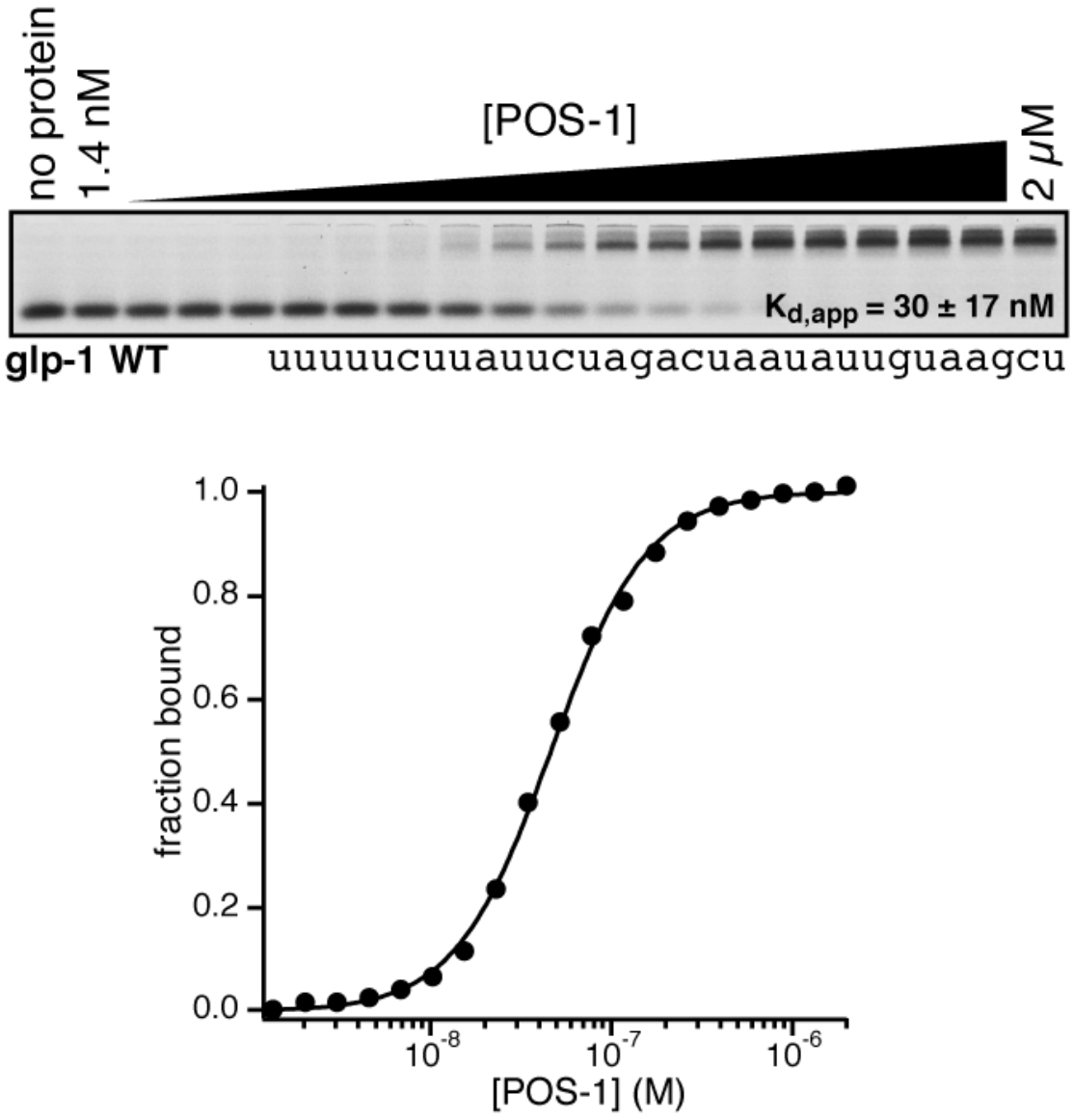

Figure S1. POS-1(80-180) binds the glp-1 fragment with a similar affinity to that of POS-1 1-206. Top, gel shift image labeled with the POS-1 concentrations (top) in each lane, and the RNA sequence beneath. The reported Kd,app is the average ± the standard deviation of six separate replicates. Bottom, representative fit of gel shift data to the Hill Equation.

