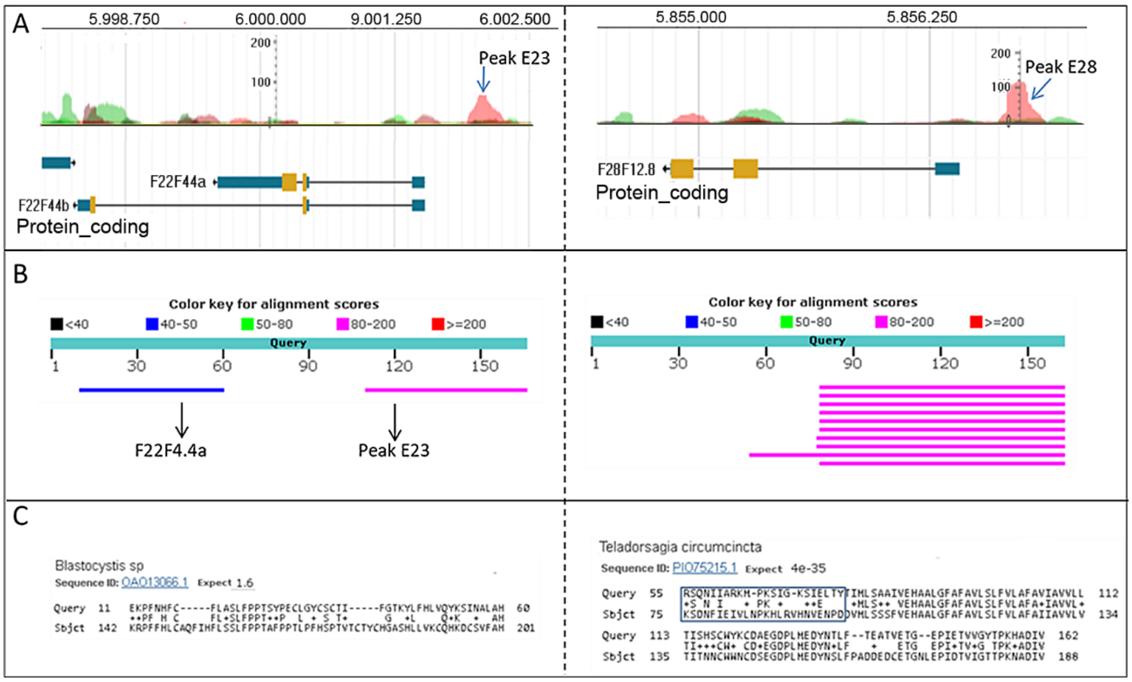
Supplementary information

Supplementary Figures



```
Blastocystis sp
Sequence ID: OAO13066.1  Expect 1.6

Query  11   EKPFNHFC-----FLASLFPPTSYPECLGYCSCTI-----FGTKYLFHLVQYKSINALAH  60
            ++PF H C     FL+SLFPPT++P  L + S T+      G  +L    Q+K +   AH
Sbjct  142  KRPFFHLCAQFIHFLSSLFPPTAFPPTLPFHSPTVTCTYCHGASHLLVKCQHKDCSVFAH  201
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Teladorsagia circumcincta
Sequence ID: PIO75215.1  Expect 4e-35

Query  55   RSQNIIARKM-PKSIG-KSIELTYTIMLSAAIVEHAALGFAFAVLSLFVLAFAVIAVVLL  112
            +S N I    + PK +    ++E     +MLS++ VEHAALGFAFAVLSLFVLAFA+IAVVL+
Sbjct  75   KSDNFIEIVLNPKHLRVHNVENPDDVMLSSSFVEHAALGFAFAVLSLFVLAFAIIAVVLV  134

Query  113  TISHSCWYKCDAEGDPLMEDYNTLF--TEATVETG--EPIETVVGYTPKHADIV  162
            TI+++CW+ CD+EGDPLMEDYN+LF    +   ETG  EPI+TV+G TPK+ADIV
Sbjct  135  TITNNCWWNCDSEGDPLMEDYNSLFPADDEDCETGNLEPIDTVIGTTPKNADIV  188
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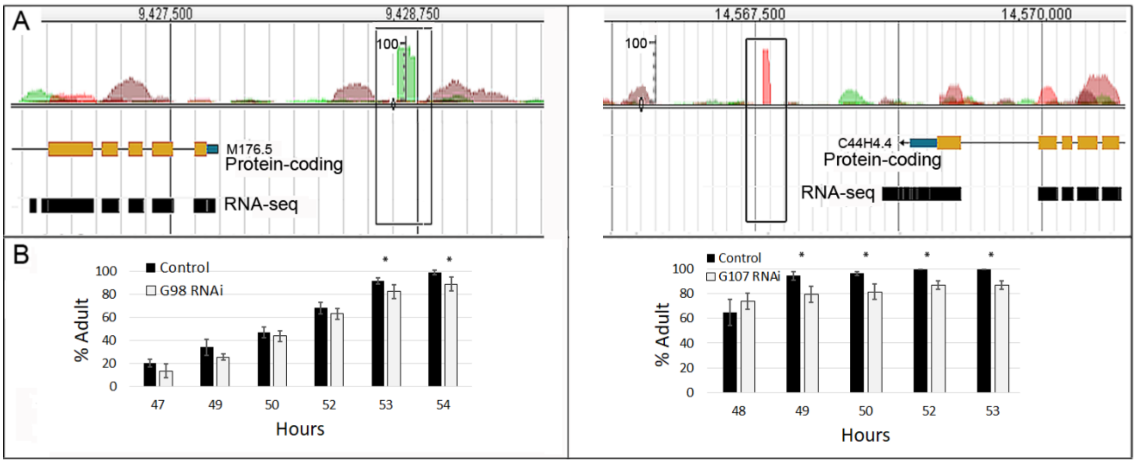
Supplementary Fig. S1. Putative new exons identified by AnABlast peaks E23 (X:6001927..6002254) and E28 (V:5856625..5856859). A) Peaks E23 (left) and E28 (right) (squared). Annotated exons of their respective adjacent genes F22F4.4a and F28F12.8 are shown. B) Top BLASTp hits of E23 (left) and E28 (right) predicted protein sequences. C) E23 (left) and E28 (right) protein sequence alignments to proteins found in the indicated specie. Exon E28 sequences is highlighted in box. Sequence ID and alignment significance (Expected E-value) are indicated.



Supplementary Fig. S2. RNAi analysis of AnABlast peaks G98 (II: 9428645..9428735) and G107 (X: 14567563-14567626). A) AnABlast profiles showing peak G98 (left) and peak G107 (right) and peaks matching exons encoding their respective adjacent protein M175.5 and C44H4. Peaks G98 and G107are indicated (squares). RNA expression data (RNA-seq) are shown. B) Average worms (%) that reaches adulthood from L1 (time 0 hours) in worms subject to E98 (left) or to E107 (right) RNAi (grey) with respect to their controls (black). Standard deviation bars are shown. * means P≤0,05.

Supplementary Tables

Supplementary Table S1. Accuracy of AnABlast in the identification of non-redundant intergenic sORFs found at http://www.sorfs.org/database for *C. elegans.* A representative sORF reference is described for the indicated genome interval. sORF length (number of amino acids), Evidences of expression reported in WormBase ("-" Not reported, "+" RNA-seq, "++" Polysomes, "+++" both), AnABlast prediction at the sORF genomic interval (Peak height: "-" Not significant, "+" 5-14, "++" 15-24) "+++" >25), and representative related coding sequence identified by BLASTp search (default parameters) against the non-redundant protein sequence data base (length of the target protein and E-value of the alignment are indicated) and remarks are indicated.

