Article

Analysis of the Gene Networks and Pathways Correlated with Tissue Differentiation in Prostate Cancer

Supplementary materials

Figure S1. Gene ontology in PCa pathology

For better visualization of the labels in gene ontology analysis, larger version of Figures 1A-C, 2B-D are shown in supplementary materials.

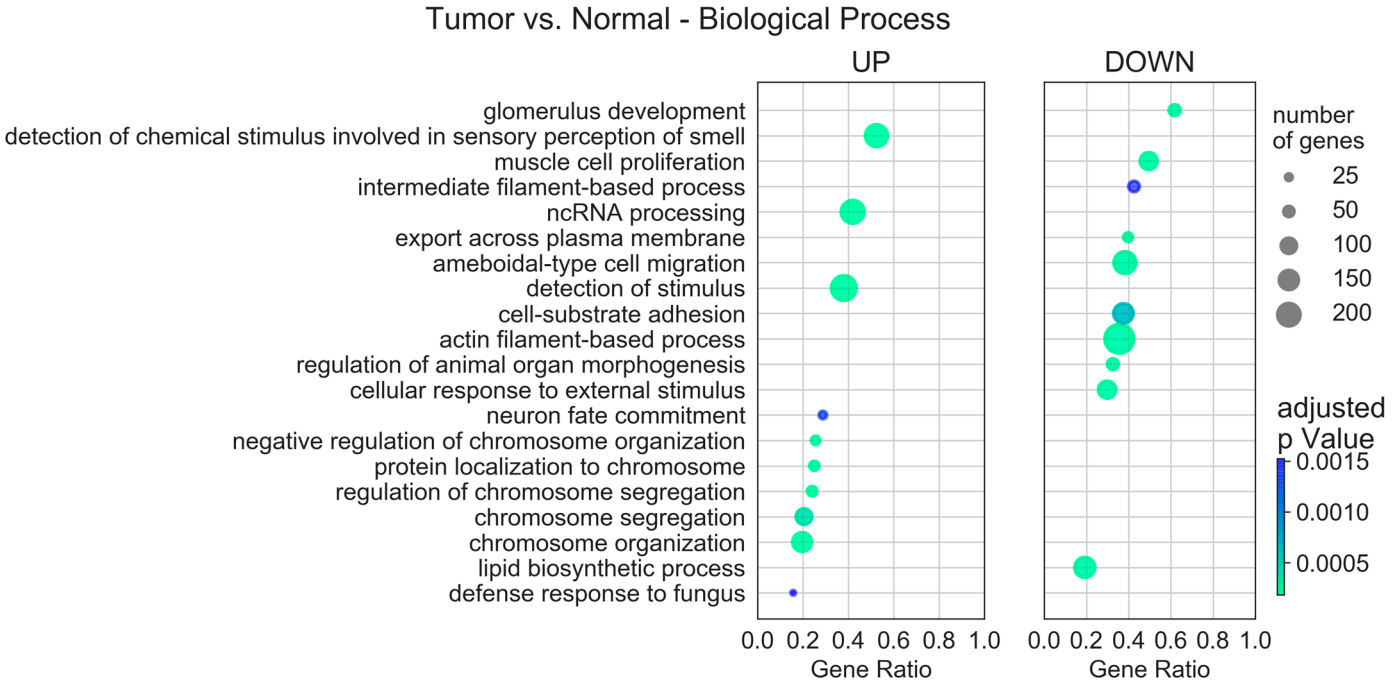


Figure 1A. Gene ontology analysis showing upregulated and downregulated set of genes associated with biological processes in normal and PCa samples.

