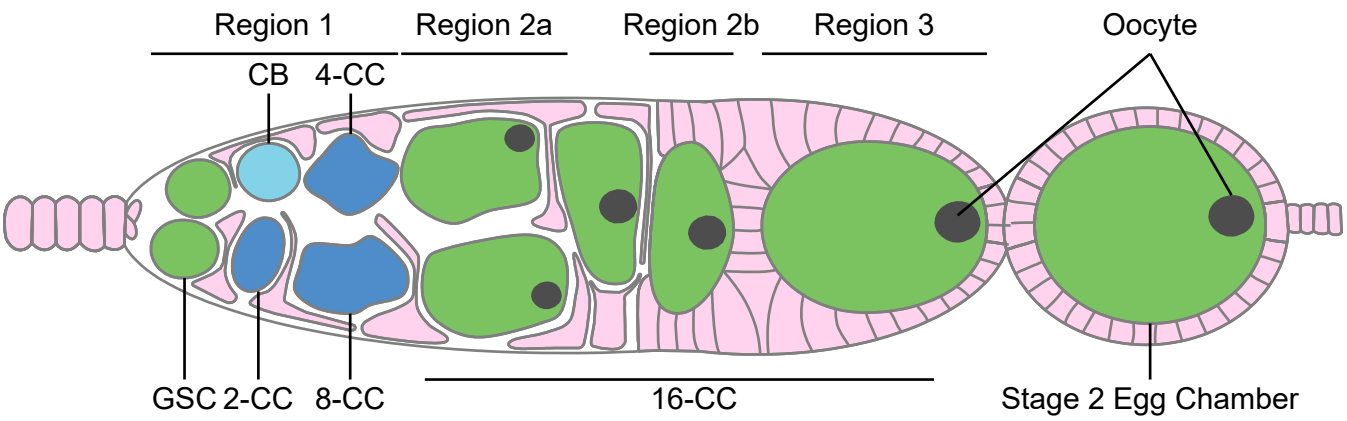
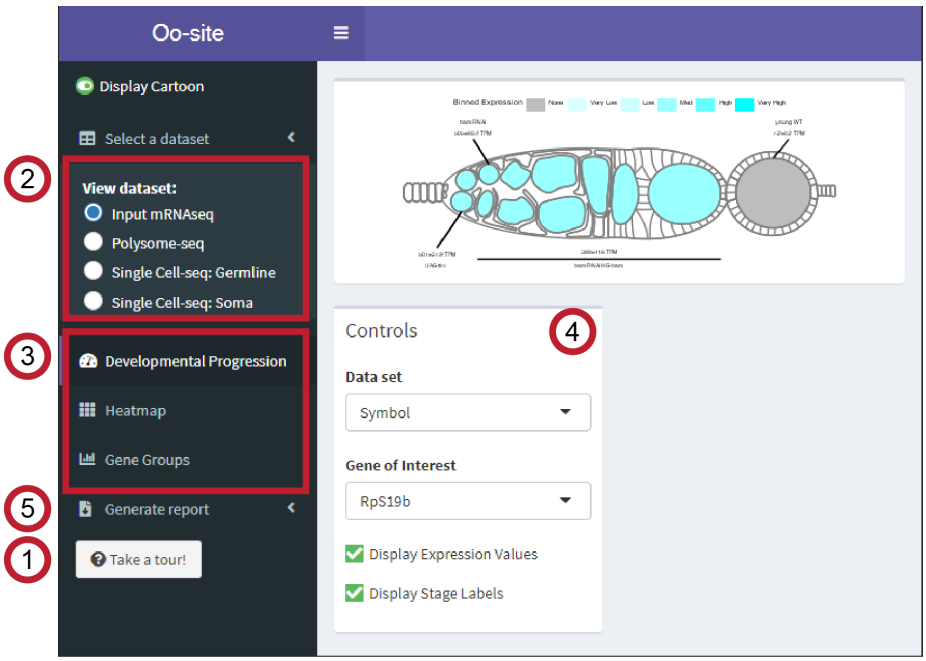
A