sORF reference	Genome interval	sORF length	Expr.	Anablast prediction	Related Coding Sequence and Remarks
arnold_c14_2014:151752	III:5094893..5095009	38	+	++	Annotated sORF CELE_F54D8.10 No similar proteins.
arnold_c14_2014:229152	IV:7053788..7053817	9	+++	++	Annotated sORF CELE_F54H12.3 No similar proteins.
arnold_n2_2014:113038	II:5758546..5758620	24	++	-	Annotated sORF CELE_F10C1.23 No similar proteins.
arnold_n2_2014:505973	X:4702799..4702855	18	-	-	Not annotated Similar proteins: -AQuaPorin (Caenorhabditis elegans) Sequence ID: NP_001359963.1 Length: 330 E-value: 1e-09 -hypothetical protein B9Z55_024173 (Caenorhabditis nigoni) Sequence ID: PIC18191.1 Length: 297 E-value: 1e-09
hendriks_2014:175563	II:2725608..2725649	13	+	-	Annotated sORF CELE_T05A8.11 No similar proteins.
hendriks_2014:175658	II:5803854..5803913	19	+	+	Not annotated Similar proteins: -TIL domain-containing protein (Caenorhabditis elegans) Sequence ID: NP_001343656.1 Length: 171 E-value: 1e-10 -hypothetical protein CRE_11990 [Caenorhabditis remanei] Sequence ID: XP_003109086.1 Length: 169 E-value: 9e-06 -hypothetical protein FL83_04414, partial [Caenorhabditis latens] Sequence ID: OZG21110.1 Length: 169 E-value: 9e-06
hendriks_2014:175699	II:8982729..8982761	10	+	-	Not annotated. No similar proteins. located at the 5' utr of gene C18E9.7
hendriks_2014:262	I:2945458..2945487	9	++	+	Not annotated No similar proteins.
hendriks_2014:331543	III:4324159..4324236	25	+	+	Not annotated. Similar proteins: -Uncharacterized CELE_H38K22.9 (Caenorhabditis elegans) Sequence ID: NP_001368690.1 Length: 25 E-value: 1e-21
hendriks_2014:331740	III:1901967..1902038	23	+	+	Not annotated. No similar proteins.
hendriks_2014:658572	V:6452777..6452872	31	+++	+	Not annotated. No similar proteins.
hendriks_2014:823799	X:5450031..5450201	56	+	+	Not annotated

					Tandem repeat of the 3’ exon of gene C25F6.6
hendriks_2014:823914	X:3025113..3025163	16	+	-	Not annotated. No similar proteins.
hendriks_2014:823999	X:4783780..4783821	13	+	-	Annotated sORF CELE_F43C9.2 No similar proteins.
hendriks_2014:824045	X:5659967..5660023	18	+	-	Annotated sORF CELE_T22B7.22 No similar proteins.
hendriks_2014:824117	X:11267038..11267298	86	+	++	Annotated sORF CELE_C03A3.9 No similar proteins.
hendriks_2014:824131	X:12148633..12148665	10	+	-	Not annotated. No similar proteins.
nedialkova_2015:108298	II:9418511..9418513	48	+	-	Annotated sORF CELE_M176.16 No similar proteins.
nedialkova_2015:108339	II:2895597..2895668	23	+	++	Not annotated. Similar proteins: -UBIQUITIN_CONJUGAT_2 domain-containing protein (Caenorhabditis elegans) Sequence ID: NP_001348718.1 Length: 238 E-value: 9e-13
nedialkova_2015:204387	III:8326386..8326598	70	+	++	Annotated sORF CELE_ZC262.13 Similar proteins: -hypothetical protein FL83_22023, partial (Caenorhabditis latens) Sequence ID: OZF89903.1 Length: 98 E-value: 2e-29 -hypothetical protein FL81_17889 (Caenorhabditis remanei) Sequence ID: POM29574.1 Length: 98 E-value: 2e-29 -Protein CBG25937 (Caenorhabditis briggsae) Sequence ID: CAS00299.1 Length: 86 E-value: 1e-27
nedialkova_2015:204436	III:2528650..2528679	9	+	-	Annotated sORF CELE_Y54F10AM.15 No similar proteins.
nedialkova_2015:27	I:10380793..10380921	42	++	+	Annotated sORF CELE_F45H11.11 Similar proteins: -Unnamed protein product (Heligmosomoides polygyrus) Sequence ID: VDP01011.1 Length: 118 E-value: 3e-08
nedialkova_2015:412435	V:14547397..14547441	14	+	-	Annotated sORF CELE_Y54F10AM.15 No Similar proteins. Located at the 5’ utr of the rbc-2 gene
nedialkova_2015:516194	X:5259950..5260078	42	+	+++	Not annotated Similar proteins: -hypothetical protein CRE_00743 (Caenorhabditis remanei) Sequence ID: XP_003117941.1 Length: 125 E-value: 1e-21 -hypothetical protein B9Z55_024276 (Caenorhabditis nigoni) Sequence ID: PIC18352.1 Length: 125 E-value: 2e-20 -Hypothetical protein CBG14648 (Caenorhabditis briggsae) Sequence ID: XP_002644667.1 Length: 125 E-value: 2e-20

stadler_2012:136758	II:8766809..8766838	9	-	-	Annotated sORF CELE_K08F8.15 No similar proteins. Located at a pah-1 gene intron (antisense)
stadler_2012:256915	III:5863632..5863715	27	+	-	Not annotated. No similar proteins. Located at the 5’ utr of the dnpp-1 gene
stadler_2012:54	I:15064721..15064759	12	++	+	Not annotated. No similar proteins.
stadler_2012:639775	X:3147194..3147226	10	+	-	Not annotated. No similar proteins. Located at the 3’ utr of the C15C7.4 gene

Supplementary Table S2. Accuracy of AnABlast in the identification of curated genes coding less than 100 amino acids length peptides. Coding genome interval, peptide length (number of amino acids), AnABlast prediction (peak height: "-" Not significant, "+" 5-29, "++" 30-89) "+++" >90), and reported sORFs entries at the coding genomic interval of the gene ("-" None, "+" 1-2, "++" 3-4, "+++" >4) are indicated.

