

Supplementary Tables and Figure Legends

Figure S1: The ODF1 gene is expressed only in the testis and not in any other tissue of the body, according to the BioGPS database (2A). The SOX11 gene is expressed only in fetal brain and not in any tissue of the adult body (2B), according to the BioGPS database, implying that it can serve as a good biomarker or immunotherapeutic for GBM.

Figure S2: Comparison between the numbers of identified plasma sHLA and tumor mHLA peptidomes of each patient (A), and between the LC-MS signal intensities of the same peptidomes (B). The intensity of the identified HLA peptides was averaged when more than 2 plasma samples of the same individual were available.

Figure S3: Comparison between the tumor proteome and mHLA peptidome (A), plasma sHLA and tumor mHLA peptidome (B), between the tumor proteome and plasma sHLA peptidome (C) of patients BCN-018 and 11-002, and comparison between the tumor proteomes of patients, CPH-09, BCN-018 and 11-002 (D). Only gene products observed as both proteins and HLA peptides are displayed. Pearson correlations are indicated in each panel and the protein levels are calculated as iBAQ intensities on a Log₂ scales. Missing values were replaced with arbitrary value of 10.

Figure S4: Fitness of the HLA peptides to different HLA alleles presenting them. Percentages of the peptides discovered in each of the tumor mHLA (A) and plasma sHLA peptidomes of the non-cancerous donors (B) that fit the sequence motifs of the HLA alleles of the patient or blood donors, according to NetMHC platform, with score below or equal 2. The colored dots represent the different patients.

Figure S5: Fitness of the identified HLA peptides to one of the six alleles of patient CPH-07, in 0.05 FDR (A), missed in 0.01 FDR (B) and 0.01 FDR analyses.

Supplemental Table S1: List of patients and non-cancerous plasma donors with their HLA typing, age, gender, disease stage, and peptides identification statistics. The raw LC-MS/MS file names are indicated in column D.

Supplemental Table S2: List of identified HLA peptides when the FDR was set to 0.05, with their LC-MS/MS signal intensities. HLA peptides that are down-regulated in the plasma after surgery are indicated in column B. HLA peptides derived from proteins, which were detected in the proteome analyses in all of the 10 tumor tissues are labeled in column C. HLA peptides derived from known TAA are marked in column D. HLA peptides derived from known CTA are marked in column E. HLA peptides that were derived from a subset of proteins that were detected in all of the GBM tumor tissues are marked in column F.

Supplemental Table S3: List of identified proteins with their LC-MS/MS signal intensities.

Supplemental Table S4: List of identified HLA peptides derived from TAA with their LC-MS/MS signal intensities.

Supplemental Table S5: List of Cancer/Testis Antigens (CTA) defined using BioGPS to be expressed at low levels in all healthy tissues.

Supplemental Table S6: Comparison between the number of shared TAAs and CTAs between the sHLA and mHLA peptidome of the same patients.

Supplemental Table S7: Comparisons of the numbers of shared HLA peptides associated with the shared HLA allomorphs of the patients.

