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Supplemental information

Identification of proteotoxic and proteoprotective bacteria that non-specifically affect proteins associated with neurodegenerative diseases

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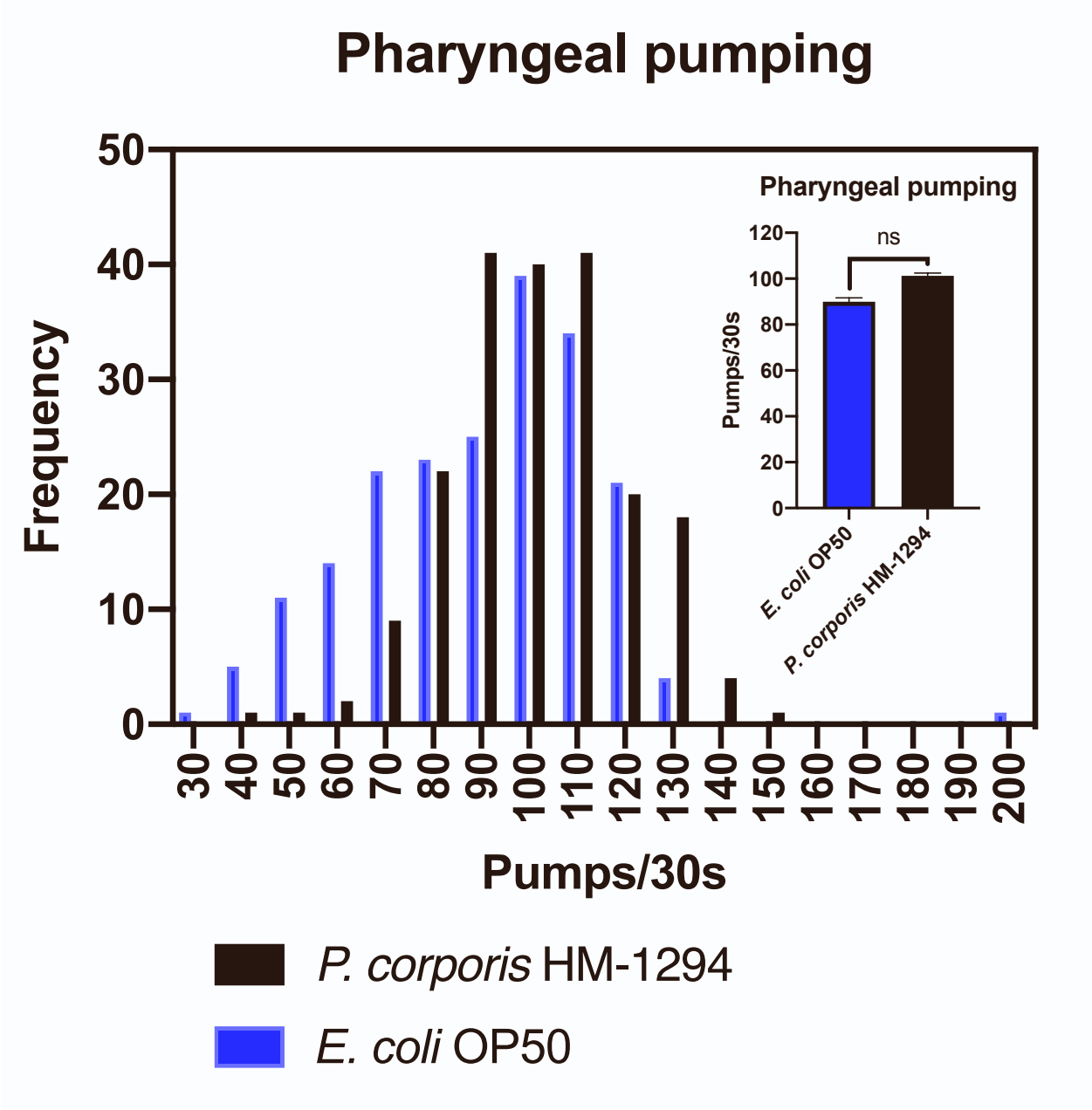

