Intergenic. Placed between two <i>Helitrons</i>
X	995	2008253	Intergenic. Contains inserted <i>Helitron</i>
X	286	5227453	Intergenic. Contains inverted satellite
X	1224	5230918-r	Intergenic. Neighbor of previous satellite. Contains inserted <i>Helitron</i>
X	580	9189061-r	Intron
X	564	12276204	Intergenic. Includes a short inversion

r indicates that it is a reverse complement sequence

**Table S5. Complete sequence of all the Cele_Fam_24_19_12 satellites:
(ATTT)₃₋₄AATTAAT (19-23 bases)**

This satellite family is specific for *C. elegans*. Its repeat is completely absent in all other *Caenorhabditis*. The AATTAAT sequence is shown in blue in this Table. Point mutations are shown in red. Related repeated sequences in some satellites are separated by an empty line. At the beginning of the Table four short satellites are shown, which were not detected by SATFIND, due to their small size. We have also recovered a related satellite (Chromosome X-5230918), which had been rejected by SATFIND due to its irregular sequence.

The first step in the appearance of this satellite was probably a partial duplication of the motif with 23 bases, which gave rise to a longer motif with 42 bases (19 + 23). Subsequent duplications originated longer satellites. Inspection of the Table demonstrates that these satellites grew further by unequal crossing-over, as shown by the distribution of point mutations, usually of fragments of about 120-200 bases. This is clearly apparent in Cele.WS201_1:12782330-12783169 and in many other satellites. In some cases point mutations appeared before crossing-over, but in other cases the satellites grew before any apparent point mutation. If we classify the satellites by the number of point mutations and the relative distribution of motifs with either three or four ATTT units, it appears that individual satellites have different ages. Old satellites have acquired more point mutations than younger satellites.

Two clearly transposed sequences in the X chromosome are shown in green. The two satellites involved are separated by about 4 Kb which contain one *Helitron* (Y2_CE4) and a LINE sequence (RTE1). These two elements might have facilitated the local transposition detected. At the end we present a few related sequences which might correspond to degraded satellites.

> 4281275 chromosome I
GGCAAAA
ATTTATTTATTTATTTAATTAAT
ATGTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTCTTTAATTAAT
ATTTTCGATGCTCT

> 1639370 chromosome IV
ATTGAGCCA
ATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATGTATTTATTTAATTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTCATTTAATTAAT
AATTATTTATTTATTTAATTAAT
CAGAACATTTTA

> 2124726 chromosome IV reverse complement
AAT
ATTTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTTATTTATTTAATTAAT
ATTTATTTATTTAATTAATTAAT
ATTTATTTATTTAATTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTA

> 4554501 chromosome V. Contains inverted repeat
TTTACCGATTTAAATAAT
ATTTATTTATTTAATTAATTAAC
ATTTATTTATTTAATTAAT
ATTTAATTATTTATTTAATTAAT
ATATATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTATTTA (Inverted)
AAATAAATAAATAAAT
ATTAATTAAATAAATAAATAAAT
ATTAATTAAATAAATAAAT
ATTAATC
ATTTACTATATA

> Rev.of:Cele.WS201_1:12782330-12783169

ATTTATTTATTTAATTAAT
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ATTTATTCATTTATTTAATTAAT
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ATTTATTTATTTAATTAAT
ATTTATTTATTTATCTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATTTATTTATTTAATTAAT

ATTTATTTATTTATTTAATTAAT
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ATTTATTCATTTATTTAATTAAT
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ATTTATTTATTTAATTAAT
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ATTTATTCATTTATTTAATTAAT
ATTTATTTATTTAATTAAT
ATTT

> Cele.WS201_2:9719108-9719711

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ATTTATTTATTTAATTAAT

ATT-ATTTAATTAAT
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ATTTATTTATTTATTTAATTAAT
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ATTTAT

> Rev.of:Cele.WS201_2:9719725-9720077. Next to previous satellite.

