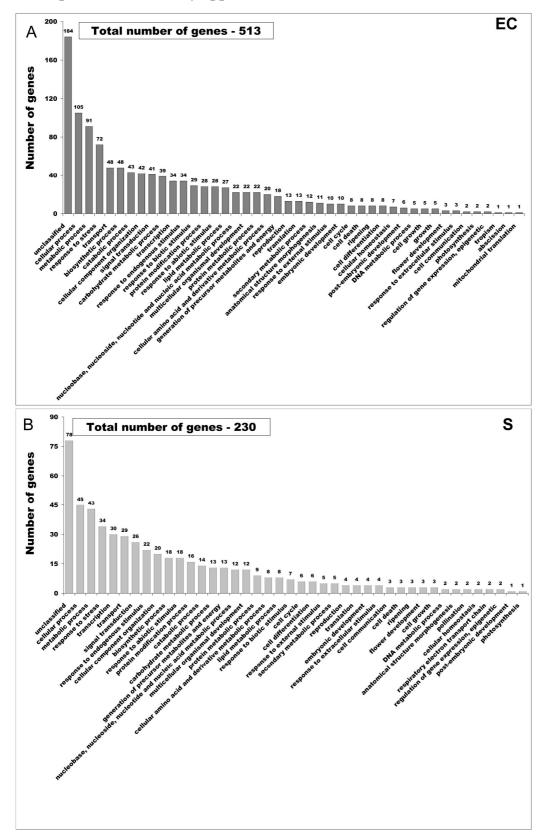
Additional file 8: Gene Ontology distribution of the gene groups identified in roots by the comparative microarray approach.



Genes were identified by microarray analysis as differentially expressed in (A) epidermis+cortex (EC) and (B) stele (S) of roots of 17-day-old *AtHMA4*-expressing tomato

(line 4) as compared with the wild-type (WT) grown in the presence of 5 μ M Zn for one week. Tomato genes were classified by GO of biological processes using the sequences from the Tomato Functional Genomics Database and GO tools available on the TFGD website.