

Additional file 1

Figure S1

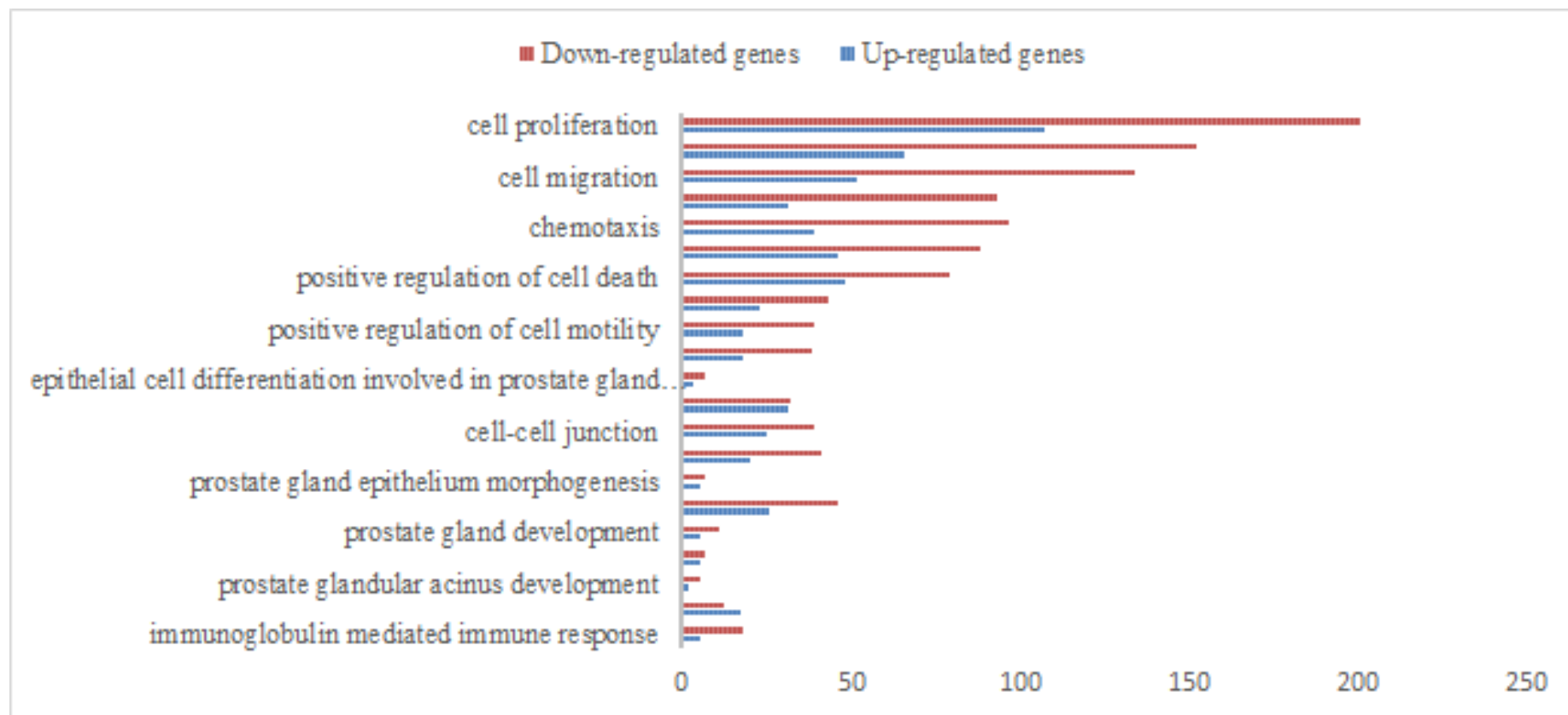


Figure S1: DE gene counts in prostate