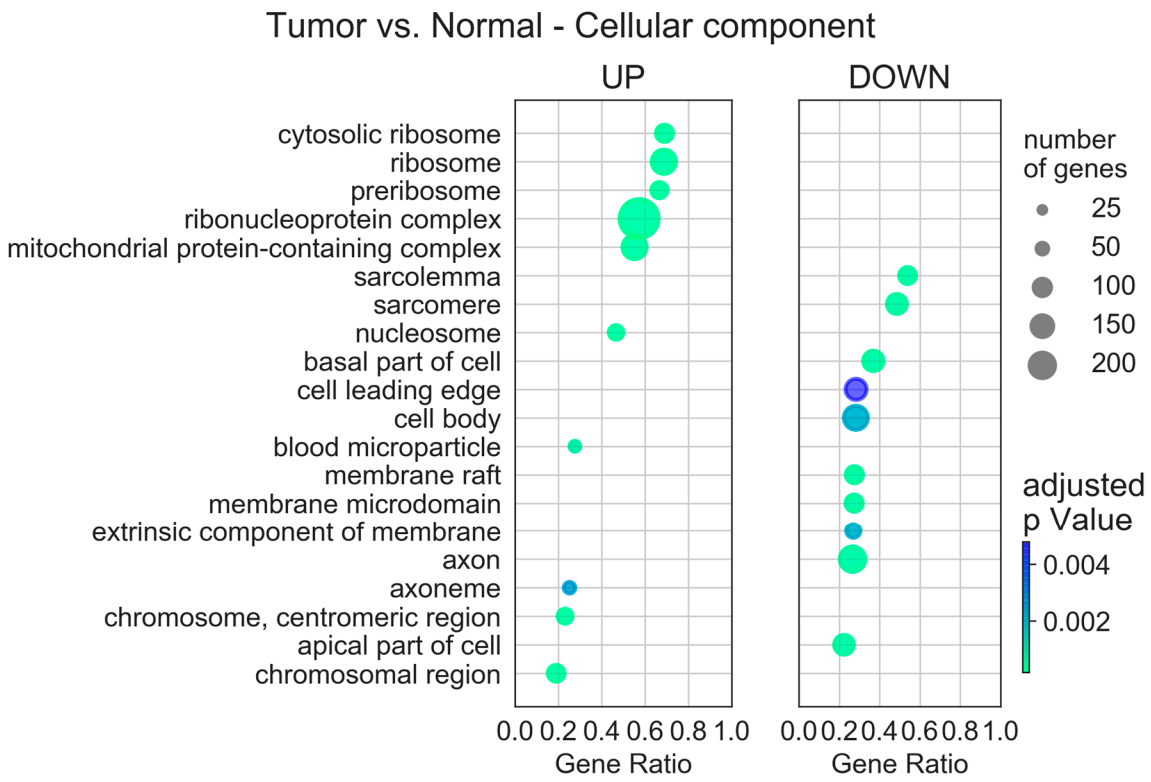


Figure 1B. Gene ontology analysis showing upregulated and downregulated set of genes associated with cellular components in normal and PCa samples.