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> Cele.WS201_6:2004045-2004604

AT

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ATTTATTT

>5230918 chromosome X reverse complement. With an inserted *Helitron* sequence

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ATTTATTTAT

> Rev.of:Cele.WS201_6:9189061-9189640

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ATTTATTTGTTTATTTAATTAAT

ATCTATTTATTTAATTAAT

ATTTATTTATTTAATTAAT

ATTTATTTATTTAATTAAT

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A

> Cele.WS201_6:12276204-12276767 Contains short inverted sequence

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AAATAAAATATTAATTAATA
AATTATTTATTTAATTAAT
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Sequences related to Cele_Fam_24_19_12

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ATTTATTTATTTAATTAAT
TTAGTTTATAAAAAT
CACGTTTGAATGAC**ATTT**CTGGGAAAACGTGGGAA**ATTT**ATTGGAAAAAAAATTCTAA

>ce6_dna range=chrIV:13456651-13456900 strand=-
CTCATATTGGGTCATTACTTTTCCTT**ATTT**ACTGTACCTTT
ATTTATTTATTTATTTATTTGATTAAT
ATTTATTTATTTATTTAAT
ATTTATTTTATTAATTT
ATTTTTATTA**ATTTATTTAATTAAT**
ATTTATTTATTTAATTAAT
ATTTATTTATTTATTTAATTAAT
ATTTATTTATTCATTTAATTAAT
AATTAATAATTAATAATAAAC**ATTT**CTGTAACTACGTGAAGCTTCTTGTACCTACTGG

>ce6_dna range=chrIV:13884851-13885050 strand=+
TGACGTCACAGACTACAAAGACTACATAGACT**ATTT**TTAAATTGAT
ATTTATTTATTTAATTAAT
TAATTAAT
ATTTTTTTATTTATTT**TAATTAAT**
ATTTATTTATTTATTTAAATAAT
ATTTATTTATTTA
TC**ATTT**ACTATATATAAA
GCGCGTGTCTTCTGTCCCTATGTAGTTTGATCTTTGATCAGAGCAACGA

>ce6_dna range=chrIV:13994001-13994200
TATTTTCACAACCTTACTTACTAA**AATATTT**CAAGTTCAGTTTCAACGCGG
AACCAAGATTTTCCAAACTCTTTTTAGCTAGAAAAAGCTTGTACATTTTC
AAAGTATTGATTAGAGAGT
TGATATTTTTAA**ATTTATTTAATTA--ATTTATTTATTTAAT**GGGTCTCTTT
TAATCTTACGACTTTCAAAAAAAAAAAAAACG

>ce6_dna range=chrV:4602651-4602850 strand=-
AAGAAGTTATG**ATTT**TTGACCCGGA**ACTTATTT**GGAGACCTAATAATTCAAAAACAAT
ATTTATTTTATTTT
TTTT**ATTTATTTAATTAATTA**
ATTTTTTTT**ATTTAATTGATGAATTAATTCATTAATTT**TTGGAAAATACTTA
ATTTGGAAAATACTCATTAGAACACAAG**ATTT**GTTACAAAATGTCTAGAGG

Table S6. Alignment of large satellite families in *Caenorhabditis*

>All.fam_Fam_1_20_5 Nr. of seq. 5 Alignment length(with gaps) = 21 Alignment score = 0.585714

```
Cbren.WS247_Fam_47_18_7      AAATTC-CG-AAAATTCT-GA
Cele.WS201_Fam_321_19_1     AAACTCGAG-AAAATTCT-GA
Cbren.WS247_Fam_33_20_9     ANCTTCCAGAAAC-TTCTAGA
Rev.of:Cbrig.WS247_Fam_11_20_22 AAATTCAG-AACATTCTAGA
Cele.WS201_Fam_319_20_1     AAATTCAG-AAGGTTCTAGT
*   **  *  **  **** *
```

