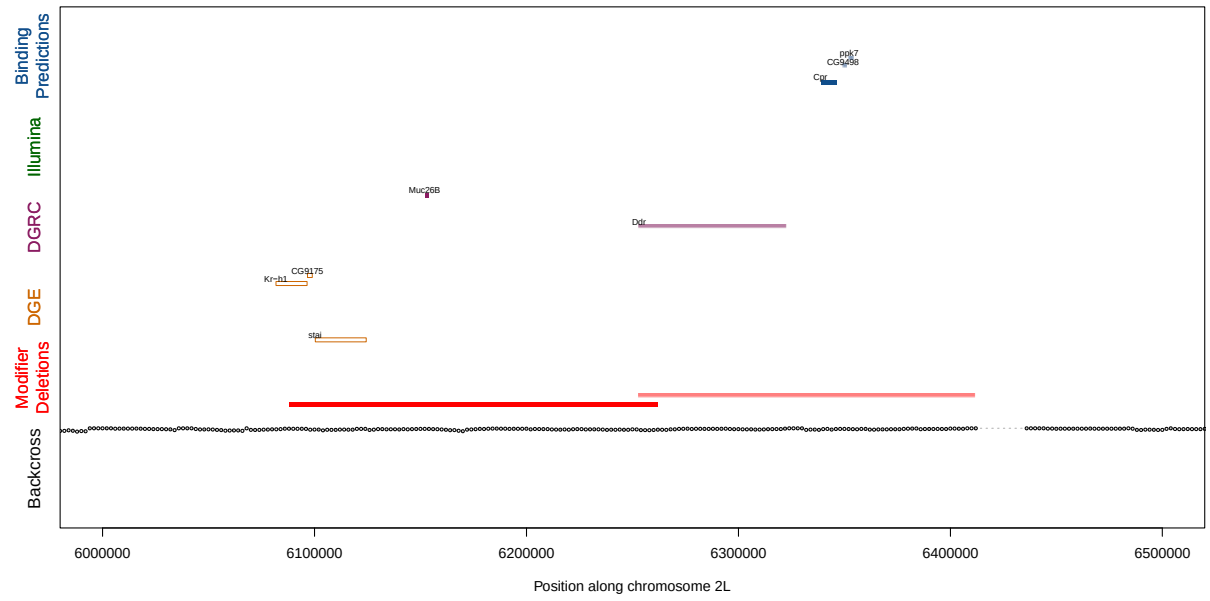
Binding Predictions
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DGRC
DGE
Modifier Deletions
Backcross
ppk7
CG9498
Cpr
Muc26B
Ddr
Kr-h1
CG9175
stai
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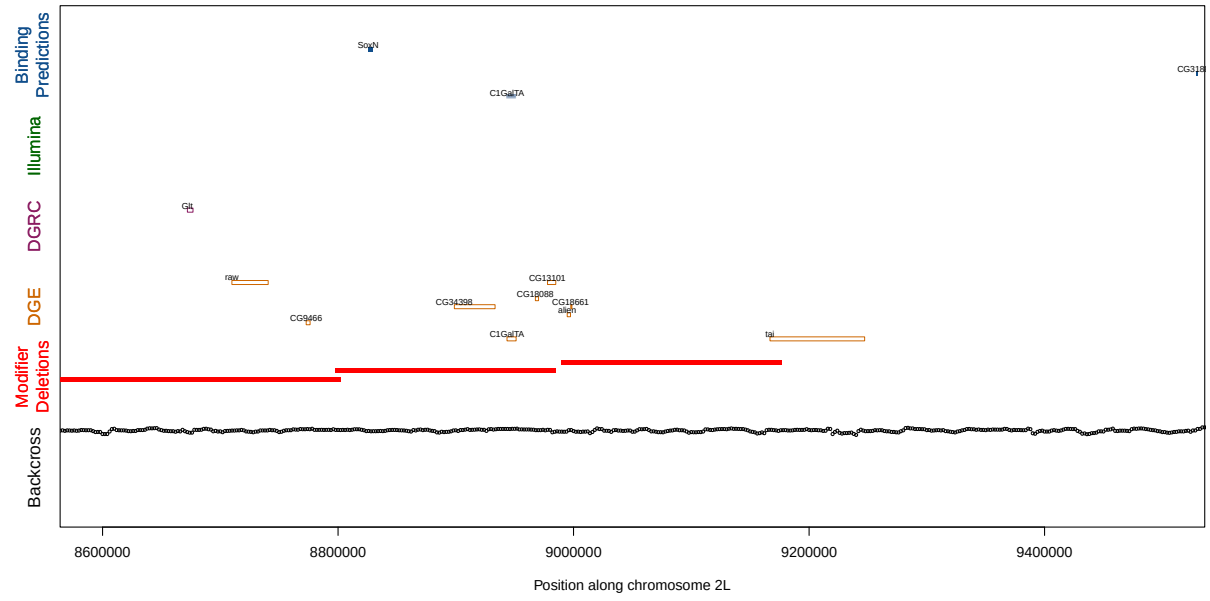
6100000
6200000
6300000
6400000
6500000
Position along chromosome 2L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DGE
Modifier Deletions
Backcross
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C1GalTA
Git
raw
CG13101
CG18088
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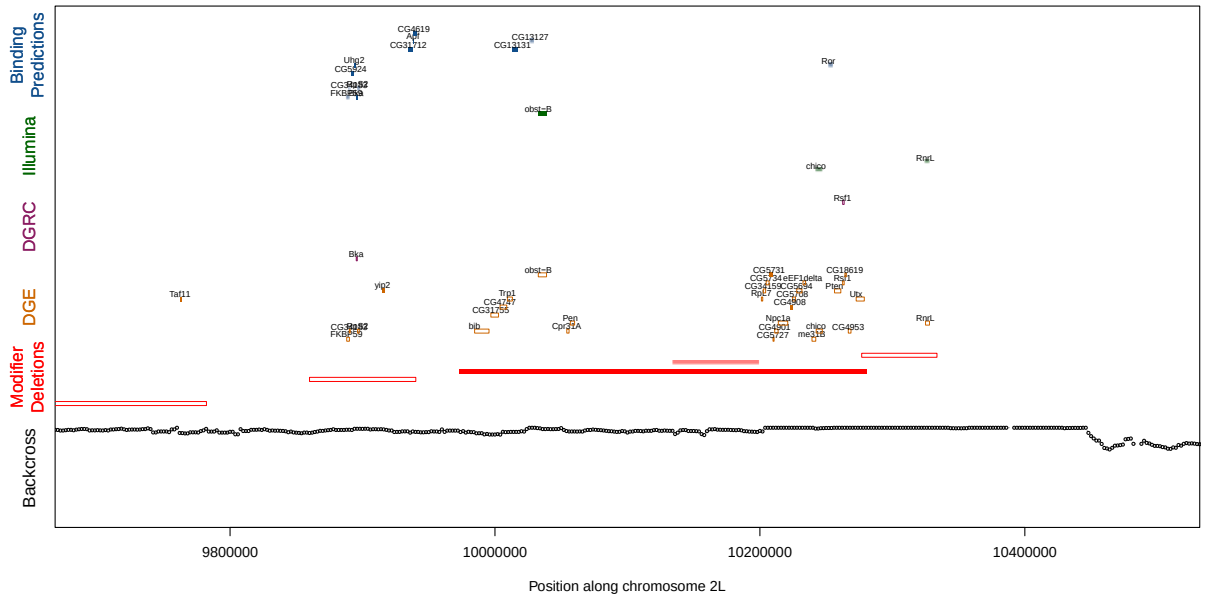
CG18661
allgh
CG9466