B

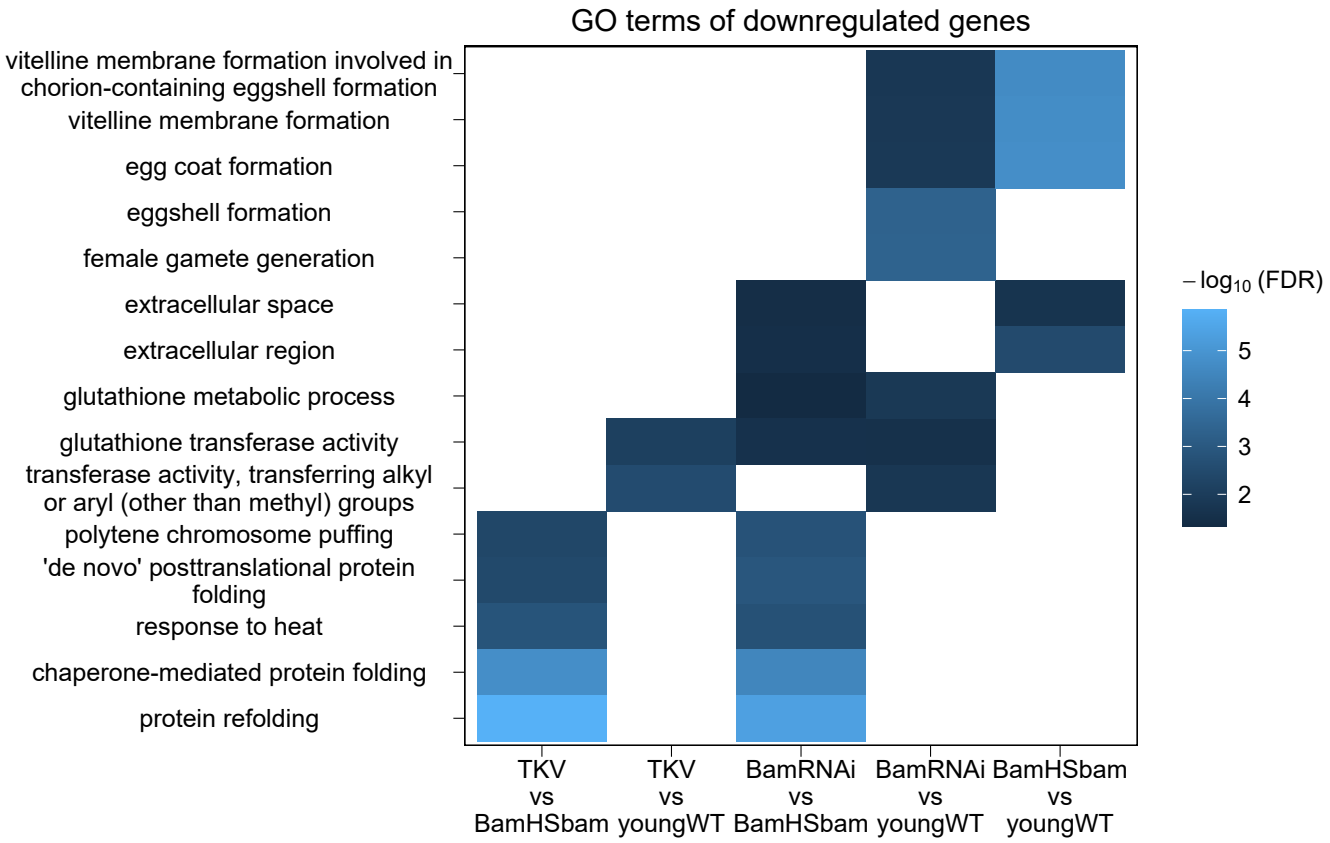


C

Sample	Enriched cell type
UAS-tkv	GSCs
bam RNAi	CBs
bam RNAi; HS-bam	Cysts
Young-WT	All early stages

Figure 1

A


GO terms of downregulated genes
vitelline membrane formation involved in chorion-containing eggshell formation
vitelline membrane formation
egg coat formation
eggshell formation
female gamete generation
extracellular space
extracellular region
glutathione metabolic process
glutathione transferase activity
transferase activity, transferring alkyl or aryl (other than methyl) groups
polytene chromosome puffing
'de novo' posttranslational protein folding
response to heat
chaperone-mediated protein folding
protein refolding
TKV vs BamHSbam
TKV vs youngWT
BamRNAi vs BamHSbam
BamRNAi vs youngWT
BamHSbam vs youngWT
−log10 (FDR)
5
4
3
2

A'

