

## Deciphering the role of c-MET in Metabolic reprogramming of Head and Neck squamous cell Carcinoma via *In Silico* analysis

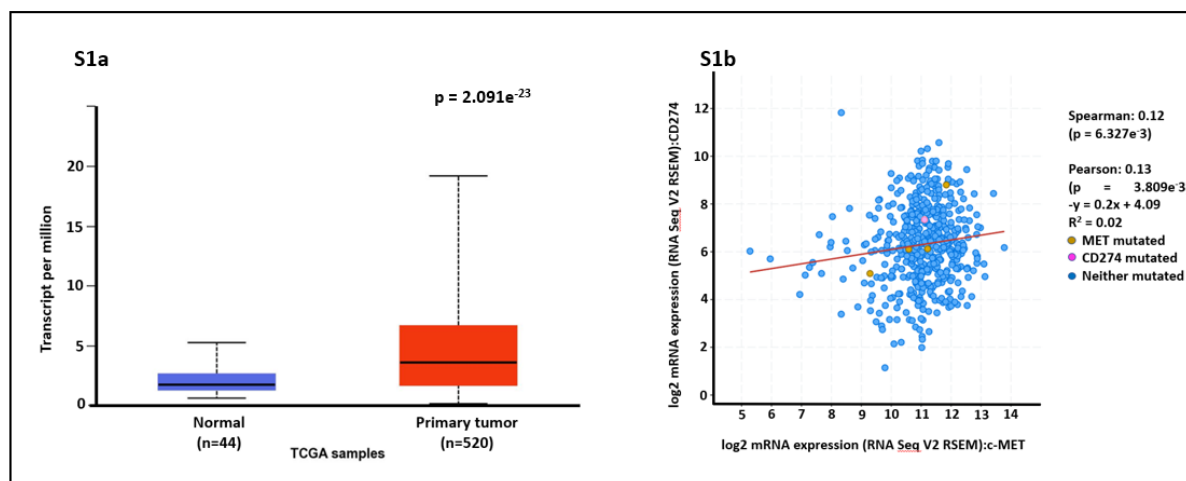
Sibi Raj<sup>1</sup>, Brijesh Rathi<sup>2</sup>, Pravesh Mehra<sup>3</sup>, Shailendra Asthana<sup>4</sup>, Dhruv Kumar<sup>1\*</sup>

<sup>1</sup>School of Health Sciences and Technology (SoHST), UPES University, Dehradun, Uttarakhand, 248007, India.