Fig. S1. The effect of proteoprotective *P. corporis* on pharyngeal pumping, related to Figure 3. Data are represented as the average number of pharyngeal pumps per 30 seconds for a total of ten data points per worm (N2) and three independent experiments for a total of 20 worms per condition. Mean pumping rates of worms fed *P. corporis* HM-1294 (101.22 pumps/30 sec +/- SEM 1.28) are not significantly different from those fed *E. coli* OP50 control (89.97 +/- 1.68 SEM) as determined by t-test ($p>0.9999$); distribution of pumping rates of worms fed *P. corporis* HM-1294 are not significantly different from those fed *E. coli* OP50 control as determined by Kolmogorov-Smirnov test ($p=0.9639$).

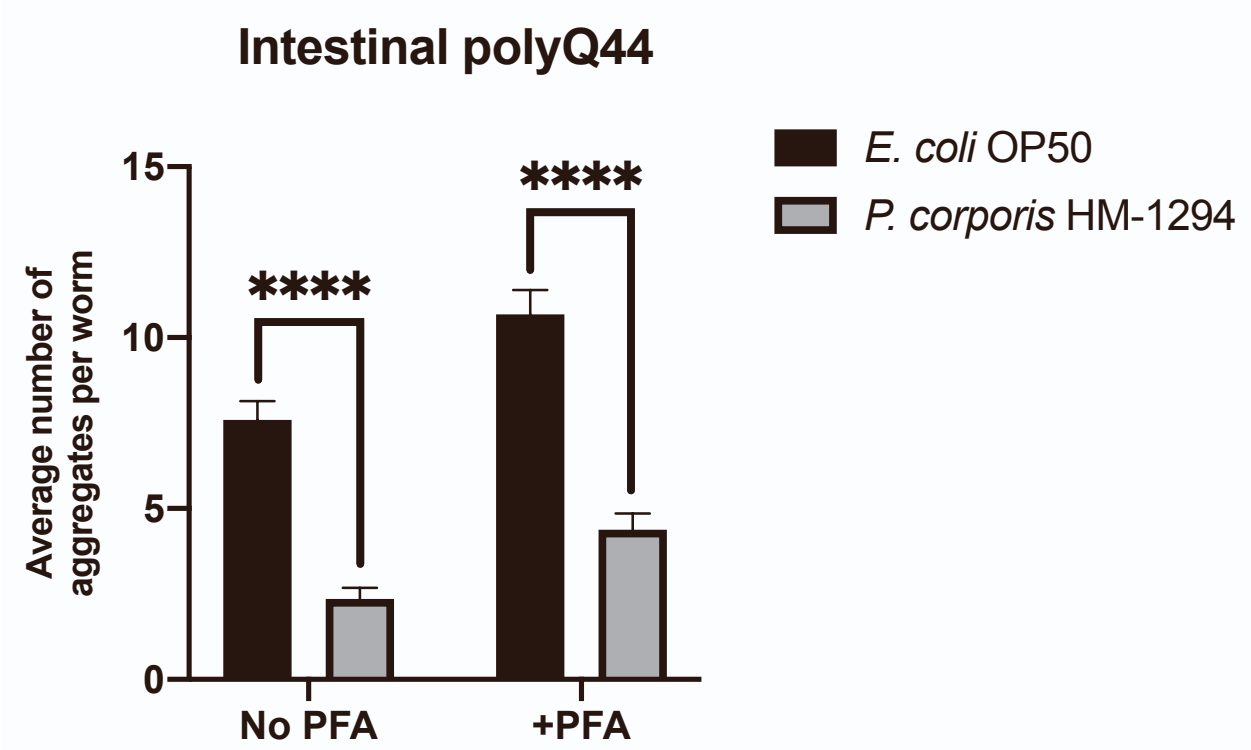

Fig. S2. The effect of PFA-killed *P. corporis* on intestinal polyQ aggregation, related to Figure 3. Data are represented as the average number of aggregates per intestinal polyQ44 worm. Each bar represents two independent experiments for a total of 60 worms. Error bars represent SEM. Statistical significance was calculated using Student's t-test (****$p<0.0001$).

