A
St. 8
St. 9
L singleton
Both L&S genes present
S singleton
35%
15%
31%
14%
54%
12%
L only expr.
L & S expr.
S only expr.
N = 932
well-annotated gene (pairs) up at st. 8
B
Stage 8
Stage 9
L activation
S activation
log2 fold increase
C
Stage 9 (all activated)
L>S
S>L
L activation
S activation
log2 fold increase
D
St. 9 primary
St. 9 all
St. 10.5
MZ Z
Proportion
P = 0.01
0.02
0.006
E
All activated
Non-maternal
Whole embryo
Epidermis
Neural progenitor
Ventral mesoderm
Endoderm
Proportion
L singleton
L only expr.
L & S expr.
S only expr.
S singleton
F
Homeolog switch proportion in lineages
All activated genes
Non-maternal genes
St. 9 activation
L only
L & S
S only
G
Proportion of genes St. 10-13
All
Non maternal
L
LS
S
Different homeolog activated in different lineages
Same homeolog(s) activated across lineages
H
log2 L/S expr
Epidermis
Neural progenitor
Ventral mesoderm
Endoderm
J
GO:0005634 Nucleus P = 2.3e-5
GO:0003677 DNA binding P = 8.6e-4
GO:0006351 Transcription P = 0.04
GO:0007275 Development P = 0.04
GO:0000981 DNA-binding TF, Pol II P = 0.01
log2 Fold enrichment
Activation from both subgenomes versus only one subgenome
I
log2 L/S expr
Epidermis
Neural progenitor
Ventral mesoderm
Endoderm
K
P = 0.15
dN/dS (log10 scale)
L
L+S
S
Activation
L
P = 0.23
CDS Percent identity
L
L+S
S
Activation