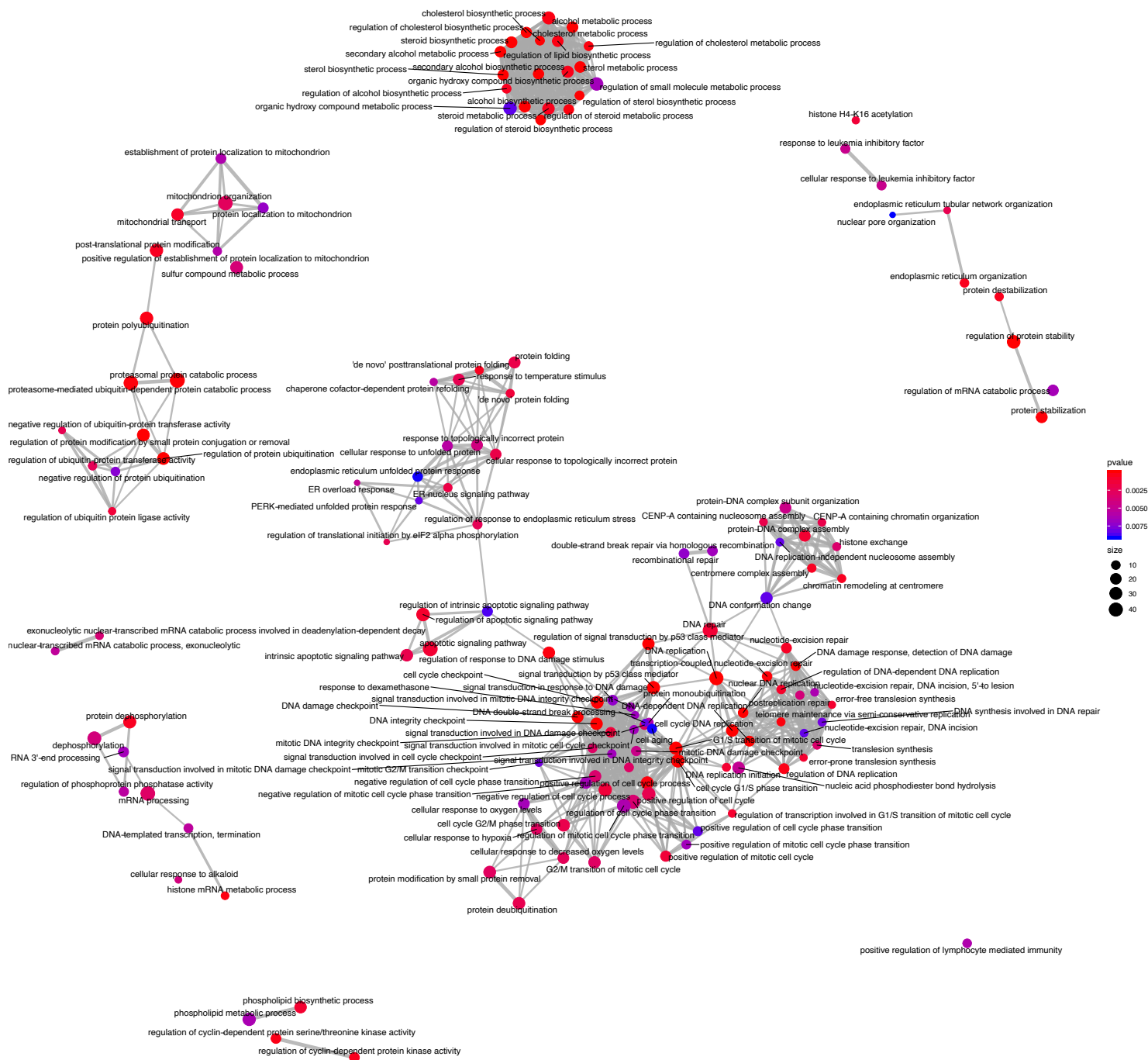
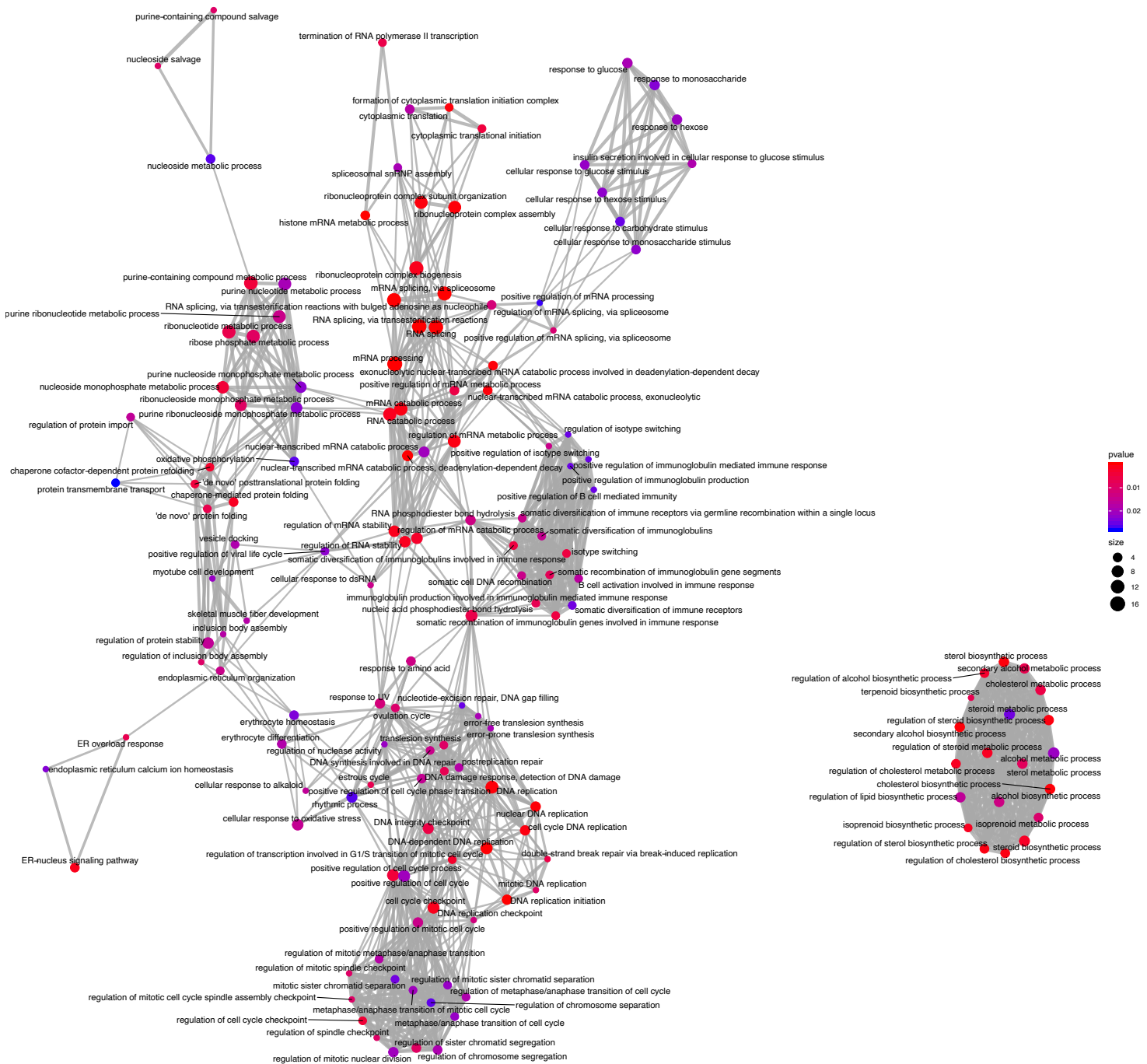


