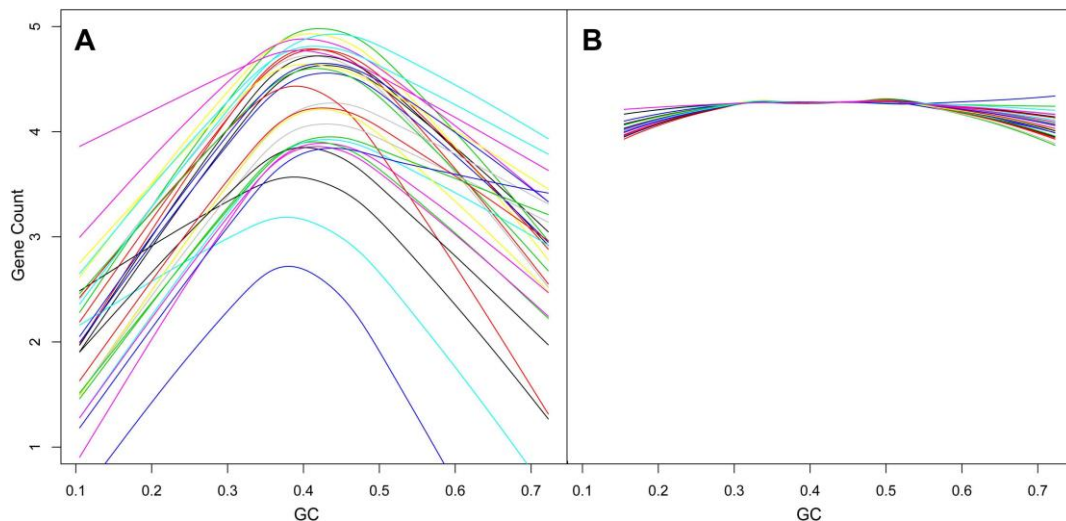
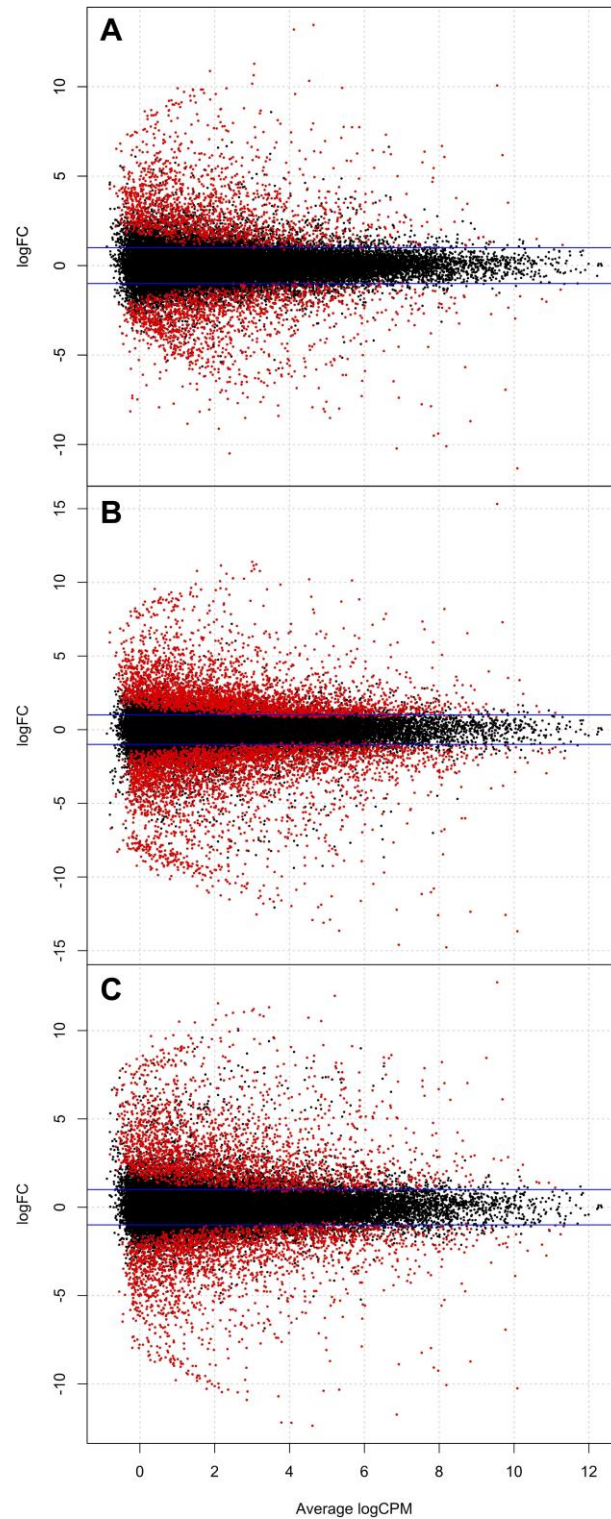