Gene	Genome interval	Encoded Peptide length	AnABlast Peak height	Reported sORFs
fipr-16	III:8590833..8590982	49	+	-
fipr-3	X:14423405..14423883	50	+	-
fipr-15	IV:10880564..10880716	50	++	-
rpl-39	V:7775742..7776079	51	+++	+++
R05D3.6	III:8350419..8350805	54	++	-
ZC262.5	III:8342224..8342610	54	+	-
T23F2.4	X:5514798..5515080	57	+++	-
tomm-7	III:7859613..7860159	58	++	+++
C04G6.5	II:5085785..5086121	59	++	-
gpc-1	X:12881126..12884989	62	++	-
mtl-2	V:14018270..14018673	63	+	++
fip-1	III:8639791..8640093	63	-	-
nola-3	I:10179042..10179236	64	+++	+++
rps-28	IV:1659691..1660011	65	+++	+++
nlp-28	V:3987900..3988312	65	-	+
sid-5	X:6904721..6905849	67	+	++
emo-1	V:10896658..10897143	68	+++	+++
flp-24	III:725022..726155	69	-	++
cpg-9	IV:3067848..3069876	69	++	++
nlp-30	V:3981980..3982741	69	+	+
rpl-38	V:15512166..15512780	70	+++	+++
ubl-5	I:5607820..5608841	73	+++	-
nlp-29	V:3984413..3984847	73	-	+
nlp-33	V:11147336..11147737	74	-	-
mtl-1	V:6691371..6691863	75	++	++
nlp-31	V:3980055..3980622	75	+	-
ins-23	III:10028247..10028600	76	+	-
ins-21	III:10023804..10024120	76	++	-
snr-7	I:2727014..2727545	77	+++	+++
ned-8	I:10373368..10373862	77	+++	+++
tmem-258	V:7063174..7063718	79	++	+++
emb-1	III:5173439..5173809	81	++	+
nlp-36	III:9488731..9489188	82	++	+++
rmo-1	II:13237404..13237907	82	+++	-
moag-4	I:2064909..2065481	82	++	+++
dss-1	III:1194367..1196292	82	++	+++
ddp-1	III:1859888..1860381	83	+++	+++
flp-23	III:8650764..8652190	83	+	-
rps-27	V:103394..104064	83	+++	+++
ins-22	III:10026289..10026673	83	++	-
kreg-1	X:8709764..8710137	83	+	-
ceh-7	II:8703368..8703829	84	+++	-
flp-26	X:7029136..7029638	84	+	-
abf-1	I:3886111..3887080	85	+	-
snr-5	III:7862070..7862577	85	+++	-
abf-2	I:3885548..3885905	85	++	-
acbp-1	I:4635722..4637328	86	+++	+++

vha-17	IV:9321801..9322528	86	+++	+++
tin-10	III:11500867..11502852	86	+++	+++
moa-2	II:7698613..7699046	87	+++	+++
rps-21	III:7189142..7189631	88	+++	+++
mai-1	X:3114668..3116538	88	+++	-
flp-19	X:10604686..10605828	89	+	+
lury-1	III:12186411..12190116	89	++	-
baf-1	III:9467464..9468058	89	+++	+++
flp-27	II:5680980..5682667	89	++	+
dlc-1	III:6462907..6463801	89	+++	+++
snr-6	III:12429172..12429630	90	+++	++
tin-9.1	IV:7044058..7044602	90	+++	++
emre-1	X:14979374..14980435	90	++	++
dlc-2	IV:12110586..12111577	90	+++	++
rpl-43	II:14155280..14155660	91	+++	+++
rpl-37	III:3528547..3528968	91	+++	-
smo-1	I:1340678..1341258	91	+++	+++
ins-11	II:5556761..5557088	91	+	-
mps-4	III:8270790..8271776	91	+	-
flp-5	X:8528250..8531033	92	+++	+
flp-16	II:13235306..13237417	92	-	-
flp-22	I:8658874..8659967	93	++	++
ufm-1	III:7858979..7859512	94	++	++
cks-1	IV:8513919..8514725	94	+++	+
dpm-3	IV:12391591..12392120	95	+++	++
tag-209	II:10787312..10787914	99	+	-

Supplementary Table S3. Genome intervals highlighted by AnABlast as putative new intergenic sORFs (82). AnABlast peak height (protomotifs accumulation), Expression evidence data, homologs/motifs, predicted amino acid sequence (ORF) and the number of residues (ORF_length) are described.

Peak	Genome interval	Peak height.	Expres.	Homolgs/ Motifs	ORF	ORF length
G5	IV:1213206..1213443	88	Polysome	-/-	MDTLAIKRRSEQKVVGSYEPTGEMGNELKRWKKERKGVLKENGGTGYRLVVREHQIFWEGEKDGLSWGDFSYYYTILRLH	80
G14	II:11736898..11737084	175	RNAseq	-/-	MEDTKRVFGILPGKLLHLSRSYSTLKHHILRASRSTFQA	39
G22	III:670901..671255	74	RNA-seq	-/-	MRHKKEGSIACELMRFESYYLLAHGGDDHHLNESLYFLYLDSLHFPCKILFSGIRKGEGRNLKVTMKIAYDTRRIISQRLVKIAFSPSTTGFAATHRLP GTSGEQFLAASPNPLTLFPRGSWSRQLFLFLQKKRERERATTNSINTDLKTSSSVFSLLQES	162
G23	III:5838386..5838494	71	RNA-seq	-/-	ISHRHEALRKSFHLINWRVNSPSHKDQEKLEKRQILPVAAK	41
G25	X:17515475..17515919	70	RNA-seq	-/-	MELECSGLLILNKKRFFSQNFLKKFVCFEIITFSSQKINEKISISRMSHYHSDQTFFKYQIVNNNSAFQSRQFPVNNQWKPLIGLSTRYGQDNILMEHKIWLKIGNIKFKKPQHTGKSPHCAQPTSSVLFGASNYFKHLLRGEKFQRA KLKEKVFEYSELYLLQNFATLHIRTG	175
