

Supplementary figures

Figure S1: Difference in mean % methylated CpG sites (mCpGs) between time points in QDL (panel A) and WDL (panel B), $\pm 95\%$ confidence intervals (estimated using a linear model); positive values mean higher % mCpGs at the later time point.

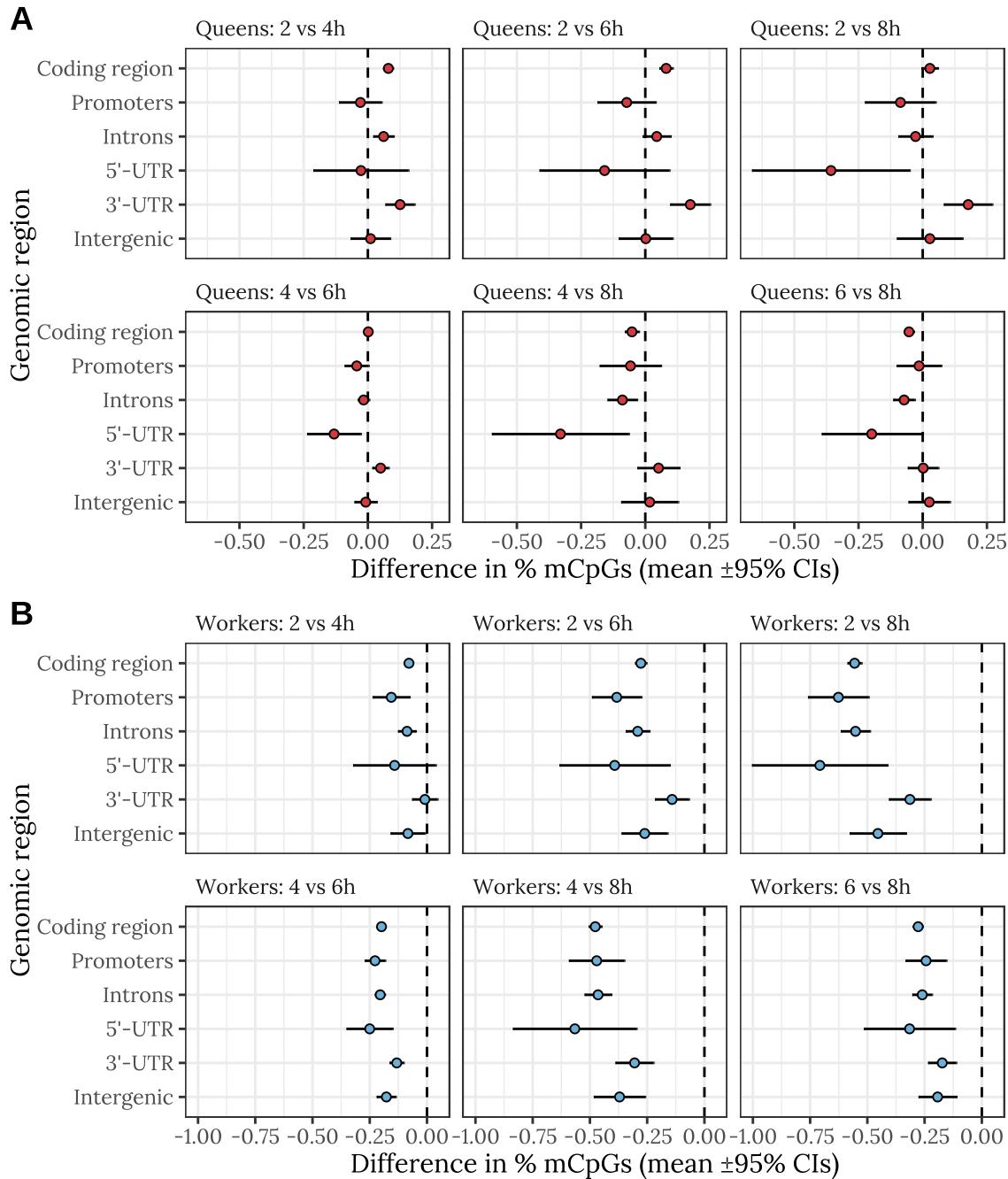


Figure S2: Similar heatmap to Figure 1C, except showing all CpG sites with at least 2.7% methylated sequencing reads ($n = 110,626$ sites).

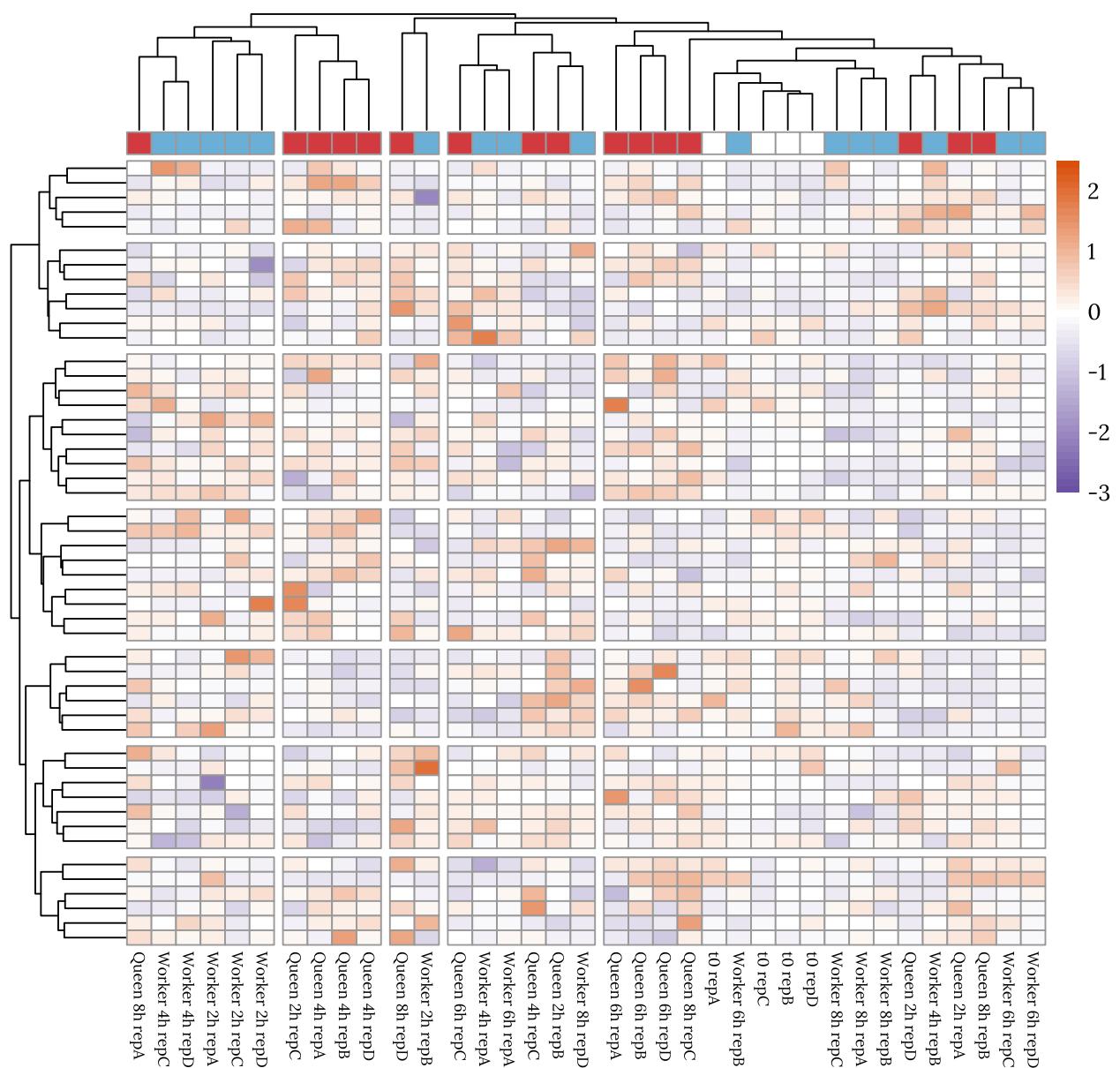


Figure S3: GO and KEGG terms that are enriched among genes showing QDL- or WDL-biased methylation (as measured by the difference in mean % CpG methylation for all sites in the introns, exons, and promoters of the gene; red: QDL-biased, blue: QDL-biased). Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction.

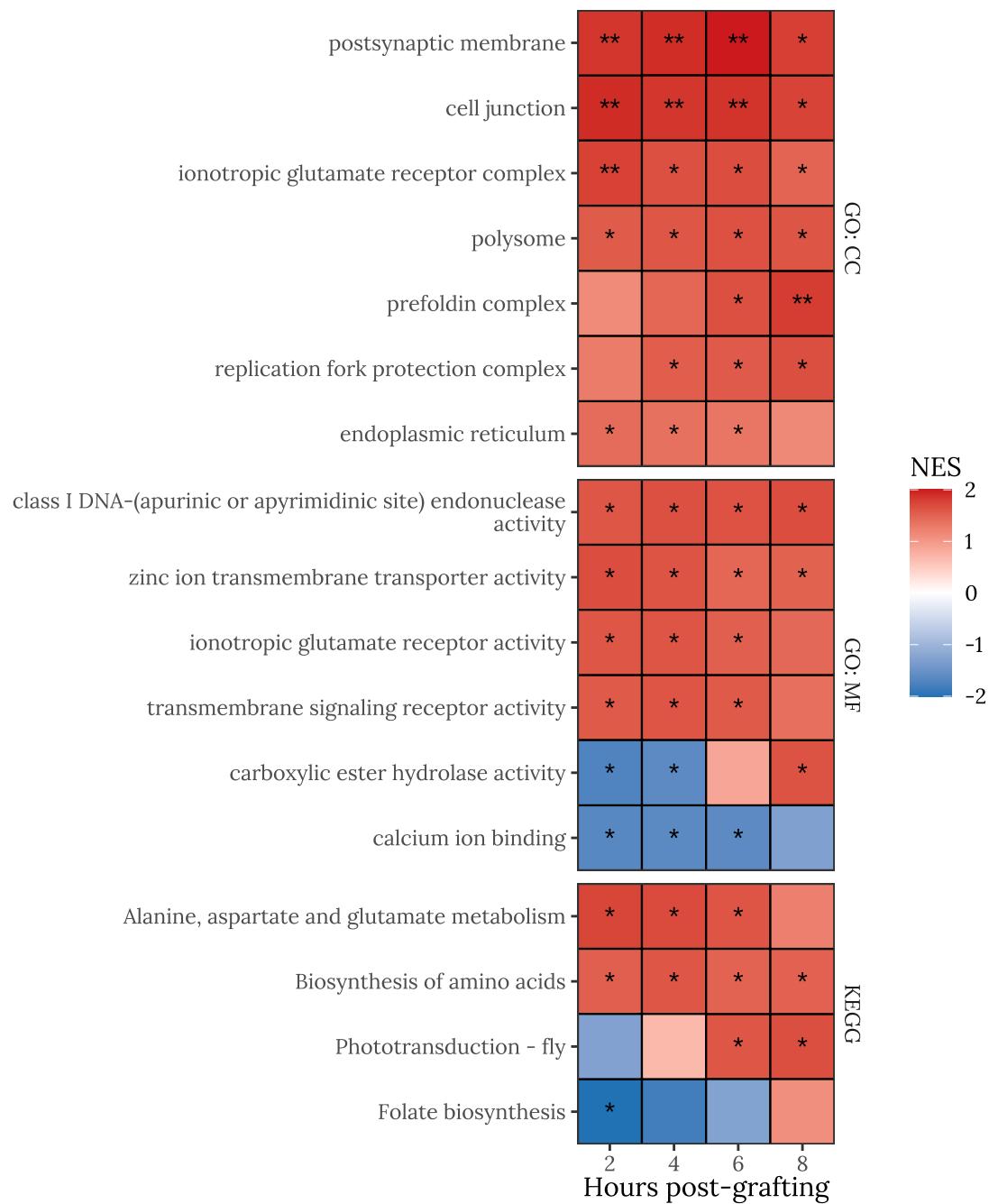


Figure S4: GO and KEGG terms that are enriched among genes showing temporally variable methylation within each treatment group (as measured by the difference in mean % CpG methylation between the 2h and 8h QDL or WDL samples for all sites in the introns, exons, and promoters of the gene). Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations. Orange indicates functional categories for which the relevant genes show increasing methylation over time, purple indicates decreasing methylation over time. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction.

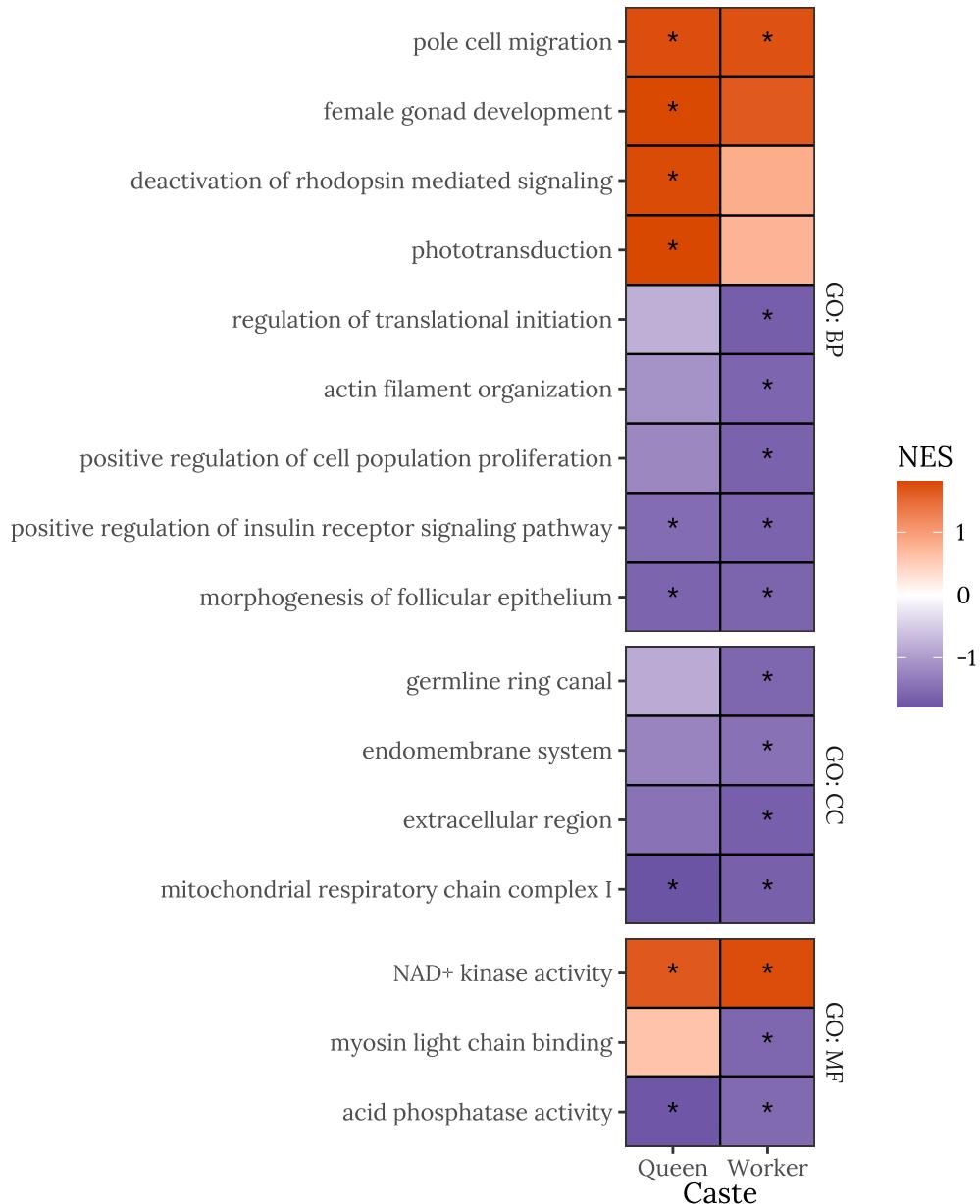


Figure S5: Results of non-metric multidimensional scaling analysis, which reduces the distance matrix between samples to three dimensions (variance explained: 96.6%). The plot suggests that queen- and worker-destined larvae have different gene expression profiles and that the transcriptome changes over time, and there is some indication that the caste difference is larger at later times post-grafting into a queen or worker cell.