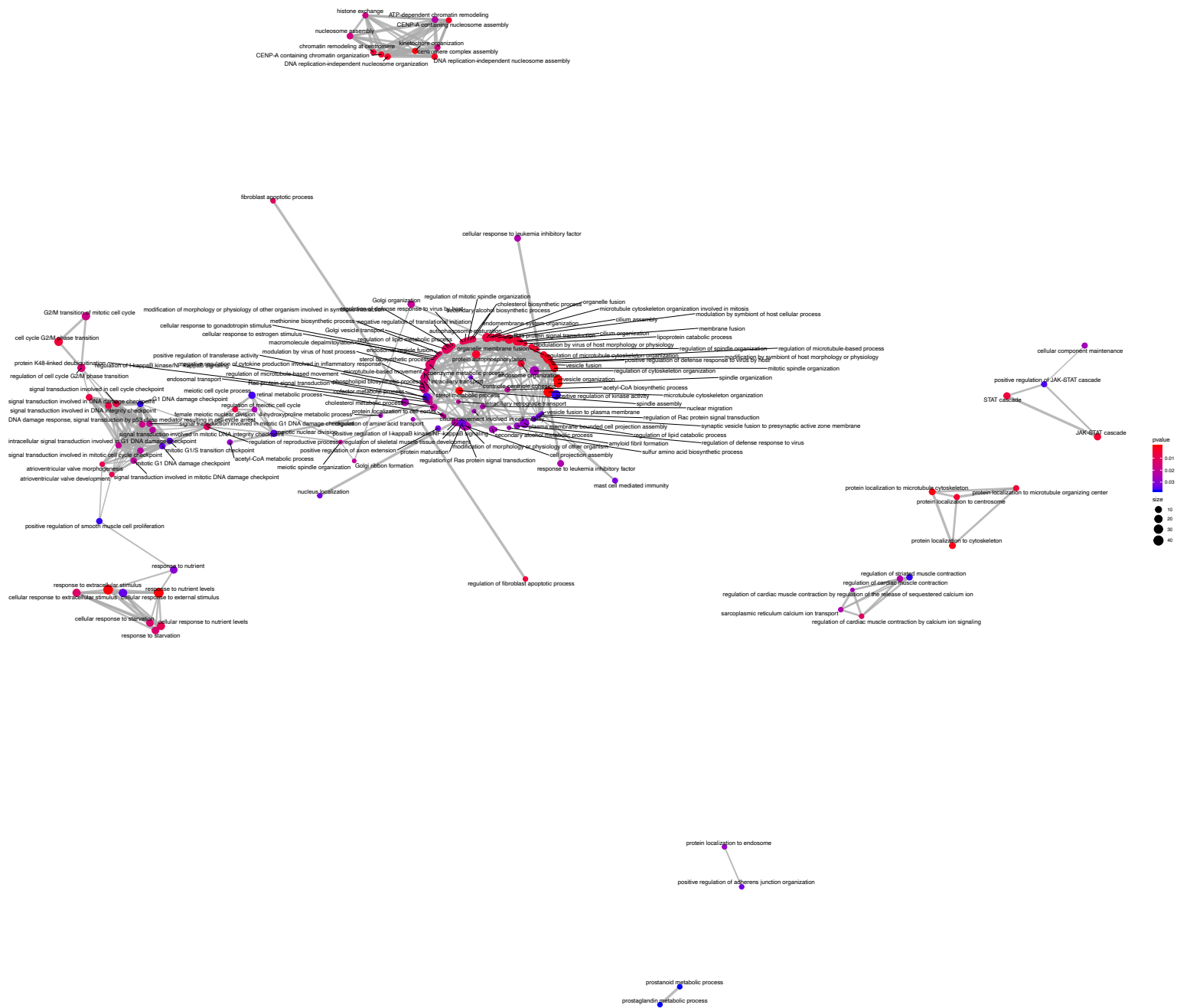
Map of the most significant GO terms (150 nodes) enriched in the union of DE genes upregulated in BxPC-3 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).