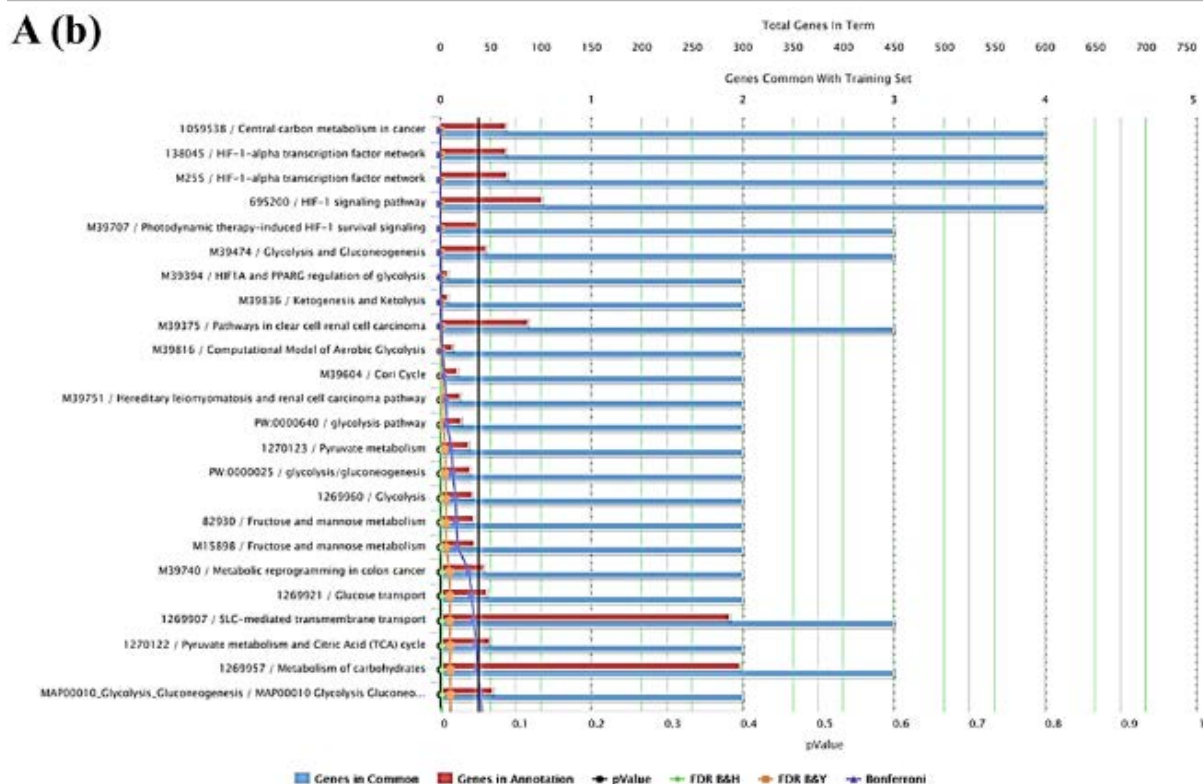
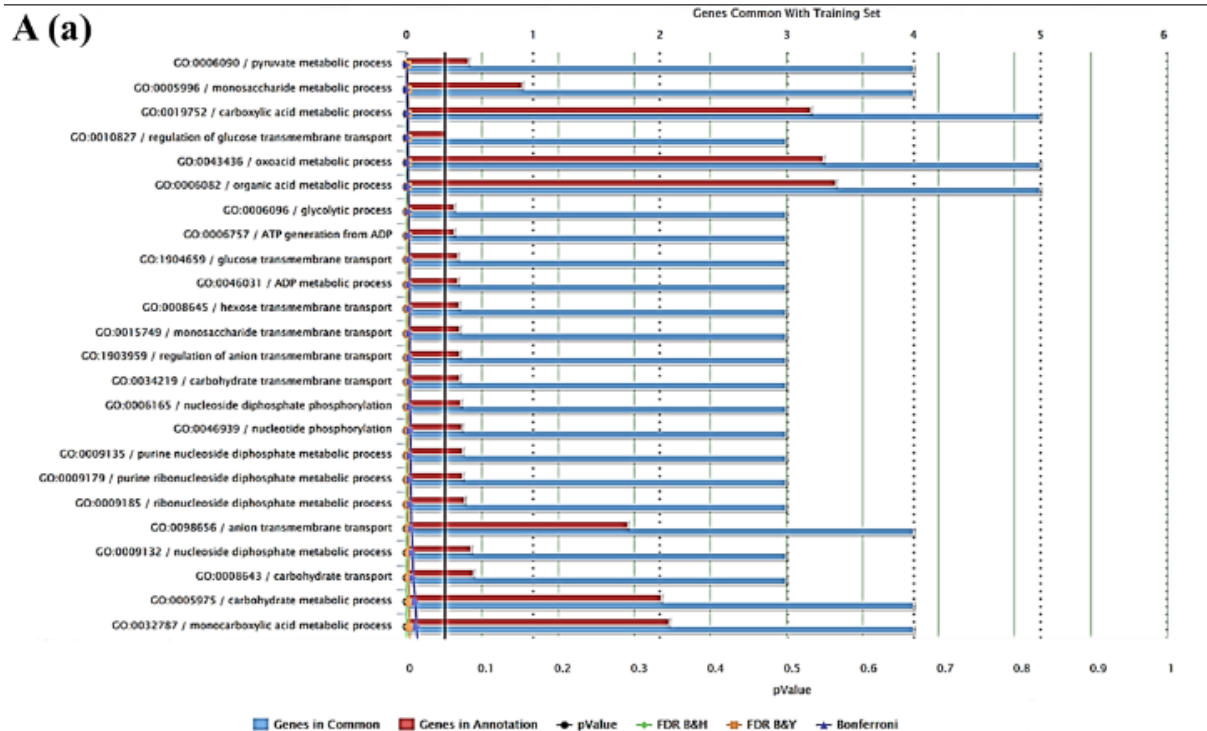
<sup>2</sup>Department of Chemistry, Hansraj College, University of Delhi, Delhi-110007, India. <sup>3</sup>Department of Oral Maxillofacial Surgery, Lady Hardinge Medical College and Hospitals, New Delhi 110001, India. <sup>4</sup>Translational Health Science and Technology Institute, Faridabad, Haryana, India