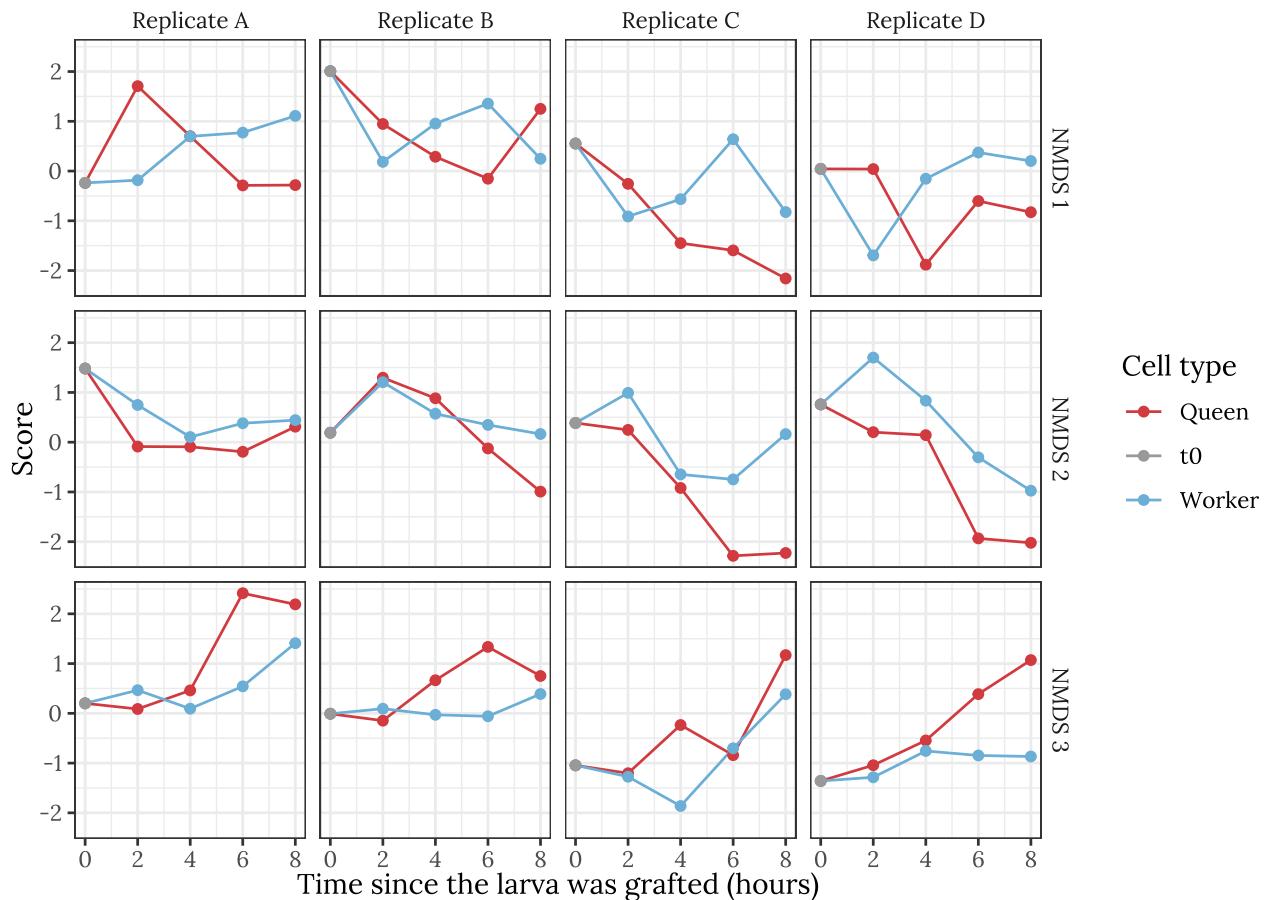


Figure S6: GO (Biological Process) terms that were enriched among genes showing a caste difference in expression. Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations; red: QDL-biased, blue: QDL-biased. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction. This figure does not include the top 50 enriched GO:BP terms that are shown in Figure 3A. The figure is split into two columns to fit onto the page.

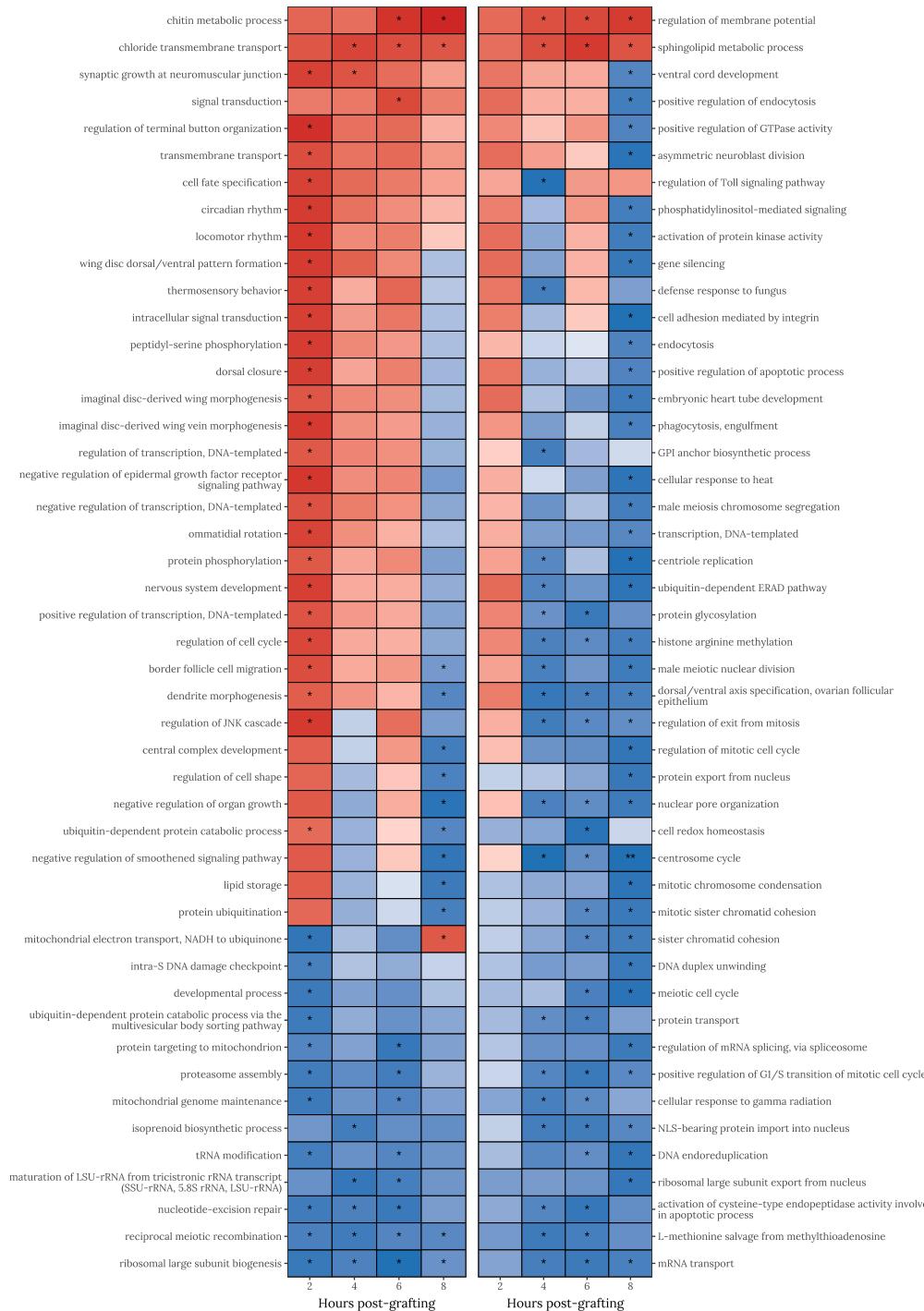


Figure S7: GO (Molecular Function) terms that were enriched among genes showing a caste difference in expression. Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations; red: QDL-biased, blue: QDL-biased. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction. The figure is split into two columns to fit onto the page.

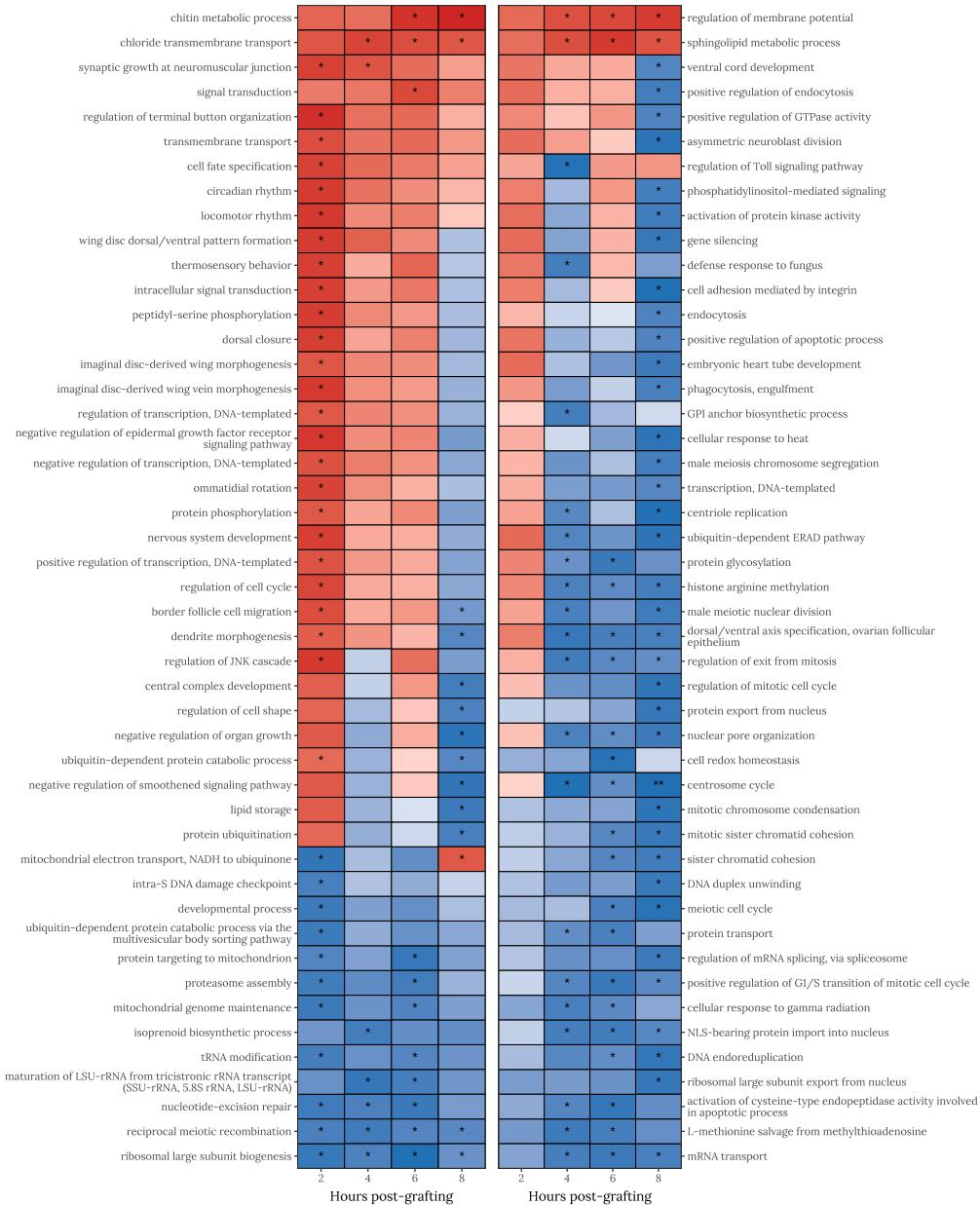


Figure S8: GO (Cellular Component) terms that were enriched among genes showing a caste difference in expression. Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations; red: QDL-biased, blue: QDL-biased. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction.

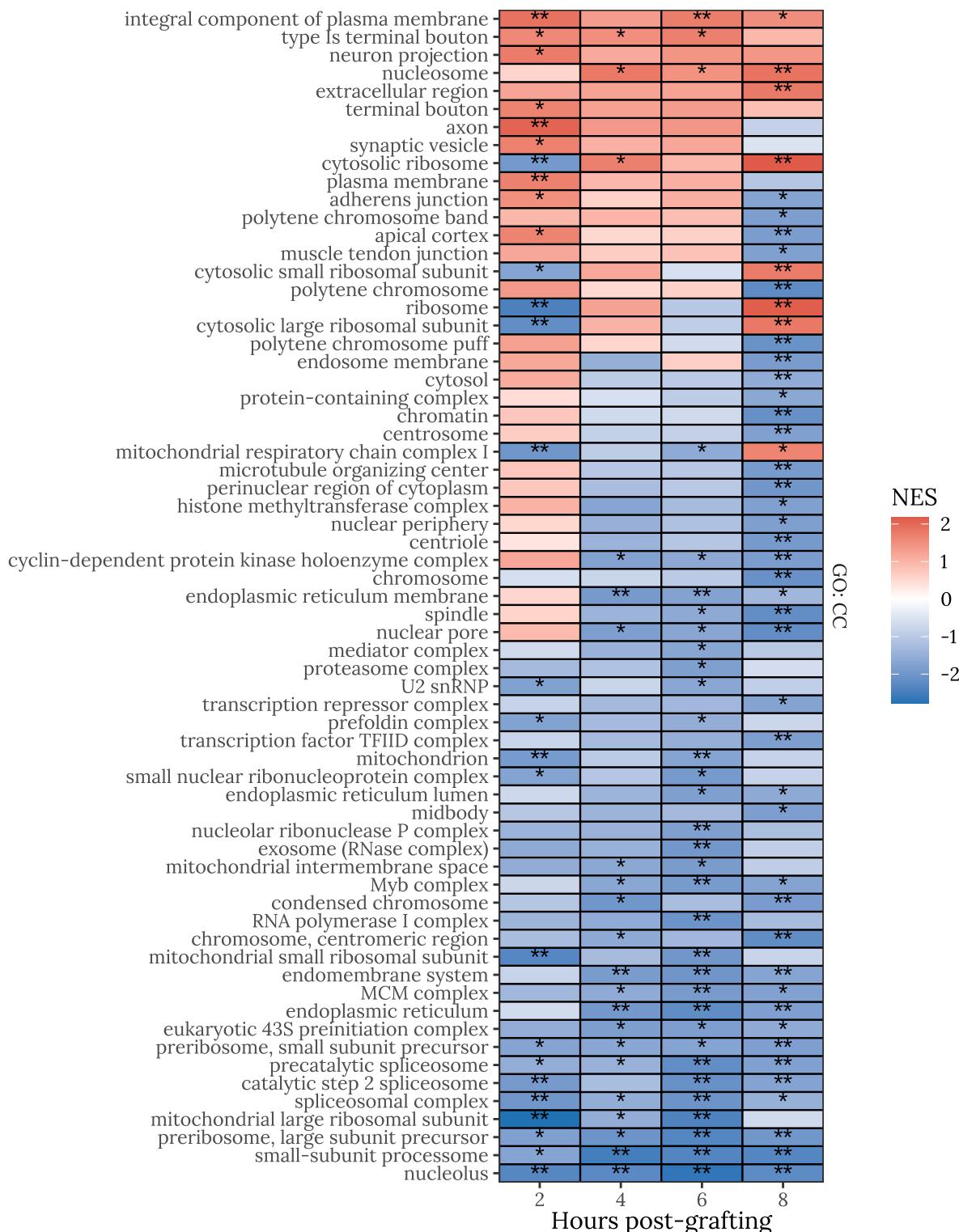
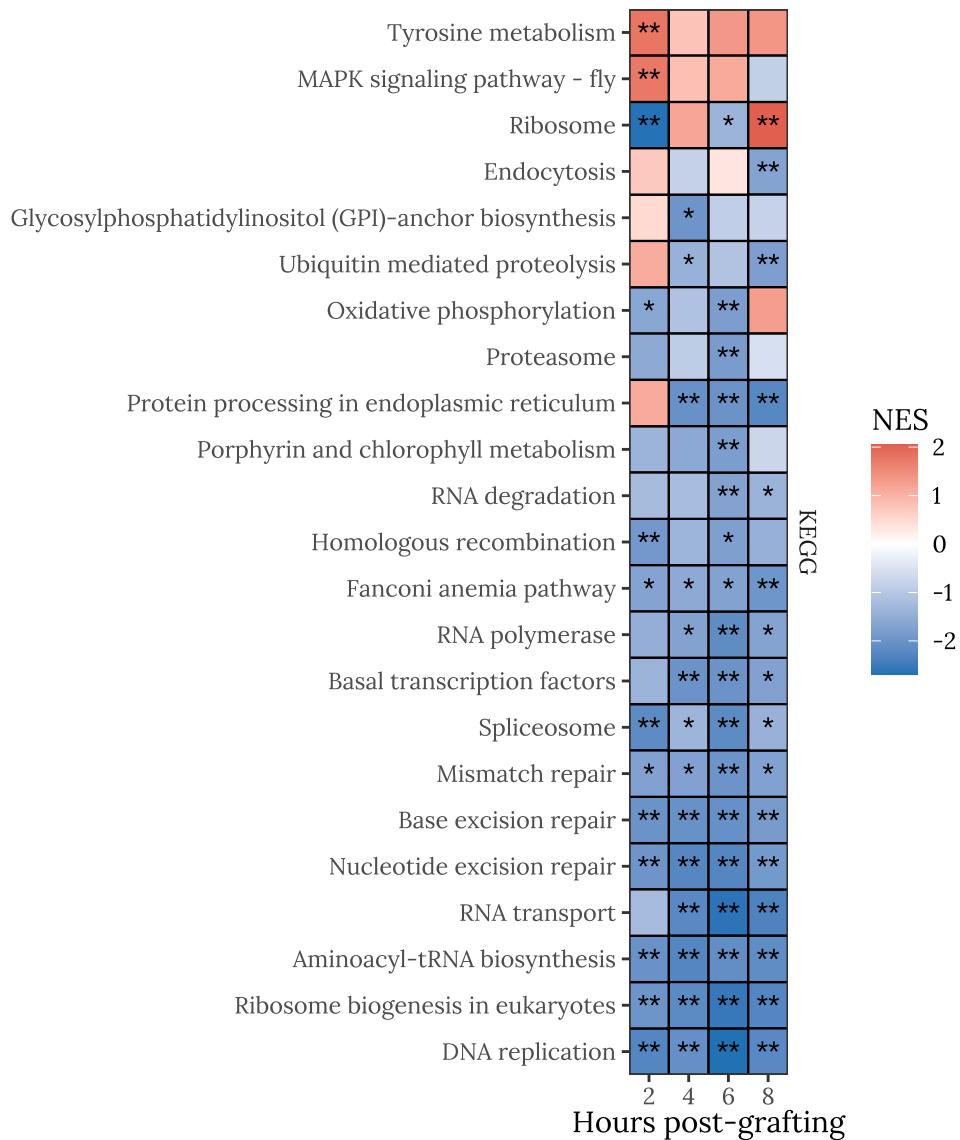


Figure S9: KEGG terms that were enriched among genes showing a caste difference in expression. Results are from Kolmogorov-Smirnov enrichment tests using our custom GO and KEGG annotations; red: QDL-biased, blue: QDL-biased. All terms passed the cutoff $p < 0.05$, and asterisks indicate results that remained significant after FDR correction.