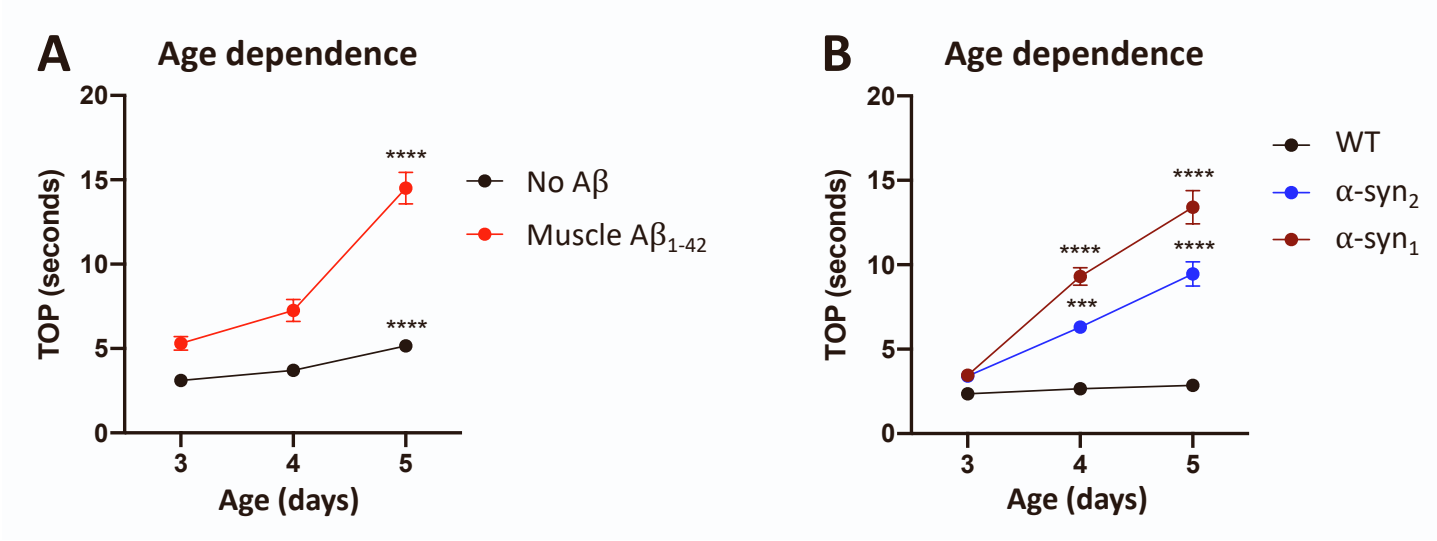

Fig. S3. Age-dependent motility defects in transgenic animals harboring aggregation-prone $A\beta_{1-42}$ and α-synuclein, related to Figures 3 and 4. Age-dependent changes in the motility of animals expressing muscle-specific (A) $A\beta_{1-42}$ and (B) α-synuclein and corresponding control animals: empty vector (No Aβ) and wild-type N2 (WT). Data are represented as the average TOP (seconds) per worm. Each data point represents two independent experiments for a total of 20 worms. Error bars represent SEM. Statistical significance was calculated using one-way analysis of variants (ANOVA) followed by multiple comparison Dunnett's post-hoc test (***$p<0.001$, ****$p<0.0001$).