Consensus:

AaatTCcaGAAnaTTCTaGa

>All.fam_Fam_2_12_5 Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.737778

```
Cbren.WS247_Fam_8_12_37     GC--TT-AGGCTTAG
Rev.of:Cbrig.WS247_Fam_108_12_2 GC--TT-AGGCTTAG
Rev.of:Cele.WS201_Fam_2_12_203 GC--TT-AGGCTTAG
Rev.of:Crema.WS247_Fam_22_12_15 GC--TT-AGGCTTAG
Cbren.WS247_Fam_389_15_1    GCTTTTCAGGCTTAG
**  **  *****
```

Consensus:

GCTTAGGCTTAG (Telomere sequence)

>All.fam_Fam_5_24_4 Nr. of seq. 4 Alignment length(with gaps) = 24 Alignment score = 0.695602

```
Crema.WS247_Fam_73_21_4     T-TGGGTCATGACCTAA-TTAAT-
Rev.of:Cbrig.WS247_Fam_3_22_70 TCTAGGTCATGACCTAA--TTTTT
Rev.of:Cbren.WS247_Fam_10_24_31 TCTAGGTCATGACCTAATTTTTTTT
Cele.WS201_Fam_280_24_1     AGTAGGTCATGACCTAATTTTTTTA
*  *****  *  *
```

Consensus:

tcTaGGTCATGACCTAAttTttTt

>All.fam_Fam_7_14_4 Nr. of seq. 4 Alignment length(with gaps) = 17 Alignment score = 0.643791

```
Cbrig.WS247_Fam_19_14_12    TGGA-ATCT-GGA-ATC
Rev.of:Crema.WS247_Fam_13_14_26 CGGA-ATCC-GGA-ATC
Cbren.WS247_Fam_4_15_56     CGGA-ATCCNGGA-ATC
Cbren.WS247_Fam_15_16_22    CGGACATCT-GGACATC
*** **  *** **
```

Consensus:

cGGAATCcGGAATC

>All.fam_Fam_8_14_4 Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.857143

```
Cbren.WS247_Fam_24_12_14    AAG-CGGAAG-CGG
Cbren.WS247_Fam_21_14_15    AAGTCGGAAGTCGG
Rev.of:Cbrig.WS247_Fam_32_14_5 AAGTCGGAAGTCGG
Rev.of:Crema.WS247_Fam_1_14_208 AAGTCGGAAGTCGG
*** ***** **
```

Consensus:

AAGtCGGAAGtCGG

>All.fam_Fam_9_12_4 Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.750000

```
Cbren.WS247_Fam_400_12_1    GCTCCGGCTCCG--
Rev.of:Cele.WS201_Fam_356_12_1 GCTCCAGCTCCA--
Rev.of:Crema.WS247_Fam_61_12_5 GCTCCAGCTCCA--
Cbrig.WS247_Fam_20_14_12    GCTCCAGCTCCAGA
***** *****
```

Consensus:

GCTCCaGCTCCa

>All.fam_Fam_10_14_4 Nr. of seq. 4 Alignment length(with gaps) = 14 Alignment score = 0.777778

```
Cbren.WS247_Fam_84_14_4      TGTAGTTTGTAGTT
Rev.of:Cele.WS201_Fam_11_14_33  TGTAGTTTGTAGTT
Rev.of:Cbrig.WS247_Fam_266_14_1  CGTAGTATGTAGTT
Crema.WS247_Fam_146_14_2      TGTAGTCTGTAATC
                               ***** **
```

Consensus:

tGTAGTtTGTAgtT

>All.fam_Fam_11_13_4 Nr. of seq. 4 Alignment length(with gaps) = 13 Alignment score = 0.602564

```
Cbren.WS247_Fam_190_10_2      TTTTT-GAAAT--
Cele.WS201_Fam_40_12_7        TTTTT-GAAATTT
Rev.of:Crema.WS247_Fam_43_13_7  TTTTTTCAAATTT
Cele.WS201_Fam_18_11_14      TTTTTGCACAT--
                               ***** * **
```

