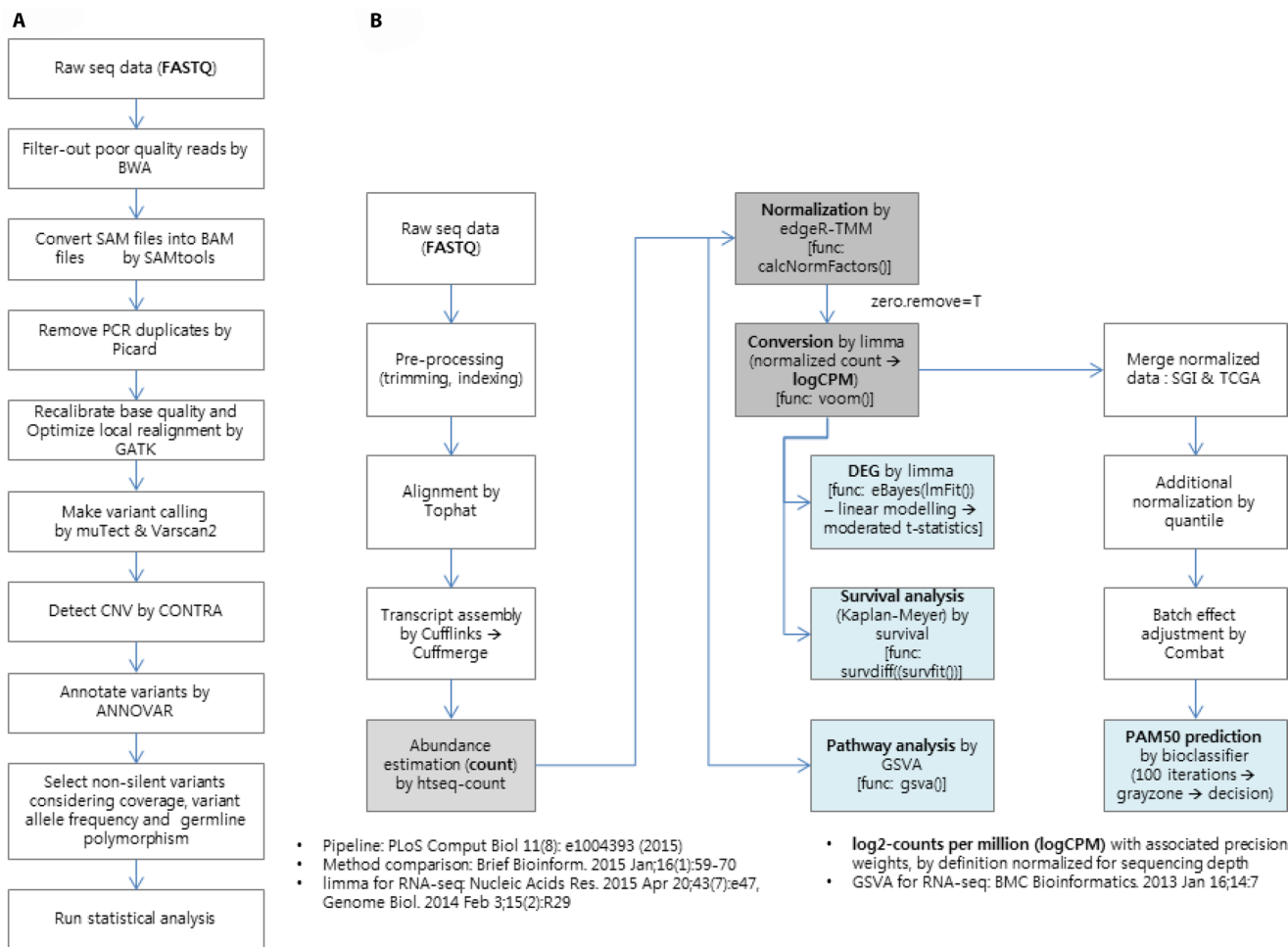
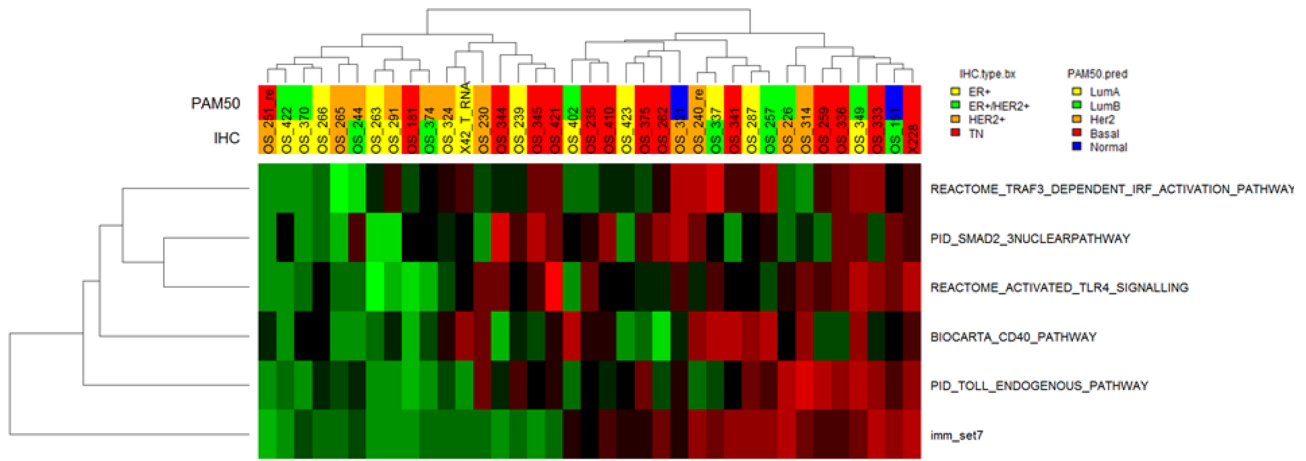


