Cell Reports, Volume *33*

Supplemental Information

Integrated Proteomic and Glycoproteomic Characterization of Human High-Grade Serous Ovarian Carcinoma

Yingwei Hu, Jianbo Pan, Punit Shah, Minghui Ao, Stefani N. Thomas, Yang Liu, Lijun Chen, Michael Schnaubelt, David J. Clark, Henry Rodriguez, Emily S. Boja, Tara Hiltke, Christopher R. Kinsinger, Karin D. Rodland, Qing Kay Li, Jiang Qian, Zhen Zhang, Daniel W. Chan, Hui Zhang, and Clinical Proteomic Tumor Analysis Consortium

Figure S1

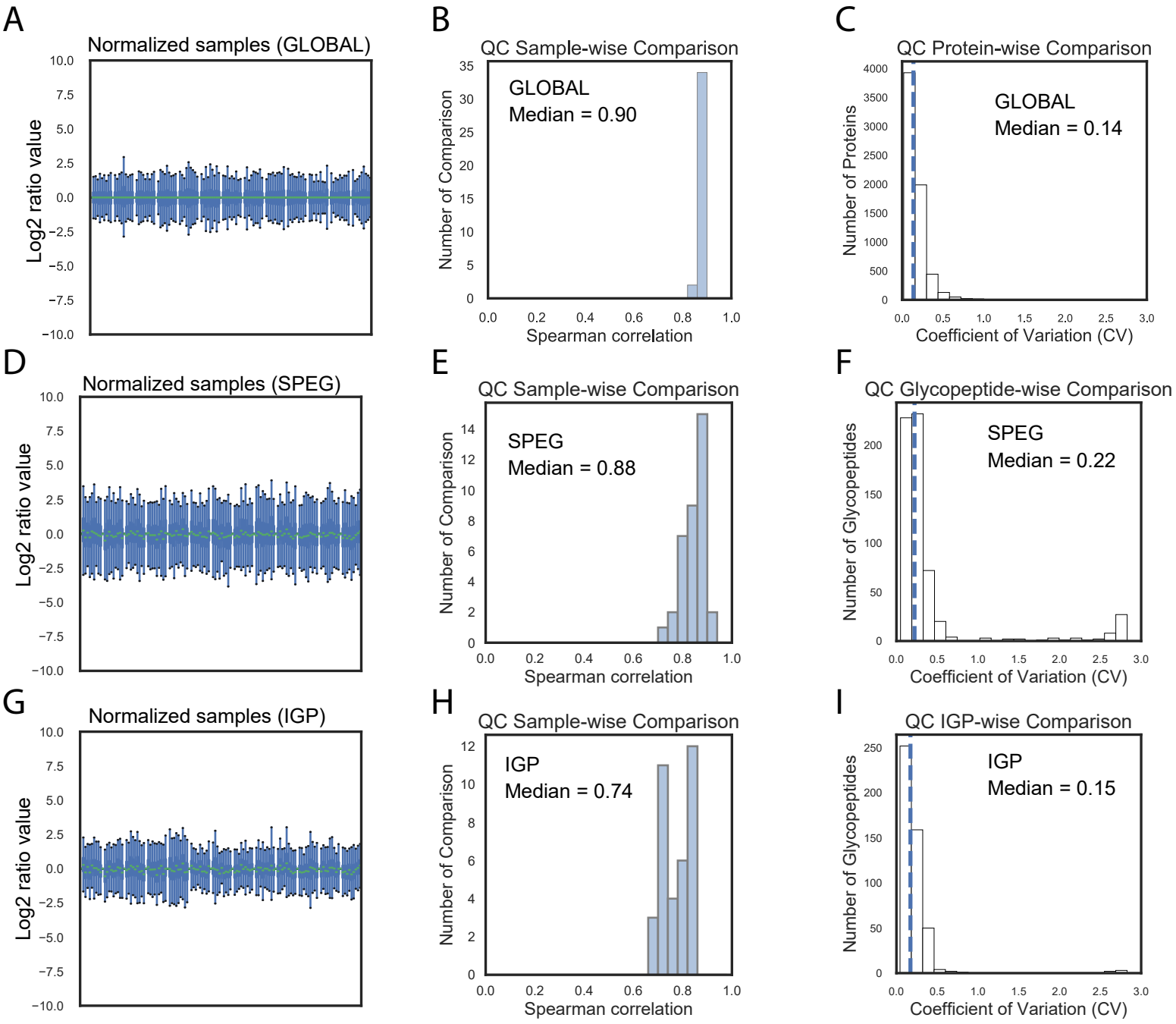

Figure S1. Quality control measurements of global, SPEG, and IGP data sets. Related to Figure 1.

A. Normalized log2 ratio of protein expression of all samples.
B. Sample-wise comparison of 9 Quality Control (QC) Samples for GLOBAL proteomic data.
C. Gene-wise comparison of genes expressed across all 9 QC samples.
D. Normalized log2 ratio values of glycosite-containing peptide expression of all samples.
E. Sample-wise comparison of 9 quality control (QC) samples for SPEG data.
F. Glycopeptide-wise comparison of glycosites expressed across all 9 QC samples.
G. Normalized log2 ratio values of intact glycopeptide expression of all samples.
H. Sample-wise comparison of 9 quality control (QC) samples from intact glycopeptide data.
I. Intact glycopeptide-wise comparison of those expressed across all 9 QC samples.