Consensus:

TTTTTncAaATtt

>All.fam_Fam_12_11_4 Nr. of seq. 4 Alignment length(with gaps) = 12 Alignment score = 0.678241

```
Cbren.WS247_Fam_68_11_5      -TCGATAAAATTA
Rev.of:Cbrig.WS247_Fam_34_11_5  -CCGGTAAATTA
Crema.WS247_Fam_27_11_13      -CCGGTAAATTA
Rev.of:Cele.WS201_Fam_359_11_1  TCCG-TTAATTA
                               ** * *****
```

Consensus:

cCGgTaAATTA

>All.fam_Fam_13_10_4 Nr. of seq. 4 Alignment length(with gaps) = 10 Alignment score = 0.822222

```
Cbren.WS247_Fam_1_10_97      TAGAAGTTTC
Rev.of:Crema.WS247_Fam_18_10_16  TAGAAGTTTC
Rev.of:Cbrig.WS247_Fam_12_10_19  TGGAATTTTC
Rev.of:Cele.WS201_Fam_64_10_4    TGGAATTTTC
                               * ** * **
```

Consensus:

TaGAAgTTTC

>All.fam_Fam_23_26_3 Nr. of seq. 3 Alignment length(with gaps) = 28 Alignment score = 0.626984

```
Cbrig.WS247_Fam_59_24_3      AATTCCCGCCAAAATATTT----TTTTG
Cbren.WS247_Fam_3_28_64      AATTCCCGCCAAANTTTTTGAATTTTTG
Crema.WS247_Fam_123_26_2     AATTCCCGCCAAAACGGAA-AA-TTTTG
                               ***** **
```

Consensus:

AATTCCCGCCAAAatntttaaTTTTG

>All.fam_Fam_28_22_3 Nr. of seq. 3 Alignment length(with gaps) = 22 Alignment score = 0.621212

```
Crema.WS247_Fam_302_20_1      GTCGATTTACGG-AGCCTCGG-
Crema.WS247_Fam_48_21_6      GTNGATTTACGGAAGCTT-TGT
Rev.of:Cele.WS201_Fam_22_22_13  GTAGATTTACGGGAGTTTCTNT
                               ** ***** ** *
```

Consensus:

GTnGATTTACGGnAGctTctgt

>All.fam_Fam_31_19_3 Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.671958

```
Cbrig.WS247_Fam_68_19_3      -TAGAGGTCCCAAAAAAAT-
Crema.WS247_Fam_9_20_29      TTAGACGTCCCAAAAAACAN-
Rev.of:Cbren.WS247_Fam_5_20_44  -TCGAGGACCAAAAAA
                               * ** * ***** *
```

Consensus:

TaGAgGtCCCAAAAAaAn

>All.fam_Fam_33_20_3 Nr. of seq. 3 Alignment length(with gaps) = 21 Alignment score = 0.650794

```
Cele.WS201_Fam_17_20_14      TTTGAATTTTTNAGTCAAAA-
Rev.of:Crema.WS247_Fam_132_21_2  TTTGATATTTTCAGTCTAAAT
Crema.WS247_Fam_92_20_3      ATTGACTTTTTTGANTCGAAA-
                               ****  ****  *  *  **
```

Consensus:

tTTGAntTTTTnAgTCnAAA

>All.fam_Fam_34_17_3 Nr. of seq. 3 Alignment length(with gaps) = 18 Alignment score = 0.660494

```
Cbrig.WS247_Fam_71_17_3      T-CTCTTTTACTACCAAG
Rev.of:Cele.WS201_Fam_14_17_18  T-CTCTTTTACTACGNN
Crema.WS247_Fam_140_18_2      TCCTCATTTACTACCGAT
                               *  **  *****
```

Consensus:

TCTCtTTTACTACcgan

>All.fam_Fam_35_17_3 Nr. of seq. 3 Alignment length(with gaps) = 17 Alignment score = 0.790850

```
Cbren.WS247_Fam_35_17_9      CTCATTGACTACATTTA
Cele.WS201_Fam_15_17_17      CTCATTGACTACCTTTG
Crema.WS247_Fam_329_17_1     CTCTTTGACTACACTTG
                               ***  *****  **
```

Consensus:

CTCaTTGACTACatTTg

>All.fam_Fam_36_16_3 Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.694444

```
Cbren.WS247_Fam_17_16_20     TCTGTATGTCTGTATG
Rev.of:Crema.WS247_Fam_143_16_2  TCTGTCAGTCTGTGTG
Cbren.WS247_Fam_37_16_9      TCTGTCTATCTGTCTA
                               *****  *****  *
```

Consensus:

TCTGTctgTCTGTnTg

>All.fam_Fam_37_16_3 Nr. of seq. 3 Alignment length(with gaps) = 16 Alignment score = 0.666667

```
Cbren.WS247_Fam_30_16_11     CTCTCAGGCTCTCAGG
Cele.WS201_Fam_342_16_1      CTCCTAGGCTCCTAGG
Rev.of:Crema.WS247_Fam_145_16_2  CTTTTAGGCTTTTTAGG
                               **  *****  ***
```

Consensus:

CTcttAGGCTcttAGG

>All.fam_Fam_41_15_3 Nr. of seq. 3 Alignment length(with gaps) = 15 Alignment score = 0.940741

```
Cbren.WS247_Fam_16_15_20     GAAACCGGACATTTTC
Crema.WS247_Fam_33_15_9      GAAACCGGACATTTTC
Cbrig.WS247_Fam_14_15_16     GAAACCAGACATTTTC
                               *****  *****
```

Consensus:

GAAACCgGACATTTTC

>All.fam_Fam_42_14_3 Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.682540

```
Cbrig.WS247_Fam_269_12_1     G-CCCTAG-CCCTA
Rev.of:Crema.WS247_Fam_26_14_13  GACCCTAGACCCTA
Rev.of:Cele.WS201_Fam_349_14_1   GTCCCTAGTCCCTA
                               *  *****  **  **
```

Consensus:

GnCCCTAGnCCcTA

>All.fam_Fam_74_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.659420

```
Crema.WS247_Fam_15_21_19     CTGAGGCTAACTGAGA-TTTTG-
Cele.WS201_Fam_123_22_2      CTGAGGCTCTCT-AGATTTTTGG
```

***** ** ** *

Consensus:

CTGAGGCTaaCTgAGAtTTTTGg

>All.fam_Fam_85_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.681818

Cbrig.WS247_Fam_5_21_47 CATTTCATGATTTT-TGGNC
Cbren.WS247_Fam_55_22_6 CATTTC AAGGTTTCTAGGC
***** * ** *

Consensus:

CATTTC AaGaTTTcTaGgC

>All.fam_Fam_91_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540

Cbrig.WS247_Fam_8_20_31 AGCCTCAGTAAAAATTCC-TA
Rev.of:Cele.WS201_Fam_320_20_1 AG-CTCAGGAAAAATTCCAGA
** ***** *

Consensus:

AGcCTCAGgAAAAATTCCagA

>All.fam_Fam_108_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.789474

Cbren.WS247_Fam_358_19_1 GAAATGCGCCAAGACACAA
Cele.WS201_Fam_16_19_15 GAATTGCGCCAAGGCACTA
*** ***** ** *

Consensus:

GAAaTGCGCCAAGaCACaA

>All.fam_Fam_126_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.718750

Cbrig.WS247_Fam_6_14_46 GGTCCCT-GGGTCCTG-
Rev.of:Cbren.WS247_Fam_179_16_2 GGTTCCTGGGGTCCTGG
*** ** *****