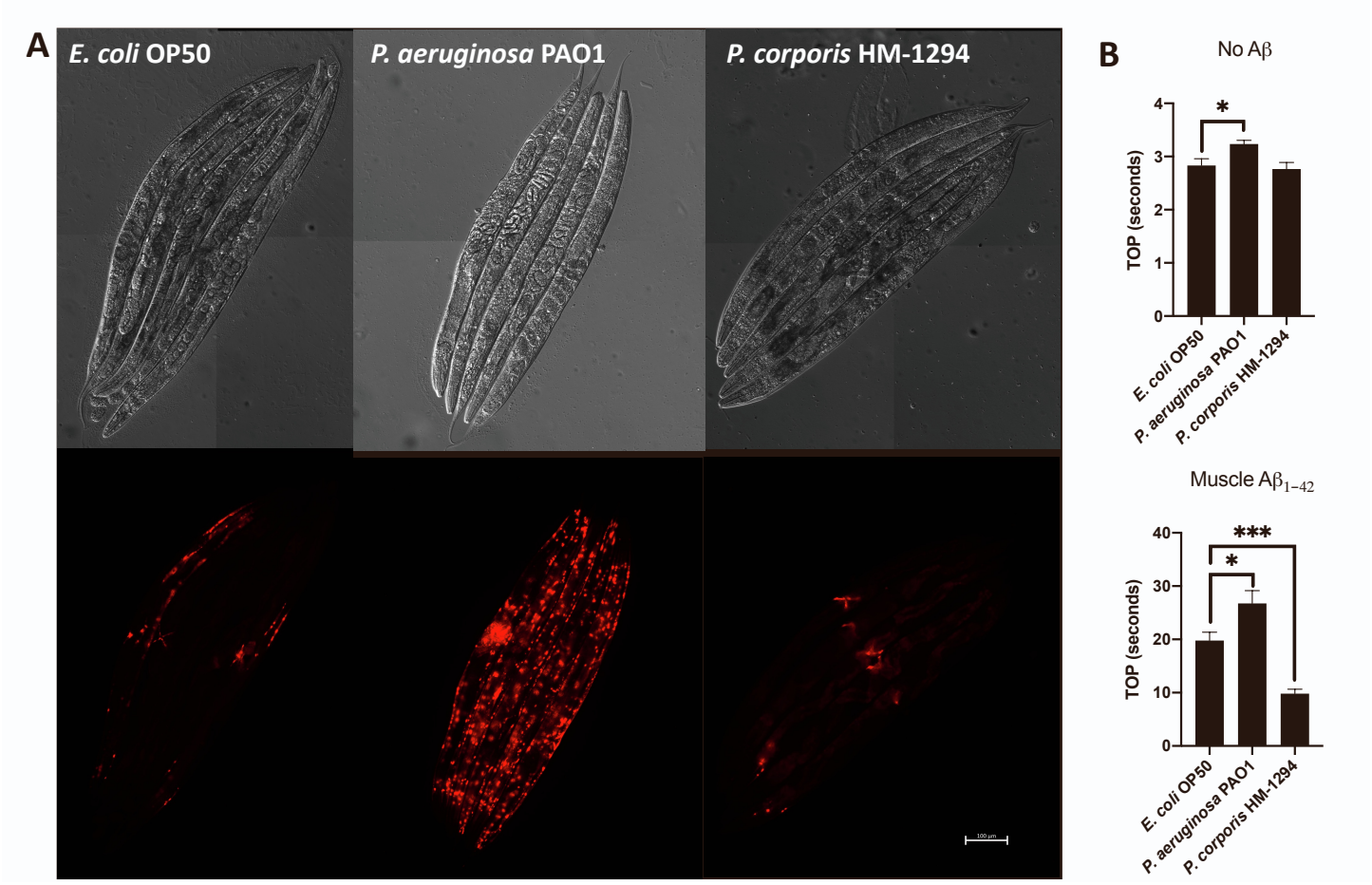

Fig. S4. The effect of bacteria on Aβ$_{1-42}$ aggregation and the associated toxicity, related to Figure 3. (A) Nomarski and fluorescent images (mScarlet) and the corresponding (B) TOP motility measurements of transgenic worms expressing muscle-specific Aβ$_{1-42}$ fed a proteoprotective strain (*P. corporis*) and a proteotoxic strain (*P. aeruginosa*). Data are represented as the average TOP (seconds) per worm. Each data point represents the average of three independent experiments for a total of 30 worms. Error bars represent SEM. Statistical significance was calculated using one-way analysis of variants (ANOVA) followed by multiple comparison Dunnett's post-hoc test (*$p<0.05$, ***$p<0.001$). Scale bar is 100 μm.