Supplementary tables

Table S1: The table shows the 46 sites for which BWASP reported a significant difference in methylation between queens and workers at one or more time points. Other columns give statistical results and annotations for the focal site. Sites were recorded as statistically significant if both their p and q values were < 0.05. See the website documenting the code for this paper for a version of this table with additional columns showing the names of genes overlapped by these sites.

seqnames	start	comparison	Diff. in % methylation (positive means Q>W)	log10 pvalue	qvalue
NC_037652.1	9383954	Q8 vs W8	39.16	11.2	0.000
NC_037643.1	16910622	Q8 vs W8	43.20	10.8	0.000
NC_037641.1	9942075	Q6 vs W6	25.00	10.4	0.000
NC_037645.1	11688425	Q4 vs W4	35.49	9.8	0.001
NC_037641.1	11217405	Q6 vs W6	36.71	9.7	0.001
NC_037641.1	11207169	Q4 vs W4	24.74	9.5	0.001
NC_037652.1	3713487	Q2 vs W2	39.66	9.5	0.002
NC_037646.1	7712369	Q4 vs W4	-27.99	9.2	0.002
NC_037647.1	417046	Q2 vs W2	40.62	9.0	0.002
NC_037648.1	586581	Q4 vs W4	37.69	9.0	0.002
NC_037645.1	7797165	Q8 vs W8	43.51	8.8	0.003
NC_037649.1	3344358	Q8 vs W8	21.58	8.8	0.003
NC_037638.1	3280105	Q4 vs W4	-36.56	8.7	0.003
NC_037645.1	11688405	Q4 vs W4	34.90	8.6	0.003
NC_037640.1	13082691	Q6 vs W6	40.79	8.6	0.004
NC_037643.1	13392591	Q6 vs W6	22.45	8.5	0.004
NC_037640.1	12275659	Q6 vs W6	37.25	8.5	0.004
NC_037641.1	9942083	Q6 vs W6	21.74	8.3	0.005
NC_037641.1	765390	Q8 vs W8	37.01	8.2	0.008
NC_037646.1	7900182	Q4 vs W4	37.90	8.0	0.011
NC_037638.1	5492379	Q8 vs W8	40.25	8.0	0.011
NC_037642.1	11358202	Q8 vs W8	40.82	7.8	0.013
NC_037638.1	3279917	Q4 vs W4	28.48	7.7	0.022
NC_037643.1	5457143	Q8 vs W8	42.18	7.6	0.021
NC_037652.1	4339735	Q2 vs W2	-28.31	7.6	0.044
NC_037640.1	11775528	Q6 vs W6	-31.33	7.5	0.029
NC_037646.1	7751142	Q4 vs W4	24.37	7.5	0.030
NC_037649.1	10695218	Q6 vs W6	-41.41	7.5	0.029
NC_037638.1	419900	Q8 vs W8	35.26	7.5	0.024
NC_037647.1	351649	Q4 vs W4	18.27	7.4	0.031
NC_037639.1	4384423	Q4 vs W4	26.95	7.4	0.031
NC_037649.1	3080211	Q8 vs W8	34.57	7.4	0.024
NC_037649.1	3267203	Q8 vs W8	32.20	7.4	0.024
NC_037651.1	5021757	Q4 vs W4	-34.78	7.4	0.031
NC_037649.1	3080213	Q8 vs W8	34.61	7.3	0.024
NC_037652.1	3627807	Q4 vs W4	36.16	7.3	0.031
NC_037643.1	5355641	Q8 vs W8	38.21	7.3	0.024
NC_037641.1	11115784	Q4 vs W4	-34.73	7.2	0.037
NC_037641.1	11115784	Q4 vs W4	-34.73	7.2	0.037
NC_037643.1	15414125	Q8 vs W8	39.02	7.2	0.026
NC_037645.1	7797150	Q8 vs W8	40.30	7.2	0.026
NC_037649.1	3993835	Q8 vs W8	39.02	7.2	0.026
NC_037648.1	11153921	Q4 vs W4	-35.69	7.1	0.041
NC_037640.1	5435533	Q8 vs W8	34.03	7.1	0.030
NC_037646.1	7712578	Q4 vs W4	-24.89	7.0	0.045
NC_037642.1	2256787	Q4 vs W4	-24.96	7.0	0.045
NC_037646.1	1634375	Q4 vs W4	36.00	7.0	0.048
NC_037638.1	15874817	Q8 vs W8	24.36	7.0	0.037
NC_037646.1	7871733	Q4 vs W4	-33.23	7.0	0.048
NC_037640.1	9850386	Q8 vs W8	25.33	6.9	0.044

Table S2: The table shows the 112 sites for which BWASP reported a significant difference in methylation between time points in queen-destined larvae. Other columns give statistical results and annotations for the focal site. Sites were recorded as statistically significant if both their p and q values were < 0.05 . See the website documenting the code for this paper for a version of this table with additional columns showing the names of genes overlapped by these sites.

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037652.1	4339735	Q2 vs Q4	43.57	13.3	0.000
NC_037641.1	11536599	t0 vs Q4	26.32	12.7	0.000
NC_037641.1	3363296	t0 vs Q4	40.29	12.1	0.000
NC_037641.1	5137830	t0 vs Q6	36.26	12.0	0.000
NC_037642.1	502052	t0 vs Q2	34.42	10.9	0.000
NC_037650.1	3053047	Q4 vs Q6	35.66	10.8	0.000
NC_037643.1	15349410	t0 vs Q8	-43.02	10.4	0.000
NC_037639.1	2270880	t0 vs Q8	26.15	9.8	0.001
NC_037646.1	10918919	t0 vs Q6	44.12	9.8	0.001
NC_037646.1	10918919	t0 vs Q6	44.12	9.8	0.001
NC_037642.1	12933629	Q4 vs Q6	44.92	9.6	0.001
NC_037643.1	13248122	t0 vs Q4	-41.50	9.4	0.001
NC_037643.1	15414125	t0 vs Q8	43.88	9.4	0.001
NC_037641.1	5430234	Q4 vs Q8	29.70	9.3	0.003
NC_037642.1	13275710	t0 vs Q4	-35.59	9.3	0.001
NC_037642.1	12933629	t0 vs Q4	-40.20	9.2	0.001
NC_037639.1	6753111	t0 vs Q8	-32.81	9.2	0.001
NC_037638.1	6942936	Q2 vs Q8	44.70	9.2	0.005
NC_037652.1	9383954	t0 vs Q8	36.30	9.2	0.001
NC_037641.1	815	t0 vs Q4	-31.19	9.2	0.001
NC_037639.1	2270880	t0 vs Q4	23.80	9.2	0.001
NC_037647.1	12059634	t0 vs Q2	26.88	9.2	0.003
NC_037643.1	16942993	Q2 vs Q6	31.79	9.0	0.009
NC_037643.1	15349397	t0 vs Q8	-38.76	8.9	0.002
NC_037645.1	6269057	Q2 vs Q4	40.83	8.8	0.004
NC_037642.1	13827846	t0 vs Q4	31.25	8.8	0.002
NC_037647.1	7571827	Q2 vs Q4	-43.08	8.8	0.004
NC_037638.1	9059711	t0 vs Q2	33.97	8.7	0.005
NC_037645.1	7317165	Q2 vs Q4	41.24	8.7	0.004
NC_037645.1	12377979	t0 vs Q8	33.64	8.6	0.003
NC_037642.1	13275710	Q4 vs Q6	36.76	8.6	0.007
NC_037639.1	2270724	t0 vs Q8	24.31	8.5	0.003
NC_037641.1	5780268	Q2 vs Q4	29.63	8.5	0.005
NC_037651.1	10481375	Q4 vs Q6	-29.95	8.5	0.007
NC_037642.1	12016507	t0 vs Q4	-35.13	8.3	0.004
NC_037650.1	2408431	Q6 vs Q8	22.73	8.3	0.040
NC_037651.1	5021757	Q4 vs Q8	40.51	8.3	0.020
NC_037641.1	3718317	t0 vs Q4	31.57	8.2	0.004
NC_037643.1	8643423	t0 vs Q4	36.33	8.2	0.004
NC_037645.1	8883315	Q2 vs Q4	-42.32	8.2	0.009
NC_037652.1	2678246	Q2 vs Q8	22.64	8.2	0.021
NC_037651.1	7186052	t0 vs Q4	36.59	8.1	0.004
NC_037643.1	14215410	t0 vs Q4	25.78	8.1	0.004
NC_037653.1	2710134	Q2 vs Q8	-42.20	8.1	0.021
NC_037638.1	14994808	Q2 vs Q6	36.10	8.1	0.036
NC_037640.1	6234369	Q4 vs Q8	25.35	8.0	0.022
NC_037651.1	5021757	Q2 vs Q4	-40.00	8.0	0.011
NC_037645.1	6538809	t0 vs Q2	23.97	7.9	0.021
NC_037643.1	13199318	t0 vs Q2	28.42	7.9	0.021
NC_037646.1	7750628	t0 vs Q4	22.38	7.9	0.007
NC_037648.1	13509923	t0 vs Q4	35.95	7.9	0.007
NC_037647.1	9167196	Q2 vs Q4	35.13	7.8	0.015
NC_037648.1	16007231	t0 vs Q6	20.00	7.8	0.038
NC_037639.1	4567893	t0 vs Q2	-26.24	7.7	0.025
NC_037638.1	25837750	t0 vs Q4	31.30	7.7	0.009
NC_037641.1	11215997	t0 vs Q6	-29.79	7.7	0.038

(continued)

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037646.1	10902771	t0 vs Q2	-27.48	7.6	0.027
NC_037640.1	12275314	t0 vs Q2	-38.49	7.6	0.027
NC_037638.1	15647091	Q2 vs Q4	24.04	7.6	0.021
NC_037645.1	6524906	Q2 vs Q4	-24.82	7.6	0.021
NC_037641.1	71660	t0 vs Q4	32.84	7.6	0.012
NC_037643.1	2343427	Q4 vs Q8	28.96	7.6	0.041
NC_037647.1	6455138	t0 vs Q6	25.97	7.6	0.038
NC_037647.1	6455138	t0 vs Q6	25.97	7.6	0.038
NC_037652.1	9336776	t0 vs Q8	16.82	7.6	0.024
NC_037648.1	586594	Q4 vs Q8	-37.93	7.6	0.041
NC_037647.1	9819144	Q4 vs Q6	-44.19	7.5	0.046
NC_037641.1	12158609	t0 vs Q6	26.26	7.5	0.038
NC_037641.1	12158609	t0 vs Q6	26.26	7.5	0.038
NC_037650.1	5267458	t0 vs Q8	18.56	7.5	0.024
NC_037645.1	6634854	Q2 vs Q4	44.27	7.5	0.021
NC_037645.1	8877259	t0 vs Q4	-27.47	7.5	0.014
NC_037642.1	13827863	Q2 vs Q4	37.57	7.5	0.021
NC_037639.1	4384423	Q2 vs Q4	26.98	7.5	0.021
NC_037647.1	9941294	t0 vs Q6	36.99	7.4	0.042
NC_037644.1	12075370	t0 vs Q2	37.42	7.4	0.035
NC_037641.1	11536774	t0 vs Q4	21.63	7.4	0.014
NC_037647.1	212762	Q2 vs Q4	31.44	7.4	0.022
NC_037641.1	10165290	t0 vs Q4	22.33	7.4	0.014
NC_037642.1	10715950	Q4 vs Q8	34.12	7.4	0.048
NC_037642.1	10715950	Q4 vs Q8	34.12	7.4	0.048
NC_037642.1	10715950	Q4 vs Q8	34.12	7.4	0.048
NC_037639.1	2264339	t0 vs Q6	18.75	7.4	0.042
NC_037646.1	12334070	t0 vs Q4	28.47	7.4	0.016
NC_037642.1	12334070	t0 vs Q4	28.47	7.4	0.048
NC_037642.1	43538	t0 vs Q8	24.33	7.3	0.033
NC_037638.1	11120226	t0 vs Q6	31.41	7.3	0.042
NC_037652.1	3706646	t0 vs Q4	29.62	7.3	0.016
NC_037645.1	9467416	t0 vs Q4	31.41	7.3	0.016
NC_037644.1	12114192	t0 vs Q2	-34.02	7.3	0.043
NC_037641.1	747345	t0 vs Q4	-29.46	7.3	0.016
NC_037641.1	5790984	t0 vs Q8	32.74	7.3	0.036
NC_037643.1	2343427	t0 vs Q4	-25.66	7.3	0.016
NC_037652.1	3768970	t0 vs Q4	28.13	7.2	0.017
NC_037639.1	2270724	t0 vs Q4	22.02	7.2	0.017
NC_037639.1	15840139	t0 vs Q8	23.71	7.2	0.036
NC_037646.1	7819627	t0 vs Q4	34.86	7.2	0.017
NC_037641.1	5509781	t0 vs Q8	37.28	7.2	0.036
NC_037644.1	12398314	Q2 vs Q4	29.52	7.2	0.037
NC_037651.1	7186052	t0 vs Q8	32.53	7.1	0.042
NC_037640.1	13541926	Q2 vs Q4	22.12	7.1	0.037
NC_037647.1	4312586	t0 vs Q4	30.30	7.1	0.021
NC_037652.1	7577290	t0 vs Q4	-35.70	7.1	0.021
NC_037653.1	6392452	Q2 vs Q4	-29.01	7.1	0.037
NC_037643.1	8669522	Q2 vs Q4	33.22	7.1	0.037
NC_037652.1	4343365	Q2 vs Q4	37.14	7.1	0.037
NC_037651.1	9028275	t0 vs Q8	27.54	7.0	0.044
NC_037642.1	5931461	Q2 vs Q4	26.29	7.0	0.037
NC_037652.1	636261	t0 vs Q8	31.13	7.0	0.044
NC_037642.1	12934078	t0 vs Q4	35.71	7.0	0.023
NC_037646.1	10957014	t0 vs Q8	20.55	7.0	0.044
NC_037640.1	8175059	t0 vs Q4	-30.62	7.0	0.023
NC_037643.1	14136824	t0 vs Q4	28.62	7.0	0.024
NC_037641.1	3371657	t0 vs Q4	25.76	7.0	0.024
NC_037652.1	3794565	t0 vs Q8	-23.81	7.0	0.045
NC_037648.1	15365774	t0 vs Q4	-33.96	6.9	0.024
NC_037638.1	419900	t0 vs Q8	33.11	6.9	0.045

(continued)

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037638.1	26847998	t0 vs Q8	17.80	6.9	0.045
NC_037647.1	212120	Q2 vs Q4	24.24	6.9	0.045
NC_037639.1	4384426	Q2 vs Q4	20.88	6.9	0.045
NC_037640.1	6102215	t0 vs Q8	-35.78	6.9	0.046
NC_037645.1	7315823	Q2 vs Q4	21.87	6.9	0.045
NC_037642.1	12933600	t0 vs Q4	-35.72	6.9	0.028
NC_037646.1	7775204	t0 vs Q4	20.50	6.9	0.028
NC_037641.1	144674	t0 vs Q4	33.75	6.9	0.028
NC_037638.1	3280105	Q2 vs Q4	-34.31	6.8	0.045
NC_037647.1	4842283	Q2 vs Q4	-30.70	6.8	0.045
NC_037639.1	15669290	Q2 vs Q4	-31.68	6.8	0.045
NC_037648.1	951944	t0 vs Q4	36.38	6.8	0.028
NC_037639.1	334653	Q2 vs Q4	23.03	6.8	0.048
NC_037646.1	6558541	t0 vs Q4	-31.45	6.7	0.034
NC_037643.1	1858380	t0 vs Q4	34.93	6.7	0.034
NC_037642.1	13827863	t0 vs Q4	33.76	6.7	0.034
NC_037639.1	15225635	t0 vs Q4	-36.36	6.7	0.034
NC_037647.1	7571827	t0 vs Q4	-35.17	6.7	0.036
NC_037643.1	13237537	t0 vs Q4	19.79	6.7	0.036
NC_037640.1	6699237	t0 vs Q4	33.60	6.7	0.036
NC_037651.1	9097782	t0 vs Q4	23.80	6.6	0.038
NC_037642.1	12954020	t0 vs Q4	-34.01	6.6	0.043
NC_037647.1	194033	t0 vs Q4	17.05	6.5	0.043
NC_037647.1	194033	t0 vs Q4	17.05	6.5	0.043
NC_037647.1	194033	t0 vs Q4	17.05	6.5	0.043
NC_037647.1	194033	t0 vs Q4	17.05	6.5	0.043
NC_037640.1	6870994	t0 vs Q4	-29.48	6.5	0.045
NC_037646.1	1235910	t0 vs Q4	25.67	6.5	0.048

Table S3: The table shows the 138 sites for which BWASP reported a significant difference in methylation between time points in queen-destined larvae. Other columns give statistical results and annotations for the focal site. Sites were recorded as statistically significant if both their p and q values were < 0.01 (note: this is lower than for Tables S1-S2; there would be 25,223 sites if we used the same < 0.05 cutoff for significance). See the website documenting the code for this paper for a version of this table with additional columns showing the names of genes overlapped by these sites.

