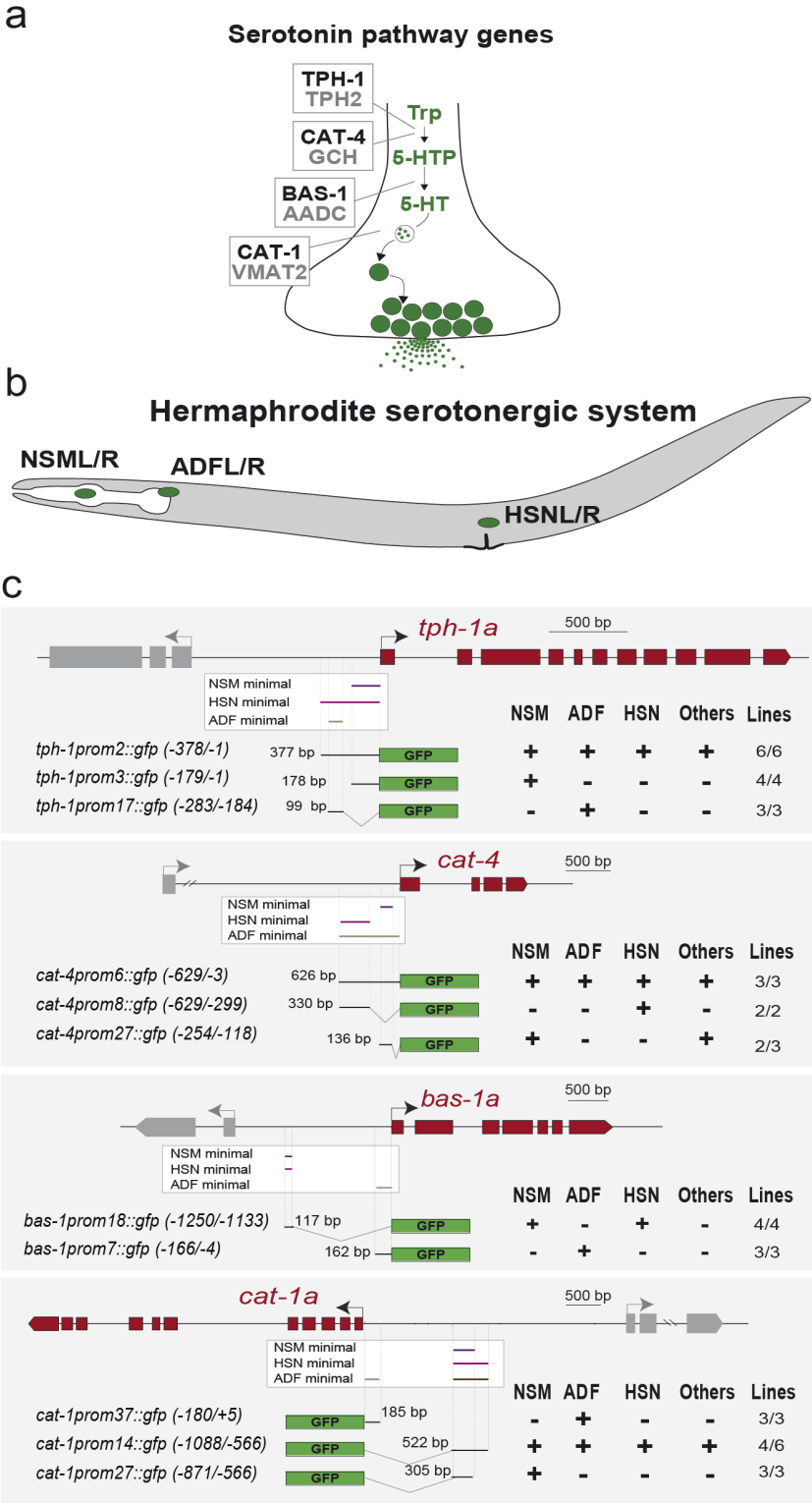
