Supplemental Figure S1 -

Fig. S1. Vulval morphogenesis defects of vab-23 RNAi larvae. (A,B) Nomarski images of RNAi control (A) and vab-23(RNAi) (B) worms at the L4 stage. Scale bar: 10 µm.

Supplemental Figure S2 -

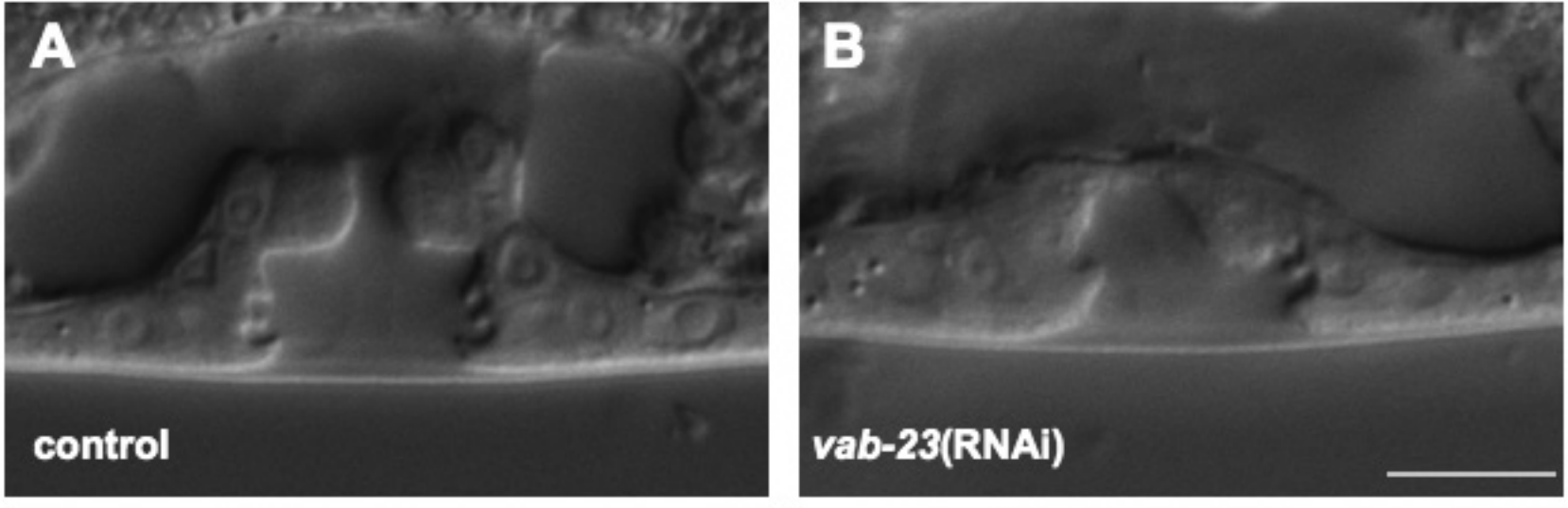
Fig. S2. ChIPseq analysis of the smp-1 and egl-26 loci. (A,B) For each gene, the read coverage is plotted over the locus. The smp-1 locus (A) contains a broad and tall peak with the highest coverage at the end of intron I, whereas the egl-26 locus (B) contains a relatively sharp but smaller peak at position -500. The control ChIP experiments did not display any significant peaks in the two genes (not shown).

