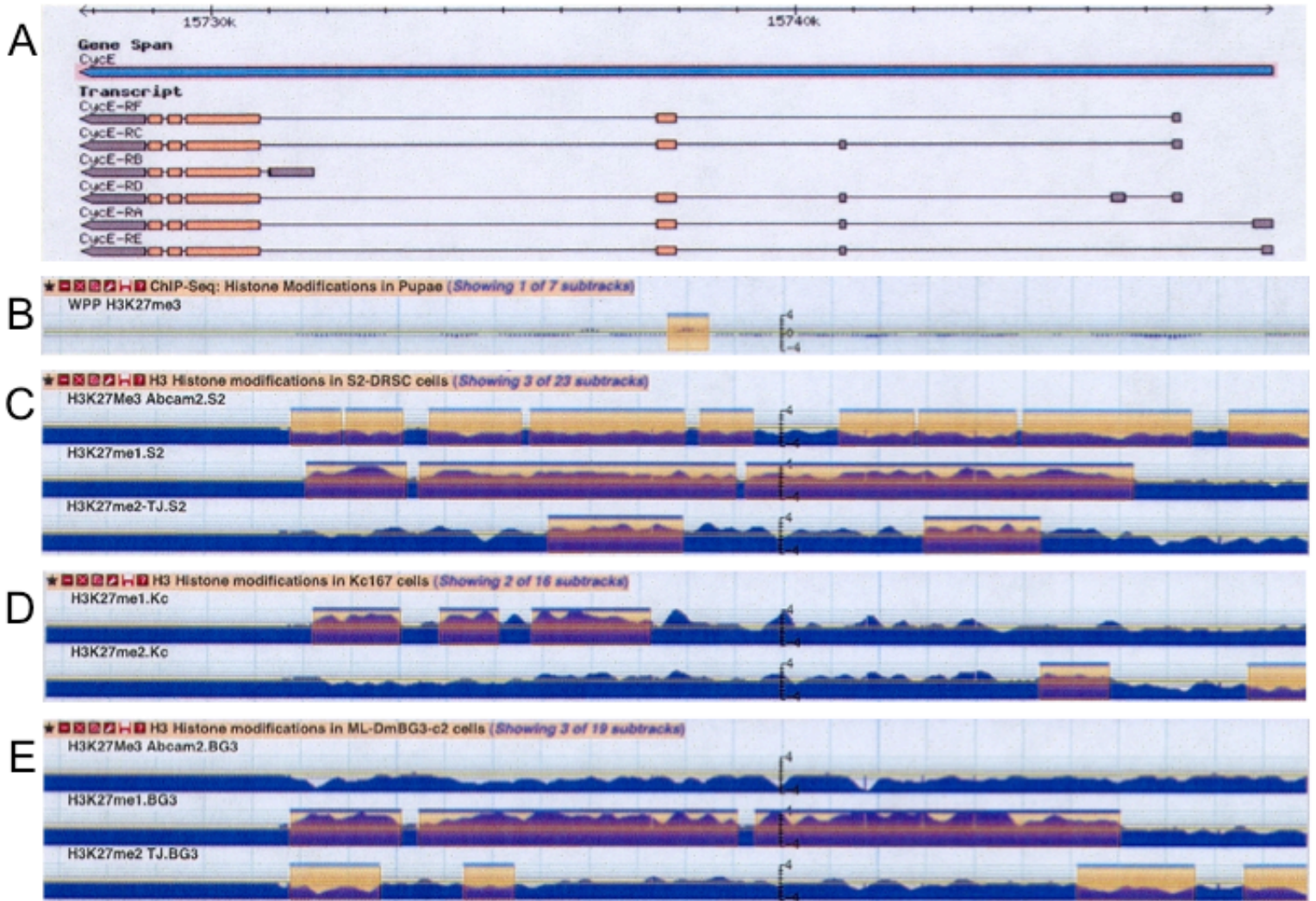
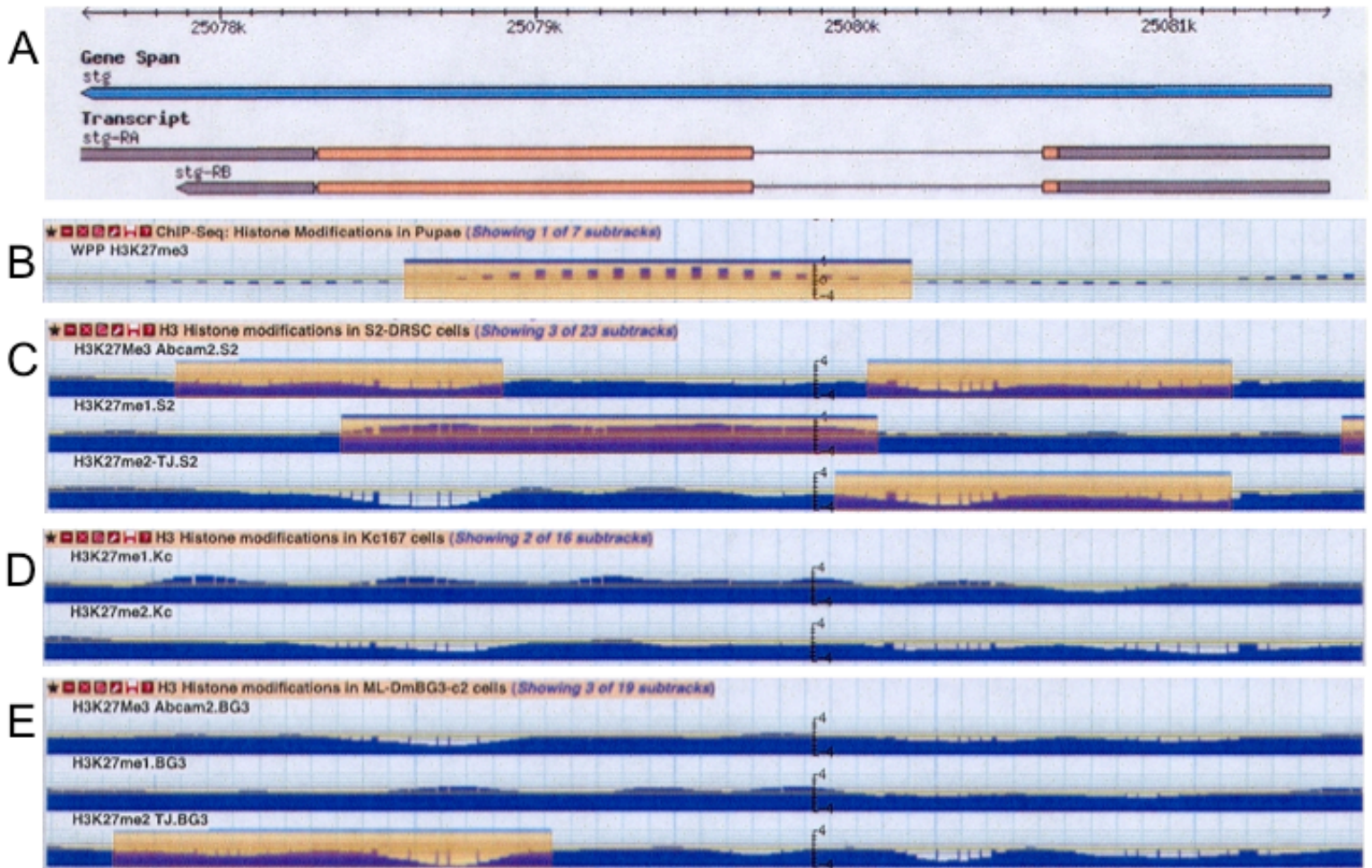