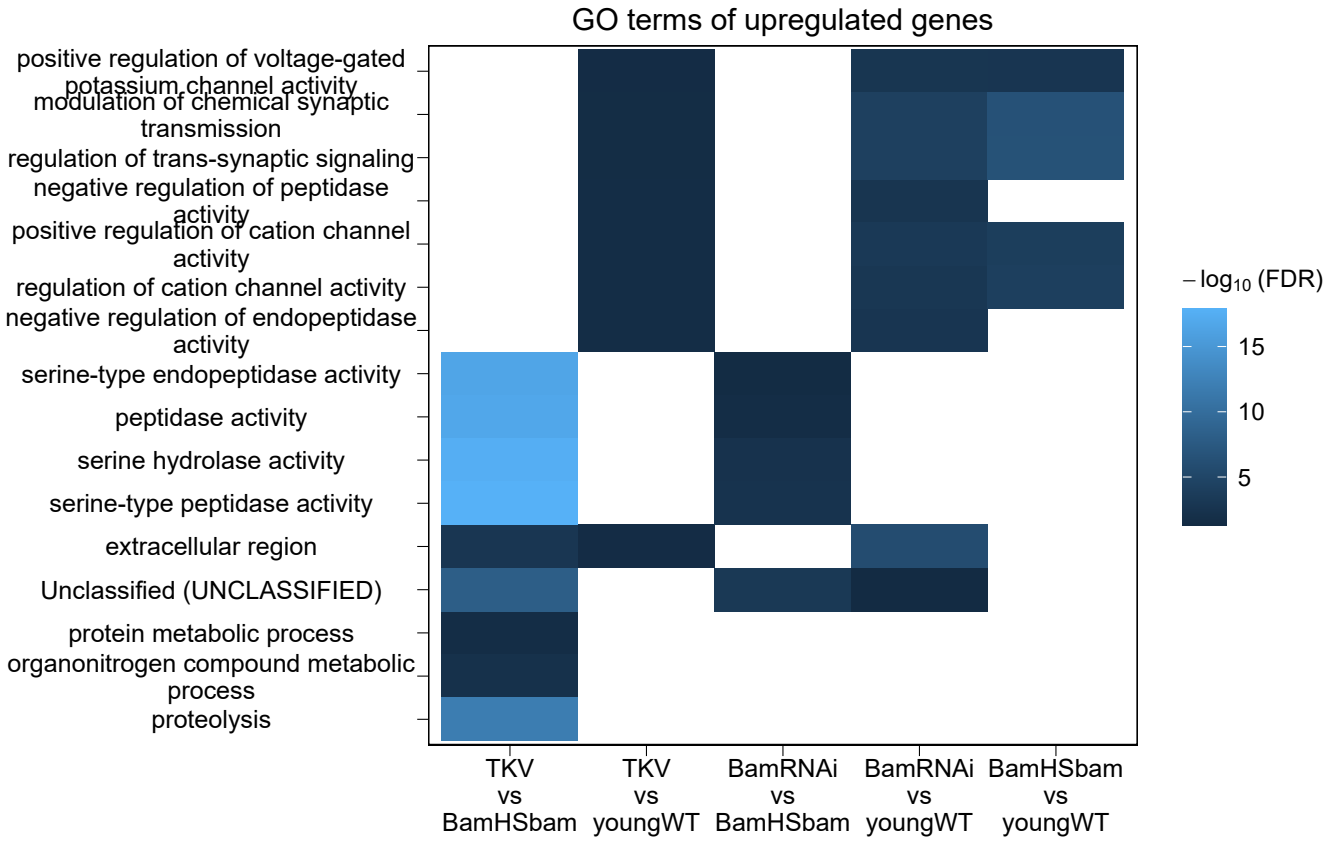
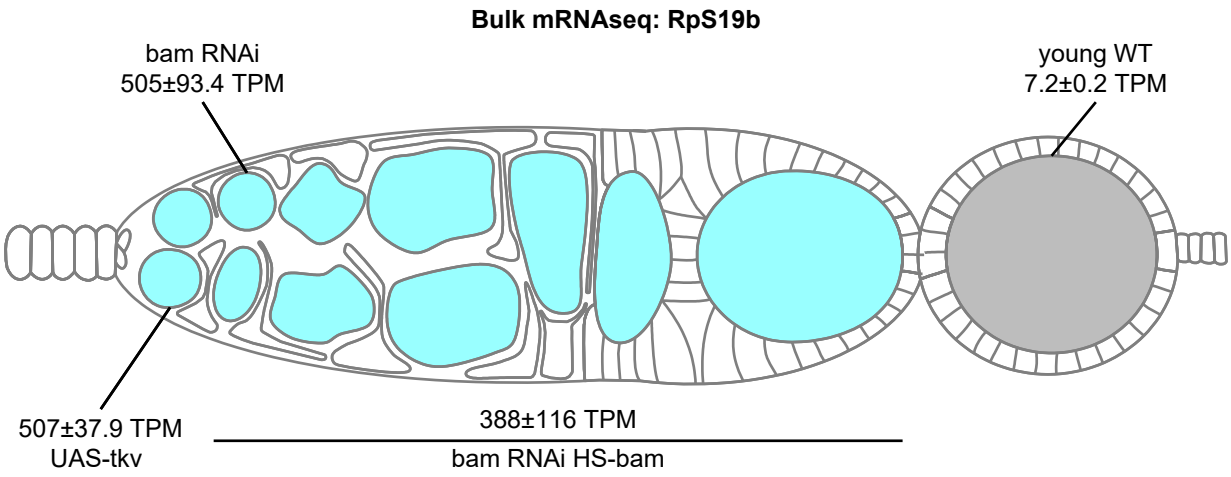
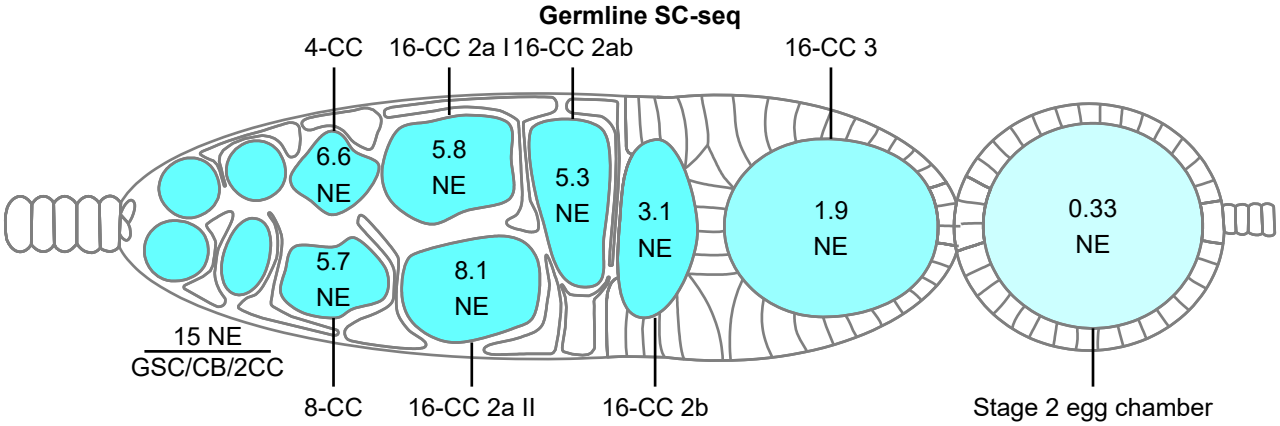

GO terms of upregulated genes
positive regulation of voltage-gated potassium channel activity
modulation of chemical synaptic transmission
regulation of trans-synaptic signaling
negative regulation of peptidase activity
positive regulation of cation channel activity
regulation of cation channel activity
negative regulation of endopeptidase activity
serine-type endopeptidase activity
peptidase activity
serine hydrolase activity
serine-type peptidase activity
extracellular region
Unclassified (UNCLASSIFIED)
protein metabolic process
organonitrogen compound metabolic process
proteolysis
TKV vs BamHSbam
TKV vs youngWT
BamRNAi vs BamHSbam
BamRNAi vs youngWT
BamHSbam vs youngWT
−log10 (FDR)
15
10
5

Figure 2

A


Bulk mRNAseq: RpS19b
bam RNAi
505±93.4 TPM
young WT
7.2±0.2 TPM
507±37.9 TPM
UAS-tkv
388±116 TPM
bam RNAi HS-bam