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037645.1	308757	W2 vs W4	50.68	13.0	0.000
NC_037638.1	21500232	W4 vs W6	-22.49	10.7	0.000
NC_037645.1	308773	W2 vs W4	45.12	10.6	0.000
NC_037640.1	11785190	t0 vs W6	-23.38	10.4	0.000
NC_037638.1	20663956	W2 vs W4	-40.32	10.4	0.000
NC_037638.1	20564094	W4 vs W6	-37.91	10.4	0.000
NC_037645.1	8628036	W4 vs W8	29.22	10.0	0.001
NC_037652.1	3767213	W2 vs W4	-41.87	9.8	0.000
NC_037646.1	7871733	W4 vs W8	-38.49	9.7	0.001
NC_037651.1	7185558	t0 vs W4	-32.32	9.7	0.001
NC_037639.1	15072595	W2 vs W6	43.75	9.7	0.000
NC_037639.1	15072595	W2 vs W6	43.75	9.7	0.000
NC_037639.1	15072595	W2 vs W6	43.75	9.7	0.000
NC_037639.1	15072595	W2 vs W6	43.75	9.7	0.000
NC_037645.1	6977070	W6 vs W8	-37.67	9.6	0.002
NC_037640.1	11782468	W4 vs W6	-28.20	9.6	0.001
NC_037639.1	13306288	t0 vs W4	40.49	9.6	0.001
NC_037649.1	914164	W4 vs W8	-22.46	9.6	0.001
NC_037644.1	13407578	W6 vs W8	36.20	9.5	0.002
NC_037648.1	12189554	t0 vs W4	19.17	9.5	0.001
NC_037645.1	2629099	W2 vs W4	-34.99	9.4	0.000
NC_037640.1	11786400	t0 vs W6	-33.44	9.4	0.002
NC_037651.1	8634088	t0 vs W4	24.92	9.3	0.001
NC_037651.1	5514070	W4 vs W6	-29.18	9.2	0.001
NC_037652.1	3627807	W2 vs W4	-39.25	9.1	0.001
NC_037649.1	7674388	t0 vs W4	-23.08	9.1	0.001
NC_037643.1	9032020	W6 vs W8	-24.60	9.1	0.002
NC_037642.1	7447184	W6 vs W8	36.63	9.1	0.002
NC_037644.1	11024732	W2 vs W4	35.16	9.0	0.001
NC_037642.1	7076859	W6 vs W8	36.00	9.0	0.002
NC_037649.1	8506682	W2 vs W6	40.77	8.9	0.000
NC_037638.1	9241710	t0 vs W4	23.66	8.9	0.001
NC_037648.1	5021688	W4 vs W6	21.06	8.9	0.002
NC_037643.1	14142840	t0 vs W4	-35.87	8.8	0.002
NC_037641.1	3684568	W2 vs W4	-35.99	8.8	0.001
NC_037648.1	15099765	t0 vs W4	23.72	8.8	0.002
NC_037647.1	216337	W2 vs W4	-45.65	8.7	0.002
NC_037648.1	11153921	W4 vs W8	-37.74	8.6	0.004
NC_037641.1	9942075	W6 vs W8	20.33	8.5	0.005
NC_037646.1	7757780	W4 vs W8	-23.26	8.5	0.004
NC_037638.1	9073490	W4 vs W8	-24.14	8.5	0.004
NC_037646.1	7871735	W4 vs W8	-35.80	8.5	0.004
NC_037638.1	11493447	t0 vs W4	-35.27	8.5	0.002
NC_037641.1	10165494	W2 vs W6	-37.14	8.5	0.000
NC_037648.1	6578371	t0 vs W4	-35.33	8.5	0.002
NC_037643.1	13199490	t0 vs W4	31.24	8.4	0.002
NC_037649.1	3344358	W6 vs W8	-20.02	8.4	0.005
NC_037640.1	13541876	W4 vs W6	-29.97	8.4	0.006
NC_037647.1	11426540	W2 vs W4	24.48	8.4	0.003
NW_020555859.1	295349	W4 vs W6	-26.54	8.3	0.006
NC_037643.1	13199828	t0 vs W4	42.79	8.3	0.003
NC_037647.1	11492955	W2 vs W4	-25.72	8.3	0.003
NC_037638.1	9073490	t0 vs W4	23.63	8.3	0.003
NC_037640.1	5290061	W6 vs W8	30.09	8.3	0.006
NC_037645.1	8878435	W4 vs W8	27.15	8.3	0.006

(continued)

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037648.1	11147246	t0 vs W4	34.85	8.2	0.003
NC_037646.1	1578357	t0 vs W4	34.76	8.2	0.003
NC_037643.1	9062599	W6 vs W8	22.28	8.2	0.006
NC_037652.1	7577290	t0 vs W4	-35.80	8.2	0.003
NC_037642.1	13119508	W4 vs W6	-19.51	8.2	0.007
NC_037646.1	7751211	W4 vs W6	32.97	8.2	0.007
NC_037640.1	10648489	t0 vs W4	21.47	8.1	0.003
NC_037648.1	10591367	W4 vs W8	37.03	8.1	0.007
NC_037643.1	6485995	t0 vs W4	-31.39	8.1	0.003
NC_037647.1	11289892	W4 vs W6	-35.37	8.1	0.007
NC_037650.1	2111386	W4 vs W8	-40.90	8.1	0.007
NC_037640.1	11788212	W2 vs W4	45.38	8.1	0.004
NC_037645.1	308757	W4 vs W6	-38.87	8.1	0.007
NC_037650.1	2180336	W6 vs W8	31.18	8.1	0.008
NC_037651.1	7185558	W4 vs W8	28.10	8.0	0.007
NC_037645.1	296138	W4 vs W6	41.18	8.0	0.008
NC_037648.1	10448638	W4 vs W8	21.24	7.9	0.009
NC_037645.1	12349714	W4 vs W6	24.07	7.9	0.009
NC_037642.1	9331827	t0 vs W4	23.08	7.9	0.005
NC_037647.1	11310693	W2 vs W4	-37.83	7.8	0.008
NC_037643.1	13253903	t0 vs W4	-24.29	7.8	0.006
NC_037648.1	11068831	t0 vs W4	32.37	7.7	0.006
NC_037638.1	12056725	t0 vs W4	16.81	7.7	0.007
NC_037648.1	15798788	W2 vs W4	36.42	7.7	0.009
NC_037648.1	10054081	W2 vs W4	34.60	7.7	0.009
NC_037643.1	13199556	t0 vs W4	32.49	7.7	0.007
NC_037642.1	13683836	W2 vs W4	33.85	7.6	0.009
NC_037642.1	13683836	W2 vs W4	33.85	7.6	0.009
NC_037645.1	2597585	t0 vs W4	35.87	7.6	0.008
NC_037643.1	13248122	t0 vs W4	-35.50	7.6	0.008
NC_037643.1	5150009	t0 vs W4	26.60	7.6	0.008
NC_037645.1	6331489	t0 vs W4	-35.10	7.5	0.008
NC_037649.1	7959149	t0 vs W2	34.19	7.5	0.001
NC_037649.1	7959149	t0 vs W4	31.79	7.5	0.008
NC_037646.1	5863561	t0 vs W4	24.89	7.5	0.008
NC_037652.1	7449942	t0 vs W4	-34.85	7.5	0.008
NC_037646.1	5863611	t0 vs W4	24.78	7.5	0.008
NC_037651.1	7717032	t0 vs W4	-21.39	7.4	0.009
NC_037643.1	15349397	t0 vs W2	-32.51	7.3	0.001
NC_037646.1	7710344	t0 vs W2	-33.36	7.3	0.001
NC_037651.1	8355911	t0 vs W2	34.25	7.3	0.001
NC_037640.1	4301325	W2 vs W6	-32.54	7.0	0.002
NC_037647.1	417046	W2 vs W6	31.77	7.0	0.002
NC_037649.1	8650196	t0 vs W2	-27.31	6.9	0.003
NC_037647.1	7065109	W2 vs W6	32.98	6.8	0.003
NC_037647.1	945225	t0 vs W2	31.01	6.8	0.003
NC_037638.1	20547546	W2 vs W6	21.80	6.7	0.003
NC_037649.1	8506682	t0 vs W2	-32.41	6.6	0.004
NC_037642.1	502052	t0 vs W2	23.86	6.6	0.004
NC_037640.1	8114990	W2 vs W6	29.07	6.6	0.003
NC_037640.1	11773321	W2 vs W6	-26.83	6.5	0.003
NC_037640.1	621001	W2 vs W6	-18.96	6.4	0.003
NC_037644.1	11002942	W2 vs W6	31.91	6.4	0.003
NC_037646.1	8650049	W2 vs W6	-37.23	6.4	0.003
NC_037640.1	5413171	W2 vs W6	20.54	6.4	0.003
NC_037641.1	158799	W2 vs W6	20.05	6.4	0.003
NC_037639.1	15138292	W2 vs W6	-39.72	6.3	0.003
NC_037647.1	232727	t0 vs W2	27.91	6.3	0.006
NC_037645.1	6467948	t0 vs W2	-29.45	6.2	0.006
NC_037641.1	8483354	t0 vs W2	22.55	6.2	0.006
NC_037647.1	229642	t0 vs W2	19.95	6.1	0.007

(continued)

seqnames	start	comparison	Diff. in % methylation (positive means increase over time)	log10 pvalue	qvalue
NC_037640.1	8340208	t0 vs W2	-35.96	6.0	0.007
NC_037640.1	8329666	W2 vs W6	-30.10	6.0	0.005
NC_037649.1	8090734	t0 vs W2	-31.33	6.0	0.007
NC_037641.1	3363296	t0 vs W2	26.74	6.0	0.007
NC_037639.1	15138242	W2 vs W6	-37.52	6.0	0.005
NC_037648.1	10424975	W2 vs W6	35.39	6.0	0.005
NC_037645.1	11705240	t0 vs W2	-34.48	6.0	0.007
NC_037638.1	20547530	W2 vs W6	20.05	6.0	0.005
NC_037639.1	139016	W2 vs W6	-28.71	6.0	0.005
NC_037640.1	13541876	W2 vs W6	-25.82	6.0	0.005
NC_037646.1	7502184	W2 vs W6	-29.87	5.9	0.005
NC_037646.1	7517975	t0 vs W2	43.69	5.9	0.008
NC_037644.1	10653121	W2 vs W6	-31.56	5.9	0.005
NC_037649.1	7763967	W2 vs W6	28.77	5.9	0.005
NC_037640.1	8186030	W2 vs W6	22.58	5.9	0.005
NC_037651.1	8241212	t0 vs W2	-29.03	5.8	0.008
NC_037651.1	6575238	W2 vs W6	15.32	5.8	0.005
NC_037641.1	165628	t0 vs W2	29.13	5.8	0.008
NC_037640.1	3231791	W2 vs W6	-33.56	5.8	0.005
NC_037640.1	648785	W2 vs W6	-22.82	5.8	0.005
NC_037639.1	15138298	W2 vs W6	-37.61	5.8	0.005
NC_037642.1	7447184	W2 vs W6	-30.33	5.8	0.005
NC_037646.1	7751211	W2 vs W6	32.15	5.8	0.005
NC_037647.1	7714648	t0 vs W2	-22.76	5.8	0.008
NC_037645.1	11745842	t0 vs W2	13.86	5.8	0.008
NC_037646.1	6078706	W2 vs W6	-24.76	5.8	0.005
NC_037648.1	10064363	W2 vs W6	-31.48	5.8	0.005
NC_037648.1	10064363	W2 vs W6	-31.48	5.8	0.005
NC_037645.1	8441586	t0 vs W2	-23.69	5.8	0.008
NC_037639.1	1926952	W2 vs W6	29.54	5.7	0.005
NC_037648.1	216101	t0 vs W2	17.15	5.7	0.008
NC_037642.1	12111715	W2 vs W6	-31.59	5.7	0.005
NC_037651.1	6467172	W2 vs W6	-35.58	5.7	0.005
NC_037644.1	10958396	t0 vs W2	27.01	5.7	0.008
NC_037640.1	3223981	W2 vs W6	-17.72	5.7	0.005
NC_037638.1	1624522	W2 vs W6	-18.18	5.6	0.006
NC_037650.1	1246209	W2 vs W6	-20.07	5.6	0.007
NC_037645.1	3845206	W2 vs W6	27.59	5.6	0.007
NC_037652.1	5820708	W2 vs W6	29.77	5.6	0.007
NC_037638.1	24656365	W2 vs W6	30.82	5.5	0.008
NC_037647.1	6322326	W2 vs W6	-31.88	5.5	0.008
NC_037647.1	6322326	W2 vs W6	-31.88	5.5	0.008
NC_037640.1	8331454	W2 vs W6	-26.20	5.5	0.008
NC_037642.1	7311791	W2 vs W6	-26.21	5.4	0.008

Table S4: The table shows the results of GO and KEGG gene set enrichment analyses on the gene-level caste difference in DNA methylation between QDL and WDL, using the GO/KEGG annotations for *Apis mellifera*, as calculated by BWASP (separately at each of the 4 time points). Only results with $p < 0.05$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to be more methylated in QDL relative to WDL (negative values mean WDL > QDL).

Test type	GO or KEGG term	Code	Time	NES	pval
GO:BP	cilium assembly	GO:0060271	6	1.72	0.00076
GO:BP	spliceosomal snRNP assembly	GO:0000387	4	1.70	0.00189
GO:BP	cell cycle	GO:0007049	8	1.66	0.00377
GO:BP	iron-sulfur cluster assembly	GO:0016226	8	1.67	0.00446
GO:MF	transmembrane signaling receptor activity	GO:0004888	4	1.81	0.00037
GO:MF	iron ion binding	GO:0005506	8	1.66	0.00867
GO:CC	cell junction	GO:0030054	2	1.75	0.00008
GO:CC	postsynaptic membrane	GO:0045211	2	1.75	0.00008
GO:CC	prefoldin complex	GO:0016272	8	1.81	0.00021
KEGG	Alanine, aspartate and glutamate metabolism	KEGG:00250	4	1.81	0.00044
KEGG	Phototransduction - fly	KEGG:04745	8	1.62	0.00697
KEGG	beta-Alanine metabolism	KEGG:00410	6	1.61	0.00736

Table S5: The table shows the results of GO and KEGG gene set enrichment analyses on the gene-level caste difference in DNA methylation between QDL and WDL, using our custom GO/KEGG annotations using information from *Drosophila melanogaster*, as calculated by BWASP (separately at each of the 4 time points). Only results with $p < 0.05$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to be more methylated in QDL relative to WDL (negative values mean WDL > QDL).