**Figure S1** The H3K27me status on the *dE2f1* gene (A; Region surveyed: 3R:17444026..17488127) during the white prepupal (WPP) stage (B) and in *Drosophila* SL2 (C), Kc (D) and BG3 (E) cells. These results are obtained from the ChIP-chip and ChIP-Seq data sets provided by Drs. Gary Karpen, Vincenzo Pirrotta, and Kevin White laboratories from the modENCODE Project (<http://modencode.oicr.on.ca/fgb2/gbrowse/fly/>). Note: H3K27me3 is enriched at the *dE2f1* locus during the WPP developmental stage (B), and the enrichment of H3K27me1/2 in *dE2f1* locus in all the three cell lines analyzed (C/D/E).



**Figure S2** The H3K27me status on the *dCycE* gene (**A**; Region surveyed: 2L:15712959..15762958) during the WPP stage (**B**) and in *Drosophila* SL2 (**C**), Kc (**D**) and BG3 (**E**) cells. Note the enrichment of H3K27me3 in *dCycE* locus during the WPP stage (**B**), and the enrichment of H3K27me1/2 in *dCycE* locus in all the three cell lines analyzed (**C/D/E**).



**Figure S3** The H3K27me status on the *stg* gene (A; Region surveyed: 3R:25064521..25114520) during the WPP stage (B) and in *Drosophila* SL2 (C), Kc (D) and BG3 (E) cells. Note the enrichment of H3K27me3 in *stg* locus during the WPP stage (B), and the enrichment of H3K27me1 in *stg* locus in SL2 cells (C).