B


Germline SC-seq
4-CC
16-CC 2a I
16-CC 2ab
16-CC 3
6.6 NE
5.8 NE
5.3 NE
3.1 NE
1.9 NE
0.33 NE
5.7 NE
8.1 NE
15 NE
GSC/CB/2CC
8-CC
16-CC 2a II
16-CC 2b
Stage 2 egg chamber

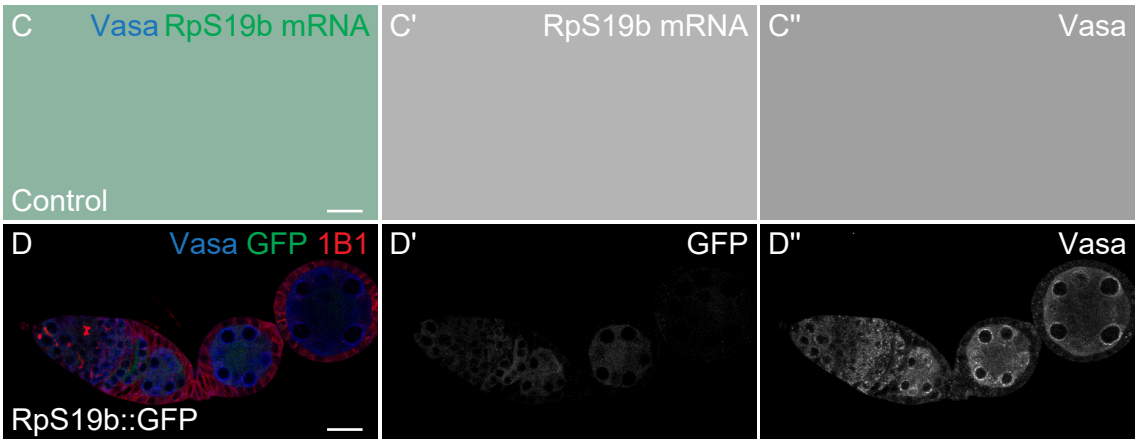
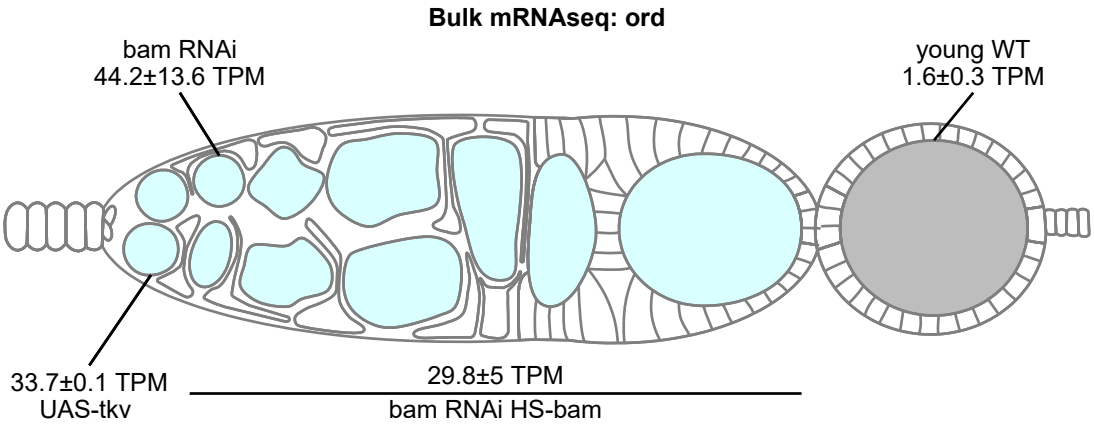
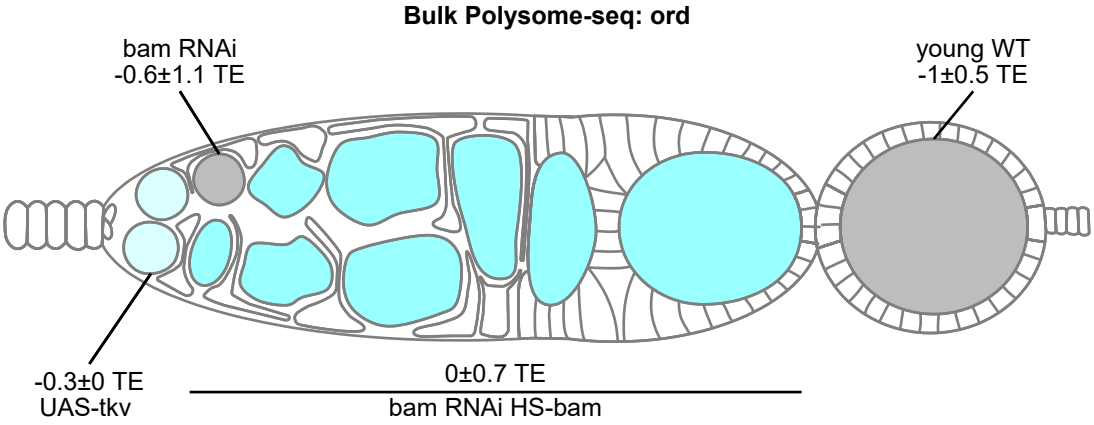

C Vasa RpS19b mRNA
Control
C' RpS19b mRNA
C'' Vasa
D Vasa GFP 1B1
RpS19b::GFP
D' GFP
D'' Vasa

Figure 3

A


Bulk mRNAseq: ord
bam RNAi
44.2±13.6 TPM
young WT
1.6±0.3 TPM
33.7±0.1 TPM
UAS-tkv
29.8±5 TPM
bam RNAi HS-bam

B


Bulk Polysome-seq: ord
bam RNAi
-0.6±1.1 TE
young WT
-1±0.5 TE
-0.3±0 TE
UAS-tkv
0±0.7 TE
bam RNAi HS-bam

