

Table S1. Summary annotation statistics for the gene sets defined by the expression

patterns in Fig. 3A. The genes in each section of the Venn diagram (“Expression Set”) were inspected for annotations derived as described (7) from BLAST analyses of the chicken IPI and GGA Unigene databases. Total: the number of genes in each gene expression set. IPI and GGA Unigene: the number (and percent) of this set that have annotations derived from the respective databases. Total with Annotations: number (and percent) with annotations from either IPI or GGA (or both). No Annotations: the number (and percent) that either have no detectable ortholog in other species or align with unannotated regions of other genomes. Note that in the subsequent GO term analyses we considered only the major four expression patterns (Novel Up and Down, Habituated Up and Down) and did not further subdivide those groups into “specific” versus overlapping subsets.

Expression Set (Fig. 3A)	total	IPI	GGA Unigene	Total with Annotations	No Annotations
Novel-specific UP	81	58 (72%)	59 (73%)	66 (81%)	15 (19%)
Novel-specific DOWN	318	66 (21%)	128 (40%)	135 (42%)	184 (58%)
Habituated-specific UP	1467	792 (54%)	1005 (69%)	1029 (70%)	425 (29%)
Habituated-specific DOWN	1456	916 (66%)	1082 (74%)	1138 (78%)	309 (21%)
(Novel + Habituated) UP	64	42 (66%)	47 (73%)	51 (80%)	13 (20%)
(Novel + Habituated) DOWN	143	35 (24%)	71 (50%)	73 (51%)	70 (49%)
Up-Down or Down-Up	10	8 (80%)	9 (90%)	10 (100%)	0 (0%)