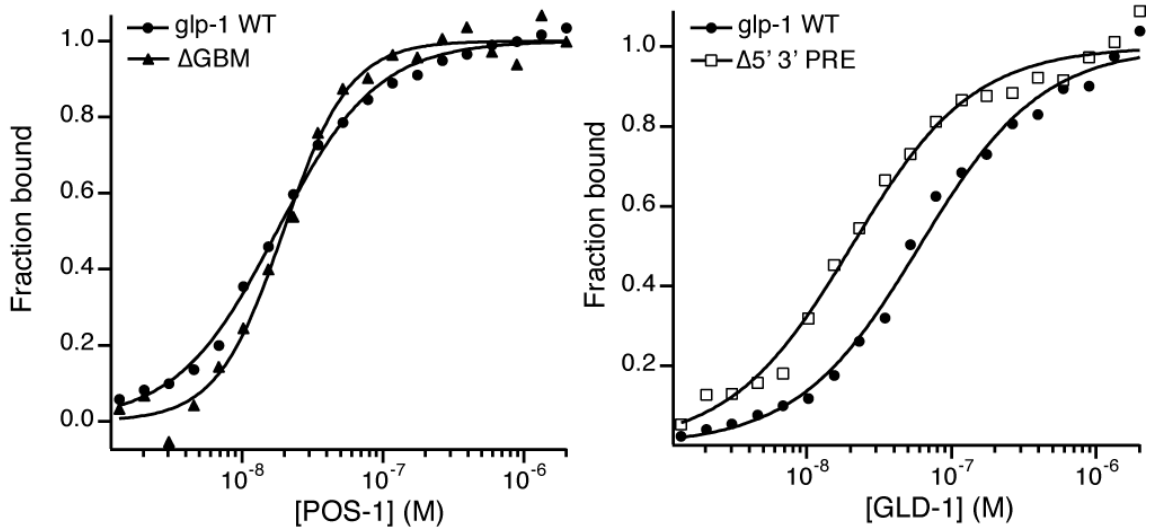

Figure S2. POS-1 or GLD-1 specific mutations in the glp-1 3′ UTR. Left, representative EMSA fits for POS-1(1-206) binding to glp-1 WT RNA (filled circles, Kd,app = 19 ± 2 nM) and ΔGBM RNA (filled triangles, Kd,app = 21 ± 1 nM). Right, representative EMSA fits for GLD-1(135-329) binding to glp-1 WT RNA (filled circles, Kd,app = 70 ± 10 nM) and Δ5′ 3′ PRE RNA (open squares, Kd,app = 20 ± 4 nM). Reported Kd,app values are means ± one standard deviation of three independent replicates.

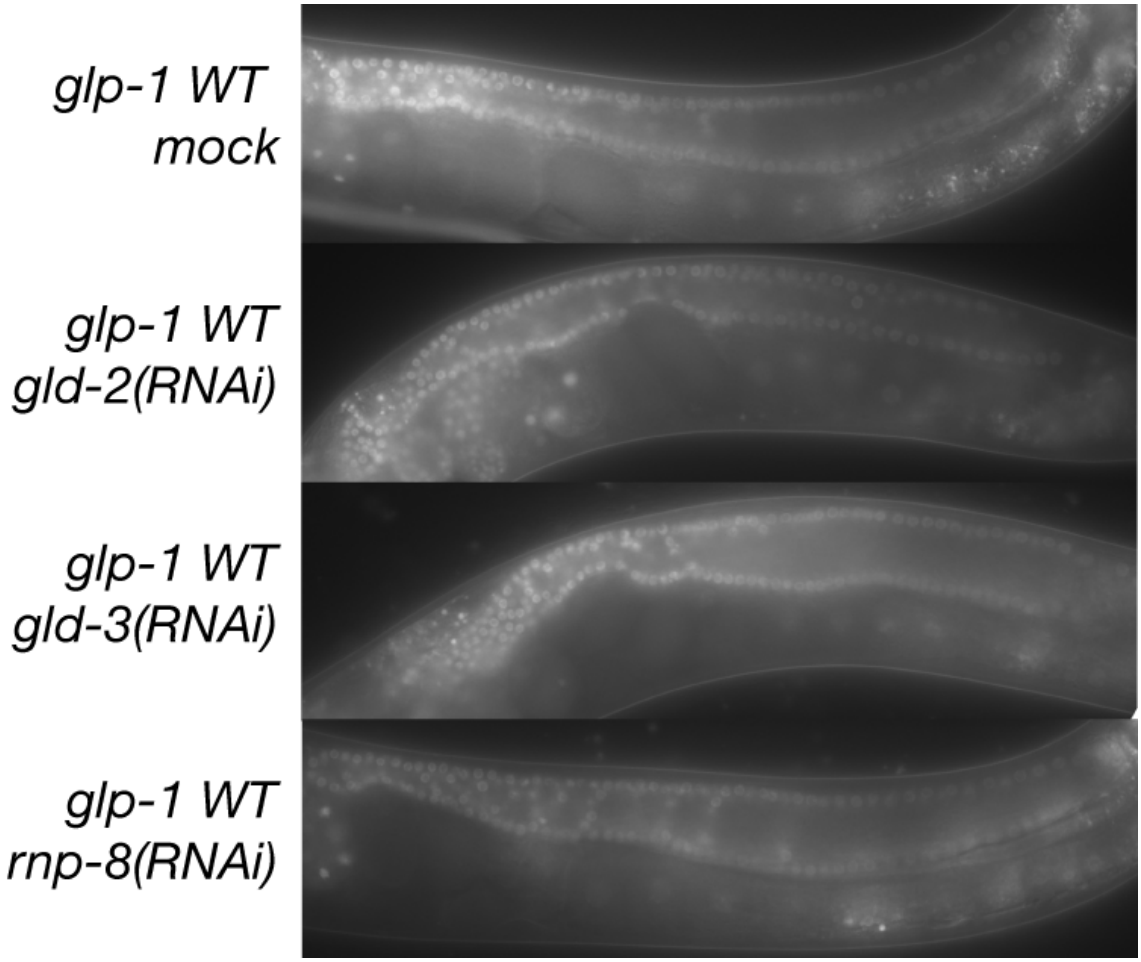

Figure S3. GLD-2 cytoplasmic poly(A) polyermase complexes are not required for translational activation of *glp-1* mRNA in the distal germline. Representative widefield fluorescence images for each of the listed experimental conditions. Each image is oriented with the distal most point of the germline at the upper left.