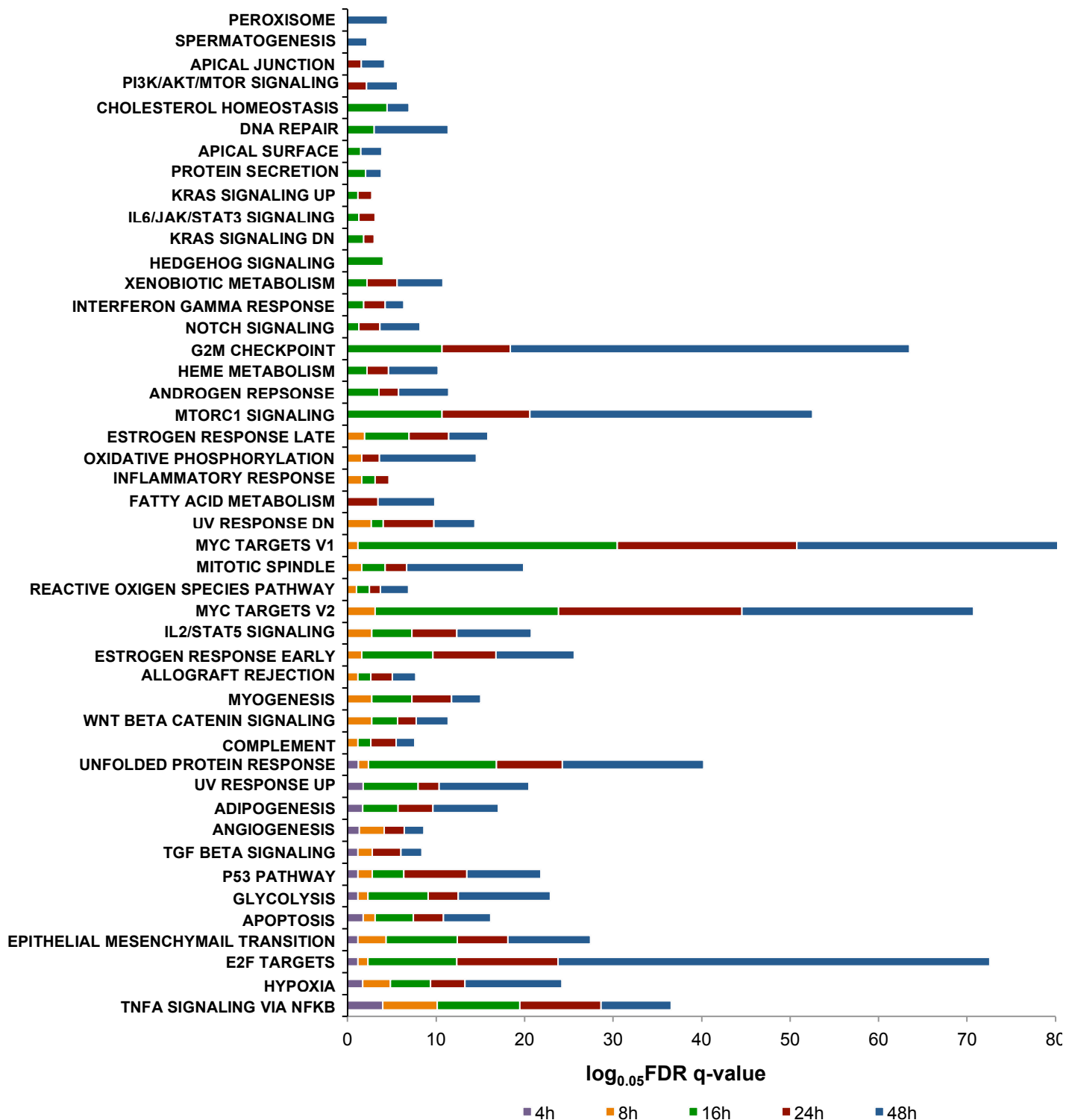


Appendix

Table of contents: Appendix Figure S1



Gene Set Enrichment Analysis of MYC target genes upon Omomyc induction in BT168FO cells

Enrichment of MSigDB hallmark gene sets (left) among genes that present a MYC peak – at promoter, intragenic, and intergenic regions – in BT168FO cells and whose mRNAs are modulated upon Dox treatment (estimated by CuffDiff2; q -value ≤ 0.05). FDR q -values were computed through GSEA; only gene sets with FDR q -value ≤ 0.05 were included. Colours correspond to the different Dox treatment durations (0 - 48 h). The height of coloured bars to the right of each gene set represents the $\log_{0.05}$ of the FDR q -value of that gene set at the various times of Dox treatment.