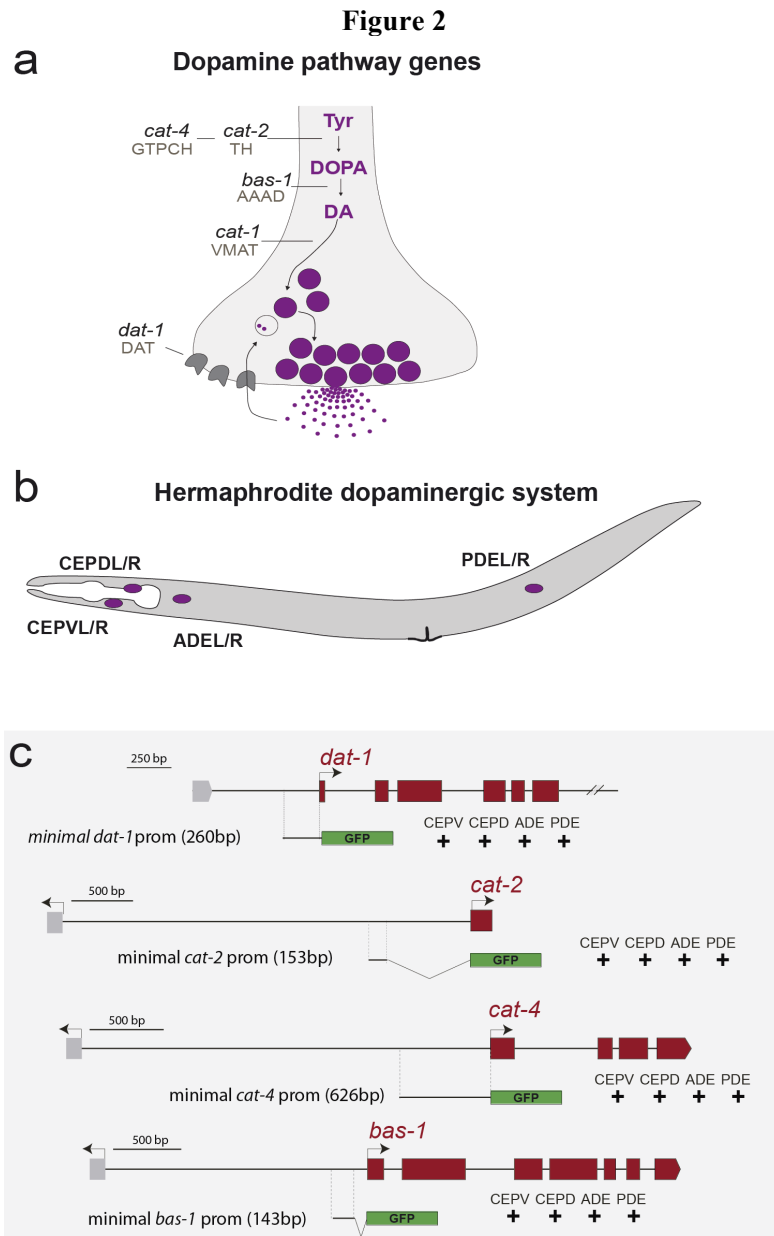