G26	II:11717583..11718477	297	RNA-seq	-/ PF07735 (F-box associated)	MVAVELNISYQTQCCVRFRNHSVNIKIDFPNGYYWNGTRRLCEEIELRYTEIDMFQRPYRWFWFMPKVSARYVDHILKTFNRGKVLRLKIDCDAREFMNLNEFNDIRFESLWIRKLRNANYFFNLKEFINQAYSLLLRDSEFTTLPKFQIDFCQNQERIELWSFSMNLNTLLLCNFKEISLITSINLADINLFTK	199
G30	II:13644506..13644671	196	RNA-seq	(O02112_CAEEL)/-	IQAFFFVFSAVLDFVVKLYLNFFSDGIERVDCSDGYDIERNDGLLATVFYQNMGTDFFVWHDRFPTYSHRNLPST	75
G31	I:12928143..12928563	164	RNA-seq	(G8JLX0_CAEEL)/ PF07735 (F-box associated)	LIINYSNWFNLDYLLKSDSVNIHLYDFVWNPADLNRFLRSWLLSESNVKLTFLEVNIANRDSLEQILDLPEDSIVRNEEENRYSANKFVLKSCLFWQRTICNCMFLSRRVKNPTKRRKESCTTHLFCSLARQIRLYISCCLRKYVICSRNNLNKVIIKILVTVAKKI	167
G32	V:13396252..13396714	84	RNA-seq	-/-	ILRDIEGIFCRNTDESLRGLGRLVFVDILIKTTDYRISSHEPSGLHFWGNWVGDKMEIFQNMWDKLLEKGLDRRTIGAPGLLHRRAAKTNLRPSALIHTYRQHPPPLRFAQCPSPYTHTHTQKRRRGHILCDKEGIFRQVREGDTGRRVHTLIGGRTDRGLPSRLDANTCGSLRVE	176
G43	X:15015384..15015639	233	RNA-seq	-/-	MNFAKQAKPDCFARHTRYKAYKNKNETFHISGRKTILKNQFLYRKAVYS	49
G45	III:7833431..7833716	102	RNA-seq	(Q9XWD9_CAEEL)/-	MYAWQQNFTGNHTLKLLGEAAIHDYLDIFPPCSDRDGIATCLISLGKLQKQCVARTLSHDEIRLDKWINTYLTMTLFRHYRSCILLSYSYNILLLFF	97
G46	I:7316251..7316590	70	RNA-seq	-/-	MQIRETERTVEERSKKIGWSSVTASSFLSFISQFPLNTKMRRMGCRSAIFTTQKRLSYRKAKGDMIERAADPKPKIDPQRKWLITLSSLQGFIKTFSSS RFPFKYFRREYEHCERYLGKET	122
G49	V:14367725..14368037	74	RNA-seq	-/-	ILSCGLSCSFLNKCFALRTFPQVFRPTFSIFPENRGIFIVMDMTSRIPNNKKYTLTPNSLTCCRKFQRSNRELELLKTWLPARLHDLFVLSRYIKYRYNHSLKLYQYSQYFHLNIALNL	119
G50	X:16728266..16728758	93	RNA-seq	-/-	MHRFTLNFARKCPMILQTFEQIVYPFRNQITEAKVSPQNLIVYKFHIQLLFAEYLISPPECGGVERTQKLSSVIYEVRHRCTLAKQEKGKNWKLATTMQ NSTSEVGMRIGLRKKKWGKDQRKEKI	126

G51	V:8646870..8647347	98	RNA-seq	-/-	ITVTILLNLTSKHLPSIINIPDLRKPLAQGYPKPLRRQTRTPERNQISGTRSGTTLNEVTEKVSKCVHLFSGRLTILWVYYVRDKEMMIERMFDRLYGGTYLDMISLFWKPRVFFCLLITFFCWVLHIPICVGIIRLCSFLMFLGFIFNFPRYKIKNTTTRVNIQM	165
G52	IV:379001..379340	71	RNA-seq	-/-	ILKMNLSIAHLEKLELIKFYIIFSRNSSTIHPHCHGTFKDFSLLTRVLVFYGTKKSLLVIIVITLTYNHKALRTFIVETAWMHTHPQISSNLVGDCEQKRRREIRKTERQIDSRDTNVRCFIGTQSVKDHREPRHRLICR	140
G54	III:4101011..4101389	139	RNA-seq	(A0A0U5FV96_9EURO)/-	IFINLKSQQNKLVGMAAQGISIEPIEKQTETKKKPQIFFLKSPNPSKDRRLRDRIRQEIREKQKVLRRIHNRIRGIVNDKVSEEMGFCFETLCWVHNHTFIGGEVGFVKYEKRNVKTGKQQCFNVQVLSCDGEAFKNE	138
G57	X:541358..541951	1820	-	RNA-directed DNA polymerase/ Integrase domain containing protein	MSQFLLHYRATPSNALGGLTPAEVHYGRRLRTRTSLMMPRKDHSEDSTASTLAMKDQFDKHNRAKARYFHEDEKVFAKVYERNSWSWKPGKVANKQGKVVYVNYLDDGRERAVHANQLKPRVDEKETVRVNAWKDTMSDTSELLPYDNEDYEVIERKTKLPTIMPTLKEDNSGSSSSTTPAQPVQSPVVQGPVQGDHAQQQDALVLLPNARGPSRATSPVPIRRSTRQHSIRFDPCA	59
G58	V:19477929..19478157	243	RNA-seq	-/ PF00097 (Zinc finger, C3HC4 type)	MTVGRQAILLECGHTFCIQCVENNKENSAVRYLDCFDLSAIRLRSEYMESNNLFIFSYRYTFFKVTIKRFLI	72
G61	V:10709701..10709983	424	-	-/-	MGLLKYEIKKRANSRSKSSKAIECISSKYENSHTSNILIKYSLKPYACNPFNDCFTTNSLLQLHRIIPVIQYTRCSNLDYDKSVESTETMICMCICFVI LR	102
G63	IV:1278944..1279091	363	-	-/ PS50883 (EAL domain profile.)	MGWRHPETLTNLPPSQFLPIAETTNFKFMNDVYLVEK	37
G64	I:14308479..14308887	354	-	-/-	MSTCSNQRLKHLSFTIQNFDWVTTILDLPHRETEPRKYEITRDDGVKSVCGLNRGVQFX	59
G65	V:5768239..5768632	343	-	-/-	MKMAPRLMYIIIHHSKSLSASHDLLSLSLKKRRDDTRGDGNSNVLSVVSCSLIDPLIMSFL	61
G67	V:3576900..3577317	288	-	(G0PEE4_CAEBE)/ Serpentine type 7TM GPCR chemorec.	ILSLSLQFSKCSKSETFLCCWQGLAYTSHAITAVLVSFHILGGYCILLKTPPQMASYRWPLFNLHFW	67
G68	II:6978237..6978540	271	-	-/ PF07735 (F-box associated)	VCVCVVDCLILEGEIYLPLSSAQLLAQRRILPRNFRELKLLIGIPLNDLLLTSCSSLHTYNSLSTDKDINLFLRHWTAGLKPELEFLTILNIHARIKLSILFSVASTFTFLKE	113
G69	X:14916816..14916993	271	-	(Q84LU4_GINBI)/-	MFFRHMSQGFCSWKKHRKPGDX	22
G70	V:13060163..13060498	251	-	(G0P3Q5_CAEBE)/ Peptidase_A17	IQRKSENKCKNHDMFNTWCSDYSYKSAKLIMFSDVSKNNDGLVAYI….. FEYKDGHAQSKLVMAKSRVKKSSIPYRG	46
G71	X:11701412..11701730	251	-	(Q4R178_CAEEL)/ PF07735 (F-box associated)	MNIKCEEAQIWKNNLSLQDIELFIRHWLSGNMPNFKCLRIHDYQNVRFWINALRGIDSRVRNPLSQPKTYKLFLNMYISKQGNIIX	86
