A
ATAC-seq
H3K27ac
No Ab
St. 8 r1
St. 8 r2
St. 8 r3
St. 9 r1
St. 9 r2
St. 9 r3
St. 8 r1
St. 8 r2
St. 8 r3
St. 8 r4
Pooled
Predicted enhancers
High confidence (N = 5047)
Lower confidence (N = 10607)
Accessible, no H3K27ac enrichment (N = 16823)
+/- 5Kb
RPM
0
0.5
B
Percent of enhancer pairs with syntenic flanking genes
100
80
60
40
20
0
670 / 682
1412 / 1563
926 / 1015
L&S
L specific
S specific
C
ATAC-seq
H3K27ac
All predicted enhancers
St. 8
St. 9
St. 10
St. 12
St. 8
St. 9
St. 10.5
L
S
L&S active
L-specific
S-specific
+/- 5Kb
RPM
0
0.5
D
Differential activity
Conserved activity
RNA-seq
L
S
L>S
L≈S
S>L
TSS
+/- 25Kb
0
200
Predicted enhancer density (bp per 10Kb)
log2 activation
12
E
pou5f3.3.L
sox3.L
sox3.S
pou5f3.3.S
pou5f3.2.L
pou5f3.2.S
St. 5 log2 TPM
8
4
0
Maternal transcription factors
L
S