Supporting Online Material
Tonkin and Bass

List of Strains:

wild-type, Bristol N2
adr-1(gv6);adr-2(gv42)
rde-1(ne219)
rde-1(ne300)
rde-4(ne299)
adr-1(gv6);adr-2(gv42);rde-1(ne219)
adr-1(gv6);adr-2(gv42);rde-1(ne300)
adr-1(gv6);adr-2(gv42);rde-4(ne299)
che-2(e1033)
odr-3(n2150)
che-2(e1033);rde-1(ne219)
odr-3(n2150);rde-1(ne219)

All crosses were followed by single worm PCR. Smaller than wild-type PCR products were used to follow deletions in the *adr* genes. All *rde*, *che*, and *odr* alleles are point mutations and were followed by gain or loss of a restriction site in PCR products. Direct sequencing of PCR products was used when mutations did not alter a restriction site.

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Figure S1

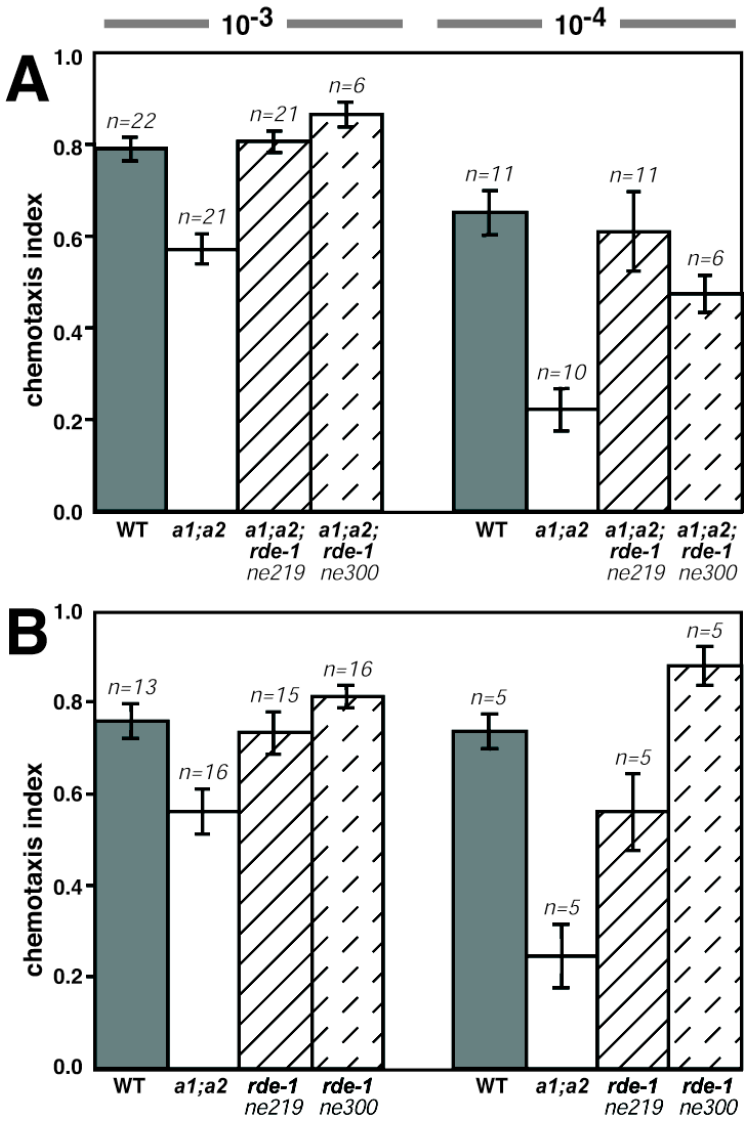

Figure S1 Legend:

Graphs show mean chemotaxis indices for assays with diacetyl at 10^{-3} and 10^{-4} dilutions. The number of trials is noted above error bars (S.E.M.). Wildtype (WT) and *adr-1(gv6);adr-2(gv42)* double-mutants (*a1;a2*) were compared with two *rde-1* rescue strains (A), or with *rde-1* strains (B). Values for rescue strains were significantly different ($P \leq .003$) from *a1;a2* strains, but not from WT. *P* values result from a student's t-test (two-tailed, unequal variance).