

Supplementary figure 1. (A) Illustration of the database constructs used for Peaks searches. Personalized databases are basez on a canonical proteome, with the addition of an ERE proteome, a small-RNA (smRNA) proteome or a cancer-specific proteome. (B) Number of MAPs identified for each HLA allele (n=53) in our dataset (n = 26).



Supplementary figure 2.

A) Percentage of the transcriptome represented at the immunopeptidomic level per cumulative samples.
Multiple random iterations (n=500) are illustrated in regard to the order of the addition of samples.
B) Histogram of the total number of MAPs generated per source gene in our dataset.



## Supplementary figure 3.

(A) Small-RNA database construction workflow. (B) Filtering steps for peptide annotation and validation for smRNA-derived MAPs. (C) Genomic mapping of ERE-derived MAPs. (D) Number of ERE-derived MAPs per ERE class. (E) Number of MAPs identified per ERE family in HR+ (red) and TNBC (blue) samples. (F) Expression level of ERE subfamilies that generate or not MAPs (t-test; p<0.001). (G) Pearson correlation between predicted and observed retention times for ERE- (r = 0.98, p<0.001) and smRNA- derived MAPs (r = 0.98, p<0.001). (H) Distribution of spectral angles for ERE-derived MAPs (mean = 0.85 vs 0.86, f-test = 0.15). (I) Distribution of spectral angles for smRNA- derived MAPs (mean = 0.84 vs 0.9, f-test = 0.001).



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	Gene ranks	NES	padj
GOBP_ACTIVATION_OF_IMMUNE_RESPONSE		1.83	9.6e-07
GOBP_CELL_CYCLE_G1_S_PHASE_TRANSITION		1.54	6.8e-03
GOBP_CELL_CYCLE_PHASE_TRANSITION		1.99	1.1e-09
GOBP_CELL_DIVISION		2.10	1.1e-09
GOBP_IMMUNE_RESPONSE_REGULATING_SIGNALING_PATHWAY		2.00	1.1e-09
GOBP_MITOTIC_CELL_CYCLE_PHASE_TRANSITION		2.02	1.1e-09
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE		1.60	6.4e-03
GOBP_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	It is which were not compared to an even construction of the compared with	-1.47	3.1e-02
GOBP_POSITIVE_REGULATION_OF_CELL_CYCLE		2.05	4.5e-09
_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE_PHASE_TRANSITION	The second	2.00	1.2e-04
GOBP_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	The second	1.78	2.6e-03
TILS GENE MARKERS (Danaher et al 2017)	) • • • • • • • • • • • • • • • • • • •	1.60	3.9e-02
	0 5000 10000 15000 20000		

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GOBP

	Gene ranks	NES	padi
GOBP ACTIVATION OF IMMUNE RESPONSE		2 23	9 0e-10
GOBP ANTIGEN PROCESSING AND PRESENTATION OF EXOGENOUS ANTIGEN	The second se	1.82	1.1e-03
GOBP ANTIGEN PROCESSING AND PRESENTATION	The second	2.00	6.8e-06
GOBP B CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	The second	1.83	3.6e-04
GOBP CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE		2.33	9.0e-10
GOBP IMMUNE RESPONSE REGULATING SIGNALING PATHWAY		2.21	9.0e-10
GOBP LYMPHOCYTE ACTIVATION INVOLVED IN IMMUNE RESPONSE		2.18	9.0e-10
GOBP MYELOID CELL ACTIVATION INVOLVED IN IMMUNE RESPONSE	· · · · · · · · · · · · · · · · · · ·	1.99	2.7e-05
GOBP_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE		1.86	4.8e-05
GOBP_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING		1.91	2.1e-05
GOBP_POSITIVE_REGULATION_OF_CELL_DEATH		1.56	1.7e-05
GOBP_POSITIVE_REGULATION_OF_FIBROBLAST_PROLIFERATION	HINE IN THE CONTRACT OF A DESCRIPTION OF A	1.61	2.8e-02
GOBP_POSITIVE_REGULATION_OF_MAPK_CASCADE		1.86	4.5e-09
GOBP_POSITIVE_REGULATION_OF_TNF_SUPERFAMILY_CYTOKINE_PRODUCTION	Binner	1.96	1.7e-05
GOBP_RECEPTOR_SIGNALING_PATHWAY_VIA_STAT	Non-second second s	2.12	2.4e-07
GOMF_MHC_CLASS_I_RECEPTOR_ACTIVITY		1.64	2.8e-02
GOBP_MAST_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	The second se	1.82	2.0e-03
TILS GENE MARKERS (Danaher et al 2017)	the second	2.55	9.0e-10
	0 5000 10000 15000 20000		

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## Supplementary figure 4.

(A) Spearman correlation between the number of MAPs identified per gene in our dataset and their frequency of mutations (as described in the breast cancer TCGA cohort). (B) GSEA enrichment analysis in all breast cancer tumors from TCGA (n = 1109) with high levels (> median) of predicted TSAs (as defined by : expression > 2 rphm and adequate HLA allele for presentation). (C) GSEA enrichment analysis in TNBC tumors from TCGA (n=158) with high levels (> median) of predicted TAAs (as defined by : expression > 2 rphm and adequate HLA allele for presentation).