G75	V:4970301..4970493	147	-	(A8WQ28_CAEBR) /Serpentine type 7TM GPCR chemoreceptor	MSQKFSKLQVEILRALTIQTLVPIVSSVLPCVICWYFPNFPNIACEL	47
G76	II:11805687..11805840	136	-	(Q9XX13_CAEEL)/-	IERVDCEDGKDVLSDDGLIATIKYKNCGIDFLVWHEKFPIDLMQRFEMRNKI	52
G78	V:6699013..6699454	134	-	-/-	MISFFQISKNTTIMISFAIKQSYSCHGVVCSVVKHEKTSVGEKYLVSSTVFLISELFAFCDLTNTFSAHRPYKKCRLHFDSRKFYGNLKSSLDTSHAFL CRLICLGF	108
G83	II:3733728..3734019	116	-	-/-	MFDIFQIRPVLPDLLDLRLIEKHSNPNFSVSLHTKYNPFLDQSRKMISFFQISKNTTIMISFAIKQSYSCHGVVCSVVKHEKTSVGEKYLVSSTVFLISELFAFCDLTNTFSAHRPYKKCRALHFDSRKFYGNLKSSLDTSHAFLCRLICLGF	154

G85	III:669337..669397	112	-	(A0A0P5LGG1_9CRUS)/ mobidb-lite	MKTNISKKNESSTKKRKTSAKRQKSVPVLPCFLPFFHTFVLFFTLLLHRYATSLFLFFFVKHHSSAFSIETCRYIKKGNLVAPPPVVRGEI	91
G86	II:4548339..4548606	111	-	-/-	IELLHYNFKNSPTFFQETLQRGLVKQKIQKTVPIRPSTDKDITNLPFNPIEDETTFDVTKNVSTKNLFVSSKTHKLWFICRIVSVWRYQNITRFF	95
G89	X:7713027..7713081	108	-	-/-	MRIRLLLHFTSHLHSISSGISVNTLIVEDTQMCKEKKTARKARTICLTIAW	51
G93	I:10067869..10067959	104	-	-/-	ILLKRLIVSHETPWTTHCTFIQNF	24
G95	II:3857180..3857426	101	-	-/-	ISFSNSIPSIRRDSVSQIASLVKRGKDTATIDVGEFYLFYFNSFSPVFYNNDTETYRYYDEKGFIYLSSLNHLTPYGLEHVRHVWTEVCAKL	92
G97	I:6983892..6983949	97	-	-/-	MLDAKMQDHSAQLLVFGNFSVISINLISFLSHFDGSRCEKX	41
G98	II:9428645..9428735	97	-	-/-	VKKQYKPRKWYSLLVVHVYFHNKFENSKKLLKSK	34
G99	X:13784500..13784599	96	-	-/-	VISHFENHILFSSVSLVTKCIFNGCYTYVMNFEKHFLVNCCC	42
G100	X:7369398..7369593	95	-	-/-	LVLTNHLSKKVCIHTLVVPLICFRYGIIPECSAPFSALFGLGRNMKTFSSSFLRIIIYLFLNIFSHKCDVLFSSVF	76
G103	III:7619994..7620480	92	-	-/-	VQKFVCVSISFVKQFSNCDEYINPNLLKGISQLCHLMVQTFCSHKQSTFTPDCHVIIFLSFLLAIFPCLSQFPLFLSSTSSTLHGHHQRPQTIIISCHKPPFSLFSIPNDLSRRILEKEREFKTLRRQCDQACQSHIVRLSHRNPIIFTFLPLIRVHNEIESPVFRGTSYVIREFMRFEI	180
G106	III:7546511..7546649	91	-	-/-	IEFYGSFTSLSVSLYTSSSLKIGRVFVAKRKYNLKVVLCFSPLLFHGLKISVIQEKIILKINQFLGQKCT	70
G107	X:14567563..14567626	91	-	(H3D5Q5_TETNG)/ -	ILSTVNFGNVLFWQQAHVFVLTGL	24
G108	II:3997148..3997499	90	-	-/-	IFAHCNGKLFEVNLNFQKEFLVSPVFAKTPSVHRNHTENYVGKYWGMVMPIETIKTDQWVKKYQEKLMVKGFENFHKFLSKIFQNALKISGRLETIFGVLKNCGKLDKVLFRYFQETLKFF	121
G109	X:16024200..16024737	90	-	-/-	MHRRSHRKCTFHVTDQHAGLGADVHVSTAVARRPAPATFLCASYTMPRSLSLCILYALSVCSPSTSLVKRWRNCVPKCNELWSIRRGEIGKAERMMEIRTTDKICYGVRVLSIIGNYWFLIYNPWFAGTILNMFLFLGNKIIYVFNHENILIASIKKSLNNFRLNKVRSPPDFSVKKFQKHMIFKLLNFPAKKFVIK	198
G110	IV:2212713..2213040	89	-	-/-	LGAGVHGSHVIYVRGSVHCGDVNELGGSVNKNWESIQKNILEIRRSYIEINKLRTDPYFKAVNTQLNLDMPESRICPLRIGMCWEFGEGSDRRSTDRPSGRDSSKF	106
G111	IV:1212666..1213077	88	-	-/-	LVGKKERGLIRFVLCCSLFFLAHHNEDTISFFPFFWQNLAHFSLTVSEIPAFFHFPKSCPVFLTVLISAAFCSTLSDFCGIFPIFRRTLLAFYSTLPTFCKTLSPFNSTLPIFCRTFPALCSTLPLWSTLPVS	133
G112	X:13380046..13380358	88	-	-/-	MIIFPTSTNKKLERAHSYPSPRFREVSKFLNALRFFDIQPFFSQDDSTSFLNRFFENLERKTFKKARVSILRVKFIRHVLTANSADLLEMTAYTLIVFNI TET	104
G114	X:14344402..14344645	86	-	-/-	MIPTHSVPTALNKRKSFKPERYQGTAQVKQITRYLPLGNGHFCCKRFRVIFSMCTNCVTVSGFQGLKVSGYYEIGVSMLDIILD	84
G115	III:214502..214871	85	-	-/-	IIGFWVRETLQTMLGRCERRKMWPDMFSSIHVPAGDPHKTHGNQVYTMSSECSEQYFKPIIPNFLRFLPKNWQHHGFETQNRLNHRFSGTTNHVRQVRELKNSEFYYQASRCPLETPRKTPHNVSTMFNYFKN	133
G116	IV:1287156..1287513	84	-	-/-	VFFDSFSKFQNISTYIISAGNPDFSTNRKLKSRFSVEFKPNLGKFSEMRIFANAGCREKPILNFISATFRKISRFFPEYYSRFRAEIFEKFPSIFSQNLENFRSRKPIFSGISAKFLRNLCKFPEM	126

G117	IV:9866734..9867040	84	-	-/-	MIAKIYTISIVYTLVFISKNRRTTSVPFQFDQNKTTLLGDEFEIRIFLKHDQFFHELLQDMSFWSYNSSIRVVFHIVMS	79
G121	IV:3654868..3655246	82	-	-/-	ILTLIFYHLSPKFFTTVQKIYANNFFTRSMETGTLQNFAIFPKKLKFFSSKLVAFSEELPQVLNKQNAIFCKSCSQSTIGCSLLRVHLWSIREQLSPTSITPLALAAPRAQPPQRTFCENRMLLTDWIRSSFSIIFLDMYSLCSFLRKKGSRGLVFCVLFGFWHVFFYFWGFQKFLAEVSRN	182
G122	X:743277..743580	82	-	-/-	MPSGVINCISRQLINPKNVLTRAQCPDLIEMVEDRNDFPLTNINNCFLIGHCCFMRKVKNLGVEYFLTRVNIICVFLTWCLLFLETILQFFSQIGFFVCK TTKSGSGIFFAVLLIKX	118
G123	III:12582510..12582588	81	-	(A0A0L8G6E5_OCTBM)/-	LVHDYFEYIFIFGGVQVFKGKIFYLKASNN	30