Test type	GO or KEGG term	Code	Time	NES	pval
GO:BP	sensory perception of touch	GO:0050975	8	1.80	0.00011
GO:BP	phototransduction	GO:0007602	8	1.85	0.00023
GO:BP	glutamine metabolic process	GO:0006541	2	1.69	0.00063
GO:BP	associative learning	GO:0008306	6	1.70	0.00240
GO:BP	regulation of membrane potential	GO:0042391	6	1.69	0.00244
GO:BP	olfactory learning	GO:0008355	2	1.76	0.00265
GO:BP	mitochondrial cytochrome c oxidase assembly	GO:0033617	8	1.73	0.00369
GO:BP	positive regulation of cell population proliferation	GO:0008284	4	1.62	0.00433
GO:BP	ion transport	GO:0006811	8	1.69	0.00449
GO:BP	cilium movement involved in cell motility	GO:0060294	6	1.61	0.00456
GO:BP	positive regulation of NF-kappaB transcription factor activity	GO:0051092	6	1.60	0.00576
GO:BP	positive regulation of insulin receptor signaling pathway	GO:0046628	6	1.63	0.00579
GO:BP	neuropeptide signaling pathway	GO:0007218	4	-1.95	0.00748
GO:BP	medium-term memory	GO:0072375	6	1.61	0.00782
GO:BP	microtubule-based process	GO:0007017	6	1.58	0.00862
GO:BP	protein import into mitochondrial matrix	GO:0030150	8	1.67	0.00895
GO:BP	protein glycosylation	GO:0006486	4	1.56	0.00937
GO:BP	cell cycle	GO:0007049	8	1.68	0.00938
GO:MF	zinc ion transmembrane transporter activity	GO:0005385	2	1.67	0.00168
GO:MF	class I DNA-(apurinic or apyrimidinic site) endonuclease activity	GO:0140078	4	1.66	0.00175
GO:MF	calcium ion binding	GO:0005509	6	-1.62	0.00213
GO:MF	ionotropic glutamate receptor activity	GO:0004970	4	1.62	0.00558
GO:MF	transmembrane signaling receptor activity	GO:0004888	4	1.62	0.00741
GO:MF	carboxylic ester hydrolase activity	GO:0052689	8	1.64	0.00784
GO:CC	postsynaptic membrane	GO:0045211	6	2.00	0.00000
GO:CC	cell junction	GO:0030054	2	1.92	0.00003
GO:CC	prefoldin complex	GO:0016272	8	1.81	0.00006
GO:CC	ionotropic glutamate receptor complex	GO:0008328	2	1.77	0.00016
GO:CC	polysome	GO:0005844	6	1.65	0.00393
GO:CC	replication fork protection complex	GO:0031298	8	1.67	0.00493
GO:CC	endoplasmic reticulum	GO:0005783	4	1.37	0.00990
KEGG	Alanine, aspartate and glutamate metabolism	dme00250	2	1.74	0.00084
KEGG	Phototransduction - fly	dme04745	6	1.61	0.00300
KEGG	Biosynthesis of amino acids	dme01230	4	1.61	0.00693
KEGG	Folate biosynthesis	dme00790	2	-2.01	0.00847

Table S6: The table shows the results of GO and KEGG gene set enrichment analyses on the gene-level temporal change in DNA methylation, using the GO/KEGG annotations for *Apis mellifera*, as calculated by BWASP (separately for QDL and WDL). Only results with $p < 0.05$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to become more methylated with time in the focal caste (negative values denote demethylation over time).

Test type	GO or KEGG term	Code	Caste	NES	pval
GO:MF	acid phosphatase activity	GO:0003993	Queen	-1.72	0.00121
KEGG	Notch signaling pathway	KEGG:04330	Queen	-1.77	0.00206
KEGG	Nitrogen metabolism	KEGG:00910	Queen	-1.66	0.00299
KEGG	Arginine and proline metabolism	KEGG:00330	Queen	1.79	0.00503
KEGG	Fatty acid elongation	KEGG:00062	Queen	-1.69	0.00812
KEGG	Arginine biosynthesis	KEGG:00220	Queen	1.63	0.03132
KEGG	Biosynthesis of unsaturated fatty acids	KEGG:01040	Queen	-1.53	0.04945
GO:MF	acid phosphatase activity	GO:0003993	Worker	-1.51	0.03279
KEGG	Fatty acid elongation	KEGG:00062	Worker	-1.75	0.00029
KEGG	Arginine and proline metabolism	KEGG:00330	Worker	2.01	0.00050
KEGG	Arginine biosynthesis	KEGG:00220	Worker	1.99	0.00075
KEGG	Biosynthesis of unsaturated fatty acids	KEGG:01040	Worker	-1.62	0.00322
KEGG	Notch signaling pathway	KEGG:04330	Worker	-1.39	0.06282
KEGG	Nitrogen metabolism	KEGG:00910	Worker	-1.38	0.08576

Table S7: The table shows the results of GO and KEGG gene set enrichment analyses on the gene-level temporal change in DNA methylation, using our custom GO/KEGG annotations using information from *Drosophila melanogaster*, as calculated by BWASP (separately for QDL and WDL). Only results with $p < 0.05$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to become more methylated with time in the focal caste (negative values denote demethylation over time).

Test type	GO or KEGG term	Code	Caste	NES	pval
GO:BP	female gonad development	GO:0008585	Queen	1.80	0.00008
GO:BP	deactivation of rhodopsin mediated signaling	GO:0016059	Queen	1.78	0.00105
GO:BP	pole cell migration	GO:0007280	Queen	1.76	0.00330
GO:BP	phototransduction	GO:0007602	Queen	1.81	0.00536
GO:BP	morphogenesis of follicular epithelium	GO:0016333	Queen	-1.60	0.01371
GO:BP	positive regulation of insulin receptor signaling pathway	GO:0046628	Queen	-1.51	0.04554
GO:BP	positive regulation of cell population proliferation	GO:0008284	Queen	-1.22	0.22575
GO:BP	actin filament organization	GO:0007015	Queen	-1.10	0.33582
GO:BP	regulation of translational initiation	GO:0006446	Queen	-0.80	0.71157
GO:MF	acid phosphatase activity	GO:0003993	Queen	-1.75	0.00069
GO:MF	NAD+ kinase activity	GO:0003951	Queen	1.67	0.00645
GO:MF	myosin light chain binding	GO:0032027	Queen	0.61	0.89121
GO:CC	mitochondrial respiratory chain complex I	GO:0005747	Queen	-1.78	0.00439
GO:CC	extracellular region	GO:0005576	Queen	-1.44	0.05282
GO:CC	endomembrane system	GO:0012505	Queen	-1.24	0.10302
GO:CC	germline ring canal	GO:0045172	Queen	-0.84	0.65962
GO:BP	regulation of translational initiation	GO:0006446	Worker	-1.66	0.00240
GO:BP	morphogenesis of follicular epithelium	GO:0016333	Worker	-1.59	0.00448
GO:BP	actin filament organization	GO:0007015	Worker	-1.58	0.00571
GO:BP	positive regulation of insulin receptor signaling pathway	GO:0046628	Worker	-1.60	0.00699
GO:BP	positive regulation of cell population proliferation	GO:0008284	Worker	-1.62	0.00992
GO:BP	pole cell migration	GO:0007280	Worker	1.73	0.03771
GO:BP	female gonad development	GO:0008585	Worker	1.66	0.05082
GO:BP	deactivation of rhodopsin mediated signaling	GO:0016059	Worker	0.84	0.65147
GO:BP	phototransduction	GO:0007602	Worker	0.77	0.77391
GO:MF	myosin light chain binding	GO:0032027	Worker	-1.56	0.00888
GO:MF	NAD+ kinase activity	GO:0003951	Worker	1.77	0.01286
GO:MF	acid phosphatase activity	GO:0003993	Worker	-1.53	0.02019
GO:CC	extracellular region	GO:0005576	Worker	-1.65	0.00071
GO:CC	mitochondrial respiratory chain complex I	GO:0005747	Worker	-1.65	0.00380
GO:CC	endomembrane system	GO:0012505	Worker	-1.45	0.00617
GO:CC	germline ring canal	GO:0045172	Worker	-1.56	0.00943

Table S8: The table shows a summary of the posterior estimate of the difference in mean module eigengenes between QDL and WDL at each of the four time points, for the co-methylation network shown in Figure 4B. There was a difference between castes in module eigengenes for modules 1 and 5 (both $p < 0.0001$), suggesting that close to 2,000 co-methylated genes acquired caste-specific methylation profiles in the first 8h post-grafting. The estimates are derived from the posterior estimates for a Bayesian multivariate generalised additive mixed model where the response variable for each sample was a length-9 vector of eigengenes for the 9 modules. The model allowed for caste-specific, non-linear changes in module eigengenes over time (see Figure 4B), and adjusted for Replicate. The eigengenes were mean-centred and scaled to unit variance, so the units in the ‘Caste difference’ column can be interpreted as the standardised effect size (Cohen’s d). Other columns show the mean deviation of data points from the estimated mean, the 95% credible interval for the mean, and the posterior probability that the true effect size has the opposite sign to the first column (similar to a one-tailed p -value).

Module	Time	Caste difference	Est.Error	Lower 95% CI	Upper 95% CI	PP
Module 0	2	-0.4008448	0.3970968	-1.0698994	0.3730978	0.15
Module 0	4	-0.4619276	0.4957985	-1.2926722	0.4922957	0.16
Module 0	6	-0.1832483	0.3873943	-0.9103133	0.5083850	0.30
Module 0	8	0.4351930	0.6112096	-0.7204993	1.6404983	0.24
Module 1	2	0.5807552	0.2591113	0.0972553	0.9956103	0.01 *
Module 1	4	0.9719140	0.3367511	0.3610842	1.4946690	0.00 ***
Module 1	6	1.1734762	0.3037786	0.5278586	1.7626823	0.00 ***
Module 1	8	1.1854419	0.4533987	0.3288729	2.1153677	0.00 ***
Module 2	2	0.2176944	0.3912341	-0.4507076	0.9964346	0.28
Module 2	4	0.2971610	0.4930746	-0.5558925	1.1984166	0.26
Module 2	6	0.2383999	0.4134920	-0.6805154	0.9338290	0.25
Module 2	8	0.0414111	0.6659021	-1.3750950	1.3251637	0.49
Module 3	2	0.4875450	0.3650392	-0.2863166	1.1244075	0.10 ~
Module 3	4	0.6285049	0.4601387	-0.3122680	1.3967142	0.12
Module 3	6	0.4228796	0.3775836	-0.3095880	1.1439543	0.14
Module 3	8	-0.1293309	0.5930406	-1.3632956	0.8746047	0.45
Module 4	2	-0.0424531	0.4215225	-0.8039642	0.6941899	0.43
Module 4	4	0.0780507	0.5338714	-0.8190800	1.0379336	0.49
Module 4	6	0.3615111	0.4606559	-0.3955768	1.1830722	0.20
Module 4	8	0.8079284	0.7446001	-0.7243154	2.0296577	0.16
Module 5	2	0.4351420	0.3018326	-0.1463666	1.0106159	0.06 ~
Module 5	4	0.8461774	0.3806579	0.1064147	1.5495253	0.00 ***
Module 5	6	1.2331060	0.3643380	0.6335591	1.8895803	0.01 *
Module 5	8	1.5959280	0.6532991	0.3686612	2.8233987	0.01 *
Module 6	2	-0.0684655	0.3899636	-0.8395728	0.8267480	0.46
Module 6	4	-0.0199331	0.4939157	-0.8555596	1.0740121	0.46
Module 6	6	0.1455973	0.4202688	-0.6264176	0.9934849	0.37
Module 6	8	0.4281258	0.6691171	-0.8985446	1.6298063	0.24
Module 7	2	0.3498870	0.4453649	-0.3860565	1.2344638	0.22
Module 7	4	0.4923079	0.5679767	-0.4711944	1.6117243	0.18
Module 7	6	0.4272628	0.4811315	-0.5404964	1.1957693	0.16
Module 7	8	0.1547517	0.7328216	-1.3314455	1.4970897	0.37
Module 8	2	-0.2145290	0.4421454	-0.9431084	0.7110450	0.28
Module 8	4	-0.2710188	0.5791029	-1.2596286	0.8691686	0.28
Module 8	6	-0.1694696	0.5130607	-1.2744873	0.8759388	0.37
Module 8	8	0.0901188	0.7123623	-1.3994490	1.2916464	0.43
Module 9	2	0.3771890	0.4416612	-0.4698772	1.1105362	0.19
Module 9	4	0.4041253	0.5462497	-0.5983493	1.2894940	0.26
Module 9	6	0.0808089	0.4181627	-0.6799001	0.9480681	0.42
Module 9	8	-0.5927602	0.6877180	-1.8517213	0.8448935	0.19

Table S9: The table lists the GO and KEGG terms that were significantly enriched among the genes that were assigned to modules 1 and 5 in the co-methylation network analysis plotted in Figure 4B (calculated using hypergeometric tests to identify GO/KEGG terms that were enriched among the genes in the module, relative to the set of genes with annotations that were used in the co-methylation analysis). The tests presented here use the standard *A. mellifera* annotations, and no terms were significantly enriched for module 5.

Module	Ontology	ID	Gene & Background ratios	Enrichment	pvalue
1	BP	regulation of transcription, DNA-templated (GO:0006355)	26/1159 54/3523	1.474	0.014
1	BP	intracellular signal transduction (GO:0035556)	9/1159 15/3523	1.830	0.028
1	CC	cell junction (GO:0030054)	9/1159 12/3523	2.290	0.003
1	CC	postsynaptic membrane (GO:0045211)	9/1159 12/3523	2.290	0.003
1	CC	nucleus (GO:0005634)	55/1159 127/3523	1.332	0.008
1	KEGG	Wnt signaling pathway (ame04310)	26/298 40/799	1.814	0.000
1	KEGG	Notch signaling pathway (ame04330)	9/298 12/799	2.042	0.009
1	KEGG	Hedgehog signaling pathway - fly (ame04341)	9/298 12/799	2.042	0.009
1	KEGG	Longevity regulating pathway - multiple species (ame04213)	11/298 16/799	1.876	0.010
1	KEGG	Phosphatidylinositol signaling system (ame04070)	12/298 18/799	1.821	0.010
1	KEGG	Neuroactive ligand-receptor interaction (ame04080)	29/298 56/799	1.430	0.016
1	KEGG	FoxO signaling pathway (ame04068)	11/298 18/799	1.663	0.033
1	KEGG	Apoptosis - fly (ame04214)	11/298 18/799	1.663	0.033
1	KEGG	MAPK signaling pathway - fly (ame04013)	20/298 39/799	1.402	0.048
1	MF	G protein-coupled receptor activity (GO:0004930)	21/1159 36/3523	1.787	0.001
1	MF	sequence-specific DNA binding (GO:0043565)	35/1159 71/3523	1.514	0.003
1	MF	protein kinase activity (GO:0004672)	9/1159 14/3523	1.962	0.016
1	MF	neurotransmitter:sodium symporter activity (GO:0005328)	7/1159 10/3523	2.135	0.018
1	MF	transmembrane signaling receptor activity (GO:0004888)	9/1159 15/3523	1.830	0.028
1	MF	ATP binding (GO:0005524)	40/1159 95/3523	1.290	0.036
1	MF	acetylcholine-gated cation-selective channel activity (GO:0022848)	6/1159 9/3523	2.032	0.040
1	MF	DNA binding (GO:0003677)	22/1159 48/3523	1.401	0.041
1	MF	nucleotide binding (GO:0000166)	5/1159 7/3523	2.176	0.043

Table S10: The table lists the GO and KEGG terms that were significantly enriched among the genes that were assigned to modules 1 and 5 in the co-methylation network analysis plotted in Figure 4B (calculated using hypergeometric tests to identify GO/KEGG terms that were enriched among the genes in the module, relative to the set of genes with annotations that were used in the co-methylation analysis). The tests presented here use our custom GO/KEGG annotations, that use information from *Drosophila melanogaster*.