Figure S2

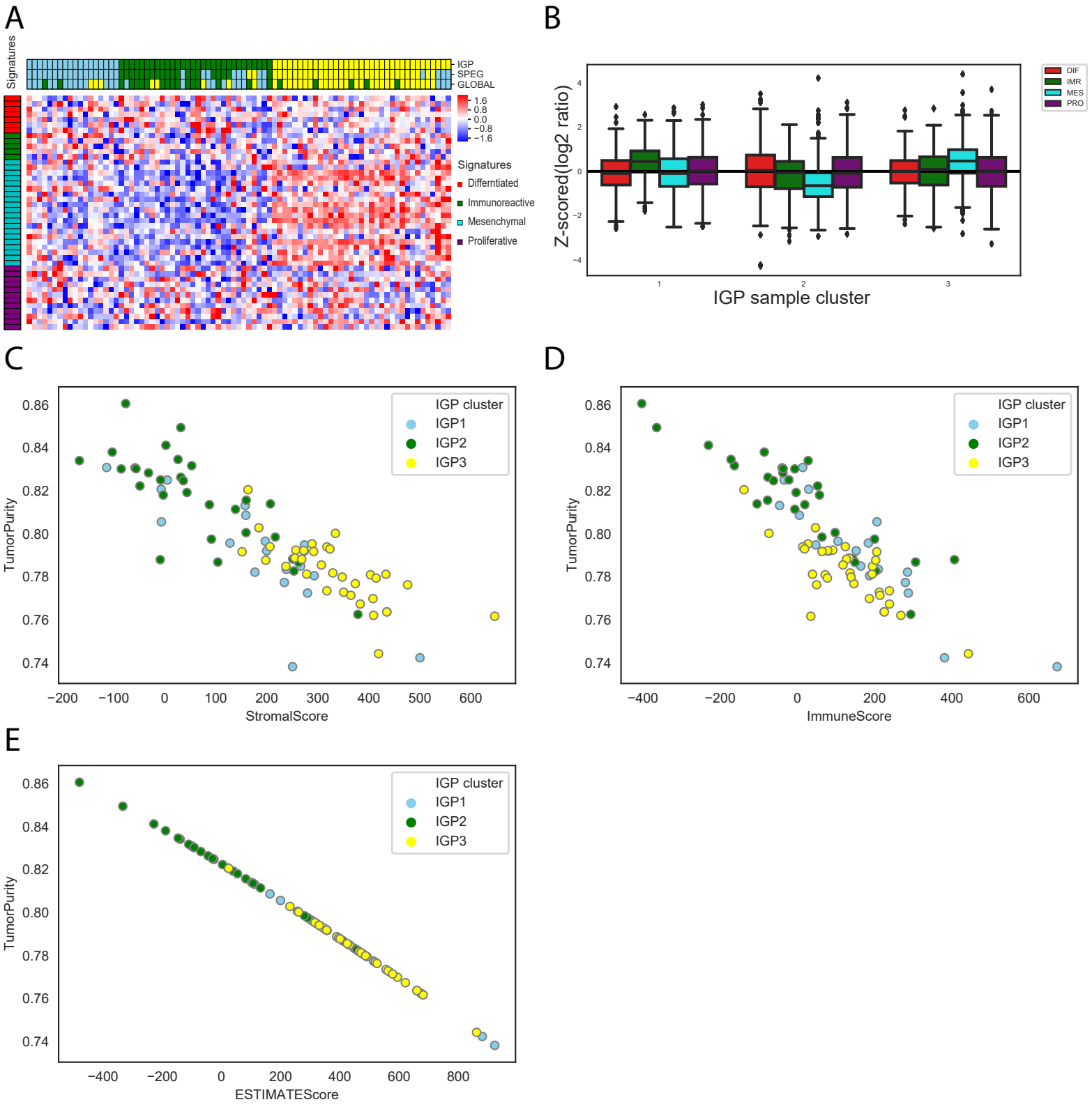

Figure S2. Tumor clustering analysis. Related to Figure 1 and 2.

A. The expression matrix of the signature protein sets of four historical subtypes (differentiated, immunoreactive, mesenchymal, and proliferative) under the order of IGP clusters.

B. The box plot of z-score transformed log2 ratio of signature proteins in IGP clusters grouped by 4 historical subtypes (DIF: differentiated, IMR: immunoreactive, MES: mesenchymal, PRO: proliferative).