Immune signature of metastatic breast cancer: Identifying predictive markers of immunotherapy response

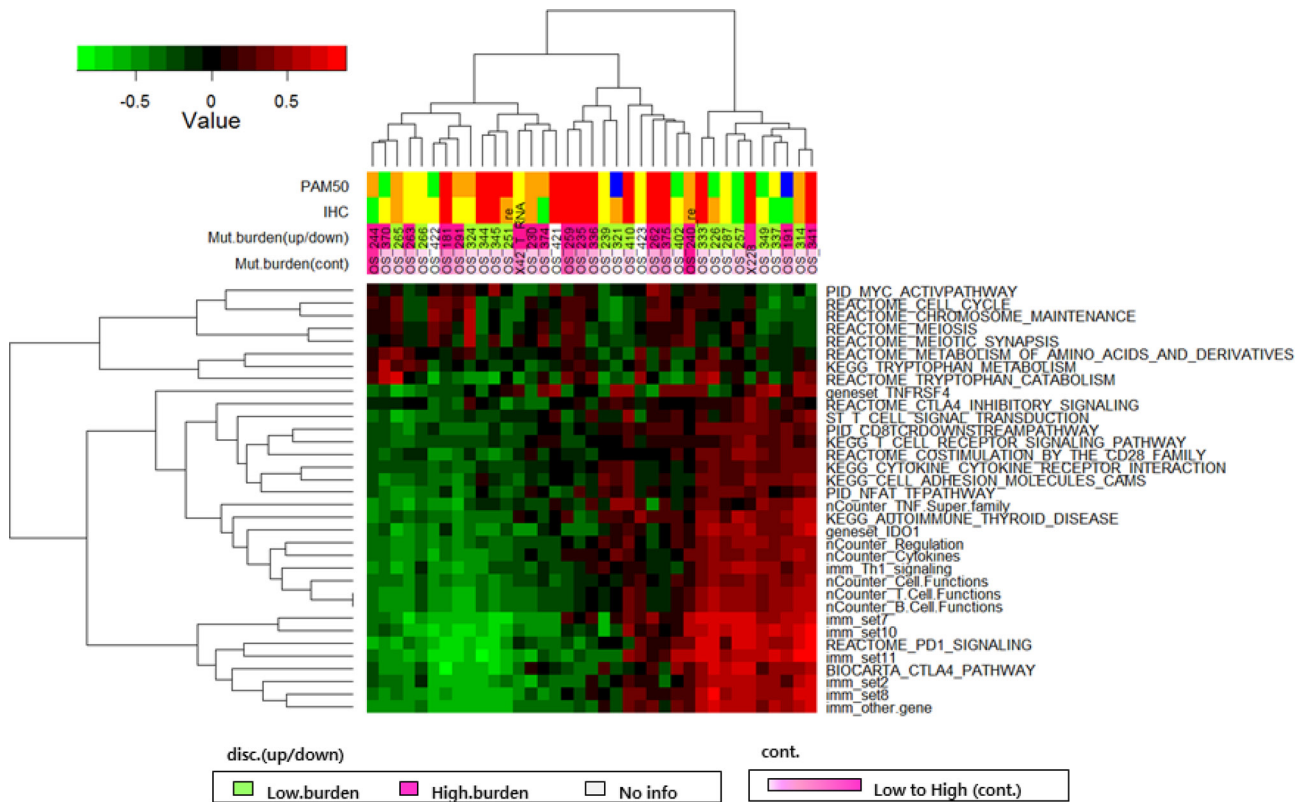
Supplementary Materials



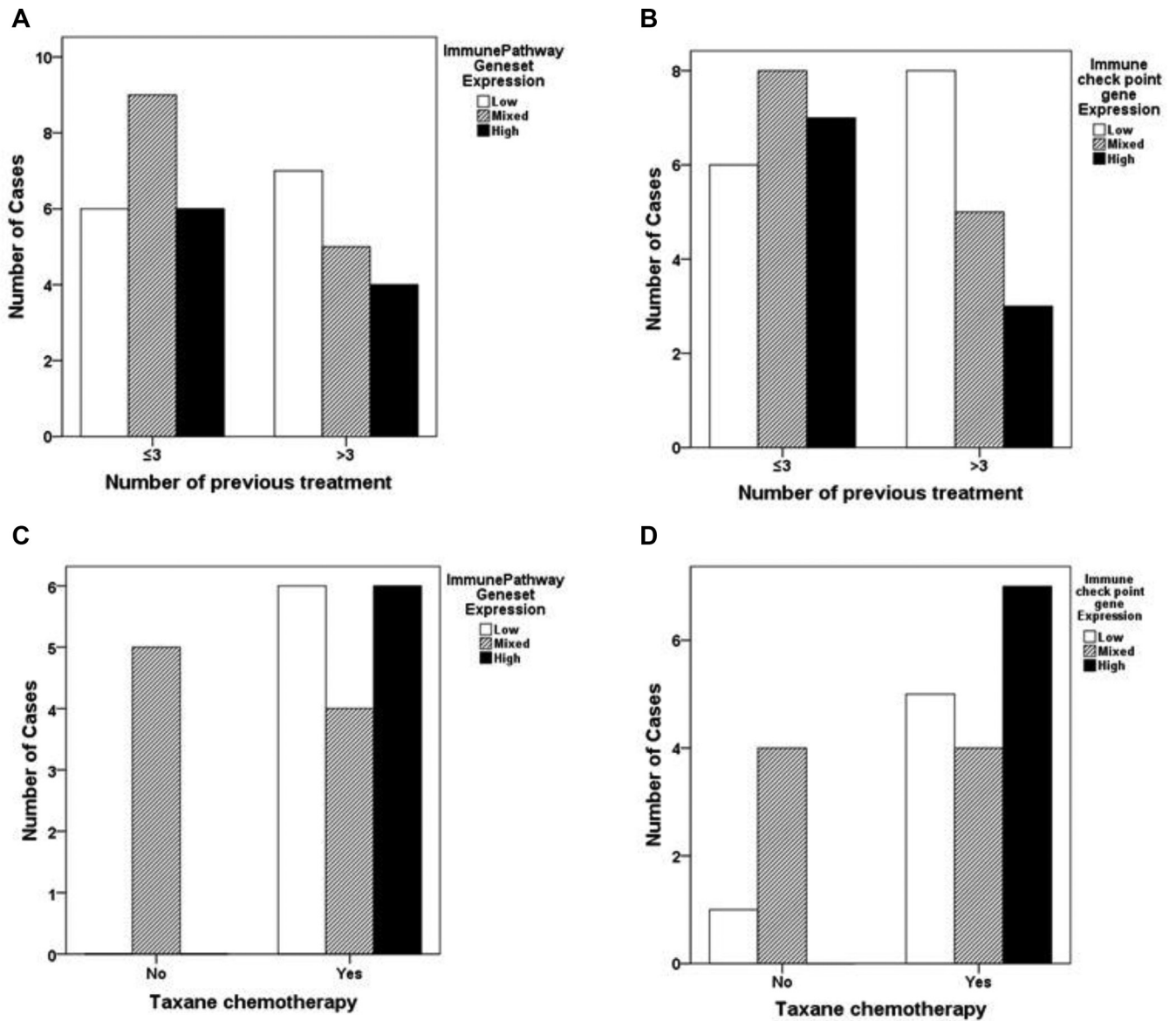
Supplementary Figure 1: Pipeline of next generation sequencing data analysis (A) whole exome sequencing (B) RNA-Seq.



Supplementary Figure 2: Immune pathway gene set expression that associated survival duration in metastatic BC.



Supplementary Figure 3: The association between mutation burden and immune gene set expression.



Supplementary Figure 4: The association between (A) immune pathway gene set expression and previous treatment; (B) immune check point gene expression and previous treatment; (C) immune pathway gene set expression and previous taxane treatment; (D) immune check point gene expression and previous taxane treatment.

Supplementary Table 1: Impact of clinicopathological characteristics on immune signature ($N = 37$). See Supplementary_Table_1

Supplementary Table 2: Clinicopathological characteristics of metastatic breast cancer $N = 37$. See Supplementary_Table_2

Supplementary Data 1: list_immune_pathway. See Supplementary_Data_1