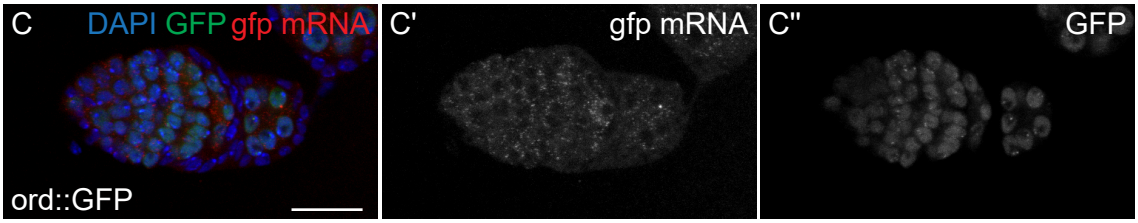
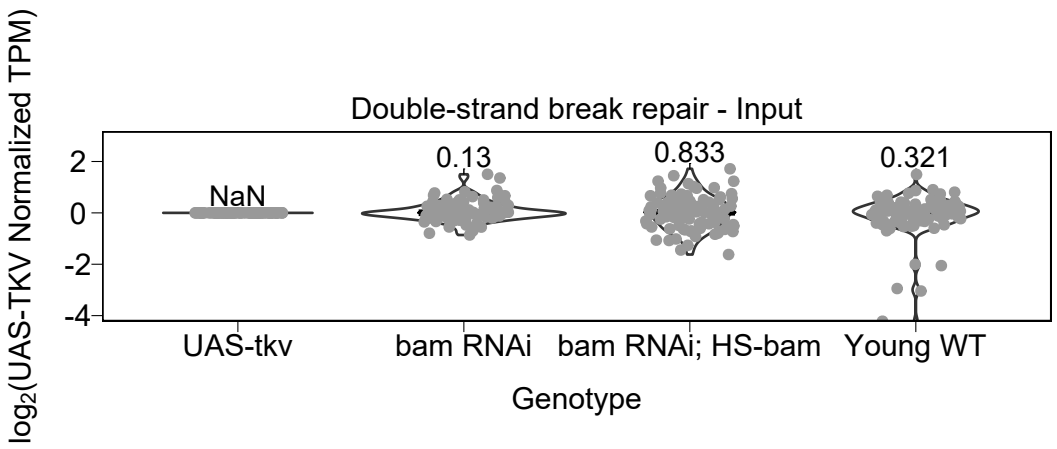
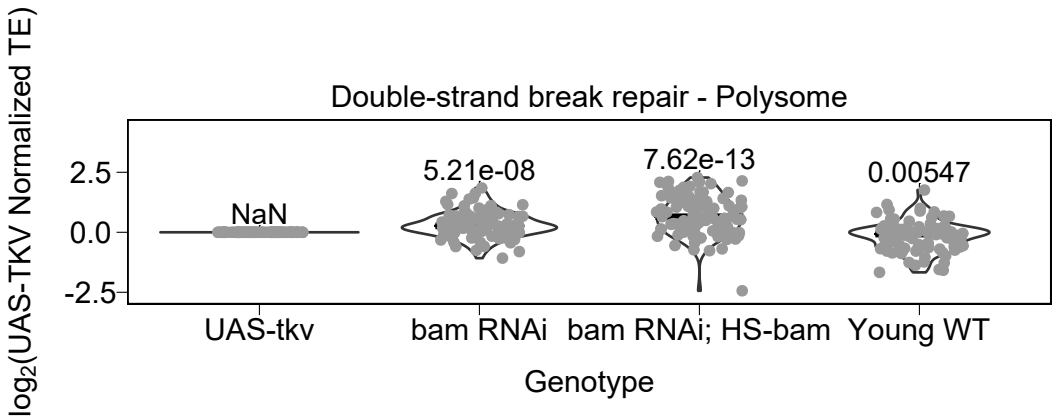

C
DAPI GFP gfp mRNA
ord::GFP
C'
gfp mRNA
C''
GFP

Figure 4

A


Double-strand break repair - Input
log2(UAS-TKV Normalized TPM)
2
0
-2
-4
NaN
0.13
0.833
0.321
UAS-tkv
bam RNAi
bam RNAi; HS-bam
Young WT
Genotype

B


Double-strand break repair - Polysome
log2(UAS-TKV Normalized TE)
2.5
0.0
-2.5
NaN
5.21e-08
7.62e-13
0.00547
UAS-tkv
bam RNAi
bam RNAi; HS-bam
Young WT
Genotype