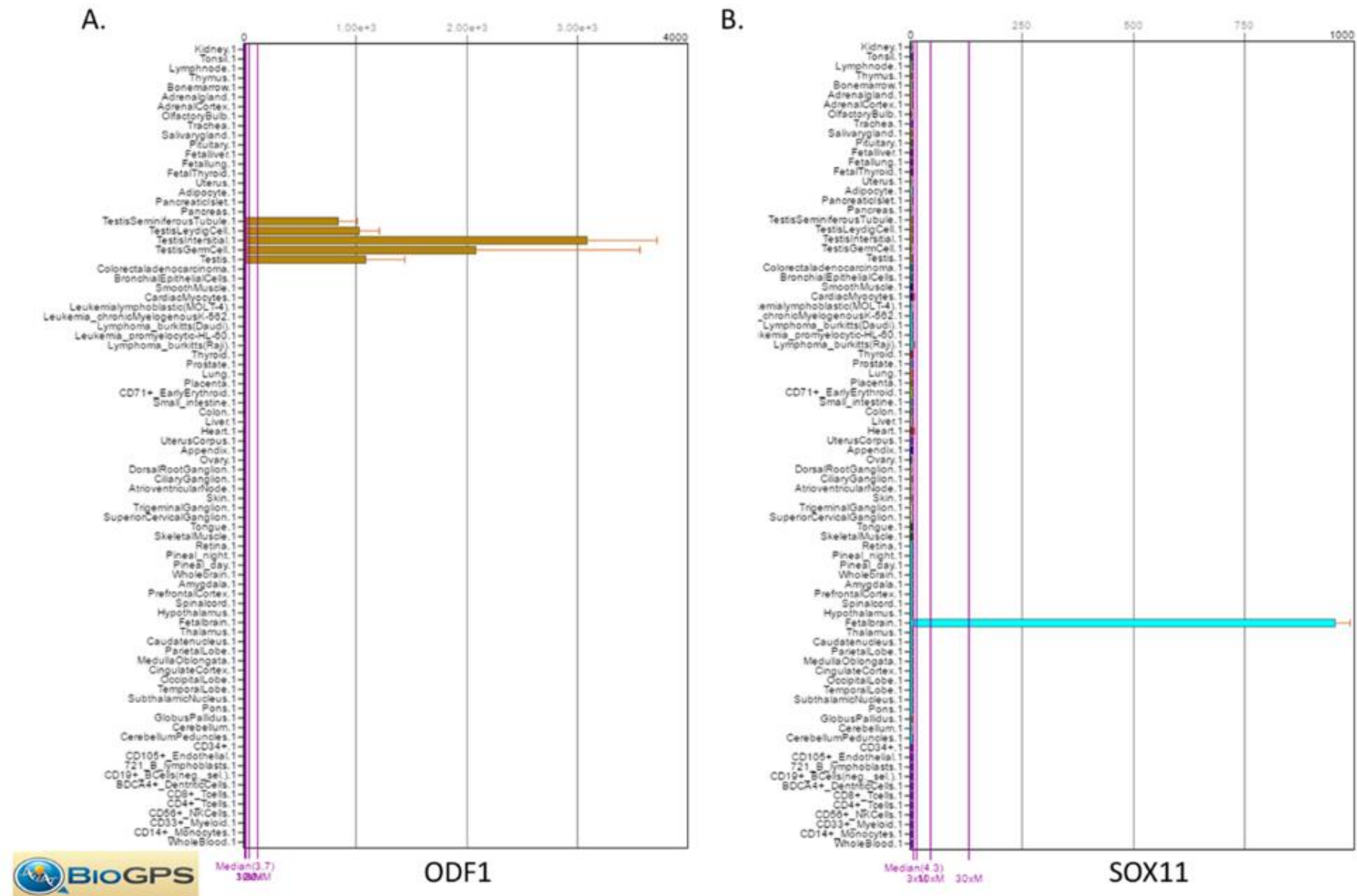
Supplemental Table S8: The percentages of the HLA peptides that fit sequence motifs of HLA alleles of each patient or plasma donor.

Supplemental Table S9: List of identified HLA peptides, when the FDR was set to 0.01, with their LC-MS/MS signal intensities.

