Supplementary Methods

RT-PCR analysis of dop-3

To isolate a cDNA for dop-3, polyA-selected RNA (from mixed-stage animals, kind gift of V. Reinke) was reverse transcribed using Maloney-MuLV reverse transcriptase and the primer 5'-AGTAAGGCAATGAC, which anneals to a site 3' of the predicted stop codon. cDNA was generated by PCR using the additional primer 5'-TCGTCTAAAATCAGA, which primes immediately upstream of the DOP-3 start codon predicted by Genefinder. One product of the predicted size was generated, isolated, and sequenced.

C. elegans dopamine receptor knockouts

dop-1, dop-2, and dop-3 deletion mutants were identified by PCR screening a library of psoralen-mutagenized animals. Mutants were outcrossed to the wild type four times to produce clean genetic backgrounds. (dop-1)vs100 is a 328 base pair deletion whose limits are 5'-AACATTGGACTACTGTTTGTCTAAAAACCG…ATGCGAATGCAACTCGCCTG AATCTTCTTT-3'. (dop-1)vs101 is a 167 base pair deletion whose limits are 5'-GTCGCCGTATAAATTACGTGATAGTTCTGG…ATGCAATTGGAAGTTCAATG GTGTCTTTCTTTT-3'. dop-2(vs105) is a 125 base pair deletion whose limits are 5'-AAGTATATTTTTATTTCAGGTA…GTGGCCATCATAGTTATGCCAT. dop-3(vs106) is a 292 base pair deletion whose limits are 5'-ACTTCCGTATTTCTACTAC…CTTAGCAGTTTCTGATTTTCTG-3'.
Complementation and allele sequencing

Mutations were tested for complementation to goa-1(n1134), eat-16(ad702), gpb-2(sa803), and dgk-1(sy428) using tester strains marked with a green fluorescent protein transgene mls13 (gift of A. Fire) so that cross-progeny could be recognized. The transheterozygous cross-progeny were placed on 40 mM dopamine plates and analyzed for spontaneous movement 5 min later. At 5 min (as opposed to the 20 min time points shown in Fig. 3, 6, 7), 100% of animals in all of the dopamine resistant strains move, whereas the wild type is 100% paralyzed. Every mutation isolated in the screen failed to complement one of the tester strains (100% resistant cross-progeny) and did complement the other three (0% resistant cross progeny). We also mated a control mls13 strain carrying no other mutations to each dopamine resistant strain and found that the cross progeny were 100% dopamine sensitive, so all mutations analyzed were recessive. Finally, we put known alleles of goa-1, eat-16, gpb-2, and dgk-1 through the same tests and each was recessive, failed to complement the tester strain for the corresponding gene, and did complement the other three. We confirmed the gene assignments of selected alleles by amplifying and sequencing genomic DNA from the corresponding genes, and in each case identified a mutation. For dgk-1, the mutations were: vs67, Gly798Arg; and vs71, stop codon at position 424. For gpb-2: vs74, Ala117Glu. For eat-16: vs65, Val385Thr; vs72, Glu171Lys; and vs83, Ser400Phe.
**Transgenes**

Primers used to amplify *C. elegans dop-1* and *dop-3* gene promoters were: for

*dop-1*: 5'-GGAATGACATGTTTGAAGCCGGAC and 5'-TTACCGAACAGGCCCCAAATAA. For *dop-3* the primers were 5'-AAACCCATATCGAAACATCAAG and 5'-TCATGTTGAAGTATGGGTTTGCC.

For rescue of *dop-3* mutant phenotype with the *dop-3* transgene we amplified

*dop-3* using the primers 5'- AAACCCATATCGAAACATCAAG and 5'-CTGTAGTAAACACCTCACCTGTG.