Supplementary Table 1. Genes down-regulated in the absence of *zld*.

Gene	symbol	FC	*p* value	Gene	symbol	foldΔ	*p* value	Gene	symbol	FC	*p* value
CG7960*	*bro*	106.0	0.00940	CG7271*		5.7	0.01100	CG12194		2.4	0.00070
CG14915*		101.3	0.01480	CG17725	*Pepck*	5.6	0.01760	CG5093	*Doc3*	2.4	0.03110
CG1502*	*tsq*	86.5	0.01900	CG3839*	*l(1)sc*	5.5	0.00510	CG10962		2.4	0.00250
CG12205*	*Bsq25A*	79.5	0.01580	CG13695	*gk*	5.3	0.02660	CG2047	*ftz*	2.4	0.00230
CG14014*		70.5	0.04580	CG3827*	*sc*	4.9	0.00060	CG13085		2.4	0.03560
CG14317*		65.4	0.01110	CG3758*	*esg*	4.8	0.00800	CG16721		2.4	0.00480
CG6885*		58.6	0.01630	CG13333		4.7	0.05300	CG3961		2.3	0.03880
CG13712*		52.1	0.01660	CG14937		4.6	0.01580	CG1849*	*run*	2.3	0.02120
CG8960*		47.4	0.00860	CG16813		4.3	0.00100	CG13252		2.3	0.00420
CG18269*		43.6	0.00260	CG1480	*bnk*	4.0	0.00280	CG1378*	*tll*	2.3	0.03120
CG31695	*scw*	34.8	0.00500	CG7343	*btsz*	3.7	0.03870	CG30184		2.3	0.05040
CG11582	*tsg like*	30.9	0.01890	CG2961	*Ipod*	3.7	0.00790	CG4210		2.3	0.00540
CG17962	*frs*	27.2	0.01310	CG1046*	*zen*	3.6	0.01040	CG2145		2.3	0.04000
CG15634*		21.5	0.01790	CG16815		3.6	0.00410	CG1623		2.3	0.02720
CG13713*		19.4	0.00280	CG5201	*Dad*	3.5	0.01080	CG18584	*koi*	2.3	0.04990
CG31253		19.3	0.03070	CG33070	*Sxl*	3.5	0.02850	CG17209		2.2	0.00120
CG7178	*wupA*	19.0	0.01360	CG7508	*ato*	3.4	0.00520	CG11275		2.2	0.01100
CG7204*	*Neu2*	18.2	0.01220	CG8066		3.4	0.00350	CG14135		2.2	0.03950
CG10393*	*amos*	17.1	0.00620	CG31743		3.1	0.04080	CG12283	*kek1*	2.2	0.02260
CG6868	*tld*	15.9	0.02390	CG12370		3.0	0.00110	CG31677		2.2	0.00200
CG13000*		15.4	0.00480	CG6494*	*h*	2.9	0.02630	CG16712		2.2	0.04990
CG15876		15.1	0.01050	CG11430	*olf186-F*	2.9	0.00500	CG15480*		2.2	0.01340
CG1944	*Cyp4p2*	15.0	0.00460	CG4702		2.9	0.04750	CG18446		2.1	0.00300
CG13716		14.9	0.00900	CG5133	*Doc1*	2.9	0.04500	CG13427*		2.1	0.04940
CG31607		14.9	0.02970	CG12179		2.9	0.02260	CG2187		2.1	0.03250
CG7428*	*halo*	14.5	0.00770	CG16778	*Tkr*	2.8	0.04080	CG15479		2.1	0.04970
CG10564	*Ac78C*	13.6	0.04070	CG5455		2.8	0.00190	CG18408	*rexin*	2.1	0.04440
CG13711*		13.2	0.04420	CG1368		2.8	0.04280	CG4429	*Rbp2*	2.1	0.02850
CG15382*		10.7	0.00540	CG3973		2.7	0.00110	CG9927	*Art2*	2.1	0.03250
CG7052	*TepII*	10.2	0.00540	CG3767	*Jhl-26*	2.7	0.00080	CG2328	*eve*	2.1	0.00680
CG1048*	*zen2*	10.2	0.02740	CG12011		2.7	0.03420	CG3096*	*Brd*	2.1	0.02350
CG4922*	*sala*	9.5	0.03520	CG31672		2.6	0.00310	CG17364		2.1	0.04840
CG13454		9.4	0.01900	CG32564		2.6	0.05280	CG1515	*l(1) G0155*	2.0	0.00020
CG14426*	*nullo*	9.2	0.01100	CG14112*	*SNCF*	2.5	0.02340	CG6936	*mth*	2.0	0.01950
CG3796	*ac*	8.4	0.01080	CG11833		2.5	0.03550	CG9914		2.0	0.00070
CG17957*	*sry-a*	8.0	0.00830	CG14427*		2.5	0.02610	CG13609		2.0	0.01330
CG1641*	*sisA*	7.2	0.01430	CG5993	*os*	2.5	0.04200	CG9506	*slam*	2.0	0.01410
CG32680	*spri*	6.5	0.01720	CG12875		2.4	0.00820	CG18522		2.0	0.02730
CG8050*	*Cys*	6.1	0.03930	CG13049		2.4	0.01470	CG15848	*Scp1*	2.0	0.00180
G9885	*dpp*	5.7	0.03530	CG6058	*Ald*	2.4	0.03640	CG12701	*zld*	4.5	0.00010