Figure 1

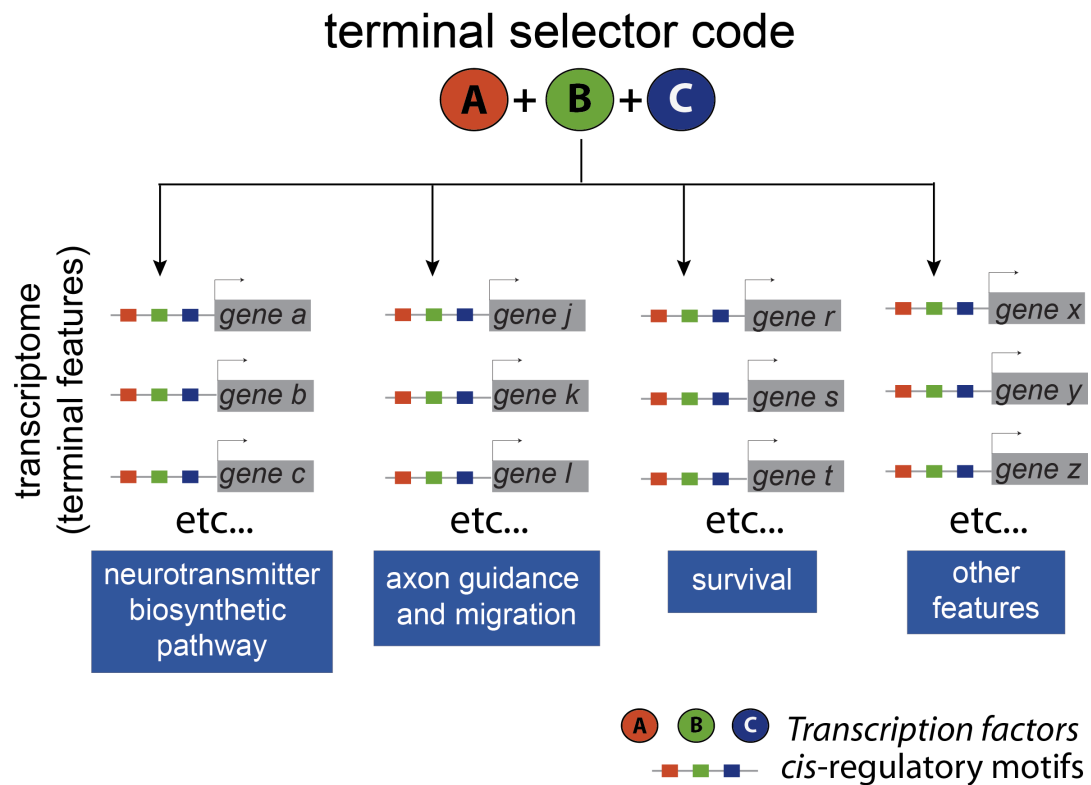


**Figure 1. a)** Schematic representation of a 5HT neuron synapse. *C.elegans* proteins appear in black case, mammalian in grey. AAAD, aromatic L-amino acid decarboxylase; GCH, GTP cyclohydrolase; TPH, tryptophan hydroxylase; Trp, tryptophan; VMAT, vesicular monoamine transporter; 5-HTP, 5-hydroxytryptophan; 5HT, serotonin. **b)** Schematic representation of *C.elegans* hermaphrodite serotonergic system composed by 3 pairs of bilateral neurons (NSM, ADF and HSN, L:left, R:right) **c)** Summary of the cis regulatory analysis of the 5HT pathway genes. For each locus exons are represented as red blocks; the upstream gene is shown in grey. At the bottom is a representation of cloned and injected constructs, and the expression pattern in 5-HT neurons of transgenic worms. Thick black lines symbolize the promoter piece placed in front of GFP (green box) and dashed lines place it in the context of the locus. White box is a summary of the CRM for each cell type. +: expression and -: no expression.



