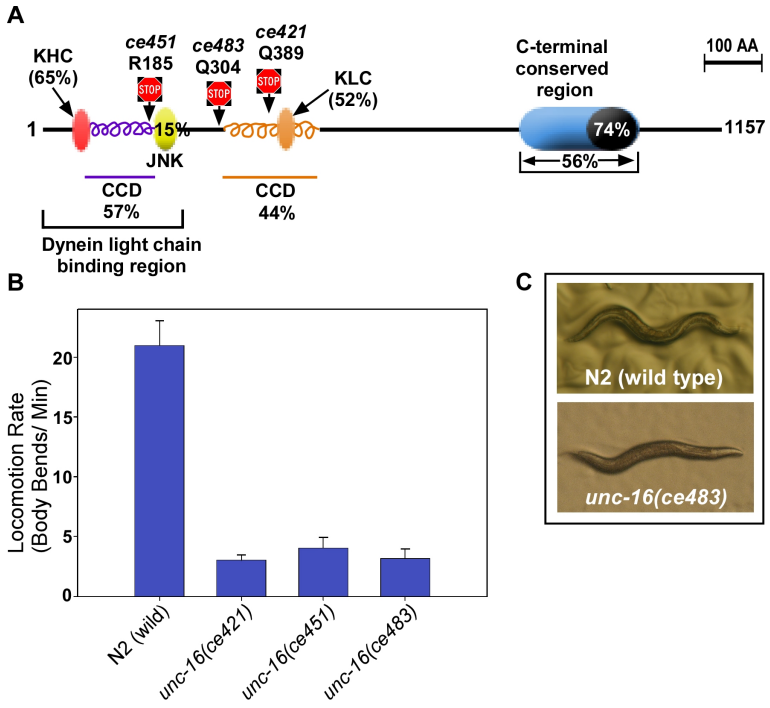

Figure S1 Three *goa-1(sa734)* suppressor mutations disrupt UNC-16, a conserved protein required for normal locomotion rates.

(A) Scale drawing of UNC-16 showing the location of nonsense mutations isolated in this study, conserved regions, and regions known to interact with other proteins from previous studies of UNC-16 and its JIP3 orthologs. Percentages refer to percent identities when comparing the indicated regions of UNC-16 (ZK1098.10b.1 from www.wormbase.org; freeze WS200; (HARRIS *et al.* 2009) to its human JIP3 ortholog (NP_003962). References for interaction sites are as follows: KHC (Kinesin Heavy Chain) (SUN *et al.* 2011); JNK (c-Jun N-terminal kinase) (KELKAR *et al.* 2000), KLC (Kinesin Light Chain) (KELKAR *et al.* 2005; NGUYEN *et al.* 2005; SAKAMOTO *et al.* 2005; VERHEY *et al.* 2001). The dynein light intermediate chain has been shown to interact with amino acids 1-240 of *C. elegans* UNC-16 (ARIMOTO *et al.* 2011). To compute percent identities we used Clustal W (THOMPSON *et al.* 1994) run through Vector NTI Advance 11.0 (InVitrogen). To predict coiled-coil domains (labeled CCD in figure) we used the COILS server on www.ch.embnet.org (LUPAS *et al.* 1991). The 100 AA scale bar indicates 100 amino acids.

(B) *unc-16* mutations confer sluggish locomotion. Graph shows spontaneous locomotion rates of N2 (wild type) compared to the indicated genotypes. Error bars are standard errors of the means (SEMs) of 10 animals each. The mean locomotion rates of the three *unc-16* mutants are not significantly different.

(C) Representative adult animals are shown for each genotype. Body length of wild type is ~1 mm, and both images have similar magnification.