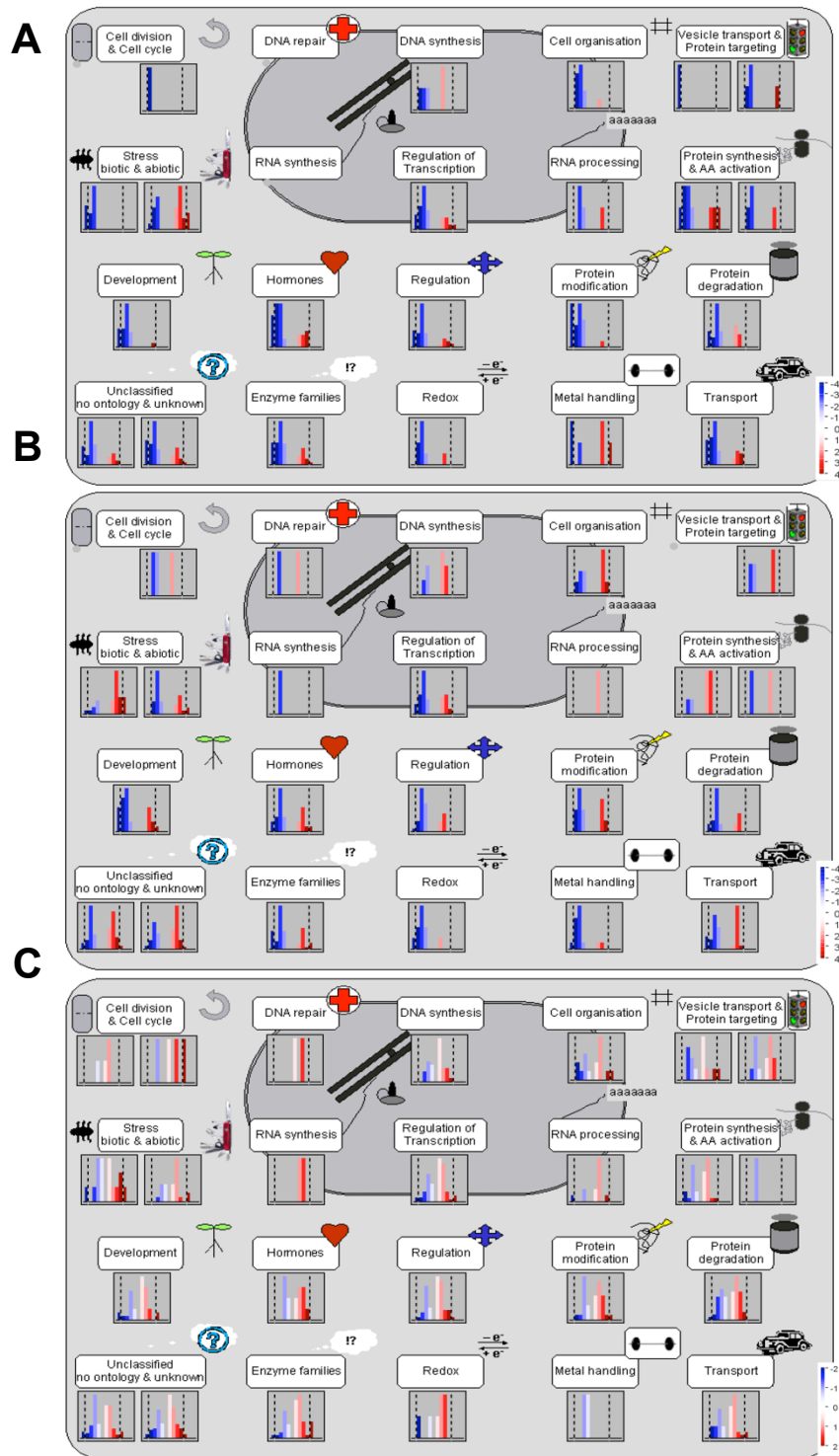




Supplementary Figure 3. Overview of cell function transcripts from tomatoes, grapes and papayas in response to ripening. Cell function transcripts from tomato (A), grape (B) and papaya (C) fruits were analysed using the MapMan software uploaded with microarrays results. Blue and red represent a decrease and an increase of expression respectively, relative to unripe fruits. It is visible 853 transcripts (from 1144) for tomato (> 2.00 fold), 992 transcripts (from 1150) for grape (> 2.00 fold) and 961 transcripts (from 1091) for papaya (> 1.25 fold). Tomato microarray data was downloaded from <http://ted.bti.cornell.edu> (Ozaki et

al., 2010); grape microarray data was downloaded from <http://biomedcentral.com> (Pilati et al., 2007).