C

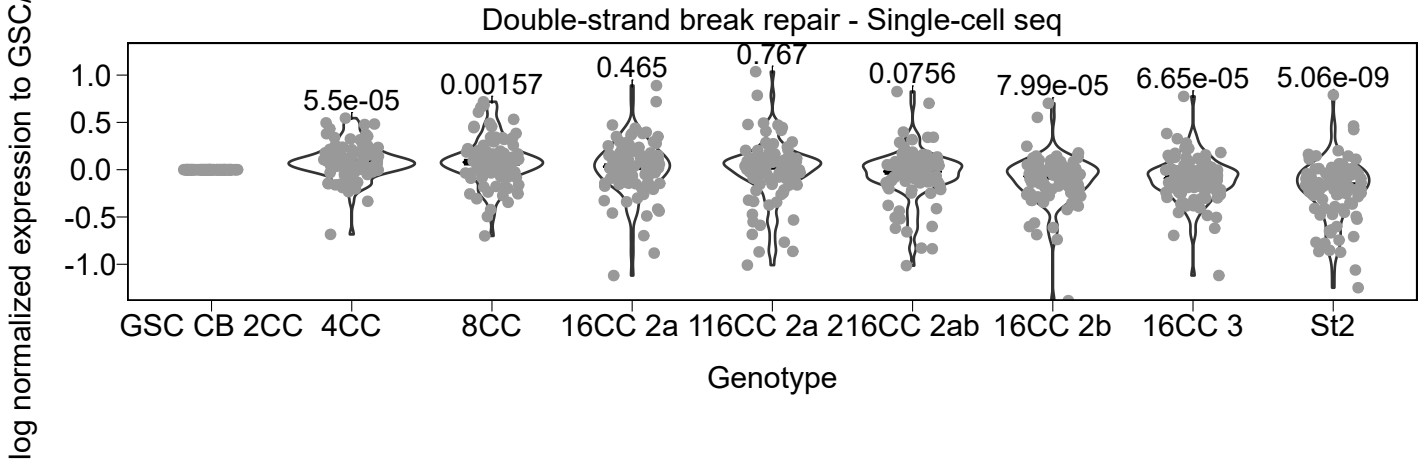
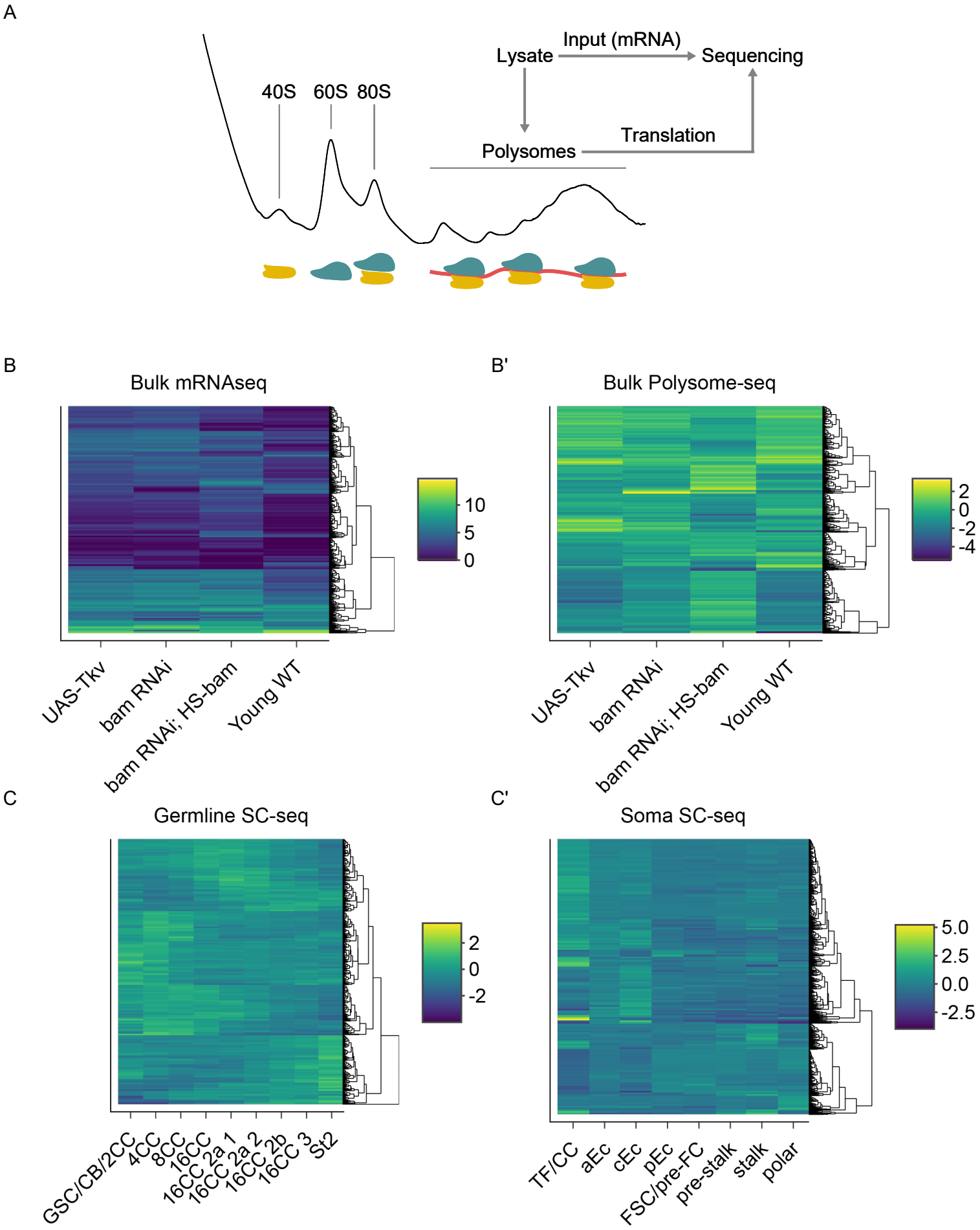
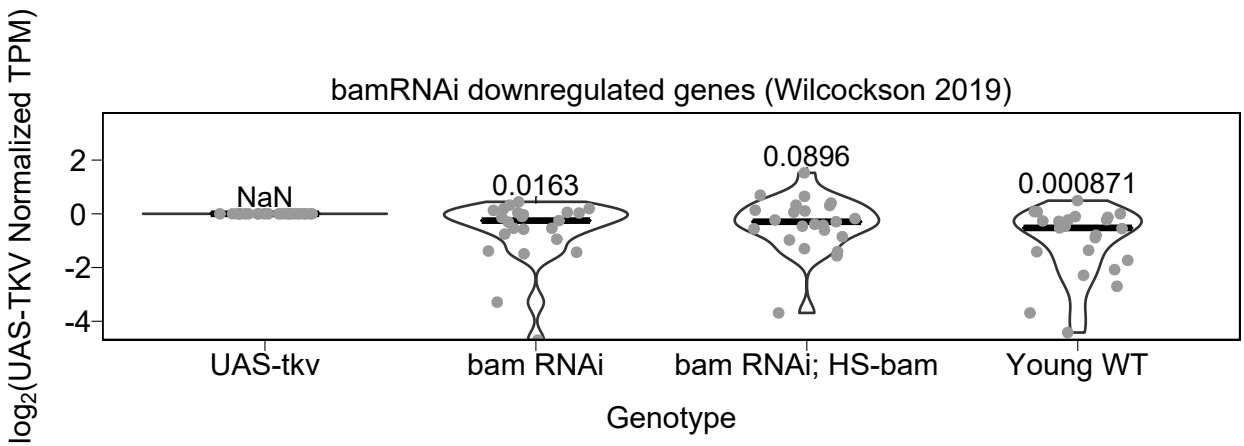

