GO MF Bar Plot: IIIC_vs_Normal_wilcox.csv structural constituent of ribosome GTPase regulator activitycadherin binding actin bindingprotein serine/threonine kinase activity MHC class II protein complex binding p.adjust GTPase binding-0.00005 rRNA binding 0.00010 0.00015 ubiquitin protein ligase 0.00020 binding SMAD binding protein phosphorylated amino acid binding DNA-binding transcription factor binding histone modifying activitytranscription coregulator binding mRNA 5'-UTR binding-25 50 75 100 0 Count