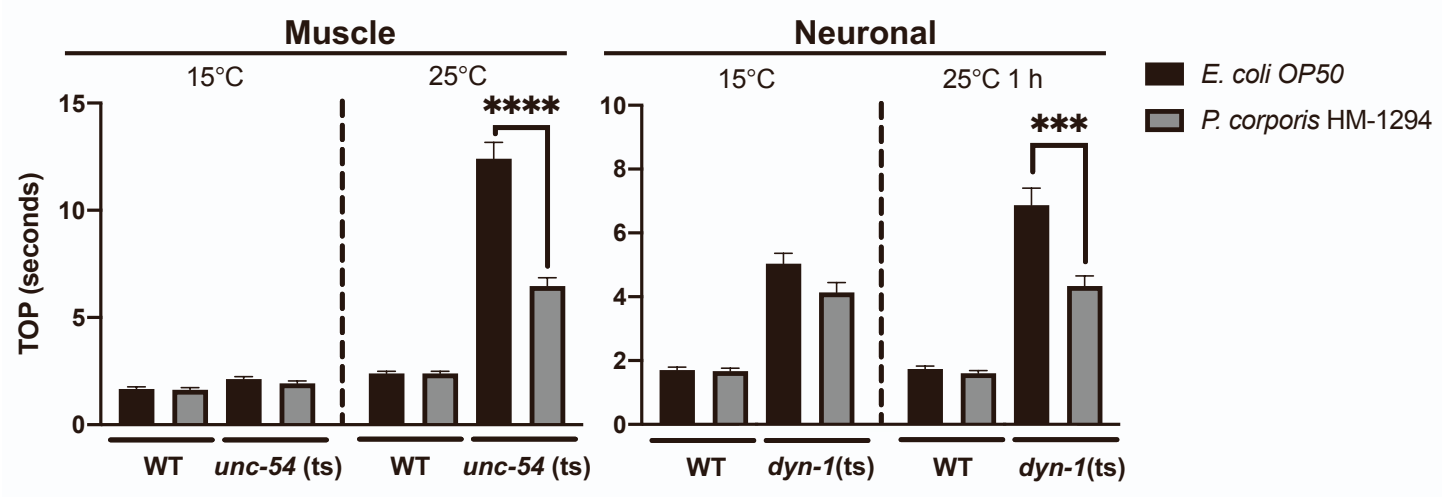

Figure S5. The effect of *P. corporis* on temperature-dependent motility defects, related to Figure 3. Temperature-dependent changes in the motility of animals expressing a muscle-specific mutation in the myosin heavy-chain gene (*e1301*) ("Muscle") and mutation in the GTPase domain (*dyn-1*) ("Neuronal"). Wild-type (WT) indicates the N2 control worms, (ts) indicates the temperature-sensitive worm strain. Data are represented as the average TOP (seconds) per worm. Each data point represents three independent experiments for a total of 30 worms. Error bars represent SEM. Statistical significance was calculated using Student's t-test (***p<0.001, ****p<0.0001).