Double-strand break repair - Single-cell seq
log normalized expression to GSC/CB/2CC
1.0
0.5
0.0
-0.5
-1.0
5.5e-05
0.00157
0.465
0.767
0.0756
7.99e-05
6.65e-05
5.06e-09
GSC
CB
2CC
4CC
8CC
16CC 2a 1
16CC 2a 2
16CC 2ab
16CC 2b
16CC 3
St2
Genotype

Figure 5

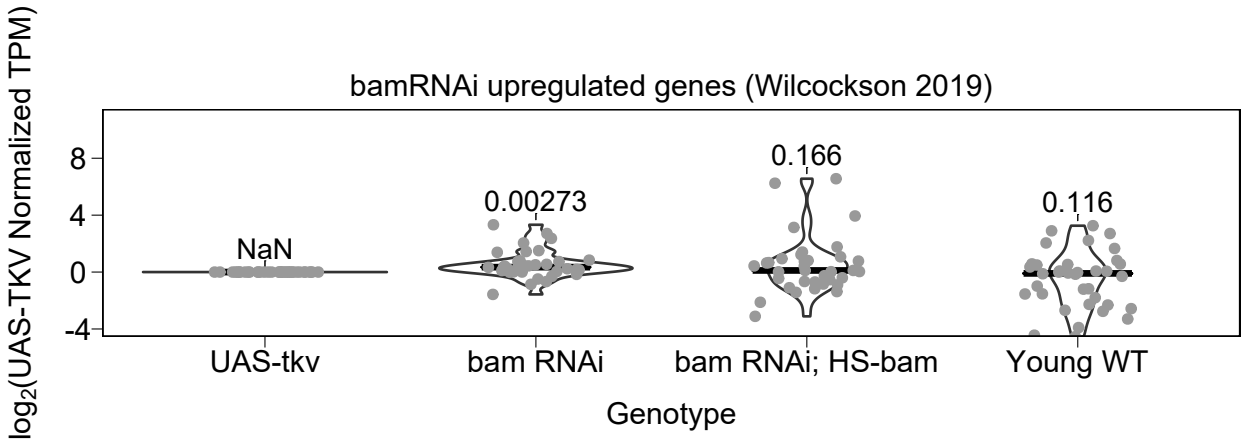


Supplemental Figure 1

A

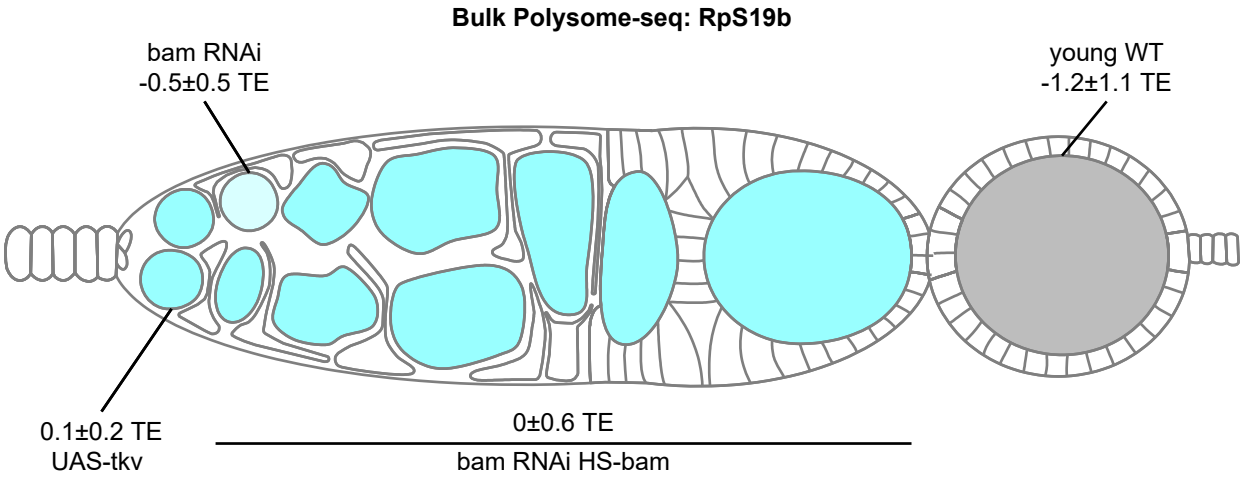


A'