### H3K27me3\_WPP\_Chip\_seq.12700 Details

Name: H3K27me3\_WPP\_Chip\_seq.12700  
Type: binding\_site  
Description:  
Source: 14111\_details  
Position: 3R:17471579..17472512  
Length: 934  
Score: 108.51  
analysis: H3K27me3\_WPP\_Chip\_seq.MACS  
load\_id: 159737658  
primary\_id: 1274681  
browse\_dbid: white.database

A

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>H3K27me3 WPP Chip seq.12700 class=Sequence position=3R:17471579..17472512
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AATCAAAACAG AGCAACTTAC GAGCAGAAAC GAGATCCAAG CTCTCTCAGA TCCCGATTTC GATCGCCTTG CTTTGGCTGT
TAAAAATATG AGAAACATT ATAACTTTTT CCGTAACACT TCTTCTCTCC OCTGGCTGGC ATTTAAGAA CTTTAGCGAT
TTATGCTCT CTCAAGCGAG CCAAGCCAAA CCTGATTTGC TCTGTACGAC CAACAGCGGC GCTTAAGGCC AGGAGGCCA
GCCAAAGTCC CAGACCTTA AAGCCGCCA CCGACTGAC GTAGCAATA AAACAGAGCC CCGTCCAAA AAGGAGGAC
AGCAGGACTC ACTACCAAT ACATGCCAGC AATCCAGCC CGACACTGC CCGCAGACAC TCCAGGACT CCTCTCTCC
ATTCGCTGC CACTGCCAC TCCGAACTTC CAGCCCTTCA CTCGCCACA TCTTGCACAC ACTGTGACAA TCAATTAAT
TAAGCCAAAT CCATCCACA CCAAAAGCCA AGGACCAAT CCAGCCGAC ACAAACCCAG CAGCAGCCG CCGAGCCGC
ATCCGATCT TCCAGCGCC AGCCAGCCCA ATGCCCTAG TCCAAAGTCT AGCTTGGTC AAGCTGGGA CCGAGCCGC
CCCGATCCA TGAGCAACT TCTTCCAGG TCCCAACAA AAGTATATG TTATGCCAA AATTCAGAC GTTTCCTAT
AAACATGAC ACTTCTTAA AGAGAAAAA ATTCTAGCC GACTAATGC TTATGCTATG ATAAATAAT ATGACTGAC
TCTTATCAT CTAATGACAA AAAAAAATA GAATACAAT CACTAATCT TCAA
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### H3K27me3\_WPP\_Chip\_seq.2385 Details

Name: H3K27me3\_WPP\_Chip\_seq.2385  
Type: binding\_site  
Description:  
Source: 14111\_details  
Position: 2L:15735620..15736449  
Length: 830  
Score: 86.76  
analysis: H3K27me3\_WPP\_Chip\_seq.MACS  
load\_id: 159739901  
primary\_id: 1267711  
browse\_dbid: white.database

B

```
>H3K27me3 WPP Chip seq.2385 class=Sequence position=2L:15735620..15736449
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CCGAACTTC TCCAGAGCA AATGTGCTCT CGATGATAT TTATTTAGAG ACGAAAGAA AAGGGAAAA CTCGGCCAG
TGATCTTGA AAGGATAGG GCTTGTCTCA ACCCTCCGCT CCGTGTCTTC GTTGTGTGG GTTTCAGCTC TGTCCCATC
CGCTAGTAC CAGCATCTC TACCATCAC CTTCCGCCA CTTCCGAGCC AATCCCTTAA ACCTTCTTGA TCTAGTCTT
CTGCTCCAG CTACCTATG ACATGCGAA TTTCAAATC TTTCAGCGGC CTTAAGGAA ATTTCCGCA GCTTATCTT
TTGAAAAAC CACCCCTCC AGAATCGGA CTTGGACTCA AGCTTGGCC CAGTGGGAA CAGCCCTTC TGTCTTCTT
CTGGCTCTC TGTCTCTCC OCTGCTCTC TTGCTCTCC CATGATAGC CTGGGATAC TGCCAAAGC
CCCTTCCGG AATTCCTTA CTCACAAAG TTCCCTGAG AGGGGGCCG ACATTTCTT GCGATGACT TTTTCTGAC
CAGATGACA TTTGTTTCC ACGGAGCCG GCGCAAAAC CATTGCCAA ACAAAAACCT CAAAAAAA ACAGCAAAA
AAATAACCA GCGAGATAC ATTGTTTCC CACAGACTG TTCTATACC CTGCTACBA CATTTAAAT TTACATATA
TCTCAGTAC AACCAAGCC ACCTATAAA
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### H3K27me3\_WPP\_Chip\_seq.13914 Details

Name: H3K27me3\_WPP\_Chip\_seq.13914  
Type: binding\_site  
Description:  
Source: 14111\_details  
Position: 3R:25077969..25079907  
Length: 1939  
Score: 916.24  
analysis: H3K27me3\_WPP\_Chip\_seq.MACS  
load\_id: 159740157  
primary\_id: 1272363  
browse\_dbid: white.database

C