cancer related GO terms

Figure S2

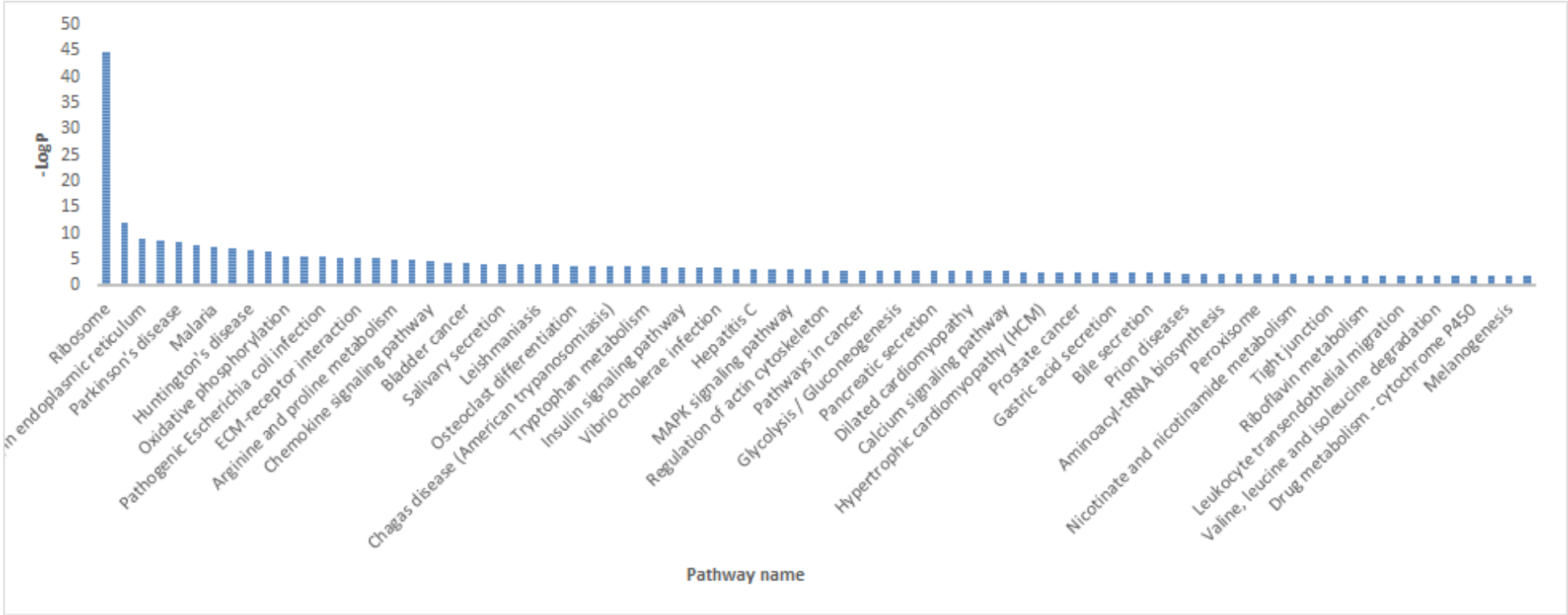
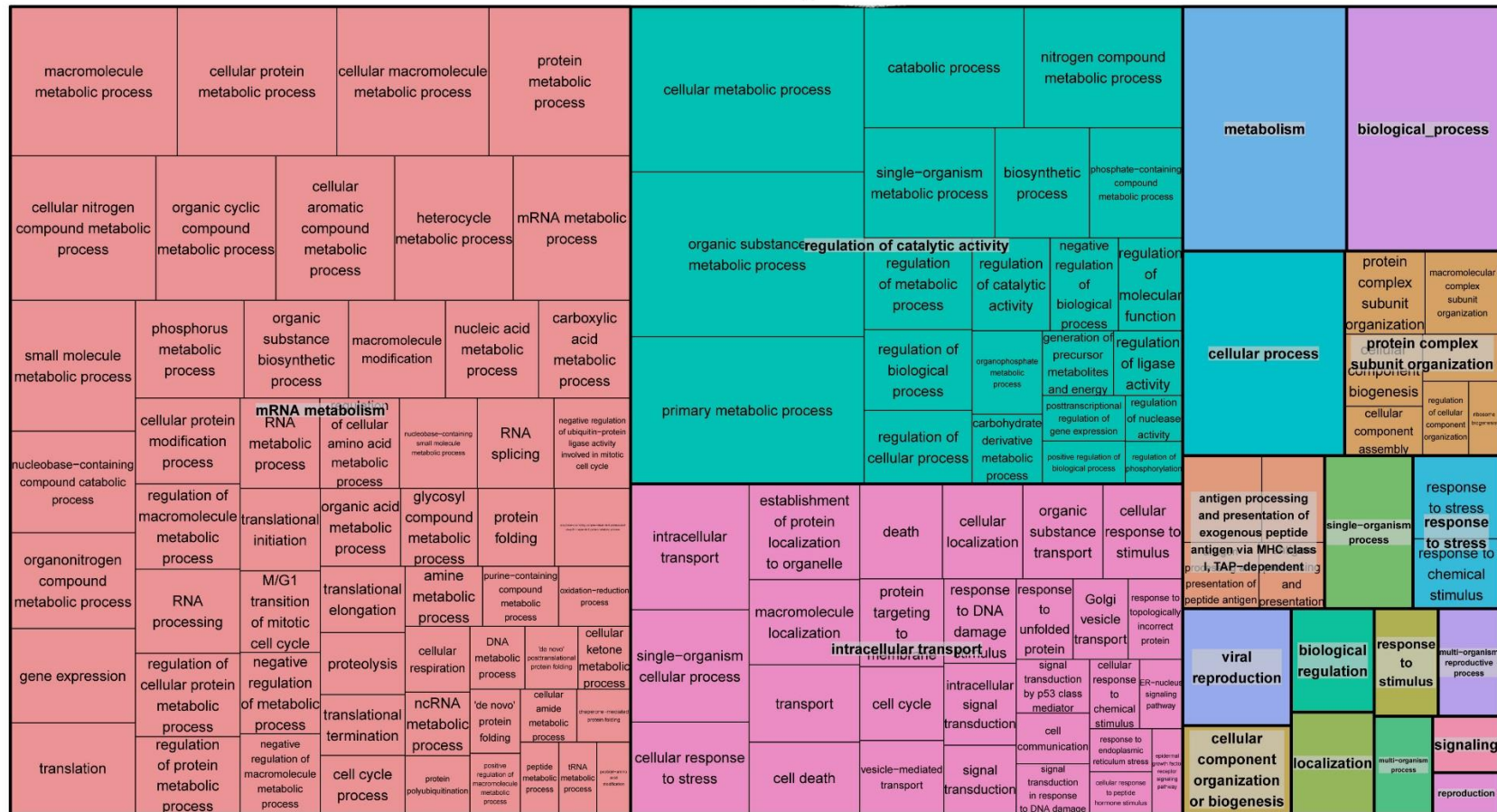