Module	Ontology	ID	Gene & Background ratios	Enrichment
1	BP	motor neuron axon guidance (GO:0008045)	25/7961 34/16840	1.
1	BP	courtship behavior (GO:0007619)	11/7961 12/16840	1.
1	BP	dendrite morphogenesis (GO:0048813)	26/7961 36/16840	1.
1	BP	compound eye morphogenesis (GO:0001745)	18/7961 23/16840	1.
1	BP	spiracle morphogenesis, open tracheal system (GO:0035277)	10/7961 11/16840	1.
1	BP	imaginal disc-derived wing morphogenesis (GO:0007476)	33/7961 49/16840	1.
1	BP	neuromuscular junction development (GO:0007528)	12/7961 14/16840	1.
1	BP	regulation of neuroblast proliferation (GO:1902692)	7/7961 7/16840	2.
1	BP	compound eye development (GO:0048749)	21/7961 29/16840	1.
1	BP	imaginal disc-derived wing margin morphogenesis (GO:0008587)	11/7961 13/16840	1.
1	BP	response to ecdysone (GO:0035075)	6/7961 6/16840	2.
1	BP	leg disc proximal/distal pattern formation (GO:0007479)	6/7961 6/16840	2.
1	BP	embryonic pattern specification (GO:0009880)	6/7961 6/16840	2.
1	BP	actin filament organization (GO:0007015)	15/7961 20/16840	1.
1	BP	potassium ion transport (GO:0006813)	8/7961 9/16840	1.
1	BP	synapse organization (GO:0050808)	11/7961 14/16840	1.
1	BP	wing disc development (GO:0035220)	9/7961 11/16840	1.
1	BP	open tracheal system development (GO:0007424)	19/7961 28/16840	1.
1	BP	axon guidance (GO:0007411)	44/7961 74/16840	1.
1	BP	imaginal disc-derived male genitalia development (GO:0007485)	5/7961 5/16840	2.
1	BP	R7 cell differentiation (GO:0045466)	5/7961 5/16840	2.
1	BP	maintenance of epithelial integrity, open tracheal system (GO:0035160)	5/7961 5/16840	2.
1	BP	positive regulation of ERK1 and ERK2 cascade (GO:0070374)	5/7961 5/16840	2.
1	BP	regulation of dendrite development (GO:0050773)	5/7961 5/16840	2.
1	BP	imaginal disc-derived leg joint morphogenesis (GO:0016348)	7/7961 8/16840	1.
1	BP	cuticle pattern formation (GO:0035017)	7/7961 8/16840	1.
1	BP	oogenesis (GO:0048477)	26/7961 41/16840	1.
1	BP	olfactory learning (GO:0008355)	13/7961 18/16840	1.
1	BP	segment polarity determination (GO:0007367)	10/7961 13/16840	1.
1	BP	associative learning (GO:0008306)	8/7961 10/16840	1.
1	BP	axon midline choice point recognition (GO:0016199)	8/7961 10/16840	1.
1	BP	potassium ion transmembrane transport (GO:0071805)	8/7961 10/16840	1.
1	BP	glial cell migration (GO:0008347)	8/7961 10/16840	1.
1	BP	positive regulation of filopodium assembly (GO:0051491)	8/7961 10/16840	1.
1	BP	synaptic growth at neuromuscular junction (GO:0051124)	11/7961 15/16840	1.
1	BP	negative regulation of transcription by RNA polymerase II (GO:0000122)	36/7961 61/16840	1.
1	BP	positive regulation of transcription by RNA polymerase II (GO:0045944)	51/7961 90/16840	1.
1	BP	positive regulation of cell migration (GO:0030335)	6/7961 7/16840	1.
1	BP	tissue development (GO:0009888)	6/7961 7/16840	1.
1	BP	positive regulation of Notch signaling pathway (GO:0045747)	6/7961 7/16840	1.
1	CC	dendrite (GO:0030425)	20/7961 28/16840	1.
1	CC	postsynaptic membrane (GO:0045211)	18/7961 25/16840	1.
1	KEGG	Neuroactive ligand-receptor interaction (dme04080)	12/135 17/312	1.
1	KEGG	FoxO signaling pathway (dme04068)	7/135 9/312	1.
1	MF	DNA-binding transcription activator activity, RNA polymerase II-specific (GO:0001228)	25/7961 35/16840	1.
1	MF	protein homodimerization activity (GO:0042803)	27/7961 39/16840	1.
1	MF	heparin binding (GO:0008201)	7/7961 8/16840	1.
1	MF	transcription regulatory region sequence-specific DNA binding (GO:0000976)	8/7961 10/16840	1.
1	MF	nuclear receptor activity (GO:0004879)	8/7961 10/16840	1.
1	MF	protein kinase activity (GO:0004672)	16/7961 24/16840	1.
1	MF	metalloendopeptidase activity (GO:0004222)	12/7961 17/16840	1.
1	MF	transcription corepressor activity (GO:0003714)	6/7961 7/16840	1.
1	MF	extracellular matrix structural constituent (GO:0005201)	6/7961 7/16840	1.
1	MF	activating transcription factor binding (GO:0033613)	6/7961 7/16840	1.
1	MF	G protein-coupled receptor activity (GO:0004930)	30/7961 50/16840	1.
1	MF	steroid hormone receptor activity (GO:0003707)	9/7961 12/16840	1.

(continued)

Module	Ontology	ID	Gene & Background ratios	Enrichment
5	CC	integral component of membrane (GO:0016021)	10/131 703/16840	1.
5	KEGG	Butanoate metabolism (dme00650)	1/1 5/312	

Table S10: This table is large, and is therefore presented as a separate .csv file. Each row lists one of the 2848 genes that was significantly differentially expressed between QDL and WDL at one or more time points (defined as FDR-corrected $p < 0.05$, calculated using empirical Bayes via `limma::eBayes`), in the analysis using `limma`. The third column lists the pairs of time points for which the gene showed significant differential expression, and the remaining columns give the log fold difference in expression at each pair of time points (positive log fold difference indicates higher expression in QDL relative to WDL).

Table S11: This table is large, and is therefore presented as a separate .csv file. Each row lists one of the 4279 genes that was significantly differentially expressed between one or more pairs of time points in QDL (defined as FDR-corrected $p < 0.05$, calculated using empirical Bayes via `limma::eBayes`), in the analysis using `limma`. The third column lists the pairs of time points for which the focal gene showed a significant difference in expression, and the remaining columns give the log fold difference in expression at each pair of time points (positive log fold difference indicates higher expression at the later time point).

Table S12: This table is large, and is therefore presented as a separate .csv file. Each row lists one of the 1364 genes that was significantly differentially expressed between one or more pairs of time points in WDL (defined as FDR-corrected $p < 0.05$, calculated using empirical Bayes via `limma::eBayes`), in the analysis using `limma`. The third column lists the pairs of time points for which the focal gene showed a significant difference in expression, and the remaining columns give the log fold difference in expression at each pair of time points (positive log fold difference indicates higher expression at the later time point).

Table S13: The table shows the results of GO (Biological Process) gene set enrichment analyses on results of differential expression analysis using limma, comparing QDL and WDL. The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression in QDL relative to WDL (negative values mean WDL $>$ QDL).

GO term	Code	Time	NES	pval
mitotic cell cycle	GO:0000278	6	-2.20	0.00000
mRNA splicing, via spliceosome	GO:0000398	6	-2.17	0.00000
cytoplasmic translation	GO:0002181	2	-2.33	0.00000
DNA replication	GO:0006260	6	-2.60	0.00000
DNA repair	GO:0006281	6	-2.22	0.00000
rRNA processing	GO:0006364	2	-2.34	0.00000
translation	GO:0006412	2	-2.86	0.00000
translational initiation	GO:0006413	6	-2.29	0.00000
protein import into nucleus	GO:0006606	8	-2.27	0.00000
intracellular protein transport	GO:0006886	8	-1.82	0.00000
mitochondrial translation	GO:0032543	2	-2.92	0.00000
mitotic sister chromatid segregation	GO:0000070	8	-2.22	0.00001
DNA replication initiation	GO:0006270	6	-2.24	0.00001
cellular response to DNA damage stimulus	GO:0006974	8	-2.17	0.00001
microtubule-based movement	GO:0007018	8	-2.20	0.00001
axon guidance	GO:0007411	2	1.90	0.00002
double-strand break repair via homologous recombination	GO:0000724	8	-2.18	0.00003
chemical synaptic transmission	GO:0007268	4	1.91	0.00006
chromatin organization	GO:0006325	8	-2.04	0.00010
transcription by RNA polymerase II	GO:0006366	6	-2.02	0.00011
chromosome condensation	GO:0030261	8	-2.05	0.00012
chromosome organization	GO:0051276	8	-2.10	0.00014
transcription initiation from RNA polymerase II promoter	GO:0006367	6	-1.96	0.00016
protein folding	GO:0006457	6	-1.95	0.00017
ribosomal small subunit biogenesis	GO:0042274	6	-1.93	0.00019
histone acetylation	GO:0016573	8	-1.99	0.00020
eggshell chorion gene amplification	GO:0007307	4	-2.14	0.00022
learning or memory	GO:0007611	4	1.90	0.00024
chromatin remodeling	GO:0006338	8	-1.96	0.00027
regulation of alternative mRNA splicing, via spliceosome	GO:0000381	8	-1.84	0.00028
protein deubiquitination	GO:0016579	8	-1.95	0.00031
syncytial blastoderm mitotic cell cycle	GO:0035186	8	-2.04	0.00032
ribosome biogenesis	GO:0042254	6	-2.06	0.00034
DNA-dependent DNA replication	GO:0006261	6	-2.05	0.00044
central nervous system formation	GO:0021556	4	-1.95	0.00047
tRNA processing	GO:0008033	6	-1.94	0.00062
mitochondrion morphogenesis	GO:0070584	8	-1.94	0.00068
mRNA export from nucleus	GO:0006406	8	-1.97	0.00072
pre-replicative complex assembly involved in nuclear cell cycle DNA replication	GO:0006267	6	-1.86	0.00074
maturaton of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000462	4	-2.08	0.00075
negative regulation of glial cell proliferation	GO:0060253	8	-1.81	0.00079
ribosomal large subunit assembly	GO:0000027	2	-1.90	0.00081
compound eye development	GO:0048749	2	1.80	0.00082
defense response to bacterium	GO:0042742	6	-1.95	0.00085
Golgi organization	GO:0007030	8	-1.76	0.00093
double-strand break repair via break-induced replication	GO:0000727	6	-1.90	0.00098
protein sumoylation	GO:0016925	8	-1.86	0.00099
mitotic cytokinesis	GO:0000281	8	-1.87	0.00105
endoplasmic reticulum unfolded protein response	GO:0030968	8	-1.94	0.00106
centrosome cycle	GO:0007098	4	-1.92	0.00112
peptidoglycan recognition protein signaling pathway	GO:0061057	2	-1.89	0.00112
intracellular signal transduction	GO:0035556	2	1.73	0.00130
signal transduction	GO:0007165	6	1.66	0.00137
ubiquitin-dependent protein catabolic process	GO:0006511	8	-1.61	0.00140
centriole replication	GO:0007099	8	-1.91	0.00146

(continued)

GO term	Code	Time	NES	pval
cell adhesion mediated by integrin	GO:0033627	8	-1.92	0.00146
chitin metabolic process	GO:0006030	6	1.81	0.00149
regulation of Toll signaling pathway	GO:0008592	4	-1.90	0.00163
ubiquitin-dependent ERAD pathway	GO:0030433	8	-1.86	0.00167
negative regulation of smoothed signaling pathway	GO:0045879	8	-1.86	0.00172
nuclear pore organization	GO:0006999	8	-1.77	0.00179
dorsal closure	GO:0007391	2	1.74	0.00180
mitochondrial electron transport, NADH to ubiquinone	GO:0006120	2	-1.86	0.00199
protein ubiquitination	GO:0016567	8	-1.73	0.00200
dendrite morphogenesis	GO:0048813	8	-1.61	0.00206
ribosomal large subunit biogenesis	GO:0042273	6	-1.94	0.00214
developmental process	GO:0032502	2	-1.81	0.00218
negative regulation of organ growth	GO:0046621	8	-1.90	0.00224
protein targeting to mitochondrion	GO:0006626	6	-1.84	0.00228
cell redox homeostasis	GO:0045454	6	-1.89	0.00238
asymmetric neuroblast division	GO:0055059	8	-1.88	0.00243
protein transport	GO:0015031	6	-1.70	0.00257
activation of cysteine-type endopeptidase activity involved in apoptotic process	GO:0006919	6	-1.83	0.00273
nucleotide-excision repair	GO:0006289	2	-1.78	0.00293
nervous system development	GO:0007399	2	1.72	0.00305
L-methionine salvage from methylthioadenosine	GO:0019509	4	-1.78	0.00305
mitochondrial genome maintenance	GO:0000002	2	-1.80	0.00312
regulation of terminal button organization	GO:2000331	2	1.83	0.00313
ribosomal large subunit export from nucleus	GO:0000055	8	-1.83	0.00315
protein export from nucleus	GO:0006611	8	-1.81	0.00323
NLS-bearing protein import into nucleus	GO:0006607	6	-1.76	0.00338
transmembrane transport	GO:0055085	2	1.62	0.00340
meiotic cell cycle	GO:0051321	8	-1.89	0.00348
lipid storage	GO:0019915	8	-1.81	0.00355
locomotor rhythm	GO:0045475	2	1.77	0.00359
cellular response to heat	GO:0034605	8	-1.86	0.00366
sphingolipid metabolic process	GO:0006665	6	1.75	0.00374
wing disc dorsal/ventral pattern formation	GO:0048190	2	1.76	0.00375
regulation of transcription, DNA-templated	GO:0006355	2	1.53	0.00380
regulation of mitotic cell cycle	GO:0007346	8	-1.84	0.00387
mitotic chromosome condensation	GO:0007076	8	-1.87	0.00394
positive regulation of G1/S transition of mitotic cell cycle	GO:1900087	6	-1.80	0.00401
border follicle cell migration	GO:0007298	2	1.63	0.00406
protein glycosylation	GO:0006486	6	-1.79	0.00407
regulation of JNK cascade	GO:0046328	2	1.77	0.00408
isoprenoid biosynthetic process	GO:0008299	4	-1.76	0.00433
DNA duplex unwinding	GO:0032508	8	-1.79	0.00435
central complex development	GO:0048036	8	-1.76	0.00448
regulation of exit from mitosis	GO:0007096	4	-1.76	0.00450
mRNA transport	GO:0051028	6	-1.79	0.00453
maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000463	4	-1.85	0.00475
chloride transmembrane transport	GO:1902476	4	1.69	0.00487
DNA endoreduplication	GO:0042023	8	-1.83	0.00509
proteasome assembly	GO:0043248	6	-1.76	0.00538
positive regulation of transcription, DNA-templated	GO:0045893	2	1.58	0.00544
mitotic sister chromatid cohesion	GO:0007064	8	-1.80	0.00565
peptidyl-serine phosphorylation	GO:0018105	2	1.74	0.00573
ubiquitin-dependent protein catabolic process via the multivesicular body sorting pathway	GO:0043162	2	-1.80	0.00574
gene silencing	GO:0016458	8	-1.82	0.00588
phagocytosis, engulfment	GO:0006911	8	-1.70	0.00590
negative regulation of epidermal growth factor receptor signaling pathway	GO:0042059	2	1.78	0.00598
phosphatidylinositol-mediated signaling	GO:0048015	8	-1.74	0.00599
GPI anchor biosynthetic process	GO:0006506	4	-1.74	0.00601
male meiosis chromosome segregation	GO:0007060	8	-1.74	0.00616
circadian rhythm	GO:0007623	2	1.75	0.00631
regulation of mRNA splicing, via spliceosome	GO:0048024	8	-1.79	0.00637

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GO term	Code	Time	NES	pval
ventral cord development	GO:0007419	8	-1.63	0.00689
imaginal disc-derived wing vein morphogenesis	GO:0008586	2	1.76	0.00689
histone arginine methylation	GO:0034969	8	-1.73	0.00699
regulation of membrane potential	GO:0042391	8	1.74	0.00734
thermosensory behavior	GO:0040040	2	1.72	0.00742
negative regulation of transcription, DNA-templated	GO:0045892	2	1.59	0.00748
male meiotic nuclear division	GO:0007140	8	-1.77	0.00758
dorsal/ventral axis specification, ovarian follicular epithelium	GO:0008069	4	-1.82	0.00775
imaginal disc-derived wing morphogenesis	GO:0007476	2	1.56	0.00785
synaptic growth at neuromuscular junction	GO:0051124	2	1.72	0.00785
ommatidial rotation	GO:0016318	2	1.70	0.00797
positive regulation of GTPase activity	GO:0043547	8	-1.65	0.00808
sister chromatid cohesion	GO:0007062	8	-1.76	0.00822
endocytosis	GO:0006897	8	-1.66	0.00823
transcription, DNA-templated	GO:0006351	8	-1.59	0.00844
cellular response to gamma radiation	GO:0071480	4	-1.71	0.00846
regulation of cell shape	GO:0008360	8	-1.70	0.00867
defense response to fungus	GO:0050832	4	-1.74	0.00894
cell fate specification	GO:0001708	2	1.71	0.00915
positive regulation of apoptotic process	GO:0043065	8	-1.65	0.00947
positive regulation of endocytosis	GO:0045807	8	-1.75	0.00951
tRNA modification	GO:0006400	2	-1.75	0.00963
reciprocal meiotic recombination	GO:0007131	4	-1.78	0.00964
intra-S DNA damage checkpoint	GO:0031573	2	-1.72	0.00964
regulation of cell cycle	GO:0051726	2	1.67	0.00966
activation of protein kinase activity	GO:0032147	8	-1.76	0.00986
protein phosphorylation	GO:0006468	2	1.54	0.00988
embryonic heart tube development	GO:0035050	8	-1.77	0.00993

Table S14: The table shows the results of GO (Molecular Function) gene set enrichment analyses on results of differential expression analysis using limma, comparing QDL and WDL. The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression in QDL relative to WDL (negative values mean WDL $>$ QDL).

