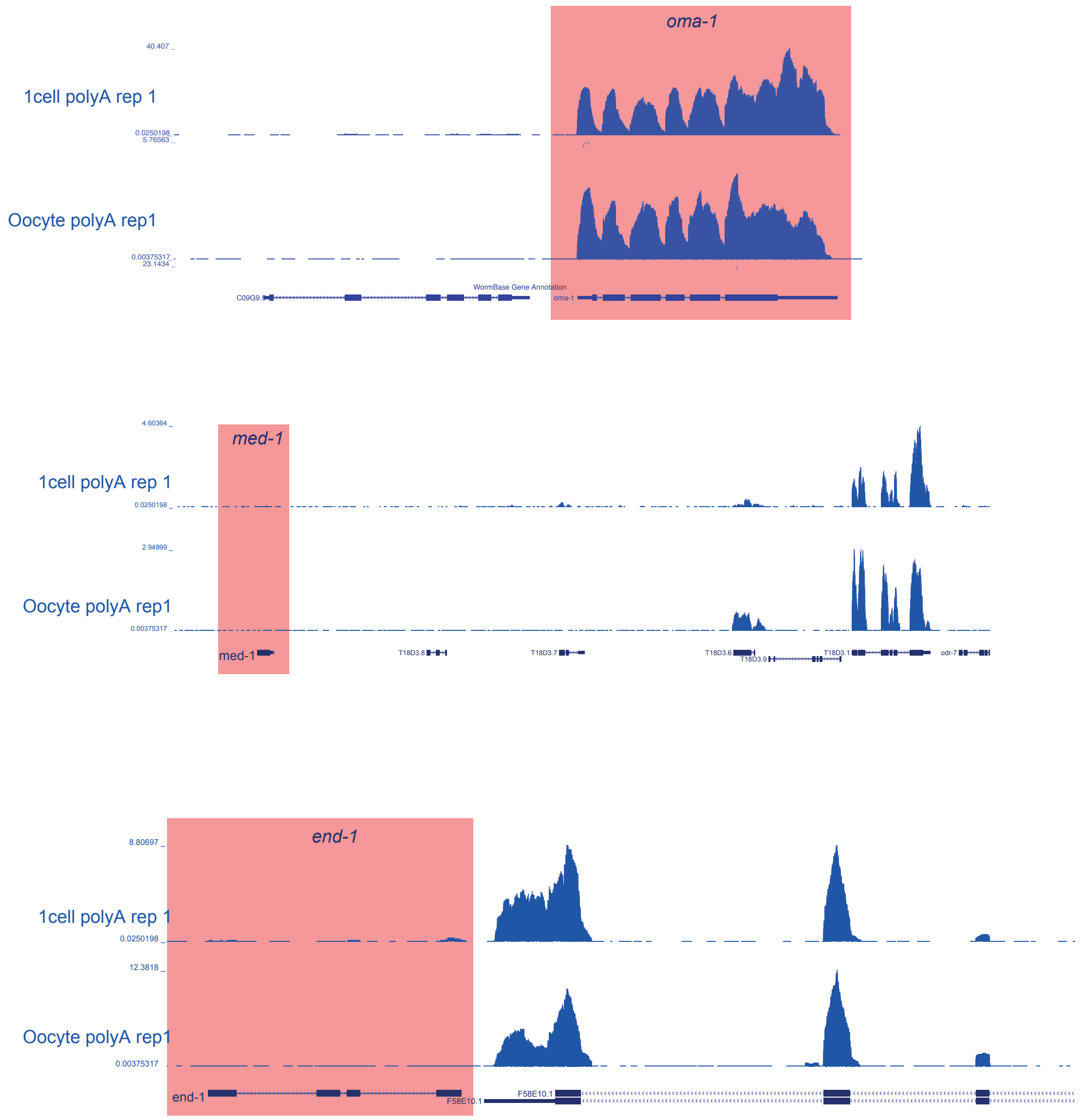
Supplementary Figure S2

A

GENENAME	oocyte_RPKM	1-cell_RPKM	2-cell_RPKM	
oma-2	1522.6	1256.1	611.3	Controls
tba-1	2265.8	1230.9	782.6	
nos-2	375.9	699.2	924.5	
pie-1	396	332.5	183.8	
oma-1	510.5	237.3	222.5	
lmn-1	289.6	219.9	283	
end-3	0.7	1.4	2.7	Zygotic transcripts or tissue markers
hlh-1	0.2	0.9	1.2	
end-1	0.3	0.8	1.1	
msp-56	0.5	0.8	1.7	
msp-81	0.6	0.7	1.5	
elt-2	0.1	0.5	0.4	
ges-1	0	0.2	0.2	
msp-10	0.4	0.2	0.6	
myo-3	0	0.2	0.1	
unc-25	0.2	0.2	0.1	
med-1	0	0.1	2.5	
med-2	0	0.1	3	
myo-2	0	0.1	0	
unc-89	0.1	0.1	0.1	

B



Supplementary Figure S2 | Assessment of sample purity.

A. The purity of our oocytes and 1-cell and 2-cell embryos was validated by checking for marker gene expression. Shown are RPKM as a measure of mRNA expression. Transcripts with ~2 RPKM are virtually only expressed at background level. We did not observe zygotic transcripts that have been described to be expressed in 4- to 8-cell embryos (e.g. *med-1*, *end-3*, *end-1*) and did not detect transcripts which are highly expressed in muscle (*myo-3*, *myo-2, hlh-1*), neurons (*unc-8, unc-25*), gut (*elt-2, ges-1*) and sperm (*msp-10*, *msp-81*, *msp-56, spe-9*). Control genes that are known to be expressed in oocytes and early embryos (*pie-1, oma-1, oma-2, nos-2)* and structural genes (*tba-1, lmn-1)* were found to be highly expressed.

B. Genome browser snapshots of the reads of our oocytes and 1-cell embryos mapping to a gene known to be highly expressed in oocytes and embryos (*oma-1*, marked in red box) and zygotic transcripts (*med-1, end-1;* marked in red box).