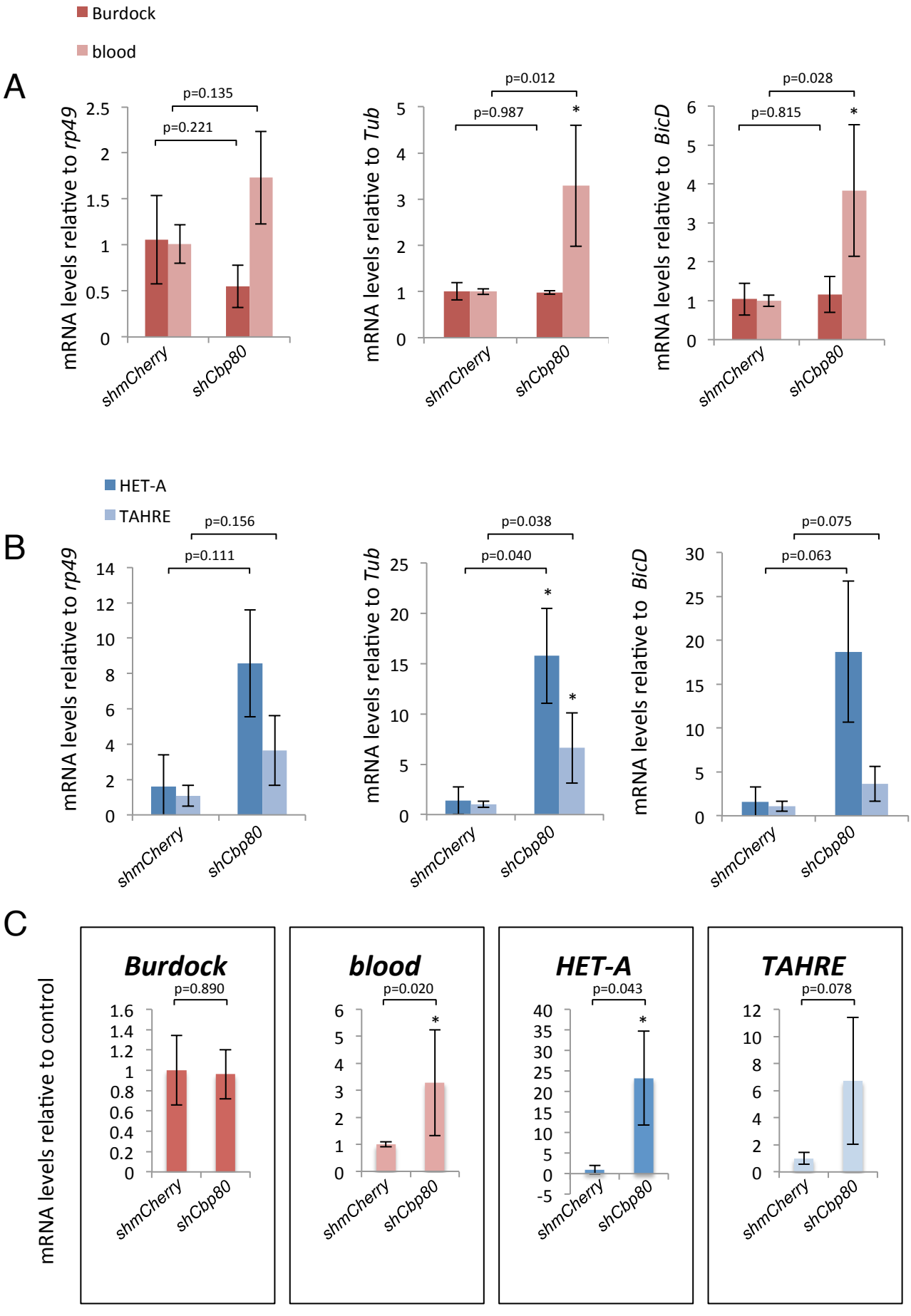
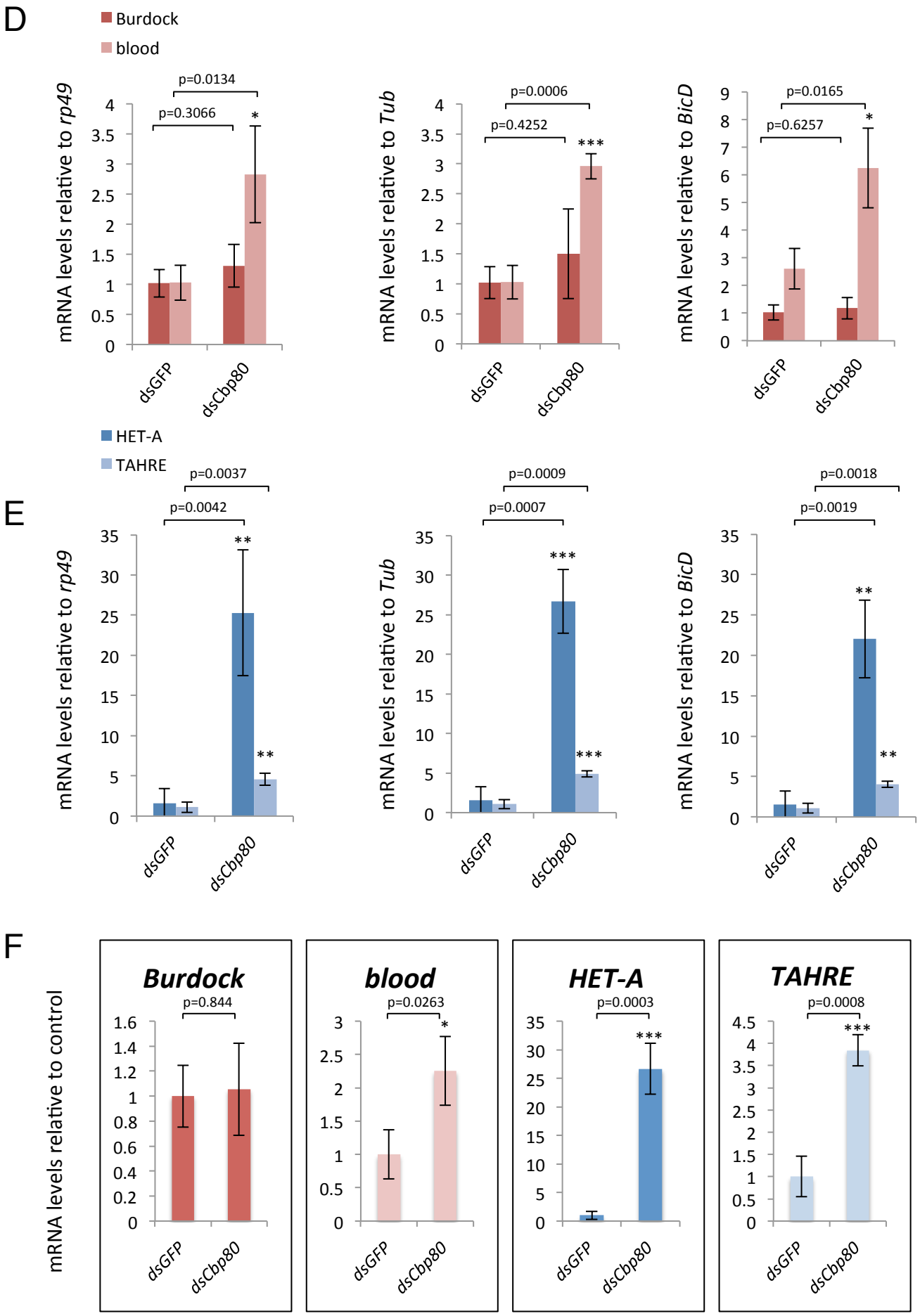
Supporting information S3




D
Burdock
blood
mRNA levels relative to rp49
p=0.0134
p=0.3066
*
mRNA levels relative to Tub
p=0.0006
p=0.4252
***
mRNA levels relative to BicD
p=0.0165
p=0.6257
*
dsGFP
dsCbp80
E
HET-A
TAHRE
mRNA levels relative to rp49
p=0.0037
p=0.0042
**
**
mRNA levels relative to Tub
p=0.0009
p=0.0007
***
***
mRNA levels relative to BicD
p=0.0018
p=0.0019
**
**
dsGFP
dsCbp80
F
mRNA levels relative to control
Burdock
p=0.844
blood
p=0.0263
*
HET-A
p=0.0003
***
TAHRE
p=0.0008
***
dsGFP
dsCbp80

Upregulation of transposons (TEs) upon *Cbp80* knockdown.
Ovaries displaying the "d" phenotype upon *Cbp80* knockdown were used in all experiments. (A-C) Fold increase in RNA levels of indicated TEs upon germline-specific RNAi-mediated knock down of *Cbp80 (*shRNA against *Cbp80*). The germline GAL4 driver alone was used as control. (A-B) Fold-changes in transposon RNA levels were normalized to *rp49, Tub* and *BicD* levels. Control ovaries expressed the *shmCherry* construct. (C) Levels of transposon transcripts relative to the control sample are shown. The same amount of total RNA was used as starting material. Error bars represent $^{+}$/- SD of 2 control and 3 biological knock down replicates. (D-F) Fold increase in RNA levels of the same TEs upon germ line specific knock down of *Cbp80* using *dsRNA.* (D-E) Fold changes relative to *rp49, Tub* and *BicD.* Control ovaries expressed a *dsGFP* RNAi construct. (F) Levels of transposon transcripts relative to the control sample are shown. The same amount of total RNA was used as starting material. Error bars represent $^{+}$/- SD of 3 biological replicates. *p<0.05; **p<0.01; ***p<0.001.