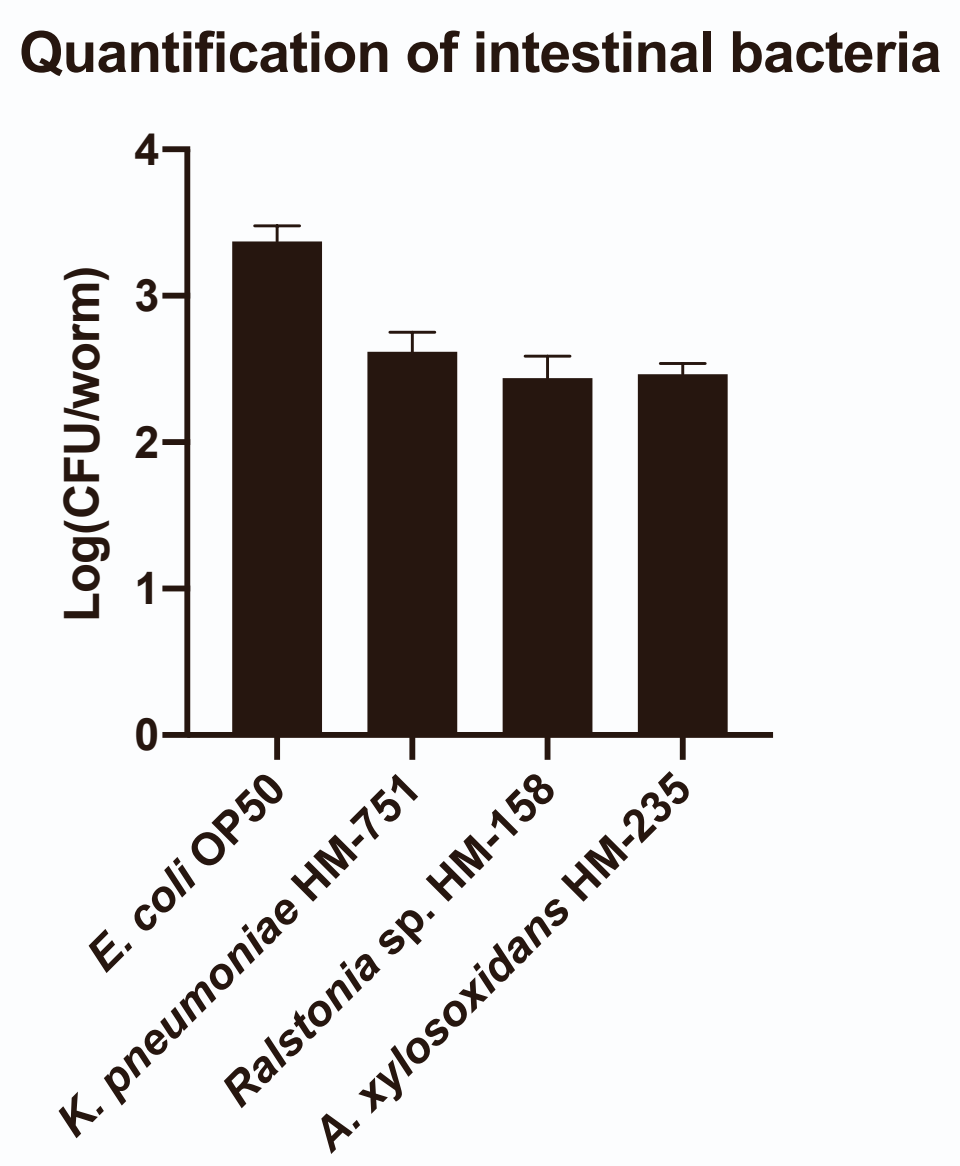

Figure S6. Enumeration of proteotoxic bacteria in the *C. elegans* intestine, related to Figure 4. Data are represented as the average bacterial load per N2 worm [Log(CFU/worm)]. Each bar represents three independent experiments for a total of 30 worms. Error bars represent SEM.