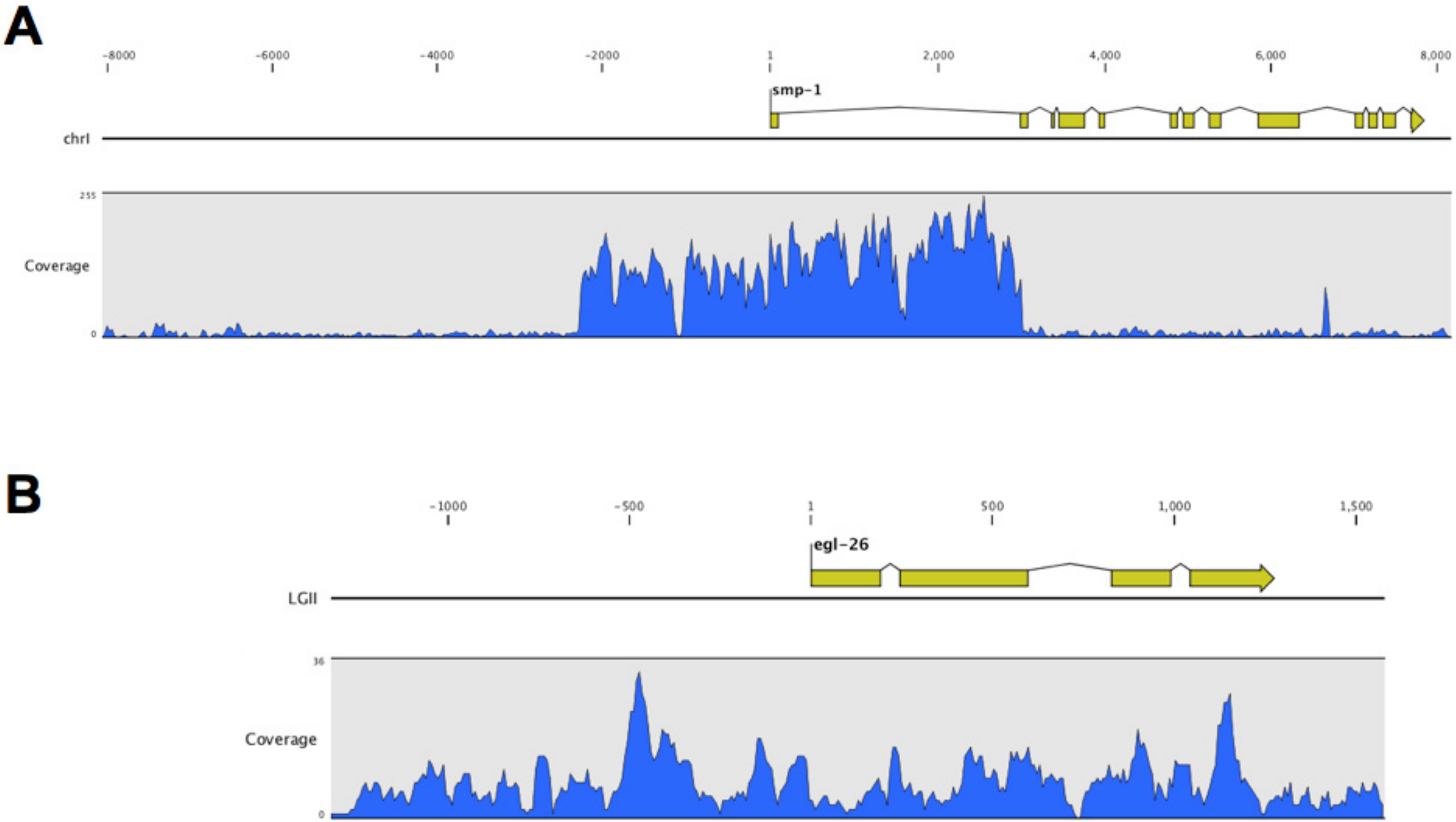
Supplemental Figure S3 -

Fig. S3. Quantification of VAB-23::GFP expression in the sos-1(cs41ts) background. sos-1(cs41); vab-23::gfp and sos-1(+) vab-23::gfp control worms were synchronized by starving them as L1 larvae, transferred to media containing Escherichia coli and allowed to feed for 27 hours at 20°C until they had reached the late L2/early L3 stage. At this time, worms were up-shifted to 25°C. VAB-23::GFP expression was scored 5 and 8 hours later in animals, which had been up-shifted after vulval fate specification and, hence, showed normal induction of P5.p, P6.p and P7.p. The expression of VAB-23::GFP was categorized as normal, reduced and weak/absent as described for Fig. 7.

Supplemental Table S1 -

Table S1. Annotated list of VAB-23 ChIPseq peaks. Peak identification was implemented in an R-script by making use of the ChIPseq package. From the computed coverage, we identified all regions with a coverage of 20 reads or more and merged neighboring regions if they were <100 bases apart. In order to reduce the false positives, we kept only regions that (a) had a less than threefold difference in the ratio of the average coverage with positive-strand-matching and negative-strand-matching reads, and (b) had a width between 50 and 300. As the read length (50) was less than the fragment length, true positive peaks are also expected to have a bias of the coverage contribution of the positive reads to the left-hand-side and negative-reads to the right-hand-side. Therefore, we required additionally (c) that for the ten left-most bases of the peak region, the positive coverage was five reads higher than the negative coverage, and vice verso for the ten right-most bases of the peak region. For each peak region, the position, width, maximum height and the genes located within 2 kb up- or downstream are listed