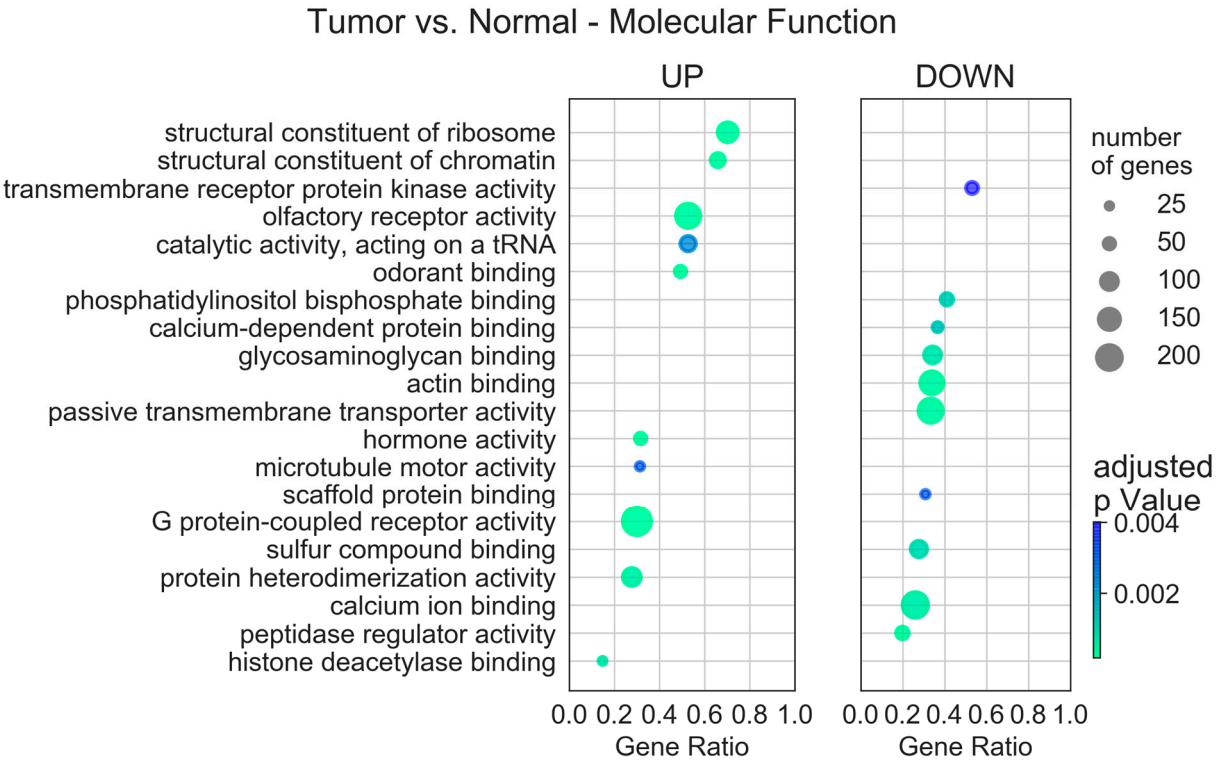


Figure 1C. Gene ontology analysis showing upregulated and downregulated set of genes associated with molecular functions in normal and PCa samples.

