



Supplemental Figure S5. Main metabolic pathways affected in the *SULTR3* mutants. The proteins were related to their metabolic pathways according to protein annotation (<http://www.arabidopsis.org>), ontological classification (Bevan et al., 1998) and established features of seed metabolism (Catusse et al., 2008). The bars indicate protein abundance variation in mature seeds of the mutants versus wild-type (log₂ volume ratios in mutant seeds versus wild-type seeds). Significant variations ($p < 0.05$) are represented by red (increase) or green (decrease) bars. For 12S globulins, bars represent volume mean of spots corresponding to At12S1 or At12S4 (log₂ volume ratios versus wild-type). The metabolites differentially accumulated during sulfate deprivation in *Arabidopsis* plants (Nikiforova et al., 2005), are shown in red (increased levels) or in green (decreased levels). * and ** indicate statistically significant variations with $p < 0.05$ and $p < 0.01$, respectively. GSH, glutathione.