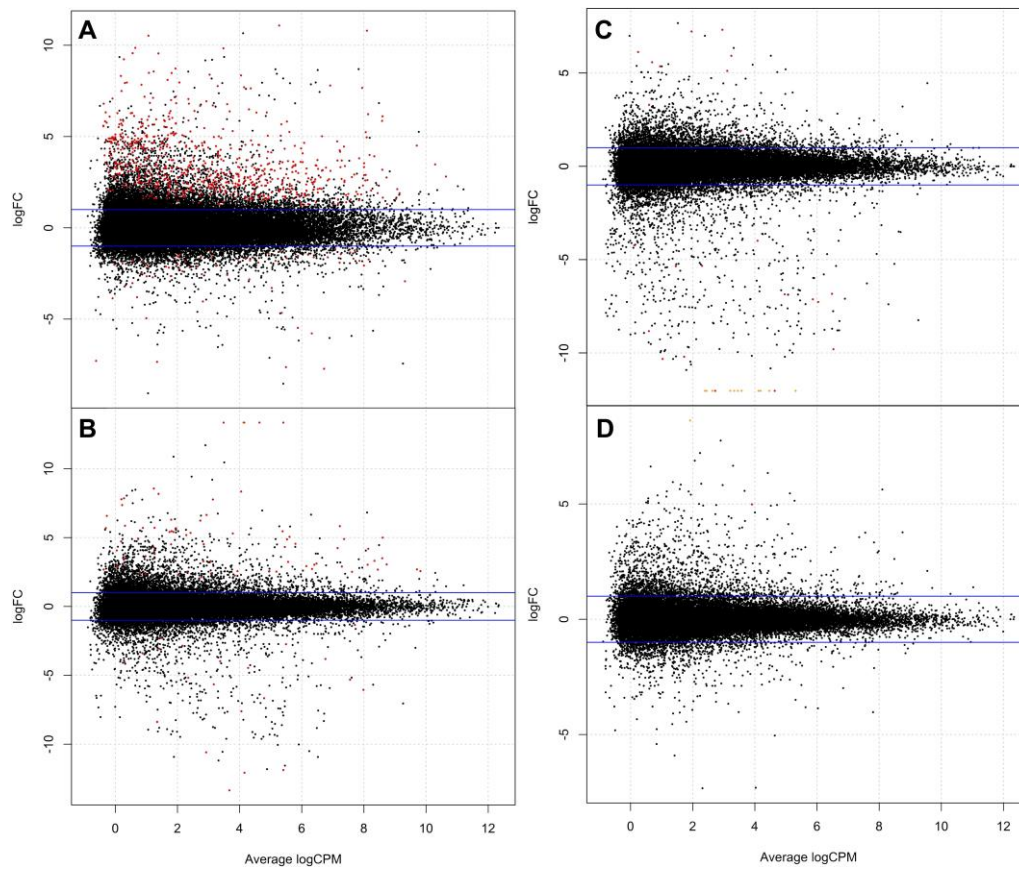
**Fig. S1.** Gene expression trajectories from short-day to long-day conditions for (A) E-strain Wnt signaling genes, (B) Z-strain Wnt signaling genes, (C) E-strain ecdysone-related genes, (D) Z-strain ecdysone-related genes, (E) E-strain insulin signaling genes, and (F) Z-strain insulin signaling genes.