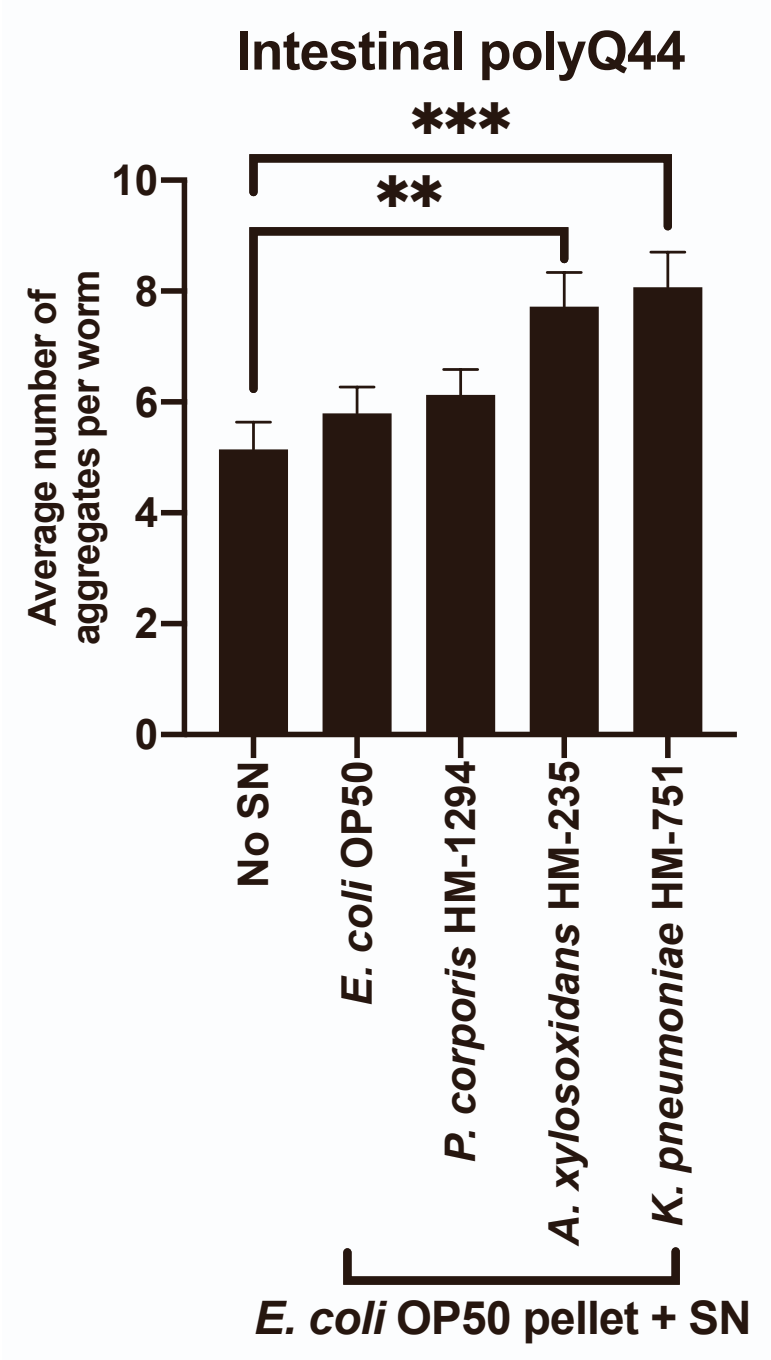

Figure S7. The effect of bacterial supernatants on intestinal polyQ aggregation in *C. elegans*, related to Figure 4. Data are represented as the average number of aggregates per intestinal polyQ44 worm. Each bar represents three independent experiments for a total of 98 worms. Error bars represent SEM. Statistical significance was calculated using one-way analysis of variants (ANOVA) followed by Dunnett's post-hoc test (**p<0.01, ***p<0.001).

Figure S8. Phylogenetic grouping reflects the effect of bacteria on host proteostasis, related to Figures 2, 3, and 4. Phylogenetic tree shows that proteotoxic bacteria predominantly cluster together, separate from proteoprotective bacteria which also form their own distinct cluster. The size of the bacterial identifiers is proportional to the magnitude of their respective proteotoxic or proteoprotective effects. Proteoprotective bacteria are indicated in blue, and proteotoxic bacteria in red. Tree analysis was performed on a large collection of human microbiome isolates in BV-BRC using maximum likelihood based on concatenated alignments of 100 single-copy genes.