G126	I:14314870..14315371	78	-	Sequence ID: NP_001361903.1 /FBA_2 domain-containing protein	MEFFLDIFNQAELTYLKLSHSGLSFLPILKDFNRFNKLVFDSDRLKSIQKYAAVAKSLKTYYVYSELLIQNFQKLKITRRPHHITLDDLLLINGERVILTAHLSSRDTNLFLKH	114
G127	III:9992028..9992310	78	-	-/-	IATLAANLQVTARRFRLPYRRCEKGALSVTVSDFSPFSLPEYRREIVLTIERKEEKEMLRRTWEQNDLHSFDGWNGTENEREIPMVDFYD	90
G129	X:15255109..15255442	78	-	-/-	MADTSQLSNCSTDPSTHVNVDMVPMSDYLKLKNTCDASIAKFARFTEAIDALICDKSPSAVPVQASNPFASVTAPSVQLVPLMSFKMHPPTFSSYSLHEISREMLSISFHSPQPSFVIIAGWKADP	127
G130	X:9603752..9604172	78	-	-/-	ISNHSQVDMSNHTNLPTIFEEGFETYLELAHVDDEASGSDLSLNTEDSTIDLEFLGTFSHYDENPNSSTFTVDFLNSSCDFSNPDAAIFEDIKSIRLGSNDLSTFPNENEAVYKTPNNQIEESADSRNAKKDESVKRWWQFWG	143
G131	II:12979623..12979845	77	-	-/-	MNTSKSTYACLKIFKETYTCLNTFDVTYACLKTYKGTFA	39
G133	II:6310391..6310769	76	-	-/-	MQTAHSMRQRSLISKIRYHLGDSSKVKVREWVRENVKRNKEENKLRKFSLLGTSFLEYAHRLPSLFPLIDGLAKKSKVETRDRMIATLYRLEKIFKLCHSDRKIFKKYLFHLNVANYFFFDIQNIFQN	128
G134	III:11729720..11729903	76	-	-/-	IGDFSRRVDFRLLFFQQILQHFKLPKISRISFQIRNQKRMFDHLNFLCSIIFQKTTIIGGKEHLNSQQISIYKIIK	76
G135	III:1446243..1446597	76	-	(A8Y423_CAEBR)/ mobidb-lite	VAWTTRAEEAAELKWSDLSQKGGDFGGKKTERKKRDQLTPNAVDSIAKRTLQKIGVDFSHHALRRG	66
G136	I:13395200..13395593	75	-	-/-	MLKKQDSKFLKMKNKKSYITEKENPQKTRRIISILGLKWKTRSSRCLRLSHYLSLIYSLYSRLKIERNWWFDRKMKMKEEGFQENKKH	88
G137	V:10032341..10032656	75	-	-/-	MMIENLPTQTMTITYFSVFPSSFMINITGDNLELTSTTKSSTGNFKQKLEELEQKRAAEHWCCVFSNYIFSVVSPVGHF	79
G138	V:8678462..8678762	75	-	-/-	MRIFSTFNITYMNSAFSSNFLPSVCQFLTNSTQFPKLQRKLPHTSHTRAQIFPKSFSPKLVNAANKIRV	69
G139	X:9646607..9646910	75	-	-/-	INSLLSFFGKQRVKWRENPPTTPHSVIMSHLRRRQRASMQIALKSEQCVPRGEQKARQQERAGSALLFLIPLPEHRGLRMKGAQLFVILTFFFSPYHYHFSCHLELFSLHNVRNATGFSKK	121
G140	I:11500352..11500649	74	-	-/-	MPKPIILPFSQLSSNNRGVYSLLPFCREEGVDPLPVLINFLSRIPGFVDEKLRISALWTKNSFLQINFFEKFEPETSFSEFASISHCAILTGAVGNRHQLDENNQSSNPGKAH	113
G141	I:12612423..12612753	74	-	-/-	MRILKENSQAKNISAKIEWNYSKRSQNSKHQCPVKHIYNLLTPINIGRQTTFNQKSSMFKNREDFFKQLNIHLCLGKFPNTQNSRISRKNGSFEVIFCLEKRGLIRRQRIEEKELCHTKNRLTFWVNDIPSTQR	135
G142	I:4819997..4820081	74	-	-/-	LETSPILETFENVKTLS	17

G144	II:1696730..1696958	74	-	-/-	ILKIVGVDGGESYFRVVSFFEVAKEQDFEVGLFKDSQLDSICHLIWFVLISIDPNEFQNFLEVLYGHHQAITDFVSLTRPLLKFNKIFR	89
G145	V:12890577..12890904	73	-	-/-	IKYTRLTAIANRESGNNESYKSSWKLKSSLNSARRLENSIKKYGRRDAKLLNNTFIFAFFSSGVNYTHLPNQCATLDNMLSLQKLVEKFQEEFGENVGVGNYTIKSCFNF	110
G146	X:1120485..1120578	73	-	-/-	MRSIIIQSCSLSRRTNVRHVPPLAFINSIIQLSFGPCLLPCHLSGPENRSALETRLVTRKERSTSPSLSVCLSTARRLPPSFPAVYCH	88
G147	V:6564739..6564919	72	-	-/-	MADWMFVSFLRFARFYNFIQAKAEKSIVVDVILAEIQKKYYDFVNIKKYLE	51
G148	I:12541606..12541939	71	-	-/-	IVERSGNYFHSNRNYSFRVFLTKLCDCKCTDRLVTYKSGTISPLCHRNLRSKHRLIGGAVSESSFVKITPVIVLDFREKICKTVDFR	87
G149	V:3831077..3831377	71	-	-/-	IGPNCIPDCHCFTTILIKFYDQALNRVCSKHKTQTQKTLQNQIKALYLQFKTQEKFLRRTLTHPQLPGVFAPSILFVYQNEVNLTNCTKISSGFQTKRFKFLWICSKHREFGV	113
G152	X:10433971..10434304	71	-	-/ mobidb-lite	LNMMTQSEKREKIHPTNALRERSGSNNAKVHLFNKLFVRPSWSMSSPNNSRMLDNKIEEVPTSSQQKIAKRAEELRKELKIIQVEAKNCIKKNAEVEECFYPYCVHENIKDIFYDKTDF	119
G154	X:854404..854797	71	-	-/ mobidb-lite	MDMLPLCFNFNKAQFNKYNKCSCQGLWSYPSSLFVSILFYPDIIQHICKMLAIESIQNKDIKQSSGNNKRTKQHHIVIRDPSSTSSSNKNEEKRKAIHNSPHKNMVGSSRAPPQREPNKSPLSHRLYRQIYSFLFCCSAAHSATGQPPPPPTLFTFGGLLLLSCCPLLLTILGVFSVS	179
G155	V:11699793..11700117	70	-	-/-	ILPNLFQSQHLIPSALPVAPYNSFSDHARGTMYRISGSTHTDPDAIKSVKSKLDVVHTNRYTLYREVSSKHNRDNSRVSGIKQIVFHLLMLKGKGHQ	97
G156	X:14348630..14348903	70	-	-/-	IEESEKGSSTVYNSFFQIFFCWYKWFPICITTIIVFIQRNKLLKNQENCLYSIHMKSQICSASKRPTSIHKMVTRSQLKPSVASTRQIDPDVLKLDRAEALEKLRGWRPPKRRELCWNLKRKMMLMFESCFLFIYIF	137
G157	X:5994407..5994674	70	-	-/-	MRICCSKVPTSQALRRYETESKNHLSLESLRYGYTSEILVNGKLQRYEKTAEKERKGVGGFFDMRFCSVWINRANTIISTYLRKMSQ	87

Supplementary Table S4. Genome intervals highlighted by AnABlast as putative new exons of known genes (10). Peak height (Protomotifs accumulation), RNA expression evidences, homologs/motifs, predicted amino acid sequence (ORF) and the number of residues (ORF_length) are indicated.