GO term	Code	Time	NES	pval
nucleic acid binding	GO:0003676	8	-1.68	0.00000
chromatin binding	GO:0003682	8	-2.31	0.00000
RNA binding	GO:0003723	2	-1.77	0.00000
mRNA binding	GO:0003729	8	-2.07	0.00000
structural constituent of ribosome	GO:0003735	2	-2.84	0.00000
translation initiation factor activity	GO:0003743	6	-2.36	0.00000
Rab GTPase binding	GO:0017137	8	-2.15	0.00000
DNA replication origin binding	GO:0003688	6	-2.23	0.00001
DNA-binding transcription factor activity	GO:0003700	2	1.87	0.00001
structural constituent of cuticle	GO:0042302	6	2.12	0.00001
DNA helicase activity	GO:0003678	6	-2.28	0.00002
single-stranded DNA binding	GO:0003697	6	-2.23	0.00002
ATPase activity	GO:0016887	8	-1.95	0.00002
unfolded protein binding	GO:0051082	6	-2.13	0.00002
rRNA binding	GO:0019843	2	-2.10	0.00005
sequence-specific DNA binding	GO:0043565	2	1.77	0.00008
RNA helicase activity	GO:0003724	8	-2.11	0.00016
thiol-dependent ubiquitinyl hydrolase activity	GO:0036459	8	-2.13	0.00018
microtubule binding	GO:0008017	8	-1.90	0.00019
thiol-dependent ubiquitin-specific protease activity	GO:0004843	8	-1.97	0.00025
RNA polymerase I activity	GO:0001054	6	-2.08	0.00031
structural constituent of nuclear pore	GO:0017056	8	-2.07	0.00034
transmembrane transporter activity	GO:0022857	2	1.86	0.00037
heme binding	GO:0020037	8	1.88	0.00043
DNA-directed 5'-3' RNA polymerase activity	GO:0003899	6	-2.05	0.00049
histone binding	GO:0042393	8	-2.02	0.00051
Ran GTPase binding	GO:0008536	8	-1.99	0.00056
DNA-directed DNA polymerase activity	GO:0003887	6	-2.09	0.00086
chitin binding	GO:0008061	8	1.88	0.00092
tRNA binding	GO:0000049	6	-1.96	0.00104
3'-5' DNA helicase activity	GO:0043138	8	-1.90	0.00104
damaged DNA binding	GO:0003684	6	-2.01	0.00109
histone acetyltransferase activity	GO:0004402	8	-1.89	0.00150
RNA polymerase III activity	GO:0001056	6	-1.91	0.00154
chaperone binding	GO:0051087	6	-2.03	0.00179
aminoacyl-tRNA editing activity	GO:0002161	8	-1.86	0.00225
iron ion binding	GO:0005506	8	1.80	0.00255
Toll binding	GO:0005121	4	-1.84	0.00257
NADH dehydrogenase activity	GO:0003954	2	-1.83	0.00283
protein disulfide oxidoreductase activity	GO:0015035	6	-1.91	0.00326
protein heterodimerization activity	GO:0046982	4	1.58	0.00358
methylated histone binding	GO:0035064	8	-1.80	0.00382
ubiquitin protein ligase binding	GO:0031625	8	-1.81	0.00383
ubiquitin protein ligase activity	GO:0061630	8	-1.59	0.00433
oxidoreductase activity, acting on paired donors, [...]	GO:0016705	4	1.73	0.00457
endonuclease activity	GO:0004519	6	-1.81	0.00466
extracellular ligand-gated ion channel activity	GO:0005230	6	1.74	0.00489
GTPase activator activity	GO:0005096	8	-1.56	0.00501
transmembrane signaling receptor activity	GO:0004888	8	1.81	0.00520
cullin family protein binding	GO:0097602	8	-1.77	0.00522
cation channel activity	GO:0005261	4	1.65	0.00614
transcription coregulator activity	GO:0003712	8	-1.71	0.00655
monooxygenase activity	GO:0004497	4	1.69	0.00687
microtubule motor activity	GO:0003777	8	-1.74	0.00706
ribosomal large subunit binding	GO:0043023	6	-1.72	0.00753

(continued)

GO term	Code	Time	NES	pval
histone methyltransferase activity	GO:0042054	8	-1.76	0.00779
phospholipid binding	GO:0005543	8	-1.73	0.00781
DNA binding	GO:0003677	8	-1.23	0.00817
cyclin-dependent protein serine/threonine kinase regulator activity	GO:0016538	8	-1.73	0.00842
RNA polymerase II core promoter sequence-specific DNA binding	GO:0000979	8	-1.77	0.00845
ribonuclease P activity	GO:0004526	2	-1.74	0.00863
3'-5' exonuclease activity	GO:0008408	6	-1.76	0.00890
magnesium ion binding	GO:0000287	8	-1.70	0.00918
peptide receptor activity	GO:0001653	6	1.65	0.00936
class I DNA-(apurinic or apyrimidinic site) endonuclease activity	GO:0140078	6	-1.69	0.00936
RNA polymerase II CTD heptapeptide repeat kinase activity	GO:0008353	4	-1.84	0.00949
methyltransferase activity	GO:0008168	6	-1.70	0.00953
guanyl-nucleotide exchange factor activity	GO:0005085	8	-1.71	0.00969

Table S15: The table shows the results of GO (Cellular Component) gene set enrichment analyses on results of differential expression analysis using limma, comparing QDL and WDL. The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression in QDL relative to WDL (negative values mean WDL > QDL).

GO term	Code	Time	NES	pval
polytene chromosome	GO:0005700	8	-2.21	0.00000
nucleolus	GO:0005730	2	-2.31	0.00000
mitochondrion	GO:0005739	2	-1.89	0.00000
mitochondrial large ribosomal subunit	GO:0005762	2	-2.77	0.00000
mitochondrial small ribosomal subunit	GO:0005763	2	-2.30	0.00000
endoplasmic reticulum	GO:0005783	4	-1.95	0.00000
cytosol	GO:0005829	8	-1.58	0.00000
ribosome	GO:0005840	2	-2.42	0.00000
endomembrane system	GO:0012505	6	-2.02	0.00000
cytosolic ribosome	GO:0022626	8	2.18	0.00000
preribosome, large subunit precursor	GO:0030687	6	-2.33	0.00000
small-subunit processome	GO:0032040	4	-2.49	0.00000
precatalytic spliceosome	GO:0071011	6	-2.16	0.00000
catalytic step 2 spliceosome	GO:0071013	6	-2.10	0.00000
chromosome, centromeric region	GO:0000775	8	-2.19	0.00001
plasma membrane	GO:0005886	2	1.68	0.00001
axon	GO:0030424	2	2.06	0.00001
integral component of plasma membrane	GO:0005887	2	1.88	0.00002
cytosolic large ribosomal subunit	GO:0022625	2	-2.17	0.00003
chromatin	GO:0000785	8	-2.12	0.00004
spindle	GO:0005819	8	-2.18	0.00005
nuclear pore	GO:0005643	8	-2.16	0.00006
spliceosomal complex	GO:0005681	6	-2.05	0.00009
chromosome	GO:0005694	8	-2.10	0.00009
endoplasmic reticulum membrane	GO:0005789	4	-1.92	0.00010
extracellular region	GO:0005576	8	1.78	0.00012
polytene chromosome puff	GO:0005703	8	-2.09	0.00012
perinuclear region of cytoplasm	GO:0048471	8	-1.98	0.00034
centrosome	GO:0005813	8	-1.79	0.00041
apical cortex	GO:0045179	8	-1.86	0.00055
mitochondrial respiratory chain complex I	GO:0005747	2	-1.99	0.00073
RNA polymerase I complex	GO:0005736	6	-2.05	0.00104
nucleolar ribonuclease P complex	GO:0005655	6	-1.81	0.00124
MCM complex	GO:0042555	6	-1.90	0.00131
exosome (RNase complex)	GO:0000178	6	-1.97	0.00136
condensed chromosome	GO:0000793	4	-2.00	0.00145
microtubule organizing center	GO:0005815	8	-1.90	0.00161
centriole	GO:0005814	8	-1.91	0.00198
nucleosome	GO:0000786	8	1.87	0.00218
Myb complex	GO:0031523	6	-1.90	0.00225
cyclin-dependent protein kinase holoenzyme complex	GO:0000307	8	-1.86	0.00261
preribosome, small subunit precursor	GO:0030688	8	-1.82	0.00271
transcription factor TFIID complex	GO:0005669	8	-1.83	0.00322
small nuclear ribonucleoprotein complex	GO:0030532	6	-1.91	0.00342
U2 snRNP	GO:0005686	2	-1.79	0.00365
endosome membrane	GO:0010008	8	-1.88	0.00368
cytosolic small ribosomal subunit	GO:0022627	8	1.75	0.00383
prefoldin complex	GO:0016272	2	-1.77	0.00416
midbody	GO:0030496	8	-1.84	0.00462
protein-containing complex	GO:0032991	8	-1.64	0.00463
type Ia terminal bouton	GO:0061177	6	1.69	0.00464
polytene chromosome band	GO:0005704	8	-1.83	0.00484
histone methyltransferase complex	GO:0035097	8	-1.79	0.00487
mitochondrial intermembrane space	GO:0005758	6	-1.87	0.00510
nuclear periphery	GO:0034399	8	-1.80	0.00517

(continued)

GO term	Code	Time	NES	pval
adherens junction	GO:0005912	8	-1.72	0.00531
mediator complex	GO:0016592	6	-1.68	0.00557
muscle tendon junction	GO:0005927	8	-1.80	0.00560
endoplasmic reticulum lumen	GO:0005788	6	-1.81	0.00656
proteasome complex	GO:0000502	6	-1.81	0.00680
eukaryotic 43S preinitiation complex	GO:0016282	6	-1.83	0.00724
transcription repressor complex	GO:0017053	8	-1.74	0.00730
neuron projection	GO:0043005	2	1.75	0.00897
synaptic vesicle	GO:0008021	2	1.67	0.00977
terminal bouton	GO:0043195	2	1.65	0.00979

Table S16: The table shows the results of KEGG gene set enrichment analyses on results of differential expression analysis using limma, comparing QDL and WDL. The enrichment tests use our custom KEGG annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression in QDL relative to WDL (negative values mean WDL $>$ QDL).

KEGG term	Code	Time	NES	pval
Ribosome biogenesis in eukaryotes	dme03008	6	-2.55	0.00000
Ribosome	dme03010	2	-2.67	0.00000
RNA transport	dme03013	4	-2.21	0.00000
DNA replication	dme03030	6	-2.69	0.00000
Spliceosome	dme03040	2	-2.17	0.00000
Protein processing in endoplasmic reticulum	dme04141	8	-2.22	0.00000
Nucleotide excision repair	dme03420	6	-2.26	0.00001
Aminoacyl-tRNA biosynthesis	dme00970	8	-2.12	0.00002
RNA polymerase	dme03020	6	-2.14	0.00010
Tyrosine metabolism	dme00350	2	1.78	0.00034
Basal transcription factors	dme03022	6	-2.00	0.00042
Base excision repair	dme03410	6	-2.06	0.00057
Mismatch repair	dme03430	6	-1.98	0.00070
Ubiquitin mediated proteolysis	dme04120	8	-1.79	0.00081
Fanconi anemia pathway	dme03460	8	-1.95	0.00083
Endocytosis	dme04144	8	-1.69	0.00084
Oxidative phosphorylation	dme00190	6	-1.80	0.00107
MAPK signaling pathway - fly	dme04013	2	1.75	0.00241
Homologous recombination	dme03440	2	-1.89	0.00473
Glycosylphosphatidylinositol (GPI)-anchor biosynthesis	dme00563	4	-1.97	0.00483
Proteasome	dme03050	6	-1.82	0.00521
RNA degradation	dme03018	6	-1.70	0.00523
Porphyrin and chlorophyll metabolism	dme00860	6	-1.79	0.00566

Table S17: The table shows the results of GO (Biological Process) gene set enrichment analyses on results of differential expression analysis using limma, comparing expression between time points within either QDL or WDL (shown in the Caste column). The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression at the later time point (negative values mean WDL > QDL).

GO term	Code	Caste	NES	pval
rRNA processing	GO:0006364	Queen	-2.30	0.00000
biological_process	GO:0008150	Queen	1.83	0.00000
protein import into nucleus	GO:0006606	Queen	-2.31	0.00002
chitin metabolic process	GO:0006030	Queen	2.18	0.00005
DNA replication	GO:0006260	Queen	-2.06	0.00015
DNA repair	GO:0006281	Queen	-1.96	0.00020
ventral cord development	GO:0007419	Queen	-1.87	0.00066
compound eye development	GO:0048749	Queen	-1.86	0.00076
regulation of transcription, DNA-templated	GO:0006355	Queen	-1.53	0.00080
mitotic sister chromatid segregation	GO:0000070	Queen	-2.07	0.00099
negative regulation of transcription by RNA polymerase II	GO:0000122	Queen	-1.66	0.00128
cilium movement	GO:0003341	Queen	-1.99	0.00189
nuclear pore organization	GO:0006999	Queen	-1.92	0.00191
regulation of Toll signaling pathway	GO:0008592	Queen	1.86	0.00192
dendrite guidance	GO:0070983	Queen	-2.06	0.00219
mitotic chromosome condensation	GO:0007076	Queen	-1.99	0.00238
compound eye morphogenesis	GO:0001745	Queen	-1.74	0.00240
chromosome condensation	GO:0030261	Queen	-1.93	0.00250
positive regulation of transcription by RNA polymerase II	GO:0045944	Queen	-1.39	0.00267
centriole replication	GO:0007099	Queen	-1.86	0.00277
microtubule-based movement	GO:0007018	Queen	-1.89	0.00299
DNA endoreduplication	GO:0042023	Queen	-2.00	0.00344
mitotic cell cycle	GO:0000278	Queen	-1.67	0.00346
embryonic heart tube development	GO:0035050	Queen	-1.99	0.00370
peptidyl-threonine phosphorylation	GO:0018107	Queen	-1.89	0.00525
DNA duplex unwinding	GO:0032508	Queen	-1.95	0.00607
meiotic cell cycle	GO:0051321	Queen	-1.86	0.00669
synaptic growth at neuromuscular junction	GO:0051124	Queen	-1.78	0.00676
regulation of alternative mRNA splicing, via spliceosome	GO:0000381	Queen	-1.62	0.00695
ganglion mother cell fate determination	GO:0007402	Queen	-1.80	0.01136
central nervous system formation	GO:0021556	Queen	1.77	0.01260
negative regulation of transcription, DNA-templated	GO:0045892	Queen	-1.59	0.01340
R7 cell development	GO:0045467	Queen	-1.47	0.10354
segmentation	GO:0035282	Queen	-1.26	0.21968
cytoplasmic translation	GO:0002181	Queen	1.19	0.24831
cytoplasmic translation	GO:0002181	Worker	-2.24	0.00000
biological_process	GO:0008150	Worker	2.09	0.00000
regulation of Toll signaling pathway	GO:0008592	Worker	1.82	0.00019
chitin metabolic process	GO:0006030	Worker	1.95	0.00044
central nervous system formation	GO:0021556	Worker	1.80	0.00044
negative regulation of transcription by RNA polymerase II	GO:0000122	Worker	-1.78	0.00073
ganglion mother cell fate determination	GO:0007402	Worker	-1.85	0.00110
regulation of transcription, DNA-templated	GO:0006355	Worker	-1.49	0.00251
positive regulation of transcription by RNA polymerase II	GO:0045944	Worker	-1.48	0.00273
negative regulation of transcription, DNA-templated	GO:0045892	Worker	-1.70	0.00280
synaptic growth at neuromuscular junction	GO:0051124	Worker	-1.79	0.00296
R7 cell development	GO:0045467	Worker	-1.92	0.00422
segmentation	GO:0035282	Worker	-1.71	0.00659
cilium movement	GO:0003341	Worker	-1.60	0.03488
ventral cord development	GO:0007419	Worker	-1.40	0.07234
mitotic sister chromatid segregation	GO:0000070	Worker	-1.46	0.09392
centriole replication	GO:0007099	Worker	-1.44	0.09605
meiotic cell cycle	GO:0051321	Worker	-1.30	0.16579
regulation of alternative mRNA splicing, via spliceosome	GO:0000381	Worker	-1.17	0.19342
DNA duplex unwinding	GO:0032508	Worker	-1.24	0.22628

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GO term	Code	Caste	NES	pval
dendrite guidance	GO:0070983	Worker	-1.18	0.28070
compound eye development	GO:0048749	Worker	-1.07	0.33953
DNA repair	GO:0006281	Worker	-1.05	0.36596
embryonic heart tube development	GO:0035050	Worker	-1.05	0.40351
DNA endoreduplication	GO:0042023	Worker	-1.03	0.41604
mitotic chromosome condensation	GO:0007076	Worker	-1.01	0.45799
protein import into nucleus	GO:0006606	Worker	-0.93	0.59197
DNA replication	GO:0006260	Worker	-0.84	0.74453
peptidyl-threonine phosphorylation	GO:0018107	Worker	0.70	0.77815
nuclear pore organization	GO:0006999	Worker	-0.74	0.78947
mitotic cell cycle	GO:0000278	Worker	-0.83	0.81250
rRNA processing	GO:0006364	Worker	-0.73	0.84906
compound eye morphogenesis	GO:0001745	Worker	-0.70	0.92157
chromosome condensation	GO:0030261	Worker	0.38	0.99706
microtubule-based movement	GO:0007018	Worker	0.36	0.99854

Table S18: The table shows the results of GO (Molecular Function) gene set enrichment analyses on results of differential expression analysis using limma, comparing expression between time points within either QDL or WDL (shown in the Caste column). The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression at the later time point (negative values mean WDL > QDL).