**Fig. S2.** GC normalization in EDaseq. (A) Lowess regression of log gene-level counts on GC content for each library. (B) Full quantile within and between lane normalization for each library.



**Fig. S3.** MA plot of differential expression within strain shown as log-fold change of expression versus average log counts per million. (A) E-strain diapause maintenance to day 1, (B) E-strain diapause maintenance to day 7, (C) Z-strain diapause maintenance to day 1, (D) Z-strain diapause maintenance to day 7. Red dots are significantly differentially expressed at  $FDR < 0.01$ .



**Fig. S4.** MA plot of differential expression between strains (A) in diapause maintenance, (B) on day 1, and (C) on day 7, shown as log-fold change of expression versus average log counts per million. Red dots are significantly differentially expressed at  $FDR < 0.01$ .

**Table S1. Enriched GO Terms and KEGG Pathways for Differentially Expressed Genes Between E and Z Strains (P-value < 0.001)**

Category	Term	Count	Size	P-value
<b>Day1</b>				
GO: biological process	proteasome-mediated ubiquitin-dependent protein catabolic process	30	83	8.39E-06
GO: biological process	cellular protein catabolic process	43	146	4.24E-05
GO: biological process	protein-DNA complex subunit organization	17	39	5.12E-05
GO: biological process	modification-dependent protein catabolic process	42	145	7.95E-05
GO: biological process	macromolecule catabolic process	54	210	2.44E-04
GO: biological process	nucleosome assembly	8	13	2.92E-04
GO: biological process	DNA endoreduplication	8	13	2.92E-04
GO: biological process	mitotic spindle assembly checkpoint	6	8	3.88E-04
GO: biological process	spindle checkpoint	6	8	3.88E-04
GO: biological process	pyrimidine-containing compound metabolic process	10	20	4.92E-04
GO: biological process	DNA packaging	19	54	5.57E-04
GO: biological process	regulation of imaginal disc-derived wing size	8	14	5.85E-04
GO: biological process	regulation of cell cycle process	39	146	8.57E-04
GO: biological process	regulation of tube size	13	32	8.64E-04
GO: biological process	canonical Wnt signaling pathway	8	21	1.35E-02*
GO: biological process	regulation of Wnt signaling pathway	15	54	2.29E-02*
GO: molecular function	glucose transmembrane transporter activity	8	11	5.78E-05
GO: molecular function	copper ion binding	10	17	9.61E-05
GO: molecular function	monosaccharide transmembrane transporter activity	9	17	6.31E-04
GO: molecular function	calcium ion binding	37	135	9.43E-04
KEGG Pathway	Proteasome	23	33	6.69E-12
KEGG Pathway	Ascorbate and aldarate metabolism	9	13	2.82E-05
KEGG Pathway	Retinol metabolism	8	13	2.76E-04
KEGG Pathway	DNA replication	12	26	3.13E-04
KEGG Pathway	Non-homologous end-joining	4	4	6.94E-04
<b>Day7</b>				
GO: biological process	amino sugar metabolic process	18	55	2.27E-07
GO: biological process	chitin-based cuticle development	22	79	2.62E-07
GO: biological process	chitin metabolic process	15	46	2.48E-06
GO: biological process	cuticle chitin catabolic process	3	3	5.82E-04
GO: biological process	regulation of hormone levels	10	43	2.34E-03
GO: biological process	regulation of tube size	10	44	2.81E-03
GO: biological process	regulation of tube architecture, open tracheal system	13	67	3.17E-03
GO: biological process	homophilic cell adhesion	7	25	3.48E-03
GO: biological process	cuticle pattern formation	7	25	3.48E-03
GO: biological process	aminoglycan catabolic process	5	14	4.25E-03
GO: biological process	pyrimidine nucleotide biosynthetic process	4	9	4.33E-03
GO: biological process	glucosamine-containing compound catabolic process	4	9	4.33E-03