Figure S2: Enriched KEGG pathways by DE genes.

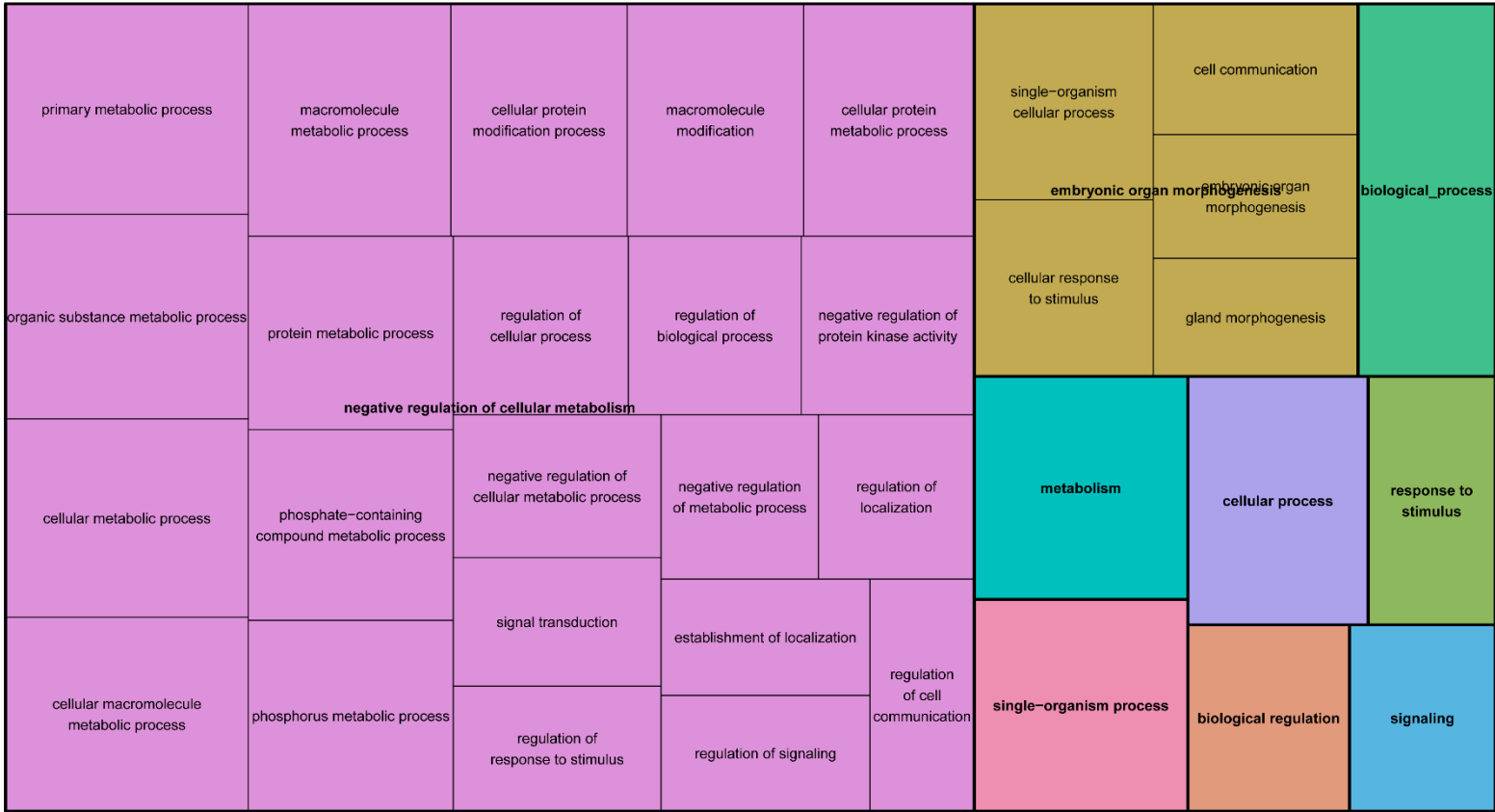
Figure S3: REVIGO treemap for enriched GO terms by DS genes. Here each rectangle is a cluster representative of loosely related GO terms.



