Supplementary

Figure S1: (A) Marginal variable effect on disease-free survival probability. The variable status "0" indicates the absence of the parameters required to define the feature. For continuous variables, the values indicated on the x-axis have been normalized and do not indicate the actual feature value. The y-axis indicated the disease-free survival probability. The x-axis rug represents the number of samples that represent the interval, therefore the robustness of the variable marginal effect for a given range of values. Ranges above the starting value (*y* value at *x=0*) are associated to a positive prognostic effect for that given feature. **(B)** Variable importance predictor coefficient for each selected feature. Higher median values are associated to a higher average impact on predictions.
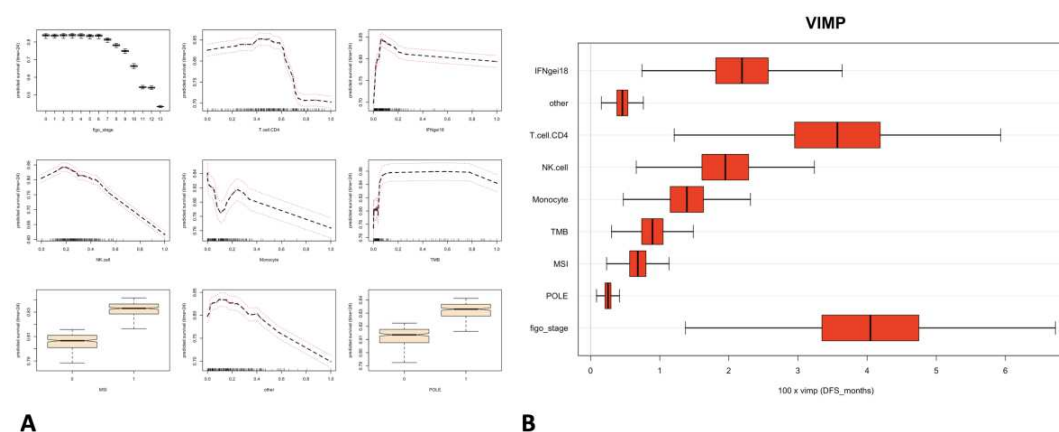

Figure S2: Comparison of cell abundances distributions in multiple in-silico deconvolution tools for shared cell populations.
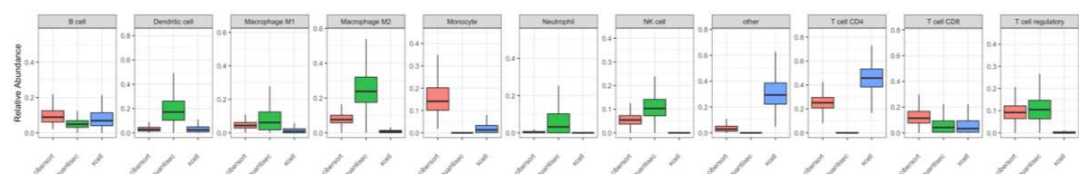

Figure S3: (A) Gene correlation network characterized relapse early stages with node size equals to 1% of the node degree. **(B)** Gene correlation network no-relapse early stages with node size equals to 1% of the node degree. **(C)** Gene correlation network unexplained relapse early stages with node size equals to 1% of the node degree.
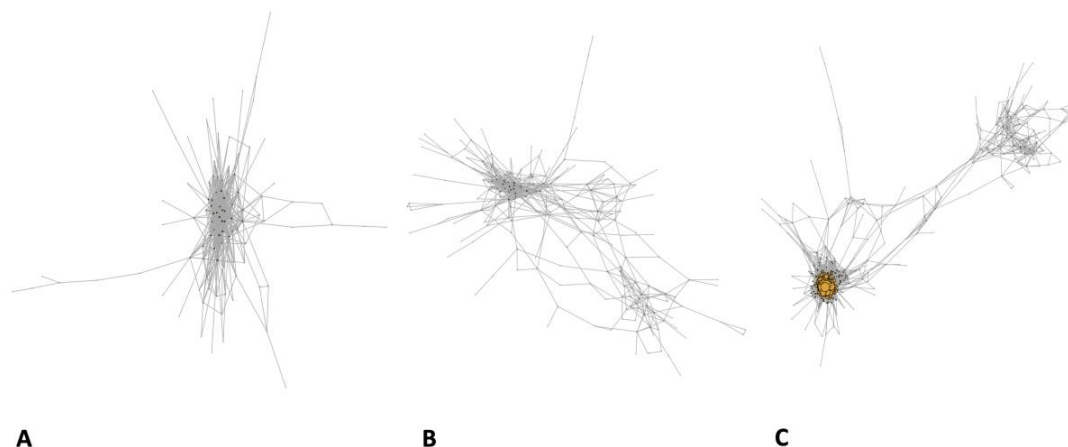
Supplemental material

