**Supplementary Legends**

**Supplementary Table 1. A targeted RNAi screen in fertile worms identifies histone demethylases that significantly worm lifespan.** These experiments are presented in Fig. 1A and Fig. 2A. For the initial RNAi screen, 30 worms per condition were used to calculate the mean lifespan. RNAi mediated knock-down of targets that resulted in greater than 10% change in average lifespan were repeated using 90 worms (30 worms in triplicate for each condition). # worms: number of observed dead worms at the end of the experiment/number of alive worms at the beginning of the experiment. The difference between both numbers corresponds to the number of censored worms (worms that underwent "matricide", exhibited ruptured vulva, or crawled off the plates). The mean lifespan and p-values were calculated by a log-rank (Mantel-Cox) statistical test. # worms: number of dead worms/number of total worms. Bold: genes whose RNAi knock-down significantly extended average lifespan.

**Supplementary Table 2. Attenuation of *utx-1* extends lifespan in adult worms in a germline-independent, insulin-dependent manner.** RNAi mediated knock-down of *T26A5.5* extends lifespan in worms; experiment 1 is displayed in Fig. 2B. *utx-1* knock-down extends lifespan in adult worms; experiment 1 is displayed in Fig. 2D. *T26A5.5(ok2364)* mutants are not long lived compared to WT worms; experiment 2 is displayed in Fig. 3A. *utx-1(tm3118)* heterozygous worms are long lived compared to WT worms;

experiment 2 is displayed in Fig. 3B. *utx-1* knock-down further extends the lifespan of *glp-1(e2141)* mutants grown at the restrictive temperature; experiment 2 is displayed in Fig. 5. *utx-1* knock-down does not extend the lifespan of *daf-16(mu86)* mutants; experiment 1 is displayed in Fig. 6B. *utx-1* knock-down does not further extend the lifespan of the long-lived *daf-2(e1370)* mutants; experiment 1 is displayed in Fig. 6A. The mean lifespan values were calculated by a log-rank (Mantel-Cox) statistical test from triplicate samples of 30 worms each. #: number of dead worms/number of total worms. Combined p-values were calculated using Fisher's combined probability test.

**Supplementary Figure 1.** RT-qPCR analysis of *utx-1* mRNA levels relative to *pan-actin* mRNA levels in WT (N2) worms treated in the absence (control) or presence of *utx-1* RNAi.

**Supplementary Figure 2. *utx-1* RNAi does not alter the levels of total H3 in WT worms.** Whole-mount immunofluorescence of worms treated with empty vector control RNAi or *utx-1* RNAi A) stained with an H3K27me3 antibody. DAPI staining was used to visualize nuclei. The worms are oriented anterior (left) to posterior (right). These results are representative of three independent experiments. The dashed line indicates the germline. Scale bar, 25 μm. B) Whole-mount immunofluorescence of worms (L3 stage) treated with empty vector control RNAi or *utx-1* RNAi and stained with an histone H3 antibody (two separate worms per condition). DAPI staining was used to visualize nuclei. L3

stage worms do not have a mature germline. The worms are oriented anterior (left) to posterior (right). Scale bar, 100 μm.

**Supplementary Figure 3. H3K27me3 levels from whole worm lysates decrease after day 12 in WT worms.**

A) Whole worm lysates were collected from age-matched cohorts of WT worms, grown on NGM plates. Lysates from worms of the indicated ages were blotted with antibodies to H3K27me3 and total histone H3 (H3) as a control for loading. Each lane represents an independent cohort of ~100 worms. The blots presented are representative of 2 independent experiments. *: band that is likely to be non-specific because it appears at random in independent experiments. Note that we cannot exclude the possibility that the lower band is a histone H3 degradation product or another histone H3 isoform. B) Quantification of H3K27me3 levels in WT worms at different ages from 2 independent experiments.