Supplementary Table 2. Distribution of TAGteam sites near transcription start sites.

absent	**0.2**	**0.4**	**0.5**	**0.8**	**1**	**1.2**	**1.4**	**1.6**	**1.8**	**2**	**FC**
CG7672											A
CG11514	**x**										A
CG13977											A
CG1283											A
CG10605											A
CG6113											A
CG13636										**x**	A
CG10704											A
CG11426					**x**						A
CG9460											A
CG8193											A
CG4984											A
CG12817											A
CG10300										**x**	A
CG8713	**xx**										A
CG15786											A
CG8850								**x**			A
CG13499								**x**		**x**	A
CG32048											A
CG7241											A
CG12565											A
CG1092											A
CG12002			**x**				**x**				A
CG11175											A
CG5973											A
CG17914									**x**		A
CG3544											A
CG3074											A
CG5171				**x**	**x**					**xxx**	A
CG4576											A
CG9444											A
CG31757											A
CG2191											A
CG13699											A
CG1124		**x**	**x**		**x**						A
CG14253						**x**				**x**	A
CG10086		**x**									A

absent	**0.2**	**0.4**	**0.5**	**0.8**	**1**	**1.2**	**1.4**	**1.6**	**1.8**	**2**	**FC**
CG10175										**x**	A
CG13506											A
CG4914											A
CG15105		**x**	**x**								A
CG5476				**x**		**x**					A

≥ 2 fold	**0.2**	**0.4**	**0.5**	**0.8**	**1**	**1.2**	**1.4**	**1.6**	**1.8**	**2**	**FC**
CG18522											2.0
slam											2.0
CG13609							**x**				2.0
CG17364		**x**			**x**						2.1
Brd	**x**		**x**								2.1
eve	**x**				**x**			**x**			2.1
Rbp2											2.1
rexin								**x**		**x**	2.1
CG15479											2.1
CG2187											2.1
CG13427	**xx**										2.1
CG18446								**xx**			2.1
CG15480	**x**	**x**									2.2
CG16712					**x**						2.2
Kek1									**x**		2.2
CG14135											2.2
CG11275		**x**				**x**					2.2
CG17209						**x**					2.2
koi					**xx**		**x**				2.3
CG1623	**x**	**x**				**x**					2.3
CG2145			**x**								2.3
CG4210			**x**			**x**					2.3
CG30184											2.3
tll	**x**	**x**				**x**					2.3
CG13252							**x**				2.3
run	**x**			**x**					**x**		2.3
CG3961											2.3
CG16721					**x**				**x**		2.4
ftz	**x**	**xx**				**x**					2.4
CG10962											2.4

Supplementary Table 2. (Continued)

≥ 2 fold	0.2	0.4	0.6	0.8	1	1.2	1.4	1.6	1.8	2	FC
Doc3	x										2.4
CG12194					xx						2.4
Ald	x				x						2.4
CG13049					x		x				2.4
CG12875						x		x		x	2.4
os									x	xx	2.5
CG14427	xx										2.5
CG11833					xx						2.5
SNCF	xx										2.5
CG32564					x						2.6
CG12011				x							2.7
Jhl-26	x						x				2.7
CG3973				x							2.7
CG1368											2.8
CG5455											2.8
Tkr											2.8
CG12179											2.9
Doc1	x										2.9
CG4702			x	x							2.9
h											2.9
CG12370											3.0
CG8066										x	3.4
ato		xx									3.4
Sxl											3.5
Dad											3.5
CG16815	x		x								3.6
zen	x	x					xxxx				3.6
btsz	xx										3.7
bnk	xx	x									4.0
CG16813		xx									4.3
CG14937	xxx										4.6
CG13333	xx										4.7
esg		x	x								4.8
sc	xxxx										4.9
gk		x			x	x					5.3
L(1)sc	xx	x									5.5
Pepck											5.6
CG7271	xx										5.7

≥ 2 fold	0.2	0.4	0.6	0.8	1	1.2	1.4	1.6	1.8	2	FC
dpp	xx	x								xx	5.7
Cys						x	x				6.1
spri											6.5
sisA	xx	xx		xx							7.2
sry-a	xx	x				xx					8.0
CG3796		x									8.4
nullo											9.2
CG13454	x										9.4
sala	xxx										9.5
zen2	x		xx	x							10.2
TepII											10.2
CG15382	xx										10.7
CG13711		xx									13.2
Ac78C											13.6
halo	xx										14.5
CG31607										x	14.9
CG13716											14.9
Cyp4p2											15.0
CG15876	xx								x	x	15.1
CG13000	x					x					15.4
tld	x	x	x					x			15.9
Neu2				x	x						18.2
wupA											19.0
CG31253	xx										19.3
CG13713	xx				x	x					19.4
CG15634	xx			x							21.5
frs	xx										27.2
tsg like	xx										30.9
CG18269	xx					x					43.6
CG8960											47.4
CG13712		x									52.1
CG6885											58.6
CG14317	xx	xxx									65.4
CG14014	x				xx						70.5
Bsq25A	xx										79.5
tsq	xxx	x									86.5
CG14915	xx				x						101.3

Table S1. Genes down-regulated in the absence of *zld*. Fold change (FC) was determined as the ratio of wt mean/M^- *zld* mean from three biological replicas. Genes with a fold change > 2 and a p-value < 0.05 were defined as significantly down-regulated. These genes were evenly distributed amongst the chromosome arms. Annotated genes are color coded by function: sex determination in green, cellular blastoderm formation in orange, and embryonic patterning in pink. The asterisks* denote genes that are also on the De Renzis *et al.*[6] (2007) list of early zygotic genes.

Table S2. Distribution of TAGteam sites near transcription start sites. TAGteam sites (CAGGTAG, TAGGTAG, CAGGCAG, CAGGTAA) were located in 200 bp intervals upstream of the transcription start site (up to 2 Kb) using FlyEnhancer.org. Genes from two categories were analyzed: genes down-regulated at least two fold in M^- *zld* embryos (in yellow), and genes absent in 1-2 hour embryos, but present in post-blastoderm genes[5] (in gray). Note that 43% of the down-regulated genes have at least one TAGteam site within 200 bp upstream of their start sites compared to 5% of the post-blastoderm genes[5] ($p=1x10^{-6}$; Fisher exact test). The genes down-regulated > 5 fold tend to have clusters of TAGteam sites within 200 bp of the start site.