A
control
B
vab-23(RNAi)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-4000
-2000
1
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4,000
6,000
8,000
smp-1
chrI
255
Coverage
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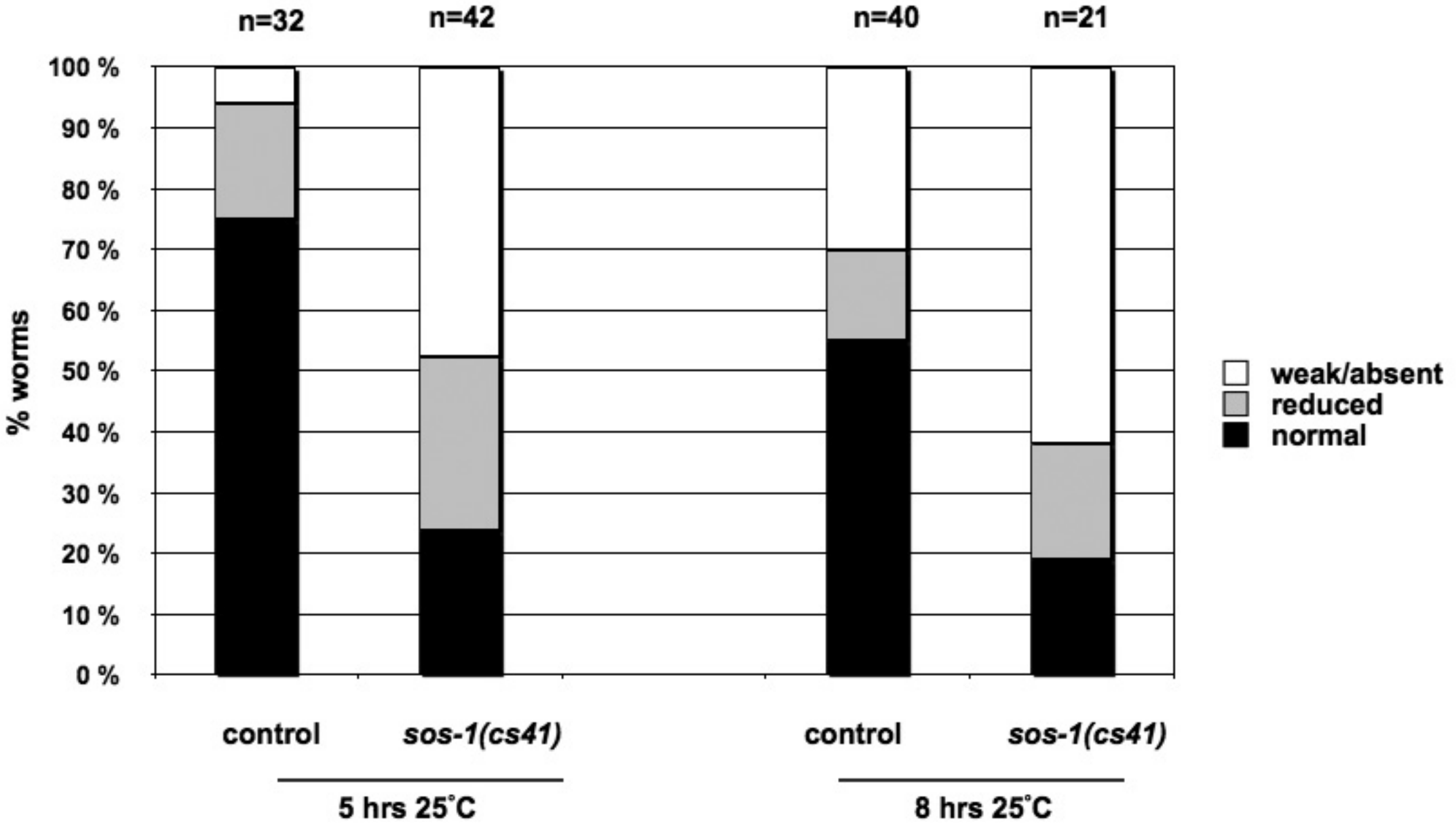
B
-1000
-500
1
500
1,000
1,500
egl-26
LGII
36
Coverage
0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90 %
80 %
70 %
60 %
50 %
40 %
30 %
20 %
10 %
0 %
% worms
weak/absent
reduced
normal
control
sos-1(cs41)
control
sos-1(cs41)
5 hrs 25˚C
8 hrs 25˚C