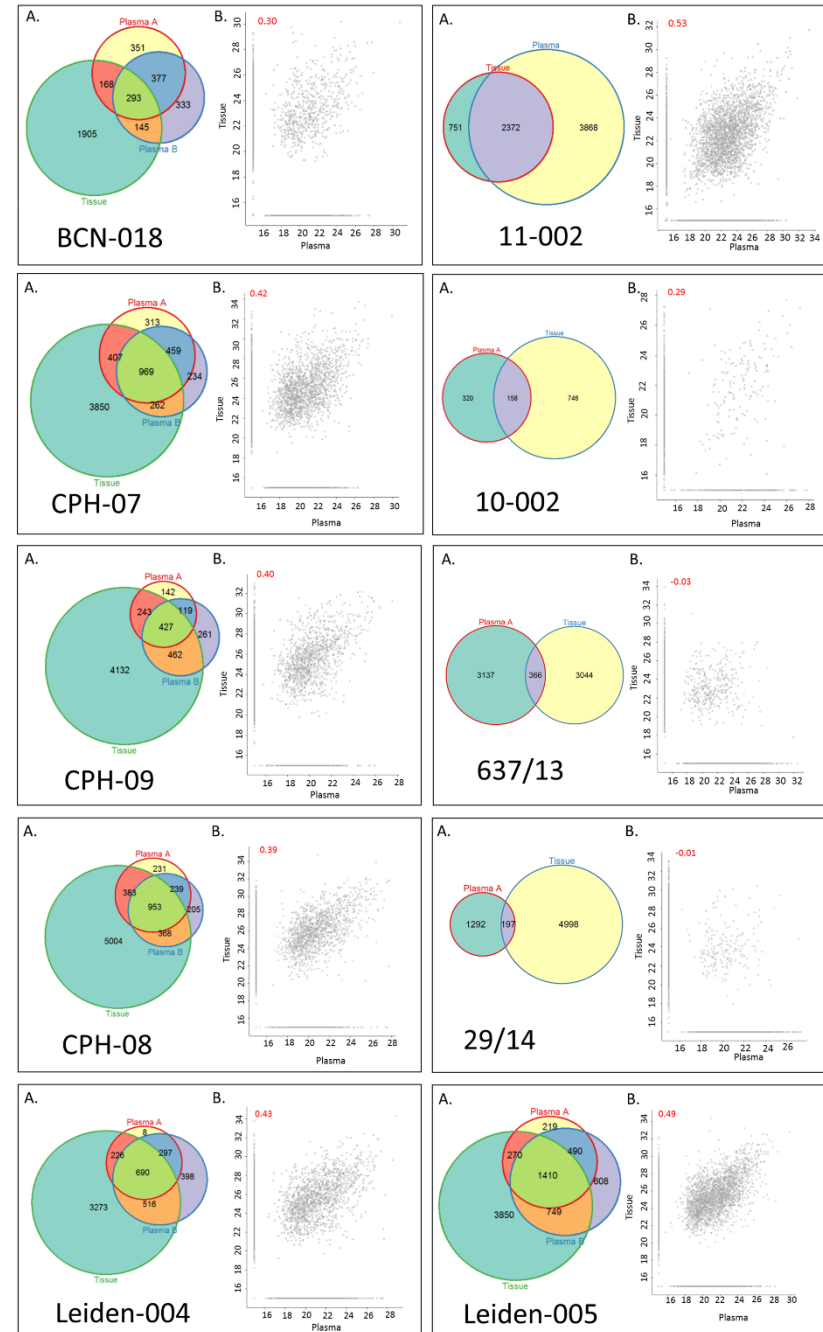
References

1. Andreatta, M., Alvarez, B., and Nielsen, M. (2017) GibbsCluster: unsupervised clustering and alignment of peptide sequences. *Nucleic Acids Res.* 41, D344–D347
2. Andreatta, M., Lund, O., and Nielsen, M. (2013) Simultaneous alignment and clustering of peptide data using a Gibbs sampling approach. *Bioinformatics* 29, 8–14

Supplemental Fig S1 Shraibman et al MCP-2018-000792R1 (Identification of tumor antigens among the HL...)