C1GalTA
tai
8600000
8800000
9000000
9200000
9400000
Position along chromosome 2L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DGE
Modifier Deletions
Backcross
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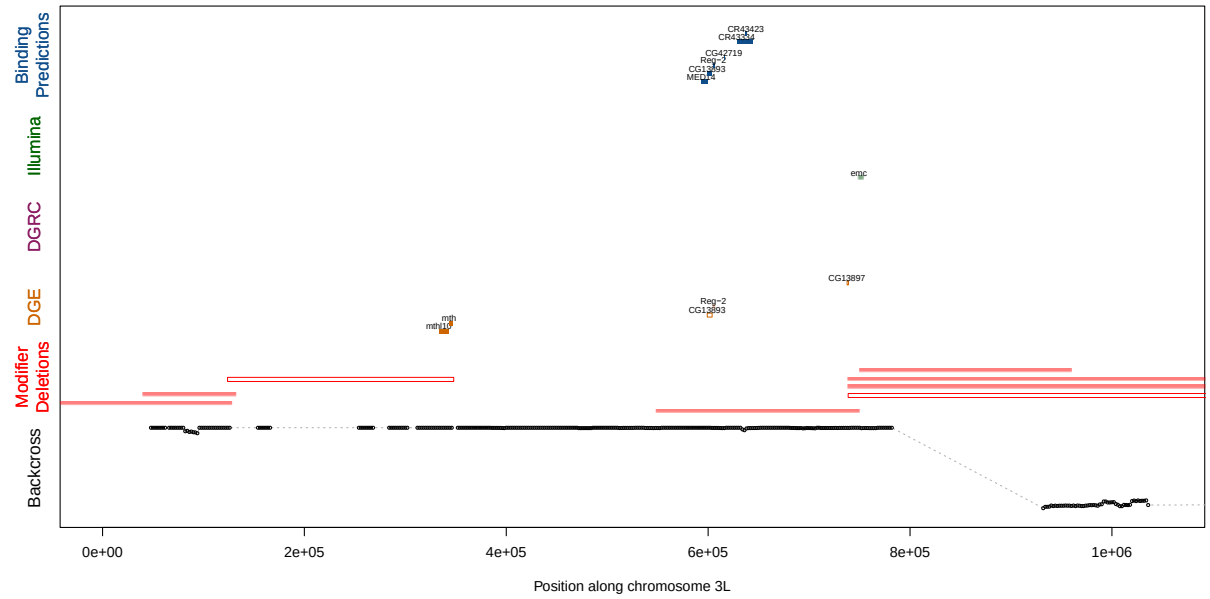
Position along chromosome 2L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DGE
Modifier Deletions
Backcross
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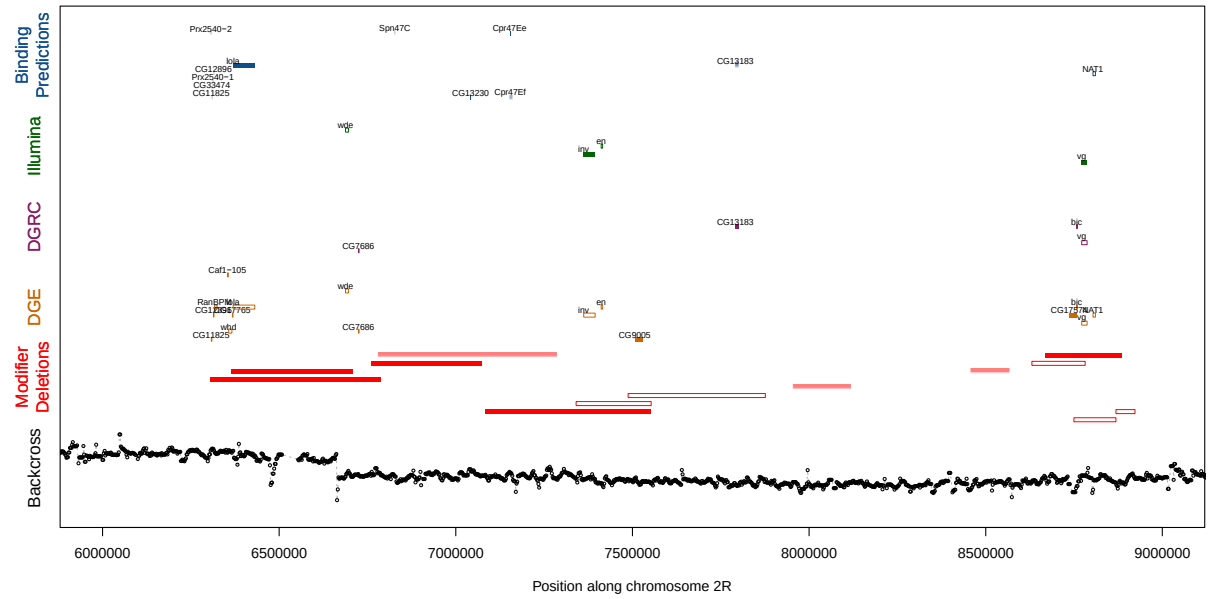
CG42719
Reg−2
CG13893
emc
CG13897
mth
0e+00
2e+05
4e+05
6e+05
8e+05
1e+06
Position along chromosome 3L


Binding Predictions
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DGRC
