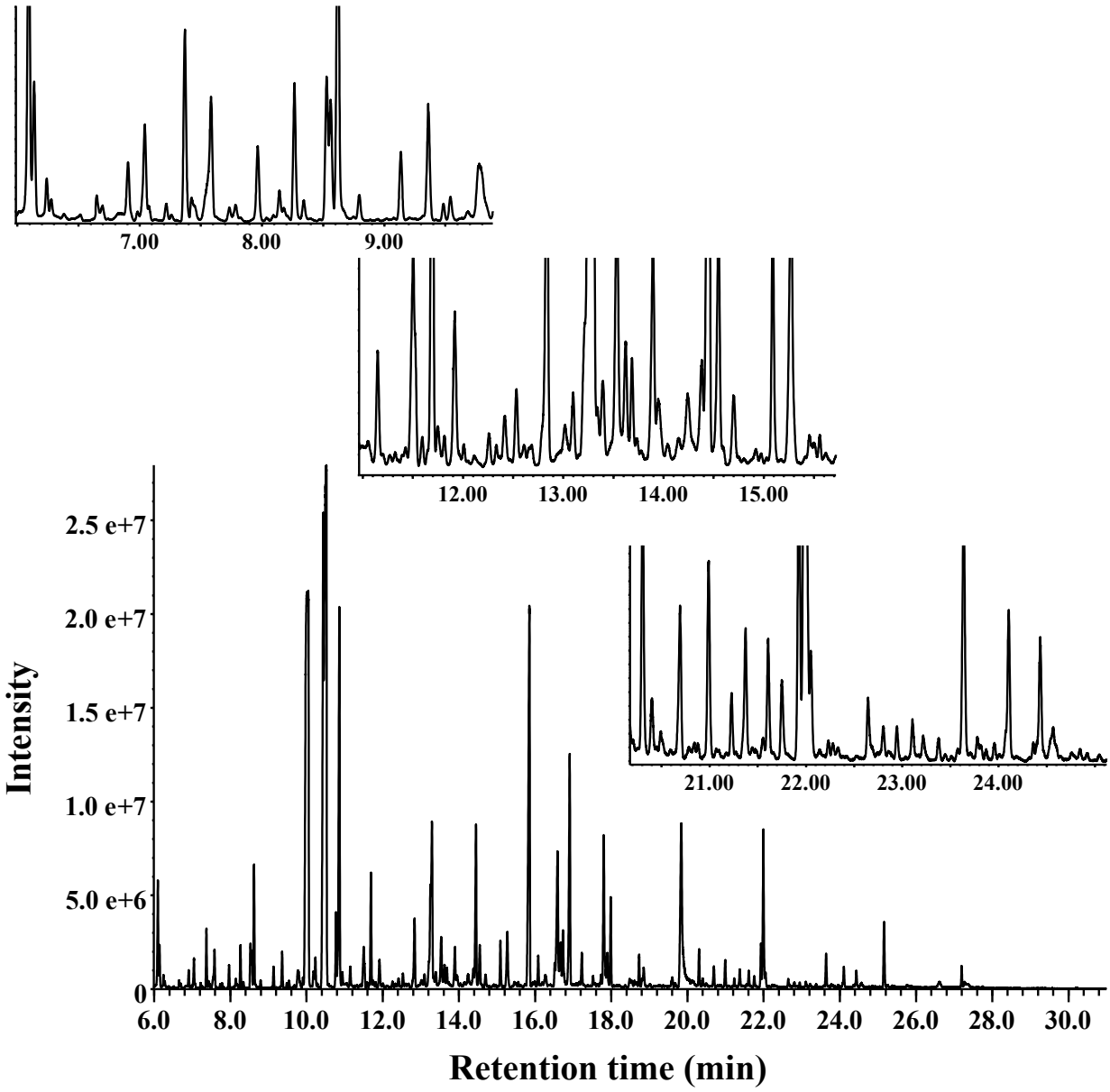
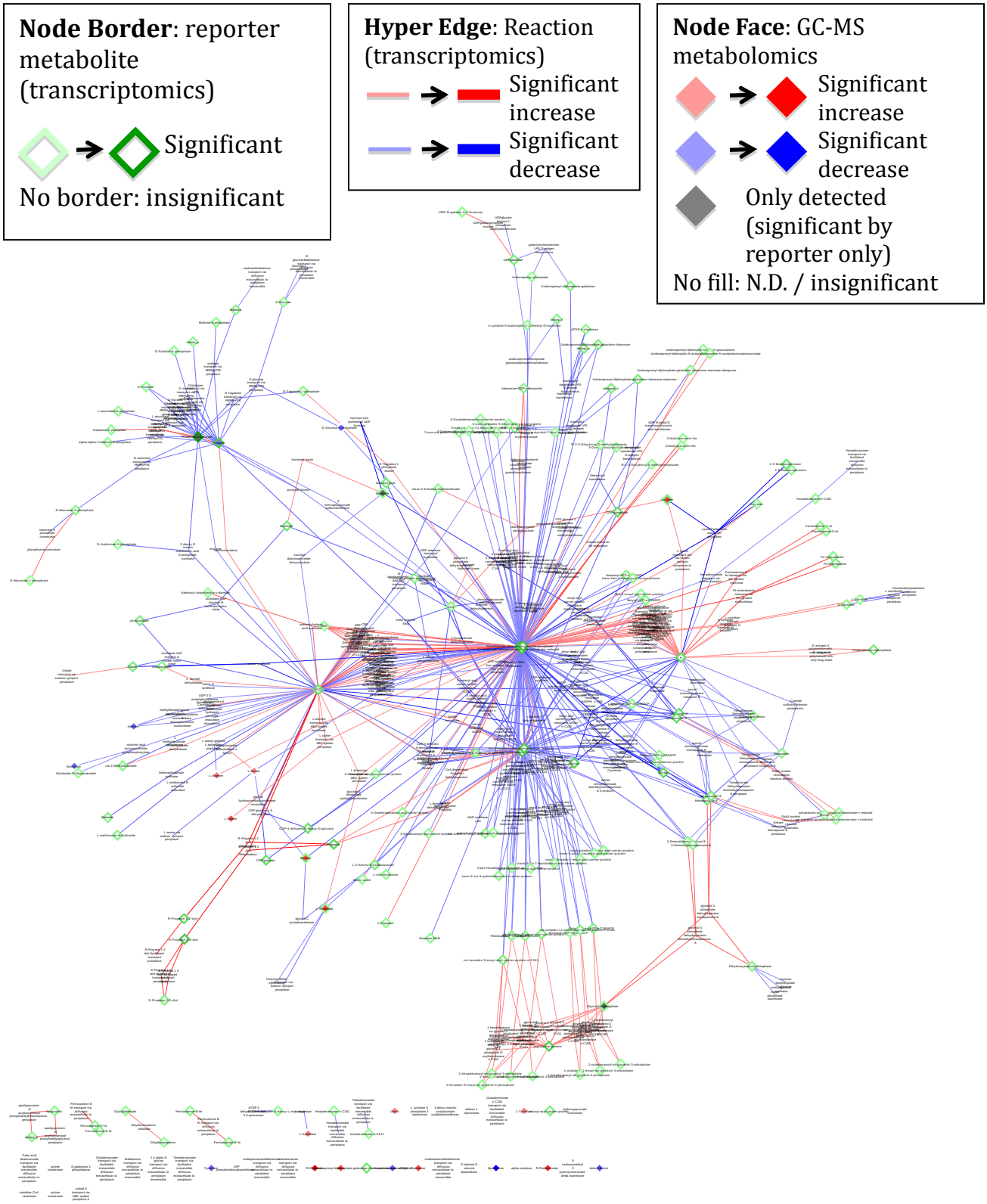
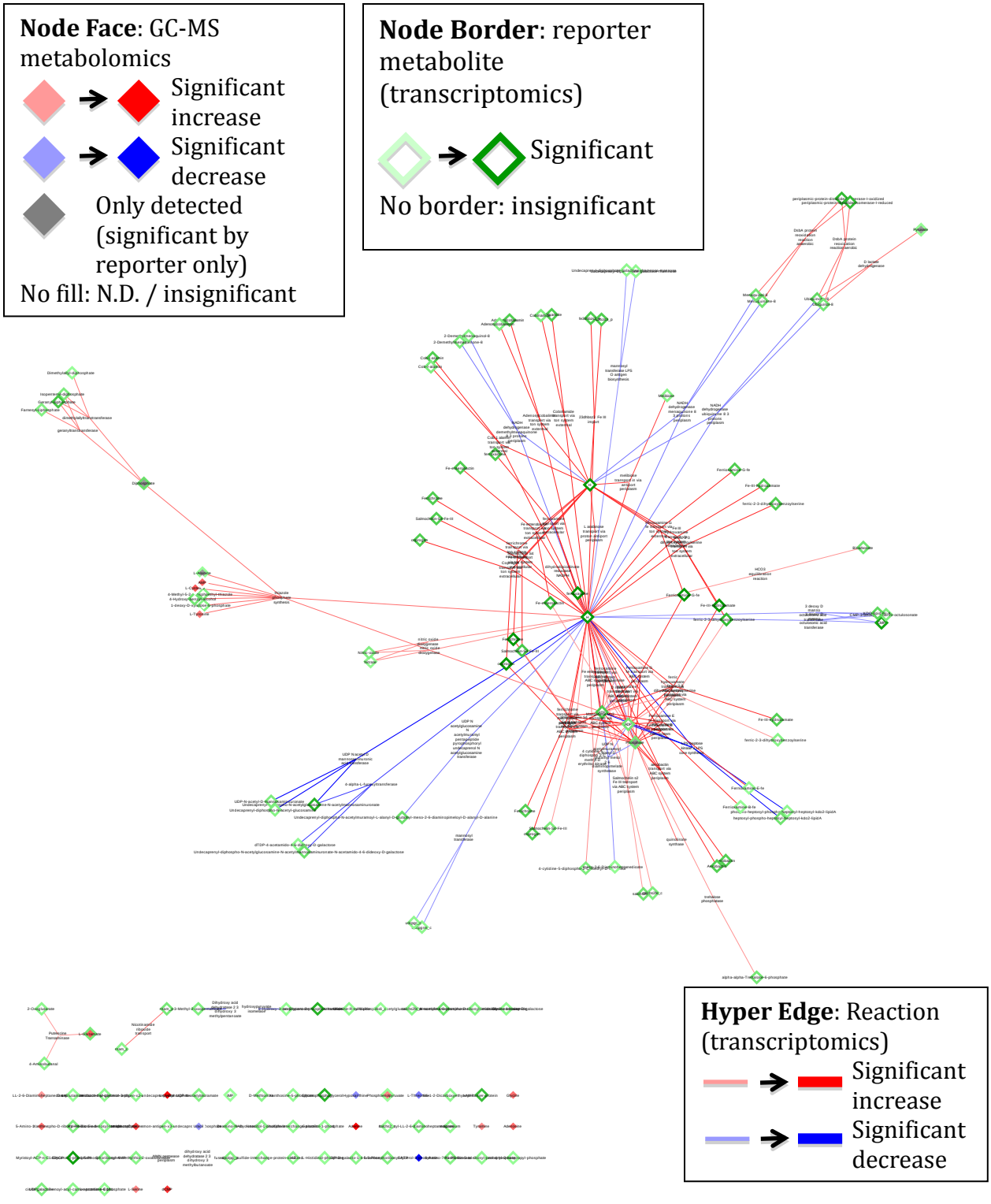



**Supplemental Figure S1. Representative GC-MS chromatogram from analysis of *S.* Typhimurium metabolites.** Cells were grown in LPM media for 20 h, isolated, and their metabolites extracted and chemically derivatized prior to analysis by GC-MS. The complete total ion chromatogram is shown, as well as select enlarged regions presented as insets.




**Supplemental Figure S2. Reporter metabolite network based on alterations in gene expression and metabolomics data in LB and LPM 4 h.** Metabolite nodes were included in the network if they were significantly altered by reporter metabolite analysis (154, $p \leq 0.05$) or metabolomics (23, two-tailed $p \leq 0.05$). Hyper edges were included if an associated reaction was significantly altered (two-tailed $p \leq 0.025$).




**Supplemental Figure S3. Reporter metabolite network based on alterations in gene expression and metabolomics data in LPM at 4 h and 20 h.** Metabolite nodes were included in the network if they were significantly altered by reporter metabolite analysis (131, $p \leq 0.05$) or metabolomics (19, two-tailed $p \leq 0.05$). Hyper edges were included if an associated reaction was significantly altered (two-tailed $p \leq 0.025$).