Peak	**Genome interval**	Peak height	**Express.**	**Homolgs/ Motifs**	**ORF**	**ORF length**
E5	X:3495047..3495548	83	RNA-seq	-/-	MVKSNFQIINTSFEIFCFQSSFEKYRKIFLSKLTKVFSRLEKLHYIDIKIKLVVPSHNISKLCIKLSQAIKNLRKLKSMTEYIETAIIFSLFPPVFSVSLKYFSQPYFPIKYTKVTKSNDFSEIT	127
E6	X:6799982..6800363	79	RNA-seq	-/E3LDB8_CAERE	MNQKSSSLLSFFLLSTRDHQTRTVNHCMYVCATSVFRMFVTKIGGNLSGCNANRFDVVVLFSSHWFPFIFILSDPTTHQNLPPSRLNMPQSSKFTTNPKIMYSIQIICQVWHTVFNSPSSSVIFLKSRGRGTLPHLKGCRFGLCVRKLYF IGCSSFSKVFDSDFYIFSRLCPY	176
E7	II:13888312..13888573	73	RNA-seq	-/-	MTENRKISIFATFSCFKVIFHRKNPQFPEIPDSIKSANTNIPTATRPQRVSPPTFPLSRHLFISFVQLYCLLCIVALSINFYFIYKITITP	92
E13	V:13768591..13768795	121	-	-/-	MWILRKISVNFLKVDKSFVTTPNNLSNQKILHQSIRYSPANSSIAVDISTQKNSFTSASCPPN	64
E14	X:10674619..10674925	80	-	-/-	MLSGFQQQPLSPSTTPARFFALPEDWLPRQQVPDISYTSHTNIKFLHQQESCFPIKTRILFLANELENFALWVVGSVSISERERESEKSSSNLRIYA	98
E18	V:7882127..7882430	79	-	-/-	MNWYNKLLSLNPETLLPRAFDGHFFWRKLYSIGSANNTMFTKEYRELIRSGIFPPGQFRNDQQVGFDFPFRWGEVITVCRKACHPNVLQPNNYTVFFIPT FQLFSSLPMFLP	114
E23	X:6001927..6002254	74	-	-/-	MKSTVPLESPHFPEKPFNHFCFLASLFPPTSYPECLGYCSCTIFGTKYLFHLVQYKSINALAHRLANMLIVEAMGGAPTRRLAPIKERRGFIFSVTSHFPSSKHLLENYGLSFDFSNFLFFLVAYIFLECGIGTRRFSKYEIIRNAH	149
E28	V:5856625..5856859	120	-	-/-	MLGPKPILKSHVKKHSDVGSGFLSNKYINCTTACVNDPSSTCISKSLNANFEIRNGCRSQNIIARKMPKSIGKSIELTYTIYF	84
E29	V:3445206..3445602	80	-	-/-	MNSIRVPFETPMLAQLGYIPQHVTKFSYPEPYLFLIFINLYILFSDFIPDLNIENLAKNISNLIKTFPIYLGWIYFSSACKHSLHISSTISRKKIVSPYWFFDAFDALYDEKVLFGYLSLSYIFDTDPIADHWMLGQSSCVYCVMIVVVLGK	155
E30	X:3170746..3171163	83	-	-/-	MNTIARFGKRRCAEKKIRHNVMYRATTEDGKKLLRFNQFVSKYFSCIPSISTDLQYTSFNNFRKHCVFEKVTKKVKRRESKQINGRREQGPIQISGGNQFQIFARGFRWSAIVIFISNLFITTFGYSNIEGRYLESRQHVFSDFFFICRFLDLTLPFSYLKTICFLFFILKNFPFKNQLPQPK	186

Supplementary Table S5. List of primers (forward and reverse) used for PCR cloning of each selected peak predicted by AnABlast as putative new sORF or exon at the indicated *C. elegans* genome interval. Primers were designed to avoid secondary target genes when expressing RNAi.

Peak	Genome interval	Forward primer	Reverse primer
G5	IV:1213206..1213443	gcagtgagcaaaaggtggtg	ttttgctttccttctggcgc
G14	II:11736898..11737084	gagtgagagagtgggcgaac	aaaaatcgacccctcggcat
G15	II:4175282..4175657	tcagtaccacgcaacagtcg	atcgacattgggattggcca
G22	III:670901..671255	gcgtgtgaactgatgcgttt	tttcgtcgtcgtcgtgtctt
G23	III:5838386..5838494	cgccaatttagtcagctgcc	gggttgtttctcgcctctca
G25	X:17515475..17515919	tggagctagaatgttcagggt	ctgtgcacagtgaggggatt
G26	II:11717583..11718477	ccgcctgaagattgattgcg	aaaacgtgagccgagtgttc
G30	II:13644506..13644671	tggccttcttgcaactgtgt	ctttctgacgagccccttgt
G31	I:12928143..12928563	actgaagagtgacagcgtga	acgagccagggaacaaaaca
G32	V:13396252..13396714	tttgcgcccatctgctctaa	tcctgctctggttttccgtg
G43	X:15015384..15015639	cttgcgtttctcatgagcgg	cctcaatgtcgtggctgtct
G45	III:7833431..7833716	gtgcacggtgtatgctgttg	tgccgtcacgatctgaacaa
G46	I:7316251..7316590	atcggttggtcatccgtcac	ggtgtgccccaattcgattg
G49	V:14367725..14368037	cttgagctgtggtctgtcgt	gggggaaaagcttctgaggt
G50	X:16728266..16728758	agatcgtctaccccttccga	cggactctttctctgtcagca
G51	V:8646870..8647347	gtgggtgtatgttcgggaca	acaaaaaggcgccattattga
G52	IV:379001..379340	cacaaggcgttgcgtacatt	gatgacccggaaactaggcg
G54	III:4101011..4101389	agagaggtacgcaggcctaa	caaaccccacttctcctcca
G57	X:541358..541586	acacggtactcgacggtaga	aagagcatttgacggcgttg
G58	V:19477929..19478157	ggagaacagcgctgtgagat	cgattgcgaatgagccaagc
G61	V:10709701..10709983	gagcaaacagtcgcagcaaa	gcagacctactggacaagtgg
G63	IV:1278944..1279091	acactctaccagtcgaccga	tttcgacaccttcttcgcga
G64	I:14308479..14308887	ttccatgcttcagctccctg	ccagtcagggaattagggcc
G65	V:5768239..5768632	gctgagaccctccaagtgtc	cttcccgttcctaacacccc
G67	V:3576900..3577317	ccgactggcaatgagttcct	aaacacggatgctaggccaa
G68	II:6978237..6978540	aagtcgcagtgcaaagttcg	cggccgtccaatgtcttaga
G69	X:14916816..14916993	ctcgacgctcttcccctttt	ccaatggcaggtgatttccg
G70	V:13060163..13060358	acgtgggaggggtagagatc	gcgcagttagtggctattgc
G71	X:11701412..11701730	cggtgaaaattgccgtccat	tcggctatcaattccacgca
G75	V:4970301..4970493	ttgcgtctatggcggcatat	cctctcgtctggacaagcag
G76	II:11805687..11805840	agcgatgacggattaattgct	tatcgtccccaccccagatt
G78	V:6699013..6699454	tccgacctgtcttacctgact	tcaaaatgaagagcacggcac

G83	II:3733728..3734019	tgtgcagccgttttcagttg	ctctgggctagagtggggat
G85	III:669337..669397	acacggttgcctatgagcaa	ttttccaactgtgccccact
G86	II:4548339..4548606	ggcactctctgatgctagcc	tcttcgatggggttgaacgg
G89	X:7713027..7713081	tgcactccatatcctccgga	acacgaatccggctgaatgt
G93	I:10067869..10067959	gtgtgttgttgttgcgacga	accaactgcataggtcacagt
G95	II:3857180..3857426	gctaccattgatgtgggggga	acggacggatcacctgaaaa
G97	I:6983892..6983949	ttcctgcacaccaattgtca	ttcacaccttgacccgtcaa
G98	II:9428645..9428735	gctacaatttgcgcttgcca	gctagccagactgacccaaa
