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HIDS 503 – Final Project Step 3

Team 1

1. Describe how this analysis was done. Include screenshots.

The CIBERSORT analysis allows us to run a multiple sample gene expression analysis matrix to identify and estimate the immune cells present in bulk tumor samples. For this analysis, I first uploaded the chosen sample files for baseline (Normal tissue) and comparison group (Bladder Cancer Surrounding Mucosa) samples. These sample files will be run as Matrix files with CIBERSORT’s signature matrix file (LM22). After my files uploaded, I went to Menu | Run CIBERSORTx. I clicked “Impute cell fractions” as my selected analysis module and ran a custom analysis for both matrix files above against the LM22 Immune cell file (signature matrix file) – each with RNA-seq not disabled and 100 permutations. Once both of these tasks were finished running, I was able to obtain heat maps, stacked bar graphs, and output files for my baseline and comparison groups. The output files include fractions for each immune cell type (per sample job run). From this, I calculated the average immune cell type fraction to find the top five immune cells affected in each group (normal and surrounding mucosa).

Graphical user interface, text, application

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A picture containing timeline

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Graphical user interface

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1. Find and list the **top 5 types of immune cells**that are most prevalent in each of the two groups
   1. *Find the average of the fractions for each cell type across all samples in a group*
   2. *Repeat this for the two groups of interest (Normal and Tumor)*
   3. *Present results as two tables sorted by fraction values (largest fractions on top)*
   4. Include these tables in a summary document

Normal cells –

|  |  |
| --- | --- |
| Cell Type – BC\_Normal | Average Immune Cell Type Fraction (sorted DESC) |
| T cells memory activated | 0.208074602 |
| Macrophages M2 | 0.165670272 |
| Mast cells resting | 0.128585614 |
| T cells CD8 | 0.10200372 |
| T cells CD4 naïve | 0.10200372 |
| Monocytes | 0.05224817 |
| Macrophages M1 | 0.051271929 |
| NK cells resting | 0.044297464 |
| T cells regulatory (Tregs) | 0.03697545 |
| B cells naïve | 0.036692412 |
| NK cells activated | 0.02806672 |
| Plasma cells | 0.02209431 |
| B cells memory | 0.020754213 |
| T cells gamma delta | 0.02052146 |
| Macrophages M0 | 0.015868161 |
| Dendritic cells activated | 0.014471262 |
| T cells CD4 memory resting | 0.010280919 |
| Neutrophils | 0.00766235 |
| Mast cell activated | 0.006379394 |
| Eosinophils | 0.00303628 |
| Dendritic cells resting | 0.002652895 |
| T cells follicular helper | 0.000488617 |

The top 5 immune cells affected in the normal bladder cancer sample group include T cells memory activated, Macrophages M2, Mast cells resting, T cells CD8, and T cells CD4 naïve.

Bladder Cancer Surrounding Mucosa –

|  |  |
| --- | --- |
| Cell Type – Bladder Cancer Surrounding Mucosa | Average Immune Cell Type Fraction (sorted DESC) |
| T cells CD4 memory resting | 0.12578013 |
| Macrophages M2 | 0.12354847 |
| Mast cells resting | 0.07916073 |
| T cells CD8 | 0.07737444 |
| T cells regulatory (Tregs) | 0.07337502 |
| Monocytes | 0.05600648 |
| Dendritic cells activated | 0.05004041 |
| T cells gamma delta | 0.04556091 |
| Plasma cells | 0.04409398 |
| Macrophages M1 | 0.04278466 |
| B cells memory | 0.04215498 |
| T cells memory activated | 0.04183767 |
| B cells naïve | 0.03850824 |
| Macrophages M0 | 0.03738479 |
| NK cells resting | 0.02694729 |
| Mast cell activated | 0.02494797 |
| T cells follicular helper | 0.02072876 |
| T cells CD4 naïve | 0.01657434 |
| Dendritic cells resting | 0.01361494 |
| NK cells activated | 0.01313873 |
| Neutrophils | 0.00392505 |
| Eosinophils | 0.002512 |

The top 5 immune cells affected in the Bladder Cancer Surrounding Mucosa sample group include T cells memory resting, Macrophages M2, Mast cells resting, T cells CD8, and T cells regulatory (Tregs).