GO: biological process	pyrimidine nucleoside monophosphate biosynthetic process	3	5	5.12E-03
GO: biological process	intercellular transport	3	5	5.12E-03
GO: biological process	septate junction assembly	7	28	6.88E-03
GO: biological process	negative regulation of hormone metabolic process	2	2	6.98E-03
GO: biological process	negative regulation of sequestering of calcium ion	2	2	6.98E-03
GO: biological process	detoxification of arsenic-containing substance	2	2	6.98E-03
GO: biological process	organonitrogen compound metabolic process	64	572	7.93E-03
GO: biological process	cellular hormone metabolic process	7	29	8.43E-03
GO: biological process	system process	35	279	9.17E-03
GO: biological process	activation of immune response	3	6	9.60E-03
GO: biological process	'de novo' pyrimidine nucleobase biosynthetic process	3	6	9.60E-03
GO: biological process	pyrimidine nucleoside biosynthetic process	3	6	9.60E-03
GO: molecular function	structural constituent of chitin-based cuticle	6	7	2.32E-06
GO: molecular function	chitin binding	13	39	1.22E-05
GO: molecular function	extracellular matrix structural constituent	7	13	3.64E-05
GO: molecular function	structural constituent of chitin-based larval cuticle	11	32	4.16E-05
GO: molecular function	serine-type endopeptidase activity	17	69	5.16E-05
GO: molecular function	serine hydrolase activity	20	91	6.74E-05
GO: molecular function	iron ion binding	16	67	1.28E-04
GO: molecular function	monosaccharide transmembrane transporter activity	7	17	3.04E-04
GO: molecular function	molybdenum ion binding	3	3	6.34E-04
KEGG Pathway	Drug metabolism - other enzymes	8	29	4.35E-04

\* Asterix indicates *P*-value <0.05

**Table S2. Gene enrichment analysis table for the seven significant STEM profiles (Bonferroni corrected P-value cutoff  $\leq 0.0001$ )**