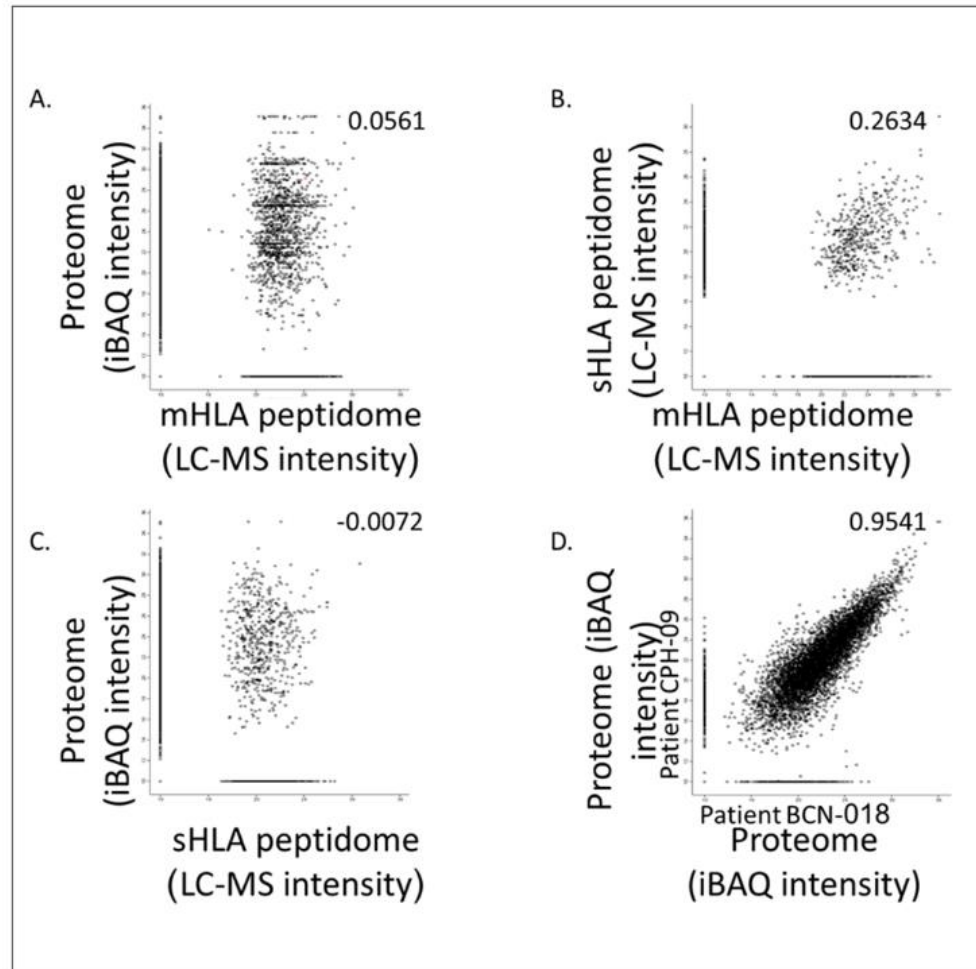


Supplemental Fig S2 Shraibman et al MCP-2018-000792R1
(Identification of tumor antigens among the HL...)

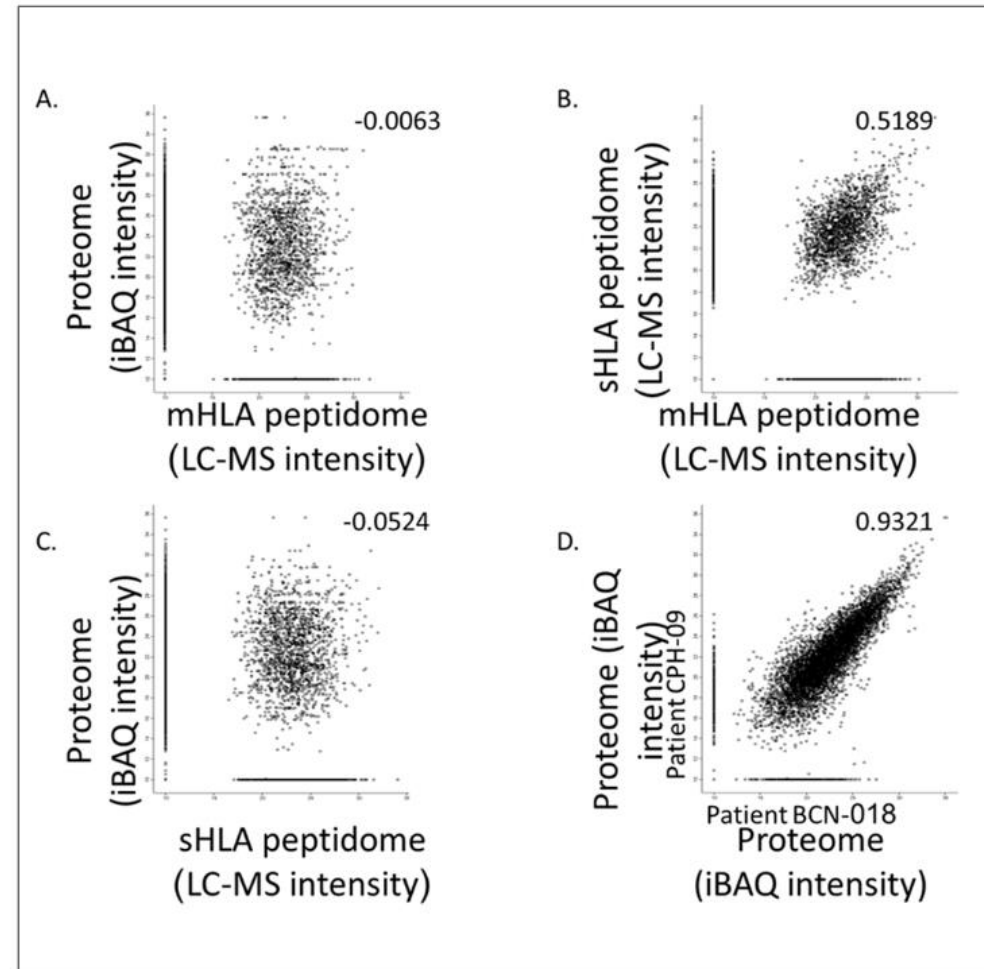


Supplemental Fig S3 Shraibman et al MCP-2018-000792R1 (Identification of tumor antigens among the HL...)

