Description of Additional Supplementary Files

Supplementary Data 1. Clinical metadata of patient samples across plasma proteomics cohort.

Supplementary Data 2. Information on TMB testing in patients for which proteomic data was available.

Supplementary Data 3. Plasma proteomics normalized proteomic expression (NPX) matrix across patient samples.

Supplementary Data 4. Relative immune proportions (mass cytometry) profiled from PBMC samples across patient samples.

Supplementary Data 5. Anatomic sites of metastases for patients for which proteomic data was available.

Supplementary Data 6. Proteins that had at least one significant linear mixed effect model covariate. A one is indicated in the appropriate column if that protein was significant for a particular term. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. Benjamini-Hochberg was used for false discovery control.

Supplementary Data 7. Proteins that had at least one significant covariate in the linear mixed effects model with the added subtype term. A one is indicated in the appropriate column if that protein was significant for a particular term. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. Benjamini-Hochberg was used for false discovery control.

Supplementary Data 8. Comparison of proteins significant for response in the original linear mixed effects models and in the linear mixed effects models with the added subtype term.

Supplementary Data 9. Proteins that had at least one significant covariate in the cutaneous-only linear mixed effects models. P-values are indicated in the appropriate column for each covariate. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. Benjamini-Hochberg was used for false discovery control.

Supplementary Data 10. Proteins that had at least one significant covariate in the SD responder linear mixed effects models. P-values are indicated in the appropriate column for each covariate. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. Benjamini-Hochberg was used for false discovery control.

Supplementary Data 11. Top 30 genes in each post-ICB protein non-negative factorization module with six components.

Supplementary Data 12. Proteins that had at least one significant linear mixed effect model covariate in the Babačić et al. data. A one is indicated in the appropriate column if that protein was significant for a particular term. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. False discovery control was not performed.

Supplementary Data 13. Proteins that had at least one significant linear mixed effect model covariate in the Nuñez et al. data. A one is indicated in the appropriate column if that protein was significant for a particular term. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. False discovery control was not performed.

Supplementary Data 14. Proteins that had at least one significant linear mixed effect model covariate in the gastric data. A one is indicated in the appropriate column if that protein was significant for a particular term. Slope coefficients are shown for each term in the rightmost columns. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. Benjamini-Hochberg was used for false discovery control.

Supplementary Data 15. P-values and slope coefficients for linear mixed effects models predicting PBMC relative immune proportions. P-values shown are associated with the F-statistic for the fixed effect of the corresponding variable in the mixed-effect model. False discovery control was not performed.

Supplementary Data 16. CellPhoneDB output file showing cell-cell interactions with significant means.

Supplementary Data 17. Pancreatitis incidence by Patient ID in the cohort, with a 1 designating patients with pancreatitis and a 0 designating patients without pancreatitis.