Strain	Profile	GO Category Name	#Genes Category	#Genes Assigned	#Genes Expected	#Genes Enriched	p-value	Corrected p-value	Fold
E	1	single-organism developmental process	1967	83	30.8	52.2	2.70E-15	1.10E-11	2.7
E	1	macromolecule metabolic process	1960	82	30.6	51.4	6.30E-15	2.70E-11	2.7
E	1	regulation of biological process	2220	84	34.7	49.3	6.10E-13	2.60E-09	2.4
E	1	regulation of cellular process	2066	79	32.3	46.7	1.70E-12	7.30E-09	2.4
E	1	organic substance metabolic process	2606	91	40.7	50.3	5.40E-12	2.30E-08	2.2
E	1	endopeptidase activity	168	19	2.6	16.4	2.90E-11	1.20E-07	7.2
E	1	proteolysis	330	26	5.2	20.8	3.10E-11	1.30E-07	5
E	1	anatomical structure development	1064	49	16.6	32.4	6.00E-11	2.50E-07	2.9
E	1	homophilic cell adhesion via plasma membrane adhesion molecules	29	9	0.5	8.5	4.20E-10	1.80E-06	19.8
E	1	developmental process involved in reproduction	520	31	8.1	22.9	4.70E-10	2.00E-06	3.8
E	1	anatomical structure morphogenesis	900	42	14.1	27.9	9.00E-10	3.80E-06	3
E	1	proteasome regulatory particle	22	8	0.3	7.7	9.40E-10	4.00E-06	23.3
E	1	plasma membrane	417	27	6.5	20.5	1.00E-09	4.30E-06	4.1
E	1	cellular macromolecule metabolic process	1726	63	27	36	1.60E-09	6.90E-06	2.3
E	1	single organism reproductive process	548	31	8.6	22.4	1.70E-09	7.00E-06	3.6
E	1	macromolecule catabolic process	214	19	3.3	15.7	1.80E-09	7.70E-06	5.7
E	1	negative regulation of cellular process	756	37	11.8	25.2	2.50E-09	1.00E-05	3.1
E	1	peptidase activity, acting on L-amino acid peptides	268	21	4.2	16.8	2.50E-09	1.10E-05	5
E	1	primary metabolic process	2469	80	38.6	41.4	2.70E-09	1.10E-05	2.1
E	1	protein binding	1272	51	19.9	31.1	2.80E-09	1.20E-05	2.6
E	1	ubiquitin-dependent protein catabolic process	131	15	2	13	2.80E-09	1.20E-05	7.3
E	1	peptidase activity	274	21	4.3	16.7	3.80E-09	1.60E-05	4.9
E	1	modification-dependent macromolecule catabolic process	136	15	2.1	12.9	4.80E-09	2.00E-05	7.1
E	1	modification-dependent protein catabolic process	136	15	2.1	12.9	4.80E-09	2.00E-05	7.1
E	1	proteolysis involved in cellular protein catabolic process	136	15	2.1	12.9	4.80E-09	2.00E-05	7.1
E	1	cellular component organization	1534	57	24	33	5.10E-09	2.10E-05	2.4
E	1	protein catabolic process	99	13	1.5	11.5	5.90E-09	2.50E-05	8.4
E	1	proteasome-mediated ubiquitin-dependent protein catabolic process	83	12	1.3	10.7	7.40E-09	3.10E-05	9.2
E	1	proteasomal protein catabolic process	84	12	1.3	10.7	8.50E-09	3.60E-05	9.1
E	1	cellular developmental process	1249	49	19.5	29.5	1.10E-08	4.60E-05	2.5
E	1	intracellular part	3372	98	52.7	45.3	1.20E-08	5.00E-05	1.9
E	1	negative regulation of biological process	844	38	13.2	24.8	1.40E-08	5.90E-05	2.9
E	1	calcium-dependent cell-cell adhesion via plasma membrane cell adhesion molecules	21	7	0.3	6.7	2.20E-08	9.30E-05	21.3
E	2	nucleus	1056	48	17.1	30.9	4.80E-10	2.00E-06	2.8
E	2	protein catabolic process	99	14	1.6	12.4	9.20E-10	3.90E-06	8.7
E	2	single-organism developmental process	1967	71	31.9	39.1	1.20E-09	5.10E-06	2.2
E	2	modification-dependent macromolecule catabolic process	136	15	2.2	12.8	7.80E-09	3.30E-05	6.8
E	2	modification-dependent protein catabolic process	136	15	2.2	12.8	7.80E-09	3.30E-05	6.8
E	2	proteolysis involved in cellular protein catabolic process	136	15	2.2	12.8	7.80E-09	3.30E-05	6.8
E	2	proteasome-mediated ubiquitin-dependent protein catabolic process	83	12	1.3	10.7	1.10E-08	4.70E-05	8.9
E	2	proteasomal protein catabolic process	84	12	1.4	10.6	1.30E-08	5.40E-05	8.8
E	2	anatomical structure development	1064	45	17.3	27.7	1.40E-08	5.90E-05	2.6
E	2	cellular response to DNA damage stimulus	234	19	3.8	15.2	1.40E-08	6.10E-05	5
E	2	macromolecule catabolic process	214	18	3.5	14.5	2.00E-08	8.40E-05	5.2