DGE
Modifier Deletions
Backcross
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Spn47C
Cpr47Ee
lola
Prx2540−1
CG33474
CG11825
CG13230
Cpr47Ef
CG13183
NAT1
wde
inv
en
vg
CG7686
Caf1−105
bic
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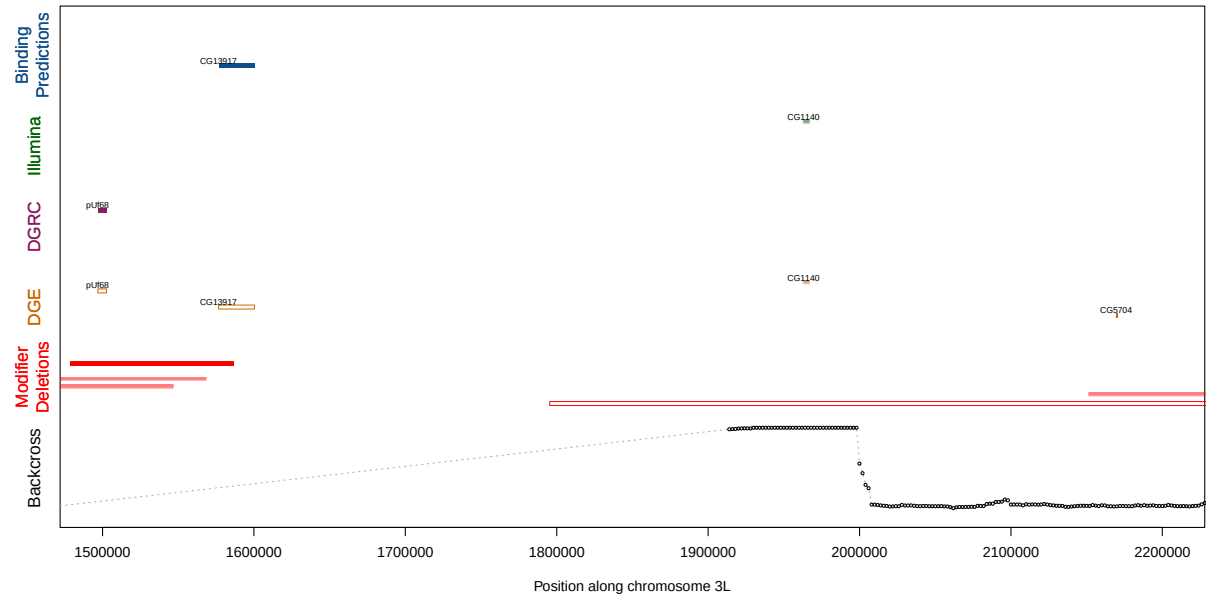
7000000
7500000
8000000
8500000
9000000
Position along chromosome 2R


Binding Predictions
Illumina
DGRC
DGE
Modifier Deletions
Backcross
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pUf68
CG5704
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1700000
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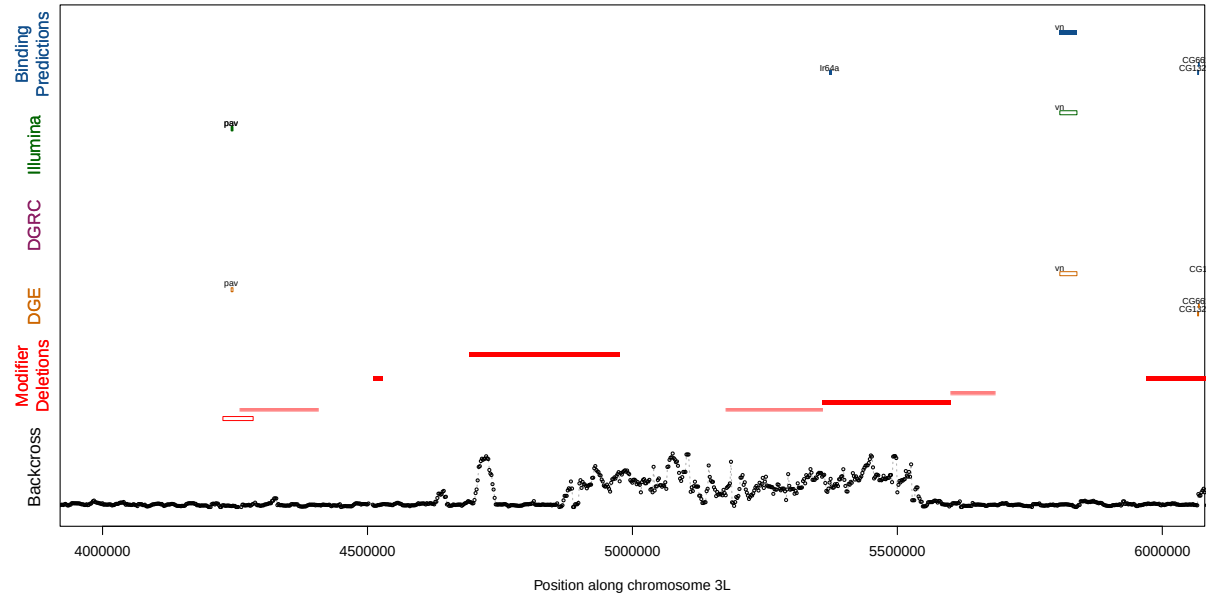
