

Description of Additional Supplementary Files

Supplementary Data 1

Description: Database of ST TNBC cohort

Supplementary Data 2

Description: Distribution of number of selected ST spots and UMIs across each ST subarray in the ST TNBC cohort

Supplementary Data 3-5

Description

-Supplementary Data 3: Contribution by percentage of pixels of each histomorphological annotation by TNBC sample in the ST TNBC cohort (*referred to Figure 3b*)

-Supplementary Data 4: Metrics related to tumor patches in ST TNBC cohort (*referred to Figure 3e*)

-Supplementary Data 5: Metrics related to stroma patches in ST TNBC cohort (*referred to Supplementary Figure 1b*)

Supplementary Data 6

Description: Contribution of different morphological compartments by percentage to each ST TNBC sample by morphological regression tool

Supplementary Data 7

Description: TNBC molecular subtypes across different compartments in ST TNBC cohort: bulk RNA-seq, global pseudobulk, tumor and stroma pseudobulks (or compartments)

Supplementary Data 8-12

Description

-Supplementary Data 8: Identification of tertiary lymphoid structures by morphological annotation and regression and by spatial localization

-Supplementary Data 9: Selected GO:BP pathways enriched in TLS compartment compared to lymphocytes compartment (*referred to Figure 5c, Supplementary Figure 5b*)

-Supplementary Data 10: Selected GO:BP pathways enriched in lymphocytes compartment compared to TLS compartment (*referred to Supplementary Figure 5b*)

-Supplementary Data 11: Selected GO:BP pathways enriched in TLS compartment compared to other non-lymphocytes compartment (*referred to Supplementary Figure 5c*)

-Supplementary Data 12: Selected GO:BP pathways enriched in other non-lymphocytes compartment compared to TLS compartment (*referred to Supplementary Figure 5c*)

Supplementary Data 13-19

Description

-Supplementary Data 13: Whole list of differentially expressed genes between TLS compartment and any other non-TLS compartment (with the highest p value and the lowest Fold-Change) (*referred to Source Data Figure 5d*)

-Supplementary Data 14: Genes excluded from ST TLS sig

- Supplementary Data 15: Distribution of the expression of various TLS signatures across the nine histomorphological compartments in the ST TNBC cohort (*referred to Supplementary Figure 6b*)
- Supplementary Data 16: AUCs of different ST derived TLS signatures to predict the presence of TLS across different methods
- Supplementary Data 17: AUCs of individual gene of ST TLS signature to predict the presence of TLS across different methods
- Supplementary Data 18: Distribution of TLS signature expression across TNBC molecular subtypes both computed on the global pseudobulk in ST TNBC cohort (*referred to Figure 5f*)
- Supplementary Data 19: Distribution of TLS signature expression computed on the global pseudobulk across TIME classes by pathologist in ST TNBC cohort (*referred to Figure 5g*)

Supplementary Data 20-23

Description

- Supplementary Data 20: Inpatient clustering characterized by the TNBC molecular subtype on individual cluster recovered by K-means and deconvolution methods (*referred to Figure 7c*)
- Supplementary Data 21: Distribution of 14 megaclusters across each ST TNBC sample by different methods of recovery (*referred to Figure 7b, Supplementary Figure 10b*)
- Supplementary Data 22: Mean AUCs of bulk RNA-seq recovery of each MC according to different number of megaclusters in the ST TNBC cohort (*referred to Supplementary Figure 11a*)
- Supplementary Data 23: AUC of bulk RNA-seq recovery of each individual MC in the ST TNBC cohort

Supplementary Data 24-27

Description

- Supplementary Data 24: Optimal number of clusters based on 23 different indices
- Supplementary Data 25: Clinical and molecular characterizations of 9 megaclusters in ST TNBC, METABRIC and SCAN-B TNBC (*referred to Supplementary Figures 19b-33*)
- Supplementary Data 26: Distribution of TLS signature expression computed on the global pseudobulk across spatial archetypes in ST TNBC cohort (*referred to Figure 8d*)
- Supplementary Data 27: Contingency table showing the reproducibility of the 9 spatial archetypes using the global pseudobulk (gold standard, y-axis) and bulk RNA-seq (x-axis) data in the ST TNBC cohort.

Supplementary Data 28

Description: Automated and manual batch corrections between the subarrays of each TNBC sample in the ST TNBC cohort