Consensus:

GGTcCTgGGGTCCTGg

>All.fam_Fam_133_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.833333

Cbrig.WS247_Fam_21_16_12 GATCCAGGGATCCAGG
Cele.WS201_Fam_87_16_3 GTTCCAGGGTTCAGG
* ***** *

Consensus:

GaTCCAGGGaTCCAGG

>All.fam_Fam_139_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.809524

Cbrig.WS247_Fam_10_14_28 TCCTTATTCCTTAT
Rev.of:Crema.WS247_Fam_4_14_69 TCCTTCTTCCTTCT
***** ***** *

Consensus:

TCCTTaTTCCTTaT

>All.fam_Fam_141_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.666667

Cbren.WS247_Fam_11_10_27 CC-GGT-CTGGT
Rev.of:Cele.WS201_Fam_352_12_1 CCTGGTCCTGGT
** ** *

Consensus:

CCtGGTcCTGGT

>All.fam_Fam_150_10_2 Nr. of seq. 2 Alignment length(with gaps) = 10 Alignment score = 0.733333

Cbren.WS247_Fam_31_10_10 GACCAGCCTA
Cbrig.WS247_Fam_115_10_2 GACCATTCTA
***** ** *

Consensus:

GACCAGcCTA

Table S7.

Satellite families shared by *M. hapla* and *Caenorhabditis*

```
>Allfam_Fam_2_10_5 Nr. of seq. 5 Alignment length(with gaps) = 15 Alignment score = 0.480000
Cbren.WS247_Fam_190_10_2          TTTTT-GAAA--T--
Cele.WS201_Fam_40_12_7            TTTTT-GAAA--TTT
Rev.of:Crema.WS247_Fam_43_13_7    TTTTTTCAAA--TTT
Mhapla.WS247_Fam_303_10_1         TTTTC-GGAA--T--
Crema.WS247_Fam_7_12_32          TTTTC-GAAAGAT--
****      ** *

Consensus:

TTTTTtgaAAT

>Allfam_Fam_43_12_3 Nr. of seq. 3 Alignment length(with gaps) = 14 Alignment score = 0.674603
Cele.WS201_Fam_33_12_8            TAAA-AATAAAAA-
Crema.WS247_Fam_149_12_2         TAAC-AATAAAAA-
Mhapla.WS247_Fam_4_14_16         TAAANAATTAAAAAT
***  ***  ****

Consensus:

TAAaAATaAAAA

>Allfam_Fam_44_10_3 Nr. of seq. 3 Alignment length(with gaps) = 13 Alignment score = 0.632479
Cbren.WS247_Fam_61_10_6            A-AAAAAATCG--
Mhapla.WS247_Fam_301_11_1         ATAAAAAATCG--
Cbrig.WS247_Fam_107_12_2         A-AAAAAATTCGAC
*  *****  ***

Consensus:

AAAAAAaTCG

>Allfam_Fam_78_23_2 Nr. of seq. 2 Alignment length(with gaps) = 23 Alignment score = 0.652174
Cbren.WS247_Fam_335_21_1          CA-AATTTTTTTTCGGGA-TTTTT
Rev.of:Mhapla.WS247_Fam_103_23_2  CAGAATTTTTTTTCCCAAGTTTTT
**  *****      *  *****

Consensus:

CAgAATTTTTTTTccaAgTTTTT

>Allfam_Fam_87_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.666667
Cbren.WS247_Fam_106_20_3          GGCAANTTGCCAGAGAAAAC--
Rev.of:Mhapla.WS247_Fam_263_22_1  GGCAATTTGCGACAAAAAACCCT
*****  *****  *  *  *****

Consensus:

GGCAAtTTGcCAcAaAAAAcct

>Allfam_Fam_98_22_2 Nr. of seq. 2 Alignment length(with gaps) = 22 Alignment score = 0.643939
Crema.WS247_Fam_291_21_1          AGGTGAAAAATTCAAATTTAT-
Rev.of:Mhapla.WS247_Fam_262_22_1  AAGTTTAAACTTTAAATTTATT
*  **  ***  **  *****

Consensus:

AaGTgaAAAaTTcAAATTTATt

>Allfam_Fam_99_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.650794
Cbrig.WS247_Fam_16_19_14          AAATTCTG--GTCCTTAAAAA
Mhapla.WS247_Fam_112_21_2         AAATTCTGATGTTTTTAAACA
*****  **  *****  *

Consensus:

AAATTCTGatGTccTAAAAA

>Allfam_Fam_108_21_2 Nr. of seq. 2 Alignment length(with gaps) = 21 Alignment score = 0.682540
Cele.WS201_Fam_132_21_2          CAACTACCACAACACTACCGTAC
Rev.of:Mhapla.WS247_Fam_44_21_3   CTTCTACCACAACAACAGCAC
*  *****  **  *  **

Consensus:

CaaCTACCACAACaCaGcAC

>Allfam_Fam_110_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.683333
Mhapla.WS247_Fam_50_18_3          NTTTTTA-TA-GGCCTAGAA
Rev.of:Cele.WS201_Fam_312_20_1    ATGTTTACTACGGCCTAGAA
*  ****  **  *****

Consensus:

aTgTTTAcTAcGGCCTAGAA
```


