

## Description of Additional Supplementary Files

### Supplementary Data 1

Description: Related to Figure 1 and the “Identification of subtypes in NSCLC patients by multiomics” section in the Results.

This includes sample clinical data and multi-omics NMF subtyping information. Additionally, it contains the results of statistical analysis (odds ratio, GSVA, and PTM-SEA) derived from the NMF subtyping results.

### Supplementary Data 2

Description: Related to Figure 2 and the “A NSCLC subtype associated with poor prognosis and frequent metastasis” section in the Results.

This includes the results of statistical comparison analysis between this study and other studies. It also includes information of combined NMF using our dataset and CPTAC dataset. Additionally, it contains the results of kinase analysis, and feature-wise survival analysis.

### Supplementary Data 3

Description: Related to Figure 3 and the “Cellular landscape of the five subtypes of NSCLC” section in the Results.

This includes the statistical results of differential expression analysis between subtypes and between tumor and normal adjacent tissue. Additionally, it contains statistical comparisons regarding cell type enrichment.

### Supplementary Data 4

Description: Related to Figure 4 and the “Proteogenomic features underlying whole-genome doubling in NSCLC subtypes” section in the Results.

It includes information on whole-genome doubling (WGD) for both our samples and CPTAC samples. It also contains the results of the association between WGD and mutations within each subtype. Additionally, it consists of the results of statistical analyses on copy number variants enrichment, geneset enrichment, and kinase activity. Also, it includes drug sensitivity results using organoid experiments about WGD.

### Supplementary Data 5

Description: Related to Figure 5 and the “Heterogeneous immune landscapes in NSCLC” section in the Results.

This includes information of the immune and cell type clusters, along with the results of statistical analyses based on this information. These analyses cover correlation, survival, gene set enrichment, and differential expression.

#### Supplementary Data 6

Description: Related to Figure 6 and the “Multiomics profiling of neoantigens and immune clusters” section in the Results.

This includes a list of cryptic MAPs and their count information across patients. It also includes the results of statistical enrichment analyses based on those information. Additionally, it includes the results of predictions for both neoantigen and cryptic MAPs.

#### Supplementary Data 7

Description: Processed and normalized gene expression data.