Size of the clusters reflects the enriched p-value of GO terms. mRNA metabolism, regulation of catalytic activity, intracellular transport, protein complex subunit organization etc can be found enriched by DS genes.

Figure S4

A



B

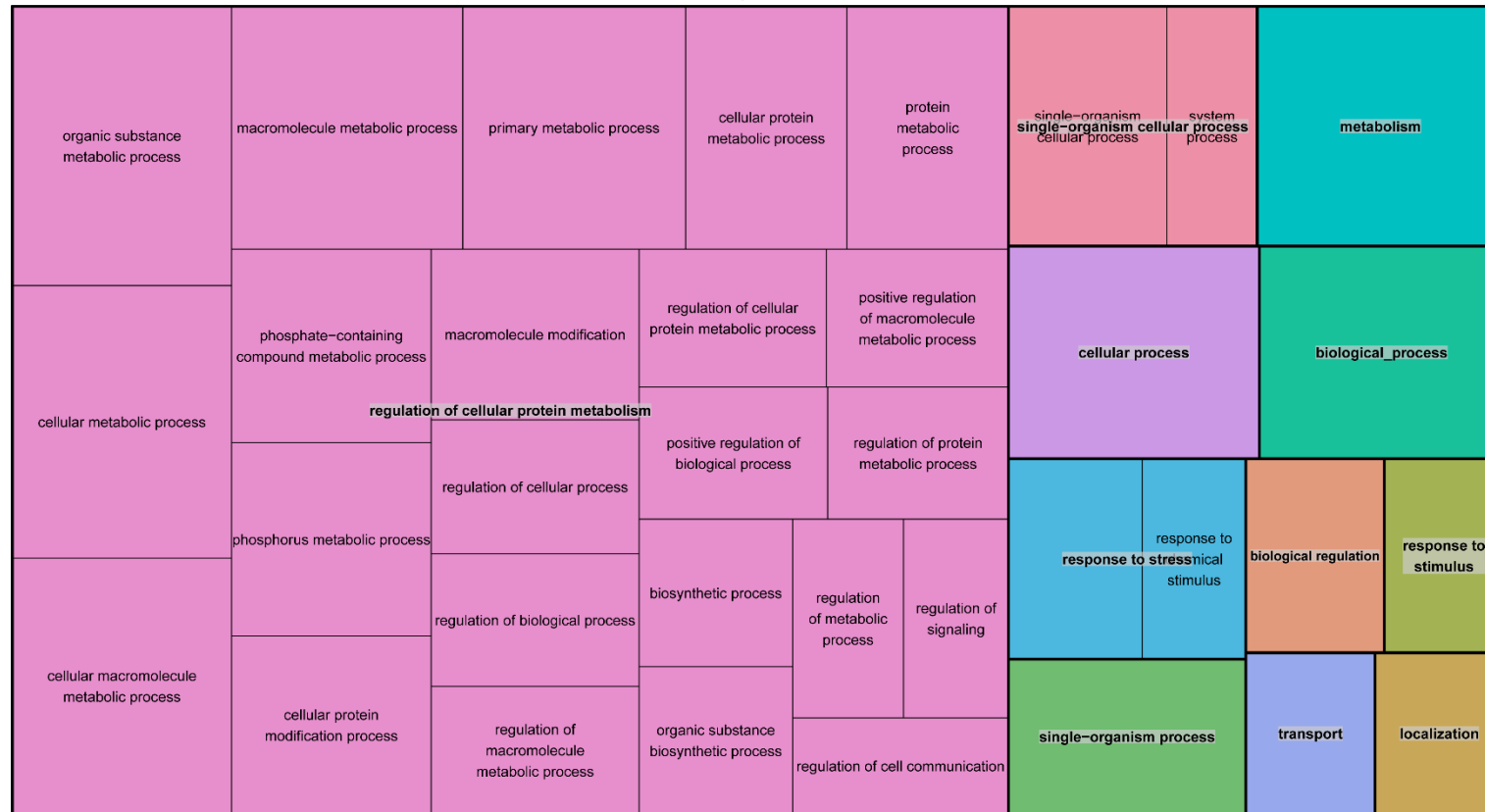


Figure S4: REVIGO treemap for enriched GO terms by DE (A) and DS (B) kinase genes. Here each rectangle is a cluster representative of loosely related GO terms. Size of the clusters reflects the enriched p-value of GO terms. Enriched clusters of DE kinases and DS kinases can be found to be opposite to each other. Enriched GO terms of DE kinases can be summarized into negative regulation of cellular metabolism