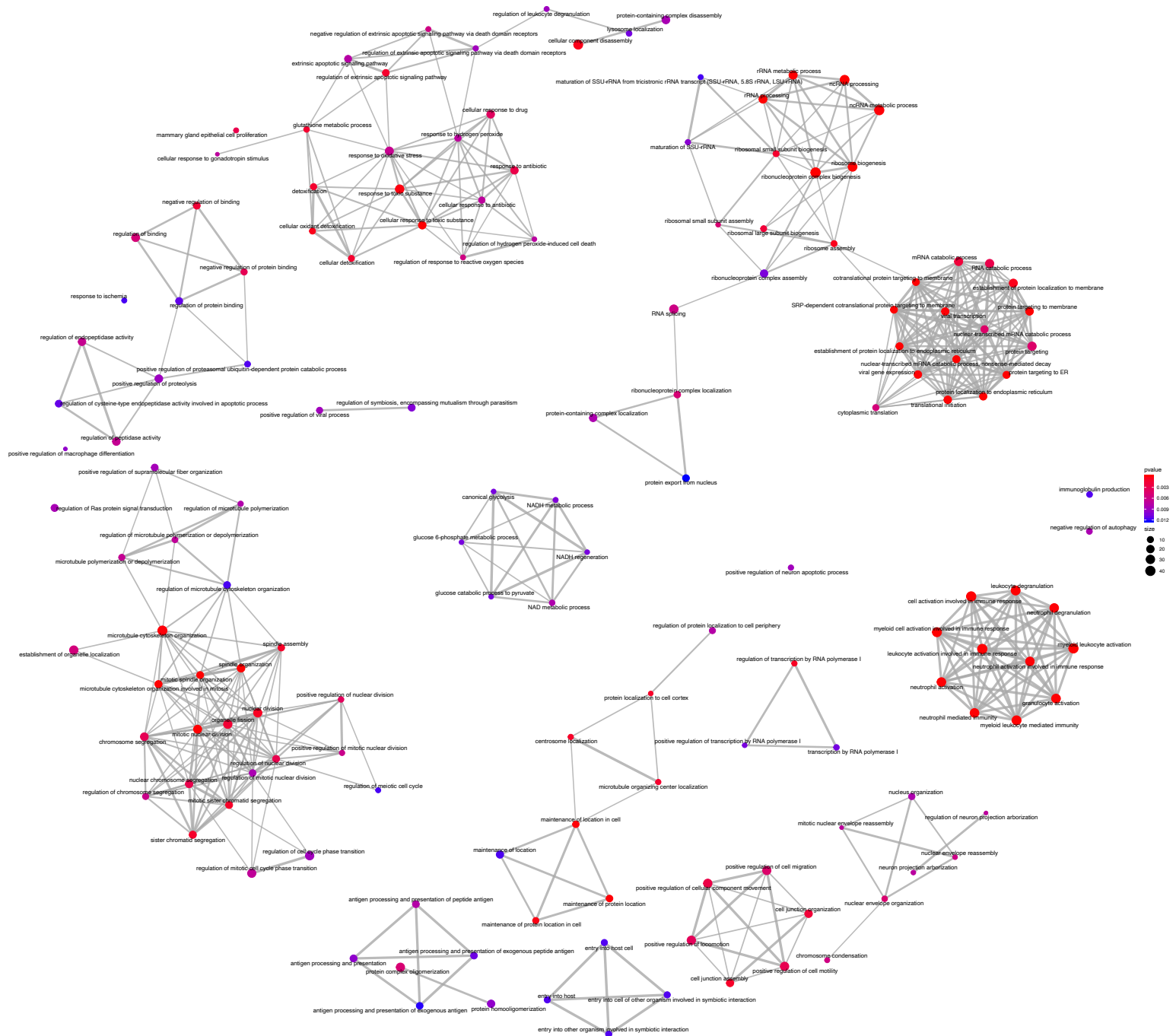
Map of the most significant GO terms (150 nodes) enriched in the union of DE genes upregulated in HCT-15 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).