C. The scatter plot of Tumor Purity and Stromal Score of 83 tumor samples calculated by ESTIMATE.

D. The scatter plot of Tumor Purity and Immune Score of 83 tumor samples calculated by ESTIMATE.

E. The scatter plot of Tumor Purity and ESTIMATE Score of 83 tumor samples calculated by ESTIMATE.

Figure S3

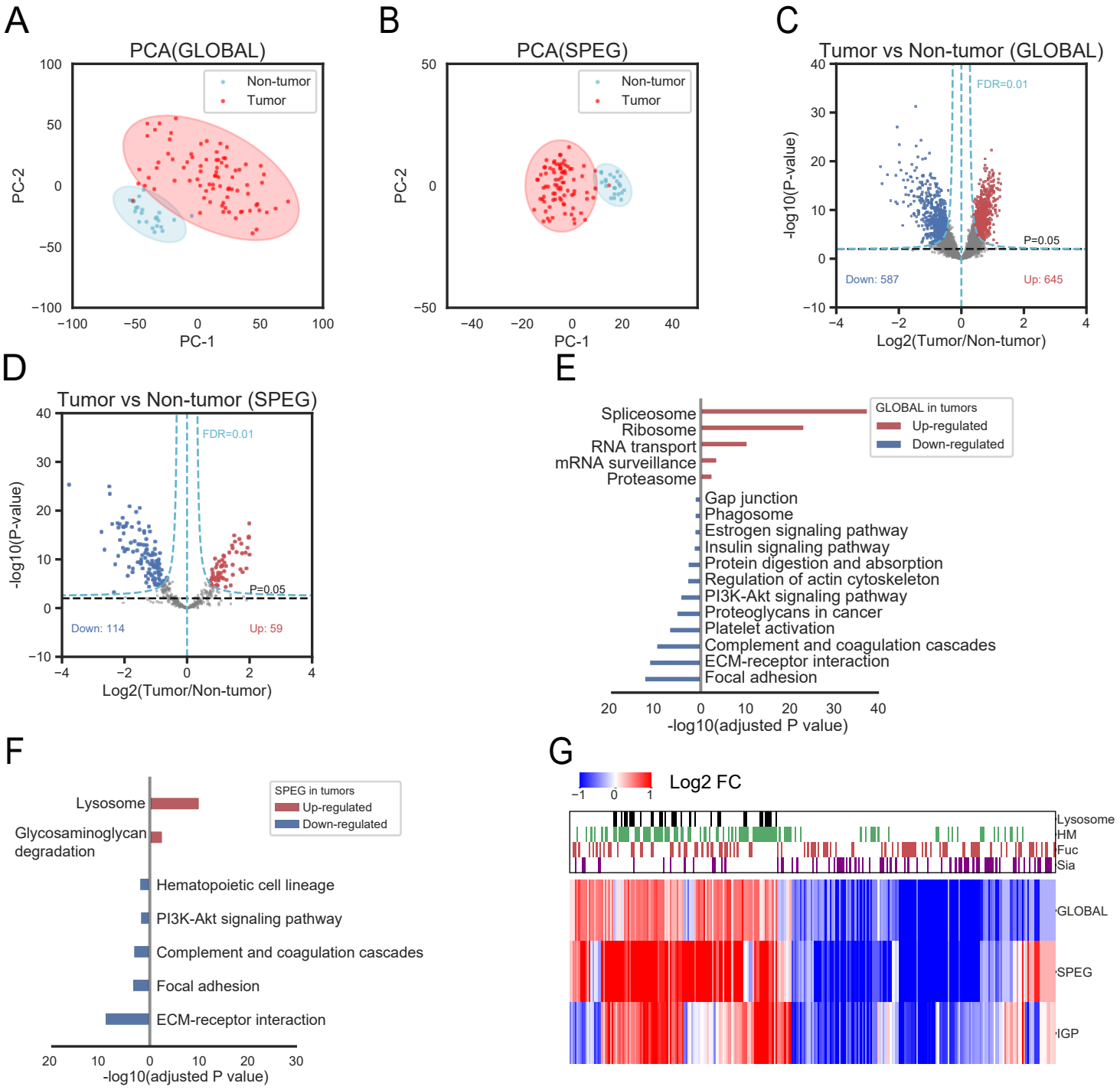

Figure S3. Proteomic and glycoproteomic analyses of ovarian tumors and non-tumors revealed alterations of proteins and glycoproteins in ovarian tumors. Related to Figure 3.

A. Principal Component Analysis (PCA) based on the abundance of proteins from GLOBAL dataset to reveal the difference between tumor and non-tumor samples.

B. Principal Component Analysis (PCA) based on the abundance of glycosite-containing peptides from SPEG dataset to reveal the difference between tumor and non-tumor samples.

C. Volcano plot of glycosite-containing peptides of tumor and non-tumor samples from GLOBAL dataset to reveal the significantly up-regulated and down-regulated proteins.

D. Volcano plot of glycosite-containing peptides of tumor and non-tumor samples from SPEG dataset to reveal the significantly up-regulated and down-regulated peptides.

E. The overrepresentation pathway analysis on up-regulated and down-regulated proteins in GLOBAL data set.

F. The overrepresentation pathway analysis on up-regulated and down-regulated proteins in SPEG data set.

G. The clustered heatmap of log2 ratio of fold changes (FC) of the median abundances of intact glycopeptides of tumors comparing to non-tumors. The enriched KEGG lysosome pathway and the associated three glycan types (HM, Fuc, and Sia) were annotated on the crytop rows.