1900000
2000000
2100000
2200000
Position along chromosome 3L


Binding Predictions
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DGRC
DGE
Modifier Deletions
Backcross
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Ir64a
pav
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4500000
5000000
5500000
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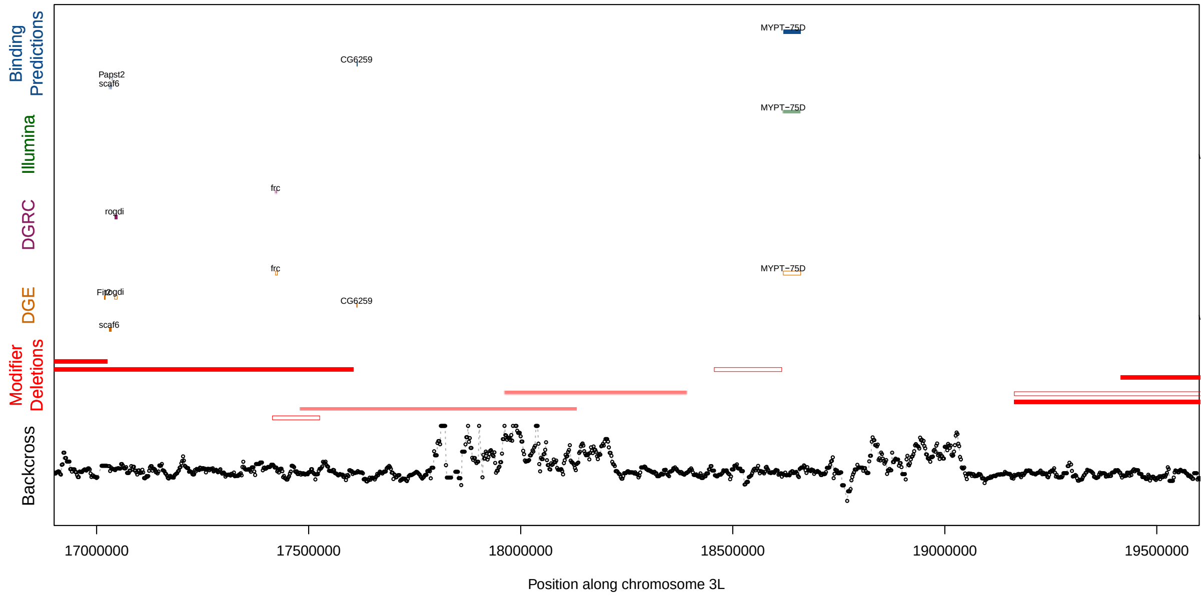
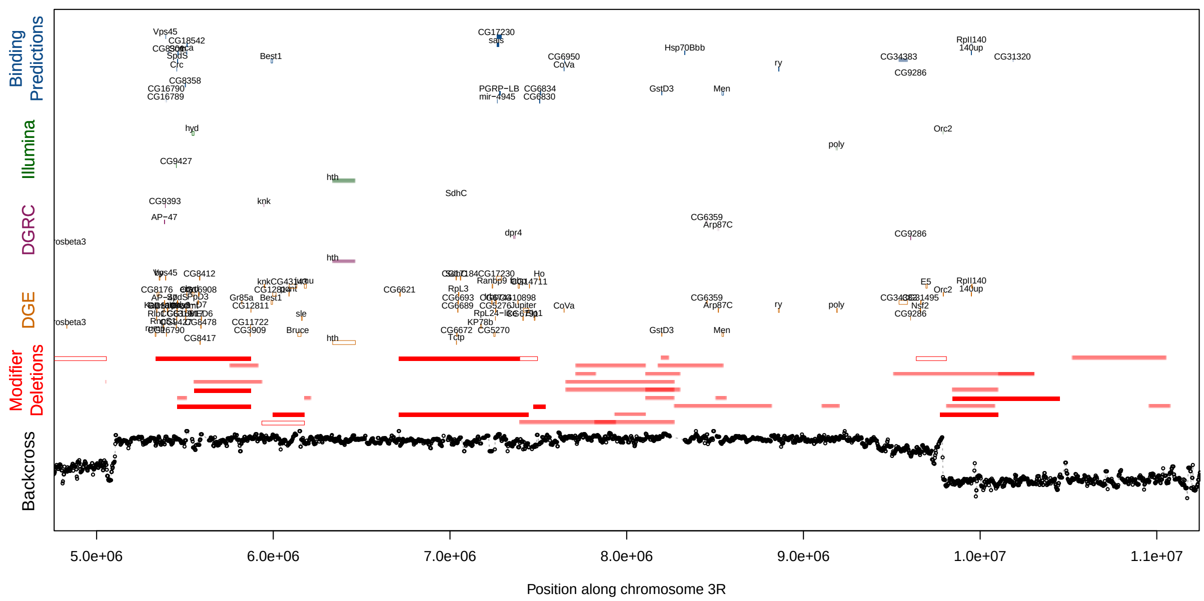
Position along chromosome 3L


Binding Predictions
Illumina
DGRC
DGE
Modifier Deletions
Backcross
17000000
17500000
18000000
18500000
19000000
19500000
Position along chromosome 3L


Binding Predictions
