



Figure 7.8. Hierarchical clustering of differentially expressed gene regulatory patterns. Experimental cell growth conditions: wild-type *E. coli* K12 strain ( $Fnr^+$ ) under aerobic conditions ( $+O_2 +Fnr$ ); wild-type *E. coli* K12 strain ( $Fnr^+$ ) under anaerobic conditions ( $-O_2 +Fnr$ ); isogenic *E. coli* K12 strain lacking the *Fnr* gene ( $-O_2 -Fnr$ ) under anaerobic conditions. Each regulatory pattern is identified by numbers that correspond to the regulatory patterns defined in Figure 7.6. The trust parameter is directly related to the mean divided by the standard deviation for each gene measurement.