including negative regulation of cellular metabolic process and metabolic process, while DS kinases are enriched in GO terms summarized by regulation of cellular protein metabolism including positive regulation of biological process and protein metabolic process.

Figure S5

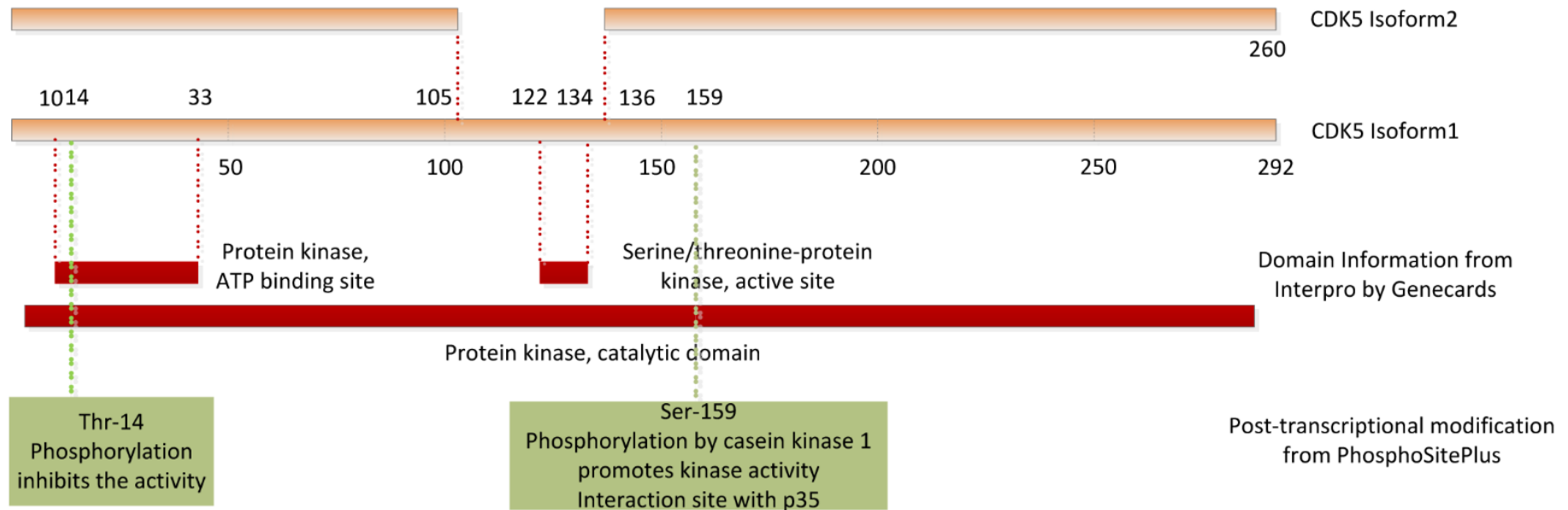


Figure S5: Kinase domain and phosphorylation site of CDK5 two protein isoforms. Exon6 of gene CDK5 encodes 32 amino acids from 105 to 136. A serine/threonine protein kinases active sit lies in this region. Here orange represents the isoforms of CDK5. Red represents the domain information from database. Green represents the post-transcriptional modification sites.