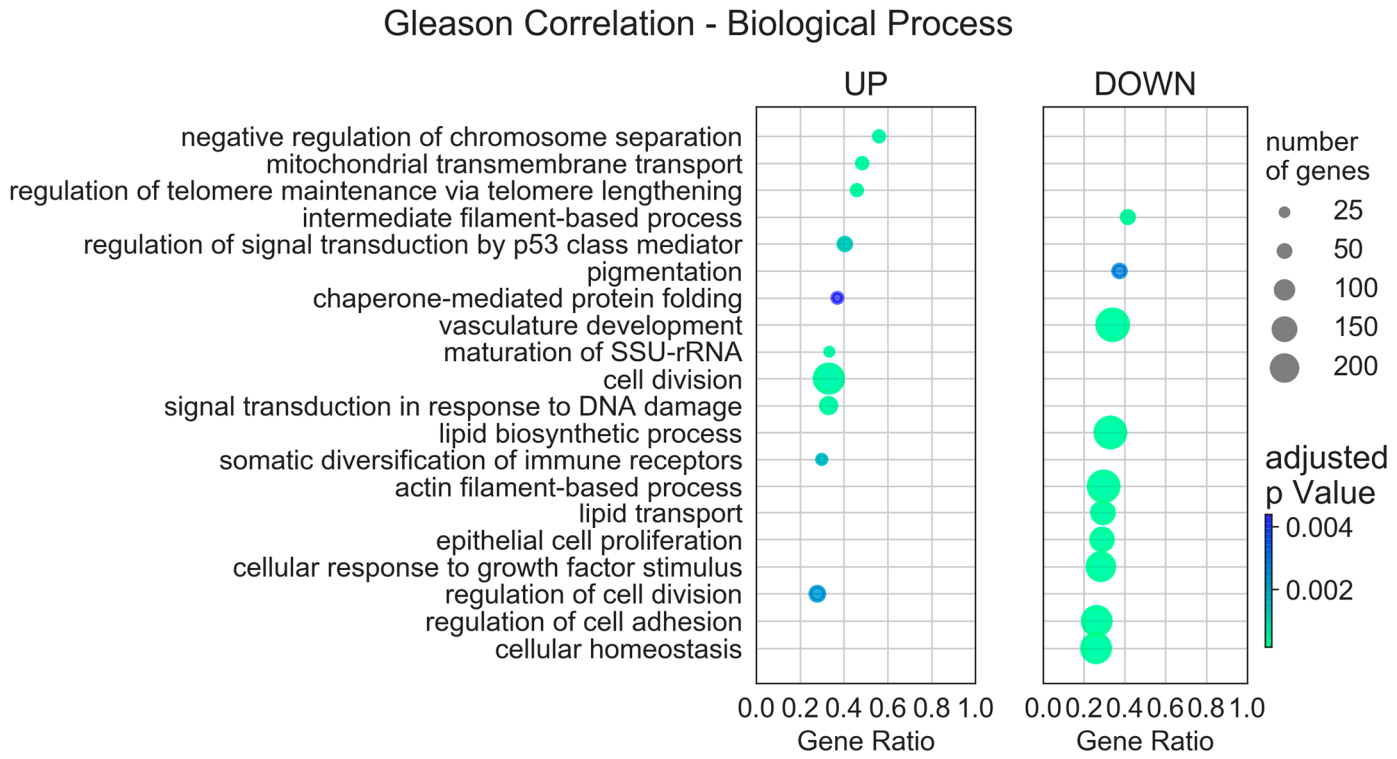


Figure 2B. Gene ontology analysis showing upregulated and downregulated set of genes associated with biological processes in Gleason grade groups.

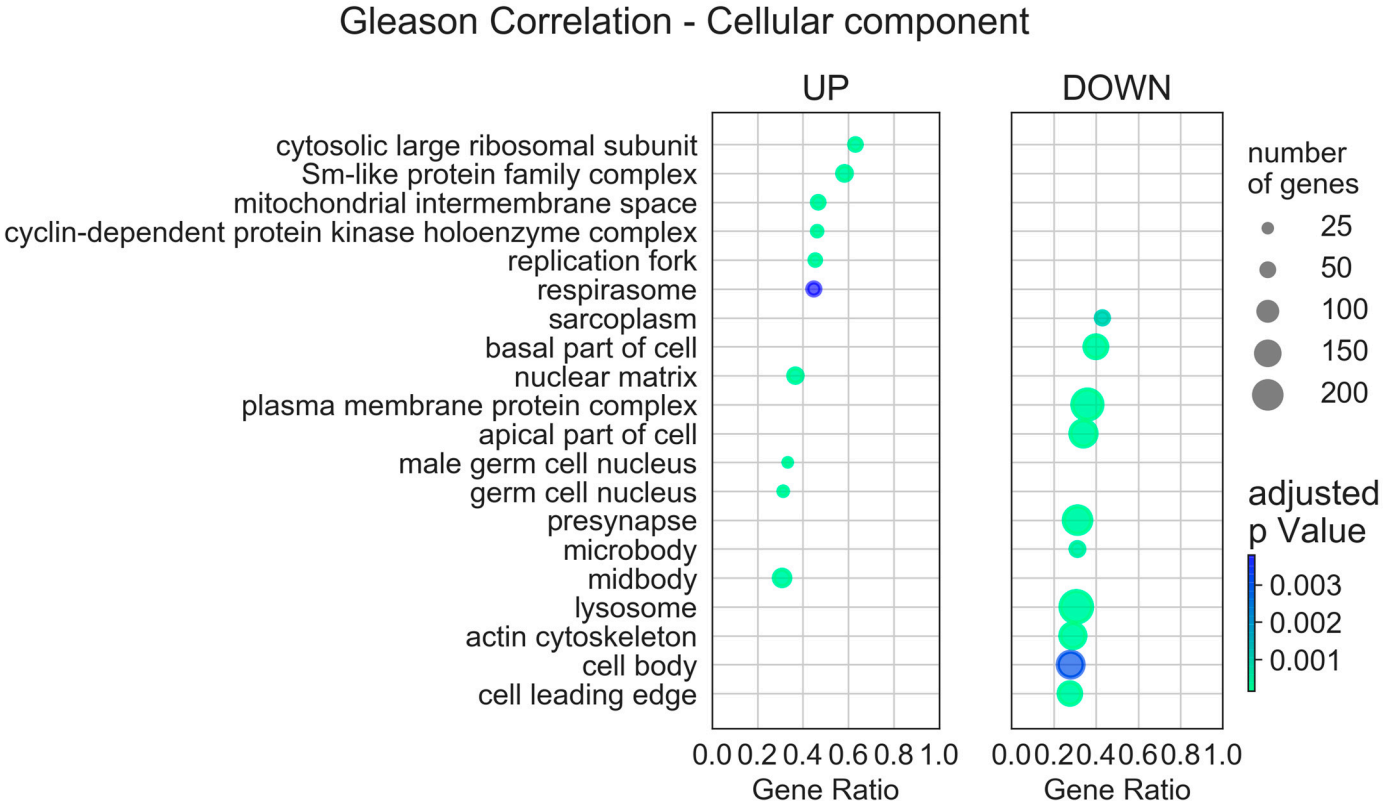


Figure 2C. Gene ontology analysis showing upregulated and downregulated set of genes associated with cellular components in Gleason grade groups.