E	3	oxidoreductase activity	380	42	6.1	35.9	3.00E-22	1.30E-18	6.9
E	3	oxidation-reduction process	325	33	5.2	27.8	1.00E-16	4.30E-13	6.3
E	3	single-organism metabolic process	1304	61	20.9	40.1	4.60E-13	1.90E-09	2.9
E	3	integral component of membrane	613	36	9.8	26.2	6.00E-11	2.50E-07	3.7
E	3	organic acid metabolic process	264	23	4.2	18.8	9.10E-11	3.80E-07	5.4
E	3	oxoacid metabolic process	264	23	4.2	18.8	9.10E-11	3.80E-07	5.4
E	3	carboxylic acid metabolic process	249	22	4	18	1.80E-10	7.40E-07	5.5
E	3	small molecule metabolic process	498	30	8	22	1.20E-09	5.20E-06	3.8
E	3	carbohydrate metabolic process	207	18	3.3	14.7	9.80E-09	4.10E-05	5.4
E	3	organonitrogen compound metabolic process	431	26	6.9	19.1	1.50E-08	6.20E-05	3.8
E	4	oxidoreductase activity	380	22	3.8	18.2	7.60E-11	3.20E-07	5.8
E	4	oxidation-reduction process	325	20	3.2	16.8	1.80E-10	7.80E-07	6.2
E	4	single-organism catabolic process	190	14	1.9	12.1	9.80E-09	4.10E-05	7.4

**Table S3. Significance (FDR) values for differentially expressed genes between E and Z strain moths in long-day conditions**

Gene Symbol	Contigs	FDR Day 1	FDR Day 7
<b>Ecdysone</b>			
<i>Usp</i>	comp37290_c0_seq1*; comp10851_c0_seq1; comp108932_c0_seq1	8.26E-03	5.41E-03
<i>Spo</i>	comp30567_c0_seq1	4.63E-07	9.21E-10
<i>Phm</i>	comp24584_c0_seq1	3.76E-06	2.69E-05
<i>Eip75B</i>	comp18210_c0_seq1; comp11010_c0_seq2*	6.48E-03	-
<i>Eip78C</i>	comp122877_c0_seq1; comp151979_c0_seq1	-	-
<i>EcR</i>	comp34369_c0_seq1	1.01E-03	-
<i>Nvd</i>	comp8057_c0_seq2	8.88E-03	2.62E-03
<b>Circadian</b>			
<i>Clk</i>	comp120765_c0_seq1	-	-
<i>Cpo</i>	comp89983_c0_seq1	-	-
<i>Cyc</i>	comp120765_c0_seq1	-	-
<i>Pdp1</i>	comp36140_c0_seq1*; comp15799_c0_seq1*	9.33E-03; 8.35E-04	-
<i>Tim</i>	comp27153_c0_seq1	-	-
<i>Vri</i>	comp23405_c0_seq1	-	-
<i>Per</i>	comp7426_c0_seq1; comp8184_c0_seq1; comp97089_c0_seq1	-	-
<b>Cell Cycle</b>			
<i>Cdk4</i>	comp127995_c0_seq1*; comp233925_c0_seq1*	2.61E-03; 1.22E-04	-
<i>CycB</i>	comp21605_c0_seq1	1.32E-07	5.73E-04
<i>Pcna</i>	comp9566_c0_seq1	2.38E-06	-
<i>Polo</i>	comp21903_c0_seq1*; comp10877_c0_seq1*	2.22E-03; 1.56E-03	-
<i>CycA</i>	comp29198_c0_seq1	-	-
<i>Trbl</i>	comp20015_c0_seq1; comp25406_c0_seq1	-	-
<b>Heat Shock</b>			
<i>Hsp83</i>	comp22537_c0_seq1	5.03E-04	-