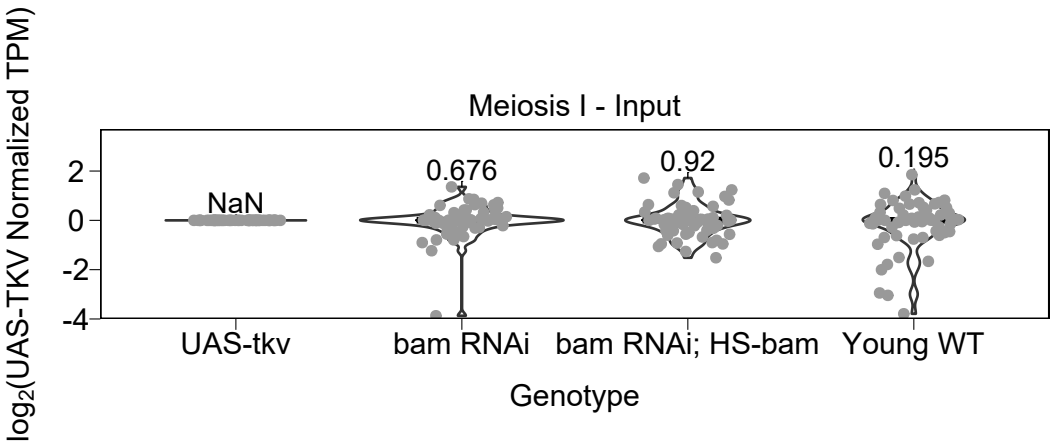
Supplemental Figure 2

A

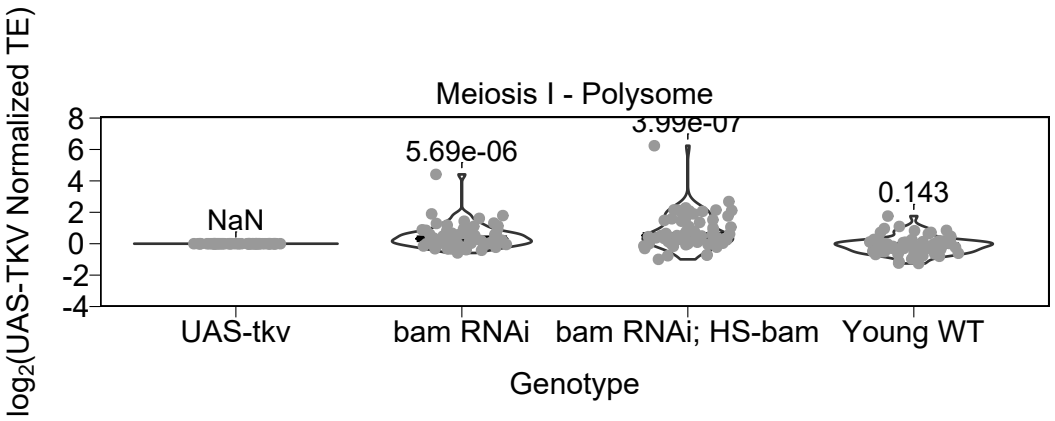


Supplemental Figure 3

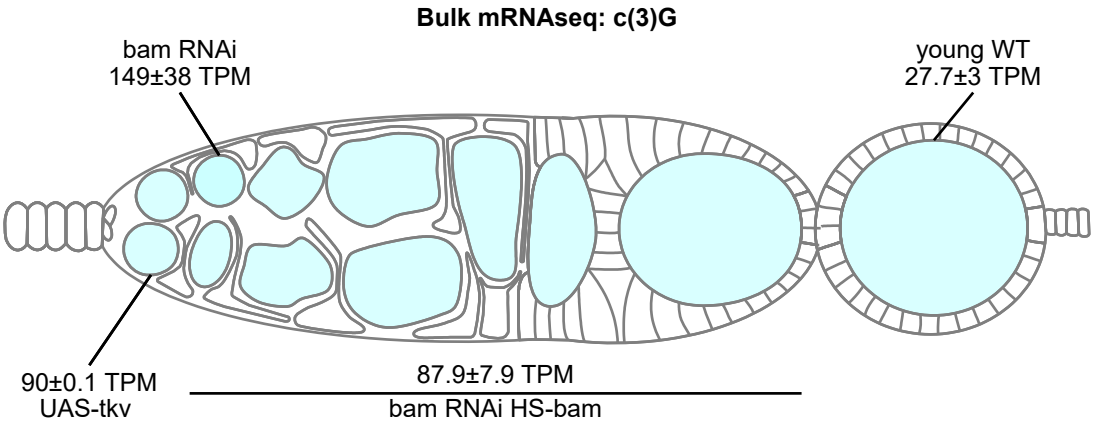
A



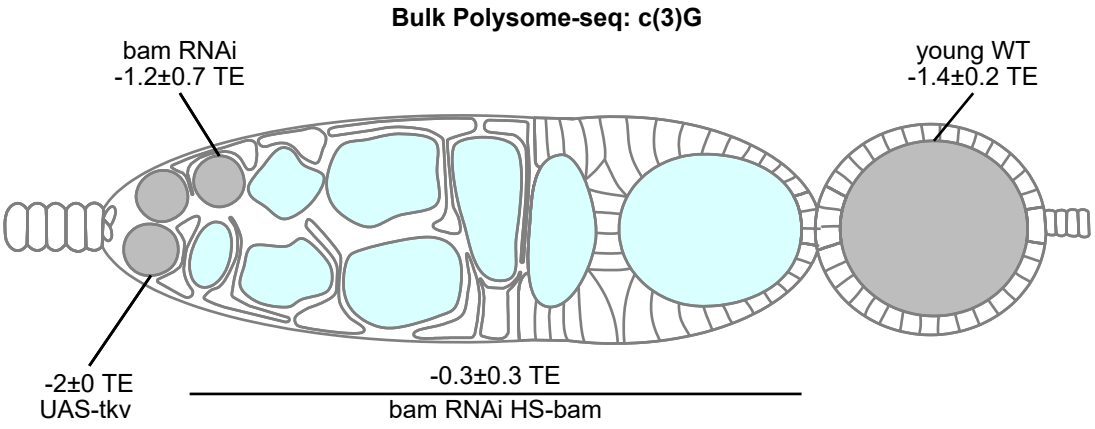
B



C



D



Supplemental Figure 4