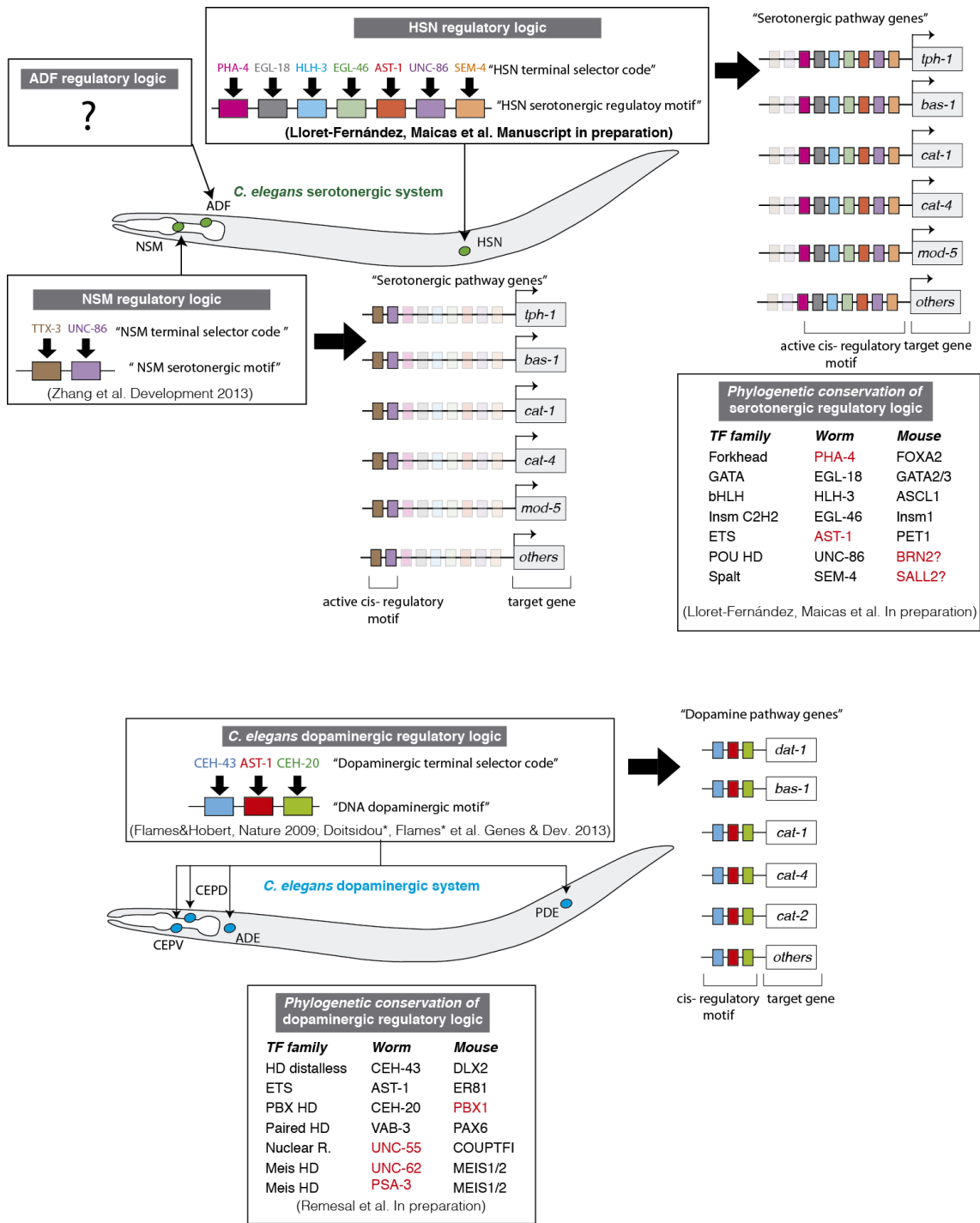
**Figure 2. a)** Schematic representation of a dopaminergic neuron synapse. *C.elegans* proteins appear in black case, mammalian in grey. AAAD, aromatic L-amino acid decarboxylase; DAT: dopamine transporter; GCH, GTP cyclohydrolase; TH, tyrosine hydroxylase; Tyr, Tyrosine; VMAT, vesicular monoamine transporter; DA, dopamine. **b)** Schematic representation of *C.elegans* hermaphrodite dopaminergic system composed by 4 pairs of bilateral neurons (CEPV, CEPD, ADE and PDE, L:left, R:right) **c)** Summary of the cis regulatory analysis of the DA pathway genes. For each locus exons are represented as red blocks; the upstream gene is shown in grey. At the bottom is a representation of the minimal cloned and injected constructs that shows expression in the DA neurons. Thick black lines symbolize the promoter piece placed in front of GFP (green box) and dashed lines place it in the context of the locus. +: expression and -: no expression.

Figure 3



**Figure 3.** Schematic representation of the terminal selector model. This model predicts that the transcriptome of each neuronal cell type is coordinately regulated by the direct action of a code of transcription factors (terminal selector code) acting directly on the regulatory sequences of the expressed genes (terminal features). Adapted from Hobert, *Annu Rev Cell Dev Biol* 2011.

Figure 4



**Figure 4.** Summary of the results produced at midterm period. Upper part summarizes the serotonin results and bottom part results regarding dopaminergic differentiation. Red case represent genes whose function on serotonergic and dopaminergic differentiation was previously unknown.