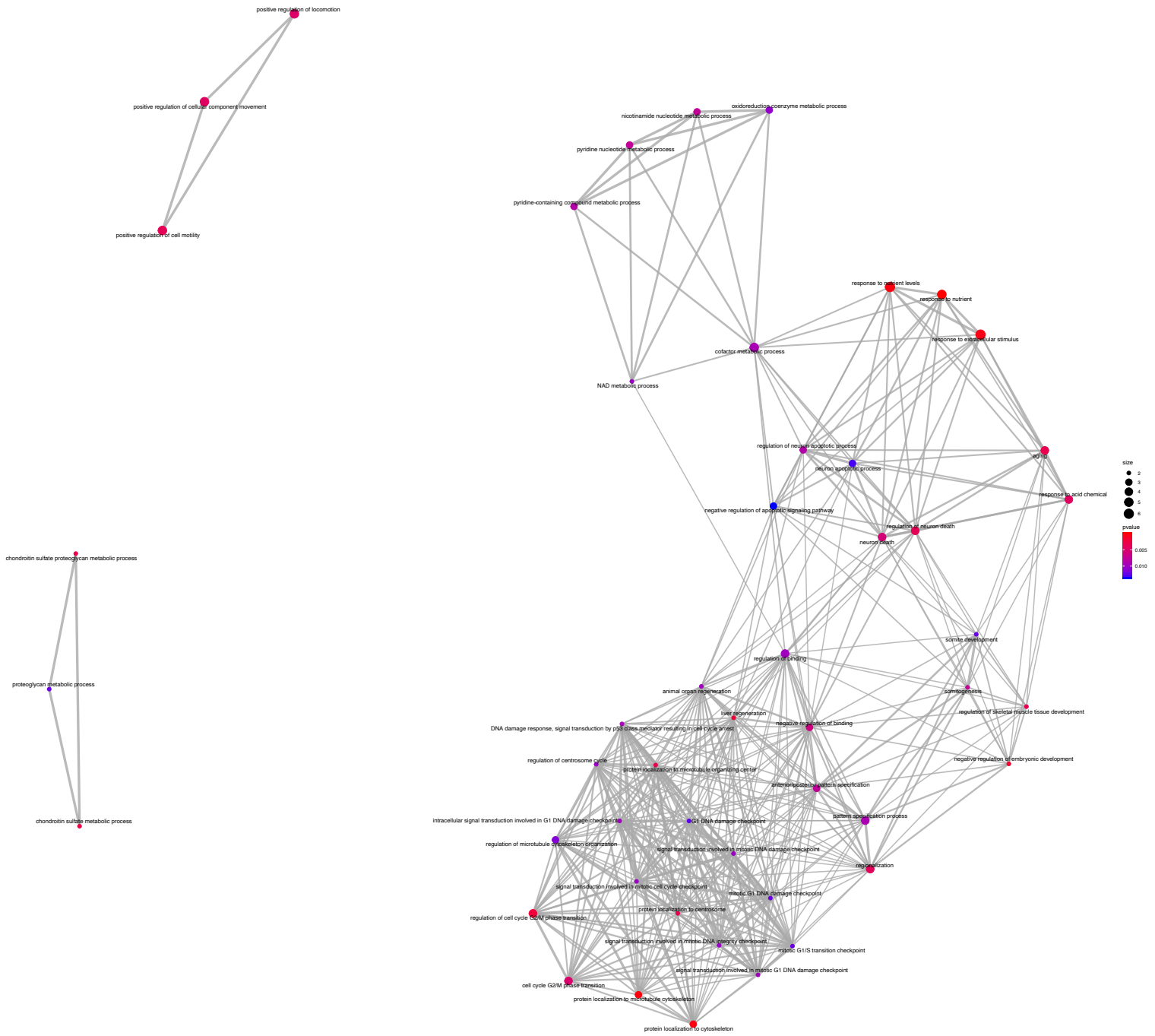
Map of the most significant GO terms (150 nodes) enriched in the union of shared DE genes upregulated in BxPC-3 and HCT-15 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).



Map of the most significant GO terms (150 nodes) enriched in the union of DE genes downregulated in BxPC-3 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).



Map of the most significant GO terms (150 nodes) enriched in the union of DE genes downregulated in HCT-15 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).



Map of the most significant GO terms (50 nodes) enriched in the union of shared DE genes downregulated in BxPC-3 and HCT-15 cells after treatment (DE genes identified after 6 h and 12 h of treatment with both **M** and **B**).