Supplemental Fig. S1. Average length of high quality expressed sequence tag (EST) sequences and unigenes showing the distribution of average lengths in nucleotides (nt) for EST sequences and unigenes from both the high P (HP) and low P (LP) libraries.

Supplemental Fig. S2. Mapping databases with top hits for gene ontology (GO) terms of expressed sequence tags (ESTs) from the high P (HP) and low P (LP) complementary DNA (cDNA) libraries.