>Allfam_Fam_113_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.641667
Cele.WS201_Fam_24_19_12 TTTATTTATTTAATT-AATA
Mhapla.WS247_Fam_30_19_4 TTTATTTTATAATTCAAG-
***** * ***** **

Consensus:
TTTATTTaTaTAATTcAAga

>Allfam_Fam_114_20_2 Nr. of seq. 2 Alignment length(with gaps) = 20 Alignment score = 0.633333
Mhapla.WS247_Fam_276_19_1 TTTTAT-TATTCGTGCGCTC
Crema.WS247_Fam_94_20_3 TTTTCTGTATTCTTGTGCAC
**** * ***** ** * *

Consensus:
TTTTaTgTATTCgTGcGCaC

>Allfam_Fam_122_19_2 Nr. of seq. 2 Alignment length(with gaps) = 19 Alignment score = 0.754386
Cbrig.WS247_Fam_244_18_1 TTTTGAAAAAAAAAATT-T
Mhapla.WS247_Fam_114_19_2 TTTTGAAAGAAAAGAATTAT
***** ***** ** *

Consensus:
TTTTGAAaAAAAaAATTaT

>Allfam_Fam_133_18_2 Nr. of seq. 2 Alignment length(with gaps) = 18 Alignment score = 0.629630
Cele.WS201_Fam_323_18_1 TTGTAGATCAACGGGGTC
Rev.of:Mhapla.WS247_Fam_52_18_3 TTGTGGTCAATGGTGGC
**** * ***** ** * *

Consensus:
TTGTaGaTCAAcGGgGgC

>Allfam_Fam_145_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.708333
Mhapla.WS247_Fam_57_15_3 ATAATTTTAAGCTT-T
Cbrig.WS247_Fam_250_16_1 AAAATTTTAGGCTTGT
* ***** ** *

Consensus:
AaAATTTTAAgCTTgT

>Allfam_Fam_151_16_2 Nr. of seq. 2 Alignment length(with gaps) = 16 Alignment score = 0.666667
Cele.WS201_Fam_88_16_3 AATTCCGCAATCGGC
Rev.of:Mhapla.WS247_Fam_282_16_1 AATTTTCGGGAAACGGG
**** ** ** **

Consensus:
AATTcCGGcAAcCGGc

>Allfam_Fam_152_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
Mhapla.WS247_Fam_299_13_1 AATTTTGTG-GC-ATT
Cbrig.WS247_Fam_263_14_1 AATTTTGTGCTAT-
***** ** **