```
>H3K27me3 WPP Chip seq.13914 class=Sequence position=3R:25077969..25079907
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AAGCCGAAAC CAATAAAACA ATATAACTA AACAAGCCG TTAATTTCCA AATGAAATTC TCTGTTTTG ATCAATGCCA
CTCTCCGCTC TGTCTCCGC TCGTCTGCA CAACCTTACT CTAGCGATA ACAAAATGAAA ATCAACAAAA ATCAACTTAA
AAGCAGCTC AATAAAATC CCTATACT CTATATATAC AATACGATA CACCCAACT TCCATAACCA ACTGCACTAA
CTTCCACA CCTACAGAT CAGTCCGAG CCGACTTCT TTAGCCGCC GTTGGCCGC CCGAGCCAT CCGCTTCA
GGACTGGAC TTGGCCGAA AATGGCAZA GCGCTGTGT TGGCCGGAT CAGCACTGT GCGTAGGCA TGTGTTCC
AGACTCAAC CTCCACTCC AAGACTCTT TGTAGCCGT CTGACGAGA TAGACTCTGG GATGTGCA CCGCGATG
GCTTGTAT TCTTCCGC ATCCGATTA CCGCAGAGC GCGCATTTT CCGTCCGCT TCCAGAGCA ATTCCACTG
GAGATAATG ATGTTCCCT TTGTCCGSA TTCCGCTTC TCGTCTCTT CCGACTCACT CTGTTGACC GTGAGACTG
CATCAGGAT CTGCTGGTG GTTACAGT TCTTGGCTCC CTGATGTGG CCGCCCTCA AATGTAAGG GTAGCCGCG
TGCATGAGC GGTAGTGGC CACTTATCC CTGAATCCG CCTTAAGAC CCGAGCCACT GTTCCCTGG AGATGCTCT
CAGATCCGA TGACACCTT CCATCAGGC CAGGGCATAG CTTTCTGTA AGTCCCGAT TNGCTGGGC TCGTTGCTT
TCTGGAGGC GCGCAGCCG GACATGATC CCGCTCTGT CAGGACATG CACTTCTCA GTGGAGGGG GTGGTAATC
GTACCTTGC TGATGGCTT CAGTCTCTT TCTCAACGC CCGCAGCCA TGGCTTTGC TCTGGATGG CTTGGATGG
CGAGCTTC CCGCATCTC CCGTCCGCG GCGCTTGAAG CAATCCCGG CAGTCTCTG GGTCTTTGT GGTGGGCTG
TGTCTCTT GTGTTCTC TCGTCTATC TGAGGCACT TCTGACCGAA GGGCCGCGA TGACAGACC CCGTGGAT
TTGGCAGG CTTGCTCTT GATCTGGCC CTGATCAGC AGTTTAGCC ACTGGGAG CCGAGCCGC TCTTGTGCT
CTGCACTCC ATCTGAGA CTTCCATGA CTCATGCTC ATGAGGACT CCAATGGAG CCAATGGAG TGTGAGGAC AGCTTGA
AGATCCGAA CCTCCGCCC CCGCTGTAT CACTTATAC TCCATGACT CCGCAATTT TCGCTCCG CAGCATCTG
AAGCTTCCG CCGAGCCCT CCGCAGAGC AGACCATCA CTTCCGACT CCGCATGCT CCGCAATTT TCGCTCCG CAGCATCTG
CGCTCTCC TGAAGGACA CTTCTCTCT GTCCATGTC ATCAGTTCA GGAACCGCG AGCAGAGCA GATCCACTA
TTTTTTAT GCTACTGAA CTGCTGCTT TATTACTCA AGAGCAACA AAGAGAGGG GAGGATTAG CAACTGTTG
ACTGCTGCT CTGTTGCTT TTTTCTTCC TAAACTCTC CCAAGAGCC CTCATTAAC CAGCTAAAA ATACTGACA
CTCAGAGCC AGTCAACT TCGTCTCTA AAAACAACA AAATACCCCA GAAATACAG AGAGCCCTTC TTCTAATTC
```

**Figure S4** The detailed results of ChIP-Seq analyses showing the enrichment of H3K27me3 in *dE2f1* (A), corresponding to the peak in Fig. S1B), *dCycE* (B), corresponding to the peak in Fig. S2B) and *stg* (C, corresponding to the peak in Suppl. Fig. 3B) loci during the WPP stage. These results are obtained from the ChIP-Seq data sets provided by Dr. Kevin White laboratory from the modENCODE Project (<http://modencode.oicr.on.ca/fgb2/gbrowse/fly/>).

**Table S1 Summary of the genetic analyses using the Exelixis *Df* lines.**

Available for download at <http://www.g3journal.org/lookup/suppl/doi:10.1534/g3.112.004333/-/DC1>.