

Supplementary Figure 1. Venn diagram showing the results for the clustering analysis comparing the non-redundant sequences from each library. For ease of interpretation, the ESTs from the reverse libraries were clustered prior to comparing to the two forward libraries. 392 of the 712 sequences in the 3F library were unique to this library, 420 of 772 sequences were unique to the 14F library, and 464 of 605 sequences were unique to the reverse (3R + 14R) libraries (212 to 3R and 252 to 14R).

Supplementary Figure 2. Gene ontology (GO) classification for the non-redundant sequences from each of the four subtractive libraries. The non-redundant sequences were annotated and assigned to three ontologies defined by the gene ontology consortium, and further summarized by assigning GO slim terms. Sequences without a GO term are referred to as unclassified.

Supplementary Figure 3. Differential GO term distribution between day 3 forward and day 3 reverse libraries.

Supplementary Figure 4. Differential GO term distribution between day 14 forward and day 14 reverse libraries.

Supplementary Figure 5. Expression patterns of *SMYD1* (A), *RTN1* (B), *MIDIIP1* (C), *HSP90A* (D), *FCon5* (E), *FOXD1* (F), *DRG1* (G) and *FCon8* (H) in brain (B), eye (E), gill (G), gut (GT), heart (H), kidney (K), liver (L), slow muscle (SM), skin (SK) and fast muscle (FM) of Atlantic salmon normalised to the geometric average of *rps29* and *rpl13*. Samples are a pool of three fish from fasted fish (0 d black), and fish fed to satiation for 8 d (white) and 21 d (grey).

Supplementary Figure 6. Expression patterns of *DNAJA4* (A), *HSPA1B* (B), *CHAC1* (C), *NHP2L1* (D), *DDX21* (E), *FCon14* (F) and *HSP30* (G) in brain (B), eye (E), gill (G), gut (GT), heart (H), kidney (K), liver (L), slow muscle (SM), skin (SK) and fast muscle (FM) of Atlantic salmon normalised to the geometric average of *Rps29* and *Rpl13*. Samples are a pool of three fish from fasted fish (0 d black), and fish fed to satiation for 8 d (white) and 21 d (grey).

Supplementary Figure 7. Expression patterns of *CEBPD* (A), *ASB2* (B), *RCon3* (C), *CTSL1* (D), *GBP* (E), *FXYD8* (F), *CCT8* (G) and *RCon8* (H) in brain (B), eye (E), gill (G), gut (GT), heart (H), kidney (K), liver (L), slow muscle (SM), skin (SK) and fast muscle (FM) of Atlantic salmon normalised to the geometric average of *Rps29* and *Rpl13*. Samples are a pool of three fish from fasted fish (0 d black), and fish fed to satiation for 8 d (white) and 21 d (grey).

Supplementary table 1. qPCR primer sequences, PCR efficiencies, amplicon size and melting temperature for candidate genes.

Supplementary table 2. Accession numbers, blastx result and GO annotation for ESTs from the 3F library. Column headings identify the Genbank accession number, sequence name (clone Id), sequence description (top blastx hit), sequence length (base pairs), minimum e-value (blastx), mean similarity between subject and top 20 blastx hits, number of associated gene ontology terms, gene ontology terms, enzyme codes and interproscan motifs.

Supplementary table 3. Accession numbers, blastx result and GO annotation for ESTs from the 14F library. Column headings identify the Genbank accession number, sequence name (clone Id), sequence description (top blastx hit), sequence length (base pairs), minimum e-value (blastx), mean similarity between subject and top 20 blastx hits, number of associated gene ontology terms, gene ontology terms, enzyme codes and interproscan motifs.

Supplementary table 4. Accession numbers, blastx result and GO annotation for ESTs from the 3R library. Column headings identify the Genbank accession number, sequence name (clone Id), sequence description (top blastx hit), sequence length (base pairs), minimum e-value (blastx), mean similarity between subject and top 20 blastx hits, number of associated gene ontology terms, gene ontology terms, enzyme codes and interproscan motifs.

Supplementary table 5. Accession numbers, blastx result and GO annotation for ESTs from the 14R library. Column headings identify the Genbank accession number, sequence name (clone Id), sequence description (top blastx hit), sequence length (base pairs), minimum e-value (blastx), mean similarity between subject and top 20 blastx hits, number of associated gene ontology terms, gene ontology terms, enzyme codes and interproscan motifs.