Consensus:
AATTTTGTgGctAtT

>Allfam_Fam_154_15_2 Nr. of seq. 2 Alignment length(with gaps) = 15 Alignment score = 0.655556
Cbren.WS247_Fam_181_14_2 TCAATAATCAATAA-
Rev.of:Mhapla.WS247_Fam_292_15_1 TCGATAATAAAAAAG
** ***** ** **

Consensus:
TCaATAATaAAaAAg

>Allfam_Fam_157_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.642857
Cele.WS201_Fam_28_12_9 CTACCTACCTAT--
Rev.of:Mhapla.WS247_Fam_295_14_1 CTACCTATATATTA
***** ** *

Consensus:
CTACCTAcaTATta

>Allfam_Fam_160_14_2 Nr. of seq. 2 Alignment length(with gaps) = 14 Alignment score = 0.714286
Cele.WS201_Fam_89_14_3 AATTTTAAATTGGA
Rev.of:Mhapla.WS247_Fam_294_14_1 AATTACAAATTGTA
**** ***** *

Consensus:
AATTacAAATTGgA

>Allfam_Fam_162_13_2 Nr. of seq. 2 Alignment length(with gaps) = 13 Alignment score = 0.641026
Cele.WS201_Fam_353_12_1 AGTTATAT-AGTA
Rev.of:Mhapla.WS247_Fam_298_13_1 AGTTATATGAGGG
***** **

Consensus:

AGTTATATgAGga

>Allfam_Fam_165_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.694444
Crema.WS247_Fam_35_10_9 TTAATTTTAA--
Rev.of:Mhapla.WS247_Fam_10_12_8 ATAATTTTAA

Consensus:

aTAATTTTAAa

>Allfam_Fam_166_12_2 Nr. of seq. 2 Alignment length(with gaps) = 12 Alignment score = 0.722222
Mhapla.WS247_Fam_302_11_1 CAGAATATA-AC
Rev.of:Cele.WS201_Fam_143_12_2 CAGAATATATTC
***** *

Consensus:

CAGAATATAtaC

>Allfam_Fam_168_11_2 Nr. of seq. 2 Alignment length(with gaps) = 11 Alignment score = 0.696970
Crema.WS247_Fam_347_10_1 TCGC-TATCTT
Mhapla.WS247_Fam_126_11_2 TCGCATAACTT
**** ** **

Consensus:

TCGCaTaaCTT

>Allfam_Fam_170_11_2 Nr. of seq. 2 Alignment length(with gaps) = 11 Alignment score = 0.651515
Mhapla.WS247_Fam_304_10_1 GCAAATATTT-
Cele.WS201_Fam_18_11_14 GCACATTTTTT
*** ** **

Consensus:

GCAaATaTTTT

Table S8. The microsatellites in *Caenorhabditis*

Species	A	AT	AC	AG	W	AAT	AAC	ATC	ACT	AAG	AGG	ACC	AGC	ACG	CCG	CG	C
<i>C.elegans</i>	50	255 [*]	125 [*]	185 [*]	12097 [*]	31	4	13	5	24	10	4	6	11	0	0	27
<i>C.briggsae</i>	8	118 [*]	115 [*]	1457 [*]	3389 [*]	25	7	15	1	220 [*]	4	1	1	0	0	0	2
<i>C.remanei</i>	22	146 [*]	19	182 [*]	4274 [*]	32 [*]	17	4	2	72 [*]	5	0	2	5	0	0	6
<i>C.brenneri</i>	59	127 [*]	49 [*]	1848 [*]	2875 [*]	14 [*]	14	20	2	101 [*]	13	3	3	3	0	0	7
<i>M.hapla</i>	23	9	0	0	101176 [*]	6	1	0	0	4	1	0	0	0	0	0	8

Number of repeats longer than 24 bases found for each motif. Values in both strands are added. The superscript (*) indicates that the maximum length is longer than 95 nucleotides.