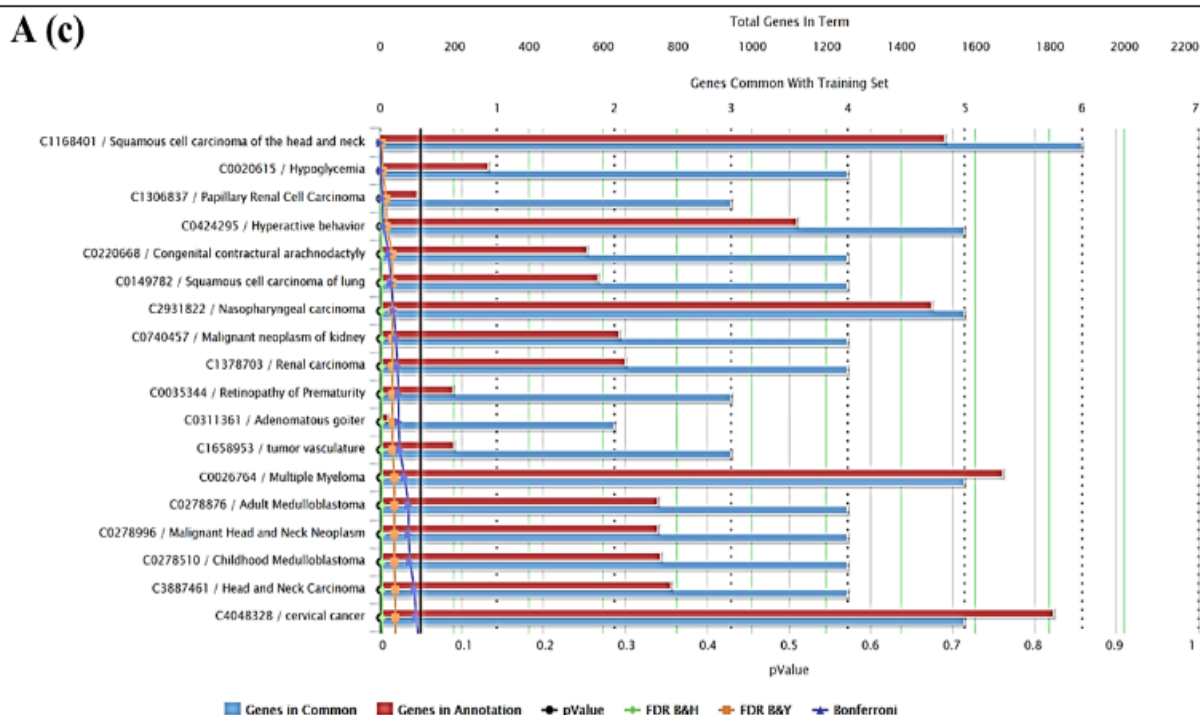
### Supplementary data

Immunotherapy with PDL-1 inhibitors has recently been explored in the treatment of multiple cancers. studies shows nearly 60% of HNSCC tumor cells expressing high levels of PDL-1, creating an immunosuppressive micro-environment around the tumor [18, 19, 20]. Data obtained from ULCAN database shows a higher expression of CD247 (PDL-1) in HNSCC patients as compared to the normal samples in the dataset (**Figure S1a**). However, c-MET expression had no significant correlation with CD247 in HNSCC patient samples (**Figure S1b**).

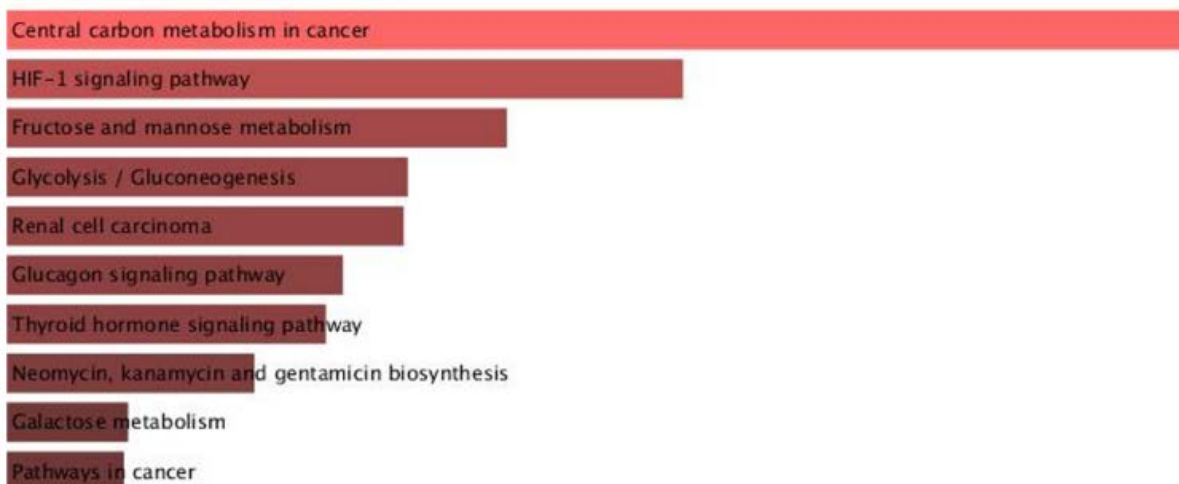


**Figure S1.** c-MET and PDL-1 gene expression analysis using different variables of TCGA HNSCC patients with ULCAN web. Box-whisker plots showing the expression of genes in sub groups of HNSCC samples. (a) Boxplot showing relative expression of PDL-1 in normal and HNSCC samples. Expression level of gene is represented as log<sub>2</sub>(TPM). (b) Correlation analysis of the c-MET and PDL-1 genes was conducted using the c-Biportal tool. c-MET and PDL-1 had no significant correlation ( $R=0.12$ ).





**B**



**Figure 3:** A. Gene ontology analysis of c-MET and metabolic genes in HNSCC patients. (a-c) The numbers of enriched genes according to the (a) biological process, (b) molecular function (c) pathway function. B. GO term and KEGG pathway enrichment analyses performed using Enrichr on c-MET and metabolic genes identified from HNSCC samples. The top 10 enriched KEGG pathway for c-MET and metabolic genes. The horizontal axis represents the number of genes, and the y-axis represents KEGG pathway names.

(Enlarged view)