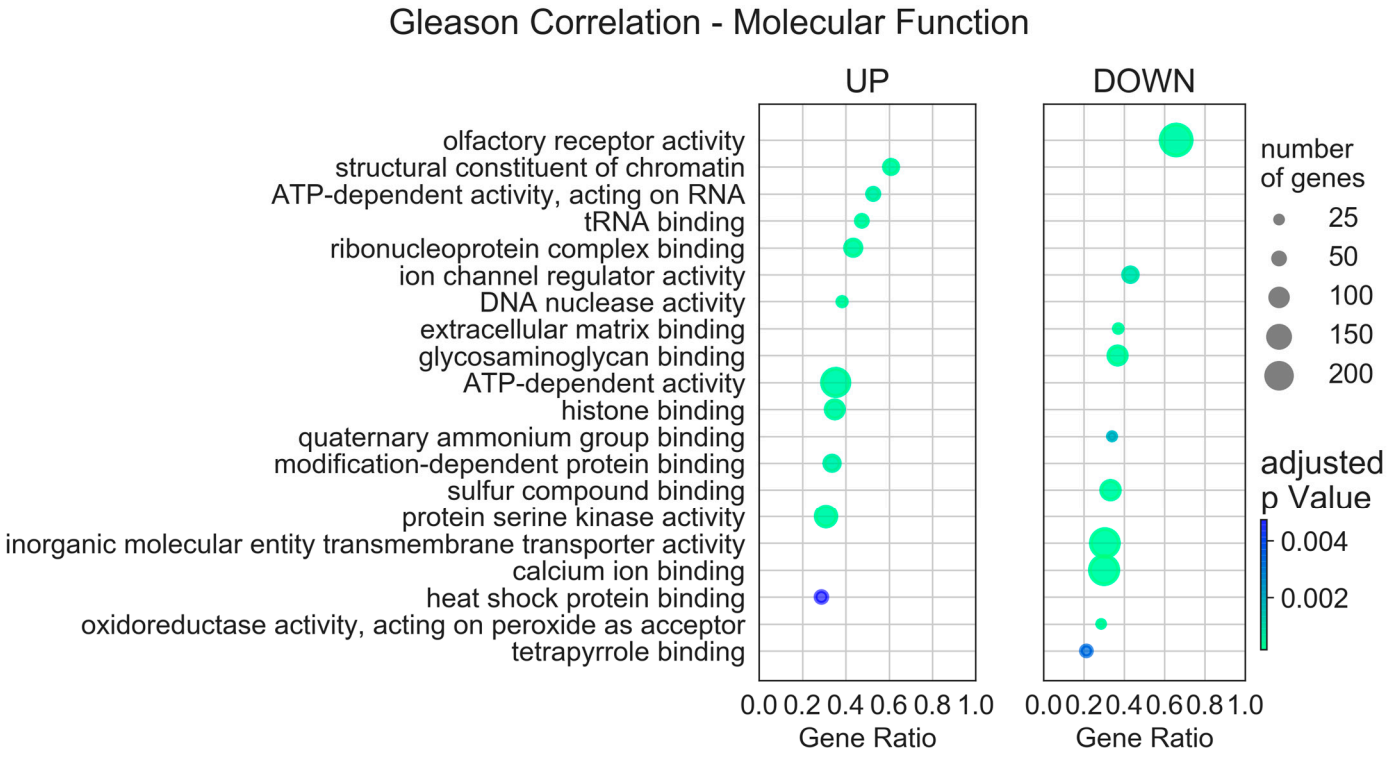


Figure 2D. Gene ontology analysis showing upregulated and downregulated set of genes associated with molecular functions in Gleason grade groups.