Figure 6 – Coupling of the methionine pathway and the nitrogen catabolite repression system in *S. cerevisiae* predicted by integration of LeMoNe and CLR networks

Figure 6: LeMoNe module 11 with genes (bottom) and predicted regulators (top) involved in the methionine pathway (regulated by Met28 and Met32) and the nitrogen catabolite repression system (regulated by Gat1, Dal80 and Gln3). The regulators are, from top to bottom: Gat1, predicted by LeMoNe, 1 target predicted by CLR; Dal80, 11 targets predicted by CLR; Gln3, 6 targets predicted by CLR; Met28, predicted by LeMoNe, 4 targets predicted by CLR; Met32, 23 targets predicted by CLR. The upregulated (green) conditions are all amino acid starvation or nitrogen depletion conditions.