Illumina
DGRC
DGE
Modifier Deletions
Backcross
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7.0e+06
8.0e+06
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1.0e+07
1.1e+07
Position along chromosome 3R

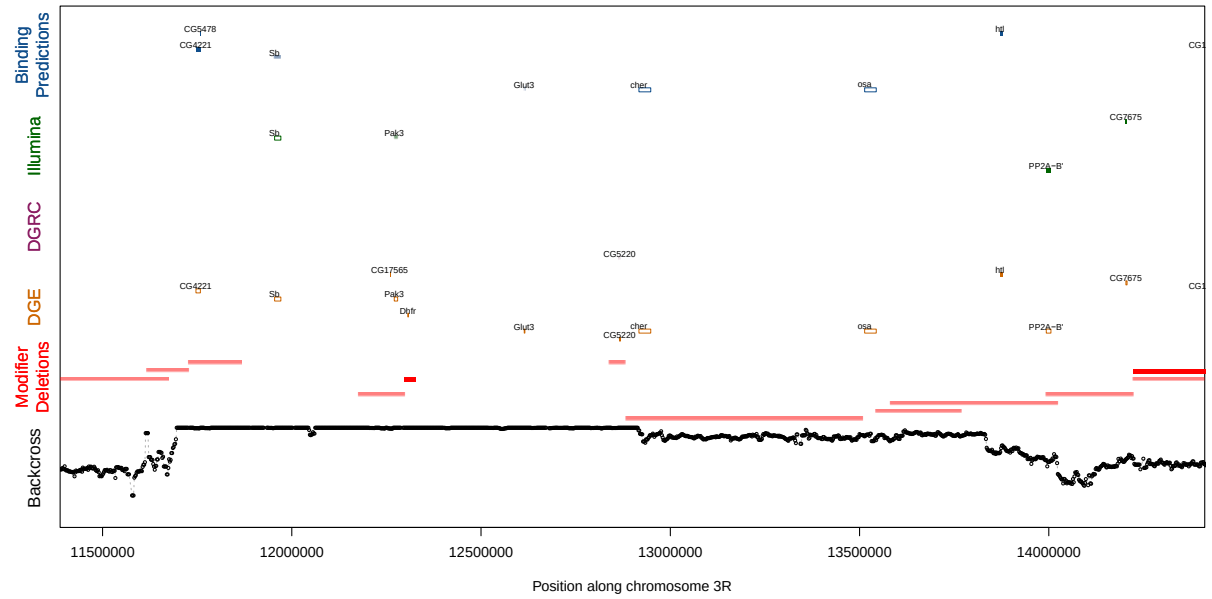

Figure S5 Integrated plots showing results of independent genomic datasets used to investigate the genetic basis of background dependence of the sd^{E3} phenotype. Backcross: Average frequency of the ORE (short-wing) allele across four short-wing introgression lines. Modifier deletions: open bars represent deletions with a significant main effect on the sd^{E3} phenotype; light shaded bars represent deletions with a significant background-dependent effect on the sd^{E3} phenotype; and dark shaded bars represent deletions in which both the main and interaction effects are significant. DGE: open bars represent genes whose transcript counts are influenced by *sd* genotype; light shaded bars represent genes showing evidence of genotype-dependent allelic imbalance; and dark shaded bars represent genes showing evidence of both an overall effect of *sd* genotype and genotype-dependent allelic imbalance. DGRC and Illumina: open bars represent genes showing evidence of an effect of *sd* genotype on expression; light shaded bars represent genes showing evidence of a genotype-by-background interaction effect; and dark shaded bars represent genes showing evidence of both the main and interaction effects. Binding predictions: open bars represent genes predicted to be overall SD binding targets (in at least one of the two genetic backgrounds); light shaded bars represent genes predicted to show differential affinity for SD between the two backgrounds; and dark shaded bars represent genes showing evidence of both overall SD binding and differential affinity between backgrounds. Only genes showing evidence of at least four significant effects across all datasets are shown.