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Table S1: In-silico deconvolution tools aggregation schema. Immune cells sub-types have been aggregated to allow for comparison.

quanTIsec	CIBERSORTx	xCell	Variation
T cells CD4+	T cells CD4 naive, T cells CD4 memory resting, T cells CD4 memory activated, T cells follicular helper	T cell CD4+ Th1, T cell CD4+ Th2, T cell CD4+ naive, T cell CD4+ memory, T cell CD4+ central memory, T cell CD4+ effector memory	8.9 %
T cells CD8+	T cells CD8	T cell CD8+ effector memory, T cell CD8+ central memory, T cell CD8+ naive	0.5%
Natural killer cells	NK cells resting, NK cells activated	NK cells	0.1%
Tregs	T cells regulatory	T cell regulatory	0.03%
Neutrophils	Neutrophils	Neutrophils	0.003 %
Dendritic cells	Dendritic cells resting, Dendritic cells activated	Myeloid dendritic cell, Plasmacytoid dendritic cell	0.07 %
Monocytes	Monocytes, Macrophages M0	Macrophages, Monocytes, Granulocyte-monocyte progenitor	0.8%
Macrophage M1	Macrophages M1	Macrophages M1	0.06%
Macrophage M2	Macrophages M2	Macrophages M2	0.02%
B cells	B cells naive, B cells memory, Plasma cells	B cell plasma, Class-switched memory B cell, B cell memory, B cell naive	0.4 %
-	T cells gamma delta, Mast cells resting, Eosinophils	T cell NK, Common lymphoid progenitor, Common myeloid progenitor, Eosinophil, Granulocyte-monocyte progenitor, Hematopoietic stem cell, Mast cell	3.8%

Table S2: Immune signature genes.

Name	Genes

IFNγ extended	CD3D,IL2RG,NKG7,CIITA,HLA-E,CD3E,CXCR6,CCL5,LAG3,TAGAP,GZMK,CD2, IDO1,CXCL10,HLA-DRA,STAT1,CXCL13,GZMB
TGFβ	ACTA2, ACTG2, ADAM12, ADAM19, CNN1, COL4A1, CTGF, CTPS1, FAM101B, FSTL3, HSPB1, IGFBP3, PXDC1, SEMA7A, SH3PXD2A, TAGLN, TGFBI, TNS1, TPM1
MPS	AKR1C3, BMP1, CRTAC1, ECEL1, ERC2, FAM110C, FUT9, GABRA2, GAP43, GREM1, HECW1, KLHL1, KRT12, LHFPL4, NEFL, NEFM, NETO1, NKX2-2, NSG2, OCIAD2, OTOP1, PDE3B, PTPRN2, PTPRT, SIGLEC15, SLC13A5, SLC9A2, SLITRK6, SNAP91, STON2, TAC1, VAT1L, WNT5A, ALX1, BRD7, DTD1, GRSF1, HCN1, LTA4H, OXCT1, PATJ, PLXNC1, SSBP4, TELO2, TMEM177
βCatenin	AKR1C3,BMP1,CRTAC1, ECEL1, ERC2, FAM110C, FUT9, GABRA2, GAP43, GREM1, HECW1, KLHL1, KRT12, LHFPL4, NEFL, NEFM, NETO1, NKX2-2, NSG2, OCIAD2, OTOP1, PDE3B, PTPRN2, PTPRT, SIGLEC15, SLC13A5, SLC9A2, SLITRK6, SNAP91, STON2, TAC1, VAT1L, WNT5A, ALX1, BRD7, DTD1, GRSF1, HCN1, LTA4H, OXCT1, PATJ, PLXNC1, SSBP4, TELO2, TMEM177