Patient BCN-018

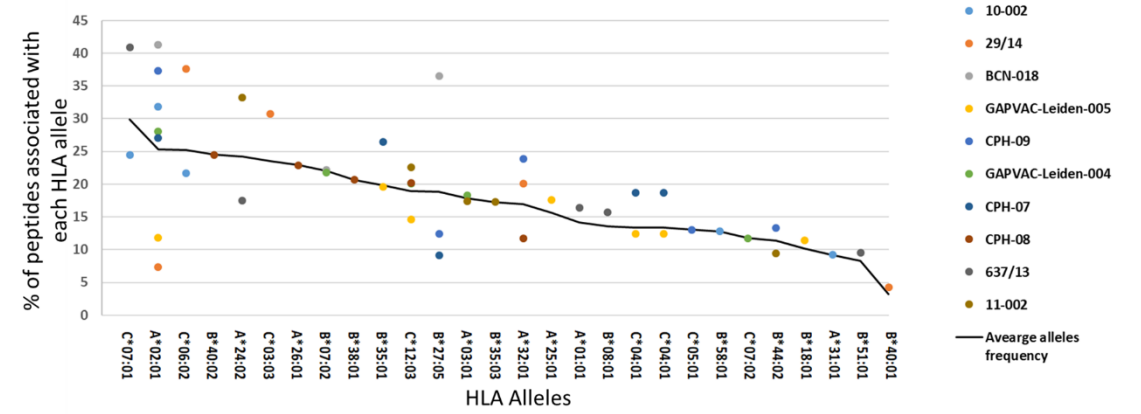


Patient 11-002

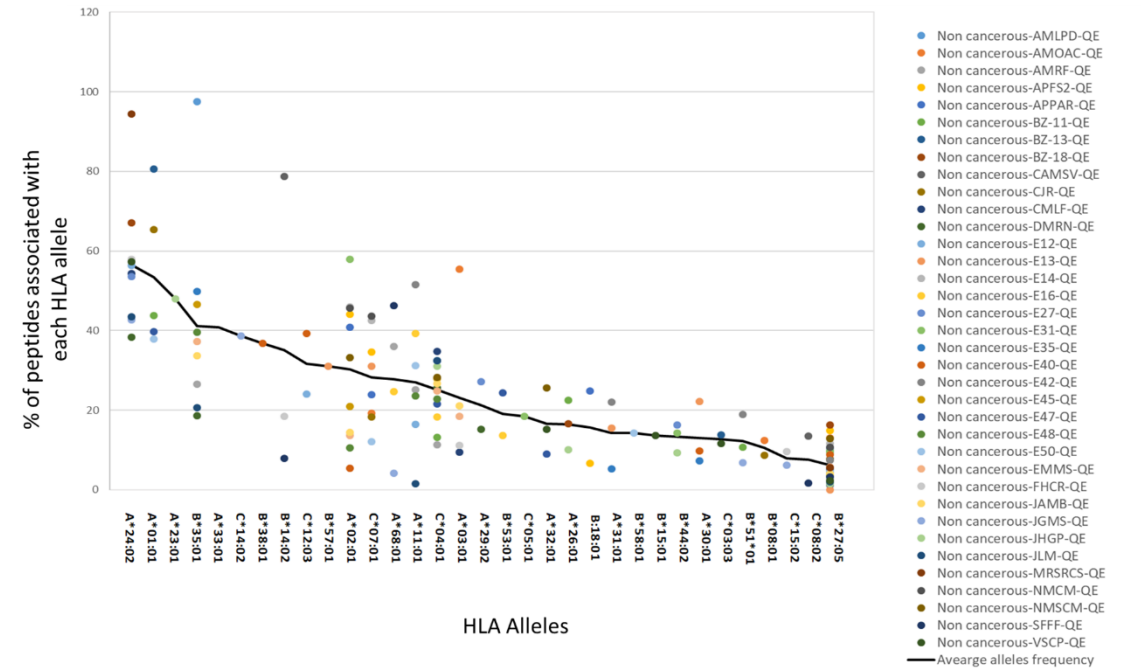


Supplemental Fig S4 Shraibman et al MCP-2018-000792R1
(Identification of tumor antigens among the HL...)

A.



B.



Supplemental Fig S5 Shraibman et al MCP-2018-000792R1 (Identification of tumor antigens among the HL...)