G99	X:13784500..13784599	tttcagcacttttcgggact	tgaatgtgggaaattcgtggt
G100	X:7369398..7369593	tcacactctcgttgtgcctc	ccgagctgacgtgaactctt
G103	III:7619994..7620480	aaccttcacacctgactgcc	ggaagacggggctctcaatt
G106	III:7546511..7546649	tgtgacccaaggaaaccaca	ggtttccagtgaaatggccac
G107	X:14567563..14567626	tgcggaatttggatttaggcg	agaagttgggatgcgtgaca
G108	II:3997148..3997499	cggaatagtggtttgcgacg	ggcatcaccatcccccaata
G109	X:16024200..16024737	ggcgcggagagataggaaaa	tggggaaaggcgaaggaaaa
G110	IV:2212713..2213040	caaagcacagaacacacggg	Cagcacatcccgatcctcaa
G111	IV:1212666..1213077	ccgttgtttggtcggcaaaa	cgcaaagtgctgcagaaagt
G112	X:13380046..13380358	gtccgaggtttcgtgaggtt	tgtgagcgtacagatgtcaca
G114	X:14344402..14344645	ttgaaagatgcggtagctgc	ccaagggcaaatatcgcgtg
G115	III:214502..214871	catgtacccgctggagatcc	gcaaccctcgaagctgagat
G116	IV:1287156..1287513	cacacacatcacggagggaa	tccgcgcgaaatctggaata
G117	IV:9866734..9867040	tggcaagacccacacagaaa	tggcaacctcgtttccatca
G121	IV:3654868..3655246	aacttcctgccaacttcccc	tgtgggggacaactgttcac
G122	X:743277..743580	ggtggaataagtgcgaccca	tcccacttccggatttggtg
G123	III:12582510..12582588	tatttgttggaacgcggcac	cctgattgcagttgcgcata
G126	I:14315133..14315517	ccgttgcgattgttccatcg	ctgctgtggccaaatcccta
G127	III:9992028..9992310	ttgggtgcgagaactttccg	tcgttttgttcccacgtcct
G129	X:15255109..15255442	ttctcagctctgccacagtg	tcaggggtctgctttccaac
G130	X:9603752..9604172	acttagagctcgcacacgtc	taccccccaaaattgccacca
G131	II:12979623..12979845	cttcaaggtgacctgtgcct	ccaacttgccgaatttgcca
G133	II:6310391..6310769	tgggtgcgtgagaatgtcaa	gcagaattgacgttggccaa
G134	III:11729720..11729903	agacgcgtagattttcggct	tccctcgcaaaacaaccaca
G135	III:1446243..1446597	aacaagtgaggaccgacgac	gtccatcagatagcgtgcga
G136	I:13395200..13395593	gtcgctccaaggcctatacc	ctccgcacccatttctctgt
G137	V:10032341..10032656	gctccagcagctactagacg	tcgtcgtgagctttcccaaa
G138	V:8678462..8678762	taccgttccagcagttgcat	tccatgttccgcatcgaaca

G139	X:9646607..9646910	taaaatggcgcgagaaccct	cggccatttgaacctatgcg
G140	I:11500352..11500649	aggagggtgtggatccgtta	tcttaccgactgcgccaatt
G141	I:12612423..12612753	atcaacattgggcggcaaac	aggaagtgtgccaaacccaa
G142	I:4819997..4820081	atagcagtgggagtacgtgc	tggaatgacgtcggtaagagt
G144	II:1696730..1696958	tccgctctctagccatctgt	agtctgtgatggcttggtgg
G145	V:12890577..12890904	aagtatggaaggcgggatgc	tttctcgtcgaacctttctgt
G146	X:1120485..1120578	cctcatgcaatcgtccagga	tcagttgagcaacgggagac
G147	V:6564739..6564919	ggaacaaaatatcgggcgcc	acattgcacgaccttttgctc
G148	I:12541606..12541939	ccccctattcgttccccaac	aatacgcgtcaccggaaact
G149	V:3831077..3831377	ccccaattaccaggcgtctt	ttccacaacaggtacgccag
G152	X:10433971..10434304	tgaaaggagtggcagcaaca	cgtcacgttttcataatgcca
G154	X:854404..854797	atgctcctgccaaggtttgt	gaagtagtgggcagcaggag
G155	V:11699793..11700117	ccgtgctcaccgtatgttct	acaccacctcgggatatcca
G156	X:14348630..14348903	tgtatgtgctgtgaactgtca	tccacccgcgaagtttttct
G157	X:5994407..5994674	tggtttgcaagagtaccccc	atcctcccactcccttcctc
E5	X:3495047..3495548	ggtgttaggcggttaaatggc	gcgccgaaatacagaatgtga
E6	X:6799982..6800363	tcaacccgagaccatcaaaca	acggacacaggcgactaaaa
E7	II:13888312..13888573	gcctcttcagtgacttttccc	ttttcgggctcggcgaag
E13	V:13768591..13768795	ttaagcggcggaactcaagt	gaacggagaagacgcagaca
E14	X:10674619..10674925	acatcccgtcaggtgacaag	tatggaaaccgagccaacca
E18	V:7882127..7882430	acatgcactccccactcaag	acaaagcgatggttgaaaaca
E23	X:6001927..6002254	acgaaccaagtcatgcataca	gtctcgttcctatcccgcat
E28	V:5856625..5856859	tgaaaatagacttccccgggc	tttttgcgctcccgttttct
E29	V:3445206..3445602	gcaacctgacacccccttgaa	cgtagcaaaactgtgatcgct
E30	X:3170746..3171163	aattcggcacaacgtcatgt	tgggctgcggtagttgattt
unc-22 Exon 20	IV: 11993323..11992879	cccaagtaccgaacgaaagac	tctgaccacaatgcttcact
unc-22 Exon 23	IV:11989007..11988644	gttctccgcgtactggaaca	gttgtcgactgggatgctga

Supplementary Table S6. Percentage of animals that reach adulthood in the indicated time (hours, grey rows). Average, Standard deviation and P-value of the differences by T-test. Normality was previously assessed.

	% Adults / Hours at 20ºC					
Control	47	48	50	52	53	54
Average	29,57	72,97	96,00	99,59	100	100
St desv	2,83	7,92	23,11	0,91	0	0
G71	47	48	50	52	53	54
Average	3,44	14,22	54,76	80,96	94,94	97,93
St desv	8,23	4,08	3,21	11,52	7,15	4,62
T-test	0,0001	< 0,0001	0,0042	0,0069	0,1528	0,3466
control	48	49	50	51	53	
Average	64,71	91,22	97,00	100	100	
St desv	10,37	3,45	1,39	0	0	
G107	48	49	50	51	53	
Average	76,33	83,04	85,03	89,68	89,68	
St desv	6,65	6,59	6,19	3,27	3,27	
T-test	0,0680	0,0222	0,00155	< 0,0001	< 0,0001	
control	47	48	50	52	53	54
Average	20,38	34,35	47,06	68,16	91,57	99,10
St desv	3,58	6,83	4,95	4,79	2,72	1,78
G98	47	48	50	52	53	54
Average	13,36	25,49	43,79	63,18	82,56	89,04
St desv	5,99	2,79	4,80	4,57	6,07	6,27
T-test	0,0914	0,0574	0,3783	0,1836	0,0352	0,0216