GO term	Code	Caste	NES	pval
nucleic acid binding	GO:0003676	Queen	-1.71	0.00000
chromatin binding	GO:0003682	Queen	-2.17	0.00000
structural constituent of cuticle	GO:0042302	Queen	2.23	0.00000
RNA binding	GO:0003723	Queen	-1.57	0.00001
heme binding	GO:0020037	Queen	2.07	0.00003
DNA binding	GO:0003677	Queen	-1.45	0.00006
chitin binding	GO:0008061	Queen	2.09	0.00008
mRNA binding	GO:0003729	Queen	-1.89	0.00009
Toll binding	GO:0005121	Queen	1.82	0.00030
helicase activity	GO:0004386	Queen	-2.01	0.00044
peroxidase activity	GO:0004601	Queen	1.81	0.00066
oxidoreductase activity, acting on paired donors, [...]	GO:0016705	Queen	1.95	0.00080
RNA helicase activity	GO:0003724	Queen	-2.02	0.00099
iron ion binding	GO:0005506	Queen	1.87	0.00141
structural constituent of nuclear pore	GO:0017056	Queen	-1.98	0.00343
histone binding	GO:0042393	Queen	-1.80	0.00425
monooxygenase activity	GO:0004497	Queen	1.79	0.00555
sequence-specific DNA binding	GO:0043565	Queen	-1.39	0.00555
Ran GTPase binding	GO:0008536	Queen	-1.91	0.00578
RNA polymerase II activating transcription factor binding	GO:0001102	Queen	-1.76	0.00823
ATPase activity	GO:0016887	Queen	-1.59	0.00823
DNA helicase activity	GO:0003678	Queen	-1.86	0.00875
molecular_function	GO:0003674	Queen	1.34	0.00898
microtubule binding	GO:0008017	Queen	-1.63	0.00954
growth factor activity	GO:0008083	Queen	1.75	0.01450
oxidoreductase activity, acting on CH-OH group of donors	GO:0016614	Queen	1.69	0.03354
carboxylic ester hydrolase activity	GO:0052689	Queen	1.57	0.06907
DNA-binding transcription factor activity, RNA polymerase II-specific	GO:0000981	Queen	-1.20	0.15748
acetylcholine-gated cation-selective channel activity	GO:0022848	Queen	-1.26	0.21728
DNA-binding transcription repressor activity, RNA polymerase II-specific	GO:0001227	Queen	-1.15	0.28205
RNA polymerase II transcription regulatory region sequence-specific DNA binding	GO:0000977	Queen	-1.09	0.30147
DNA-binding transcription factor activity	GO:0003700	Queen	-1.02	0.40816
hormone activity	GO:0005179	Queen	0.75	0.73032
G protein-coupled receptor activity	GO:0004930	Queen	0.61	0.91822
sequence-specific DNA binding	GO:0043565	Worker	-2.22	0.00000
structural constituent of cuticle	GO:0042302	Worker	2.20	0.00003
Toll binding	GO:0005121	Worker	1.94	0.00006
molecular_function	GO:0003674	Worker	1.63	0.00009
DNA-binding transcription factor activity, RNA polymerase II-specific	GO:0000981	Worker	-2.00	0.00010
DNA binding	GO:0003677	Worker	-1.54	0.00014
chitin binding	GO:0008061	Worker	1.98	0.00088
hormone activity	GO:0005179	Worker	-1.92	0.00166
DNA-binding transcription factor activity	GO:0003700	Worker	-1.51	0.00399
G protein-coupled receptor activity	GO:0004930	Worker	-1.76	0.00523
acetylcholine-gated cation-selective channel activity	GO:0022848	Worker	-1.81	0.00646
oxidoreductase activity, acting on CH-OH group of donors	GO:0016614	Worker	1.79	0.00674
RNA polymerase II transcription regulatory region sequence-specific DNA binding	GO:0000977	Worker	-1.74	0.00716
DNA-binding transcription repressor activity, RNA polymerase II-specific	GO:0001227	Worker	-1.83	0.00741
carboxylic ester hydrolase activity	GO:0052689	Worker	1.81	0.00750
growth factor activity	GO:0008083	Worker	1.83	0.00763
RNA polymerase II activating transcription factor binding	GO:0001102	Worker	-1.68	0.00903
peroxidase activity	GO:0004601	Worker	1.72	0.01253
nucleic acid binding	GO:0003676	Worker	-1.26	0.01685
iron ion binding	GO:0005506	Worker	1.60	0.02456
heme binding	GO:0020037	Worker	1.55	0.04043

(continued)

GO term	Code	Caste	NES	pval
oxidoreductase activity, acting on paired donors, [...]	GO:0016705	Worker	1.54	0.06436
chromatin binding	GO:0003682	Worker	-1.10	0.29885
monooxygenase activity	GO:0004497	Worker	1.14	0.33717
RNA helicase activity	GO:0003724	Worker	-1.06	0.35329
histone binding	GO:0042393	Worker	-1.06	0.38199
helicase activity	GO:0004386	Worker	-0.97	0.50000
structural constituent of nuclear pore	GO:0017056	Worker	-0.88	0.61916
mRNA binding	GO:0003729	Worker	-0.92	0.62658
ATPase activity	GO:0016887	Worker	-0.79	0.83495
microtubule binding	GO:0008017	Worker	-0.76	0.87083
RNA binding	GO:0003723	Worker	-0.77	0.94595
DNA helicase activity	GO:0003678	Worker	0.52	0.95161
Ran GTPase binding	GO:0008536	Worker	-0.52	0.96135

Table S19: The table shows the results of GO (Cellular Component) gene set enrichment analyses on results of differential expression analysis using limma, comparing expression between time points within either QDL or WDL (shown in the Caste column). The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression at the later time point (negative values mean WDL > QDL).

GO term	Code	Caste	NES	pval
nucleolus	GO:0005730	Queen	-2.12	0.00000
extracellular region	GO:0005576	Queen	1.99	0.00001
integral component of plasma membrane	GO:0005887	Queen	1.88	0.00002
chromosome	GO:0005694	Queen	-2.27	0.00004
nuclear pore	GO:0005643	Queen	-2.14	0.00055
chromatin	GO:0000785	Queen	-2.05	0.00064
preribosome, large subunit precursor	GO:0030687	Queen	-2.14	0.00069
condensin complex	GO:0000796	Queen	-1.98	0.00146
condensed chromosome	GO:0000793	Queen	-2.02	0.00336
centriole	GO:0005814	Queen	-1.95	0.00364
transcriptionally active chromatin	GO:0035327	Queen	-1.90	0.00515
spindle midzone	GO:0051233	Queen	-1.85	0.00625
ribonucleoprotein complex	GO:1990904	Queen	-1.83	0.00646
small-subunit processome	GO:0032040	Queen	-1.78	0.00823
apical plasma membrane	GO:0016324	Queen	1.70	0.01906
ribosome	GO:0005840	Queen	1.44	0.05501
cytosolic ribosome	GO:0022626	Queen	1.45	0.08500
cytosolic large ribosomal subunit	GO:0022625	Queen	1.00	0.46468
cytosolic small ribosomal subunit	GO:0022627	Queen	0.95	0.51952
postsynaptic membrane	GO:0045211	Queen	-0.70	0.87149
nucleosome	GO:0000786	Queen	0.54	0.91525
cytosolic ribosome	GO:0022626	Worker	-2.19	0.00003
nucleosome	GO:0000786	Worker	-2.08	0.00023
integral component of plasma membrane	GO:0005887	Worker	1.90	0.00035
extracellular region	GO:0005576	Worker	1.89	0.00040
cytosolic large ribosomal subunit	GO:0022625	Worker	-1.99	0.00055
ribosome	GO:0005840	Worker	-1.94	0.00079
cytosolic small ribosomal subunit	GO:0022627	Worker	-1.91	0.00317
apical plasma membrane	GO:0016324	Worker	1.81	0.00696
postsynaptic membrane	GO:0045211	Worker	-1.72	0.00861
ribonucleoprotein complex	GO:1990904	Worker	-1.29	0.15789
condensin complex	GO:0000796	Worker	-1.29	0.19432
spindle midzone	GO:0051233	Worker	-1.24	0.23438
centriole	GO:0005814	Worker	-1.18	0.26431
chromosome	GO:0005694	Worker	-1.14	0.31781
chromatin	GO:0000785	Worker	-1.09	0.33333
condensed chromosome	GO:0000793	Worker	-0.87	0.62972
preribosome, large subunit precursor	GO:0030687	Worker	-0.85	0.64754
transcriptionally active chromatin	GO:0035327	Worker	-0.83	0.66667
small-subunit processome	GO:0032040	Worker	0.58	0.92936
nuclear pore	GO:0005643	Worker	-0.56	0.94355
nucleolus	GO:0005730	Worker	-0.69	0.98582

Table S20: The table shows the results of KEGG gene set enrichment analyses on results of differential expression analysis using limma, comparing expression between time points within either QDL or WDL (shown in the Caste column). The enrichment tests use our custom GO annotations. Only results with $p < 0.01$ are shown, and in cases where the term was significant at multiple time points, only the most significant time point is shown. NES is the ‘normalised enrichment score’, and positive values mean that genes annotated with the focal pathway tend to show higher expression at the later time point (negative values mean WDL > QDL).

KEGG term	Code	Caste	NES	pval
RNA transport	dme03013	Queen	-2.17	0.00000
Ribosome biogenesis in eukaryotes	dme03008	Queen	-2.11	0.00012
Ribosome	dme03010	Queen	1.45	0.05202
Ribosome	dme03010	Worker	-1.84	0.00041
Ribosome biogenesis in eukaryotes	dme03008	Worker	-0.87	0.67871
RNA transport	dme03013	Worker	-0.80	0.87791

Table S21: The table shows a summary of the posterior estimate of the difference in mean module eigengenes between QDL and WDL at each of the four time points, for the co-expression network shown in Figure 4A. There was a difference between castes in module eigengenes for 9/19 modules ($p < 0.05$ or better), suggesting large, coordinated changes in muhc of the transcriptome following experimental grafting. The estimates are derived from the posterior estimates for a Bayesian multivariate generalised additive mixed model where the response variable for each sample was a length-19 vector of eigengenes for the 19 modules. The model allowed for caste-specific, non-linear changes in module eigengenes over time (see Figure 4A), and adjusted for Replicate. The eigengenes were mean-centred and scaled to unit variance, so the units in the ‘Caste difference’ column can be interpreted as the standardised effect size (Cohen’s d). Other columns show the mean deviation of data points from the estimated mean, the 95% credible interval for the mean, and the posterior probability that the true effect size has the opposite sign to the first column (similar to a one-tailed p -value).

Module	Time	Caste difference	Est.Error	Lower 95% CI	Upper 95% CI	PP
Module 0	2	0.1500303	0.2922939	-0.5229733	0.6930837	0.30
Module 0	4	0.2543403	0.3894691	-0.5421509	1.0013759	0.28
Module 0	6	0.3129299	0.3694279	-0.4440154	1.0668608	0.18
Module 0	8	0.3257993	0.5240367	-0.8487726	1.1356694	0.26
Module 1	2	-0.2810615	0.2795083	-0.7739859	0.1886244	0.18
Module 1	4	-0.4729283	0.3558779	-1.0896844	0.1067943	0.08 ~
Module 1	6	-0.5756006	0.3158462	-1.1317963	0.0448347	0.04 *
Module 1	8	-0.5890782	0.5121092	-1.4214201	0.4610965	0.10 ~
Module 2	2	-0.0132697	0.3854441	-0.8584821	0.6298396	0.43
Module 2	4	-0.2171321	0.4982881	-1.3332484	0.6971513	0.27
Module 2	6	-0.6115873	0.4449207	-1.4372646	0.2449511	0.08 ~
Module 2	8	-1.1966352	0.6733042	-2.5830835	-0.0438377	0.02 *
Module 3	2	0.2231401	0.3577019	-0.4574262	0.8362343	0.26
Module 3	4	0.0972729	0.4668677	-0.8140324	0.8392188	0.44
Module 3	6	-0.3776016	0.4270031	-1.1464522	0.3678861	0.19
Module 3	8	-1.2014833	0.6356578	-2.3798586	-0.0156032	0.03 *
Module 4	2	0.2253853	0.3739482	-0.4169929	0.9201448	0.29
Module 4	4	0.3559126	0.4840282	-0.4853831	1.3507544	0.24
Module 4	6	0.3915819	0.4505969	-0.3994254	1.3363595	0.20
Module 4	8	0.3323932	0.7133465	-0.9976017	1.7284143	0.30
Module 5	2	0.0196822	0.3111125	-0.4786219	0.6107480	0.48
Module 5	4	0.1196371	0.3986149	-0.5674617	0.9416136	0.46
Module 5	6	0.2998647	0.3497139	-0.4066501	0.9769192	0.18
Module 5	8	0.5603650	0.5423978	-0.4957856	1.5659789	0.12
Module 6	2	0.4476762	0.3031537	-0.2390612	0.9176562	0.08 ~
Module 6	4	0.8791604	0.3721647	0.0734127	1.4725559	0.02 *
Module 6	6	1.2944525	0.2994924	0.7259466	1.7721808	0.00 ***
Module 6	8	1.6935526	0.5354750	0.8719899	2.8370763	0.00 ***
Module 7	2	0.5642198	0.3417481	-0.1176975	1.1872145	0.06 ~
Module 7	4	0.8222193	0.4245555	-0.0032655	1.6094536	0.03 *
Module 7	6	0.7739984	0.3116537	0.1041834	1.2555863	0.00 ***
Module 7	8	0.4195572	0.4729857	-0.4135835	1.4571192	0.19
Module 8	2	-0.0881957	0.3705974	-0.8100672	0.5787735	0.39
Module 8	4	-0.0293632	0.4917791	-0.9644024	0.9129419	0.50
Module 8	6	0.1764973	0.4734020	-0.7185673	1.1231788	0.36
Module 8	8	0.5293860	0.7004064	-0.7763013	1.6535044	0.18
Module 9	2	0.1909431	0.2485663	-0.2719709	0.5817207	0.24
Module 9	4	0.2293279	0.3053267	-0.3916694	0.7003860	0.26
Module 9	6	0.1151544	0.2400114	-0.3666801	0.5671964	0.28
Module 9	8	-0.1515775	0.4208322	-0.9636952	0.6866461	0.33
Module 10	2	-0.4100284	0.4217513	-1.1189266	0.3984514	0.13
Module 10	4	-0.6502283	0.5316086	-1.5564199	0.3778800	0.11
Module 10	6	-0.7205996	0.4180143	-1.4999455	-0.0677258	0.02 *
Module 10	8	-0.6211423	0.6217876	-1.6922872	0.4862633	0.13
Module 11	2	0.1532437	0.3172910	-0.4512898	0.7756292	0.30
Module 11	4	0.1238408	0.4101836	-0.6475256	0.8280135	0.33
Module 11	6	-0.0882087	0.3827099	-0.7998238	0.6140031	0.44

(continued)

Module	Time	Caste difference	Est.Error	Lower 95% CI	Upper 95% CI	PP
Module 11	8	-0.4829048	0.6106772	-1.4094346	0.6453286	0.23
Module 12	2	0.5874883	0.2732333	0.0400770	1.0904430	0.01 *
Module 12	4	1.1369371	0.3484914	0.4842284	1.8236731	0.00 ***
Module 12	6	1.6483462	0.2795238	1.1797072	2.1902089	0.00 ***
Module 12	8	2.1217158	0.3922502	1.4837446	2.8912119	0.00 ***
Module 13	2	0.0711165	0.2561698	-0.4603019	0.5678001	0.39
Module 13	4	0.1886827	0.3214600	-0.4233286	0.7493699	0.27
Module 13	6	0.3526985	0.2792842	-0.1878659	0.8856238	0.09 ~
Module 13	8	0.5631640	0.4753176	-0.3346228	1.4914411	0.07 ~
Module 14	2	0.0859027	0.3336721	-0.5806216	0.7494312	0.39
Module 14	4	0.0610887	0.3954948	-0.6089174	0.8881120	0.41
Module 14	6	-0.0744421	0.2918664	-0.5575841	0.5418604	0.38
Module 14	8	-0.3206898	0.5989368	-1.6571280	0.7993705	0.29
Module 15	2	0.0867301	0.3197798	-0.5220332	0.6813220	0.36
Module 15	4	0.3674044	0.4072913	-0.4286867	1.0846584	0.19
Module 15	6	0.8420231	0.3455839	0.0761096	1.5081281	0.01 *
Module 15	8	1.5105862	0.5314711	0.4569996	2.4155585	0.00 ***
Module 16	2	-0.7256283	0.3821978	-1.3627232	-0.0837200	0.02 *
Module 16	4	-1.0100294	0.4704469	-1.7448629	-0.2102233	0.02 *
Module 16	6	-0.8532033	0.3952519	-1.7438296	-0.1526391	0.02 *
Module 16	8	-0.2551502	0.7173246	-1.7573187	1.1988860	0.33
Module 17	2	0.1100118	0.2001075	-0.2589111	0.4773094	0.30
Module 17	4	0.4395541	0.2561014	-0.0373629	0.8791860	0.06 ~
Module 17	6	0.9886267	0.2054123	0.5988282	1.3419025	0.00 ***
Module 17	8	1.7572298	0.2804798	1.2454114	2.2219627	0.00 ***
Module 18	2	-0.1324890	0.3782039	-0.8191721	0.6912406	0.36
Module 18	4	-0.1695378	0.4639272	-0.9932827	0.8473713	0.31
Module 18	6	-0.1111463	0.3508142	-0.7666660	0.6035094	0.33
Module 18	8	0.0426853	0.6018691	-0.8556599	1.2994184	0.44

```
{r} # read_csv("output/module_G0_table_expr.csv") # finish  
this... #
```