<i>Hsp60</i>	comp19138_c0_seq1	8.82E-03	-
<i>Hsp70Bc</i>	comp418731_c0_seq1; comp427912_c0_seq1	-	-
<i>Hsp70Ab</i>	comp9675_c0_seq1	-	-
<b>Canonical Wnt Signaling</b>			
<i>Fz3</i>	comp15297_c0_seq1	3.93E-03	-
<i>Arm</i>	comp17057_c0_seq1	9.38E-03	-
<i>Smo</i>	comp14234_c0_seq1	7.71E-03	-
<i>Wg</i>	comp13981_c0_seq1	1.91E-03	-
<i>Wnt6</i>	comp25466_c0_seq1	-	-
<i>Hs6st</i>	comp78453_c0_seq1	-	-
<i>Gro</i>	comp8218_c0_seq1	-	-
<i>Pan</i>	-	7.04E-03	-
<b>Insulin</b>			
<i>Akt1</i>	comp18543_c0_seq1; comp38567_c0_seq1; comp53008_c0_seq1; comp10465_c0_seq1	-	-
<i>Foxo</i>	comp19046_c0_seq1	-	-
<i>InR</i>	comp25612_c0_seq1; comp14287_c0_seq1; comp16806_c0_seq1; comp22132_c0_seq1; comp223642_c0_seq1	-	-
<i>Pi3k</i>	comp190582_c0_seq1; comp28365_c0_seq1; comp31462_c0_seq1	-	-
<i>Pten</i>	comp6369_c0_seq1; comp7648_c0_seq1	-	-
<i>SNF4y</i>	comp26437_c0_seq1	-	3.11E-03
<i>Tor</i>	comp16536_c0_seq1; comp17899_c0_seq1; comp19143_c0_seq1; comp26489_c0_seq1	-	-

\*Some genes had multiple transcripts, asterix denotes which transcript shows differential expression

**Table S4. Short read archive accession numbers**

<b>Strain</b>	<b>Days After Long-day Exposure</b>	<b>Sample Name</b>	<b>SRA Accession</b>
E	0	Shortday_E_biologicalrep1	SRX1206058
E	0	Shortday_E_biologicalrep2	SRX1206872
E	0	Shortday_E_biologicalrep3	SRX1211504
E	0	Shortday_E_biologicalrep4	SRX1211546
E	0	Shortday_E_biologicalrep5	SRX1211572
Z	0	Shortday_Z_biologicalrep1	SRX1211612
Z	0	Shortday_Z_biologicalrep2	SRX1211648
Z	0	Shortday_Z_biologicalrep3	SRX1211686
Z	0	Shortday_Z_biologicalrep4	SRX1211701
Z	0	Shortday_Z_biologicalrep5	SRX1211703
E	1	Longday1_E_biologicalrep1	SRX1211704
E	1	Longday1_E_biologicalrep2	SRX1211706
E	1	Longday1_E_biologicalrep3	SRX1211707
E	1	Longday1_E_biologicalrep4	SRX1211711
E	1	Longday1_E_biologicalrep5	SRX1211709
Z	1	Longday1_Z_biologicalrep1	SRX1211714
Z	1	Longday1_Z_biologicalrep2	SRX1211718
Z	1	Longday1_Z_biologicalrep3	SRX1211716
Z	1	Longday1_Z_biologicalrep4	SRX1211720
Z	1	Longday1_Z_biologicalrep5	SRX1211723
E	7	Longday7_E_biologicalrep1	SRX1211725
E	7	Longday7_E_biologicalrep2	SRX1211741
E	7	Longday7_E_biologicalrep3	SRX1211744
E	7	Longday7_E_biologicalrep4	SRX1211746
E	7	Longday7_E_biologicalrep5	SRX1211748
Z	7	Longday7_Z_biologicalrep1	SRX1211750
Z	7	Longday7_Z_biologicalrep2	SRX1211752
Z	7	Longday7_Z_biologicalrep3	SRX1211782
Z	7	Longday7_Z_biologicalrep4	SRX1211784
Z	7	Longday7_Z_biologicalrep5	SRX1211786