

Background

Immune checkpoint therapies target immune regulatory pathways to enhance anti-tumor immune response. These therapies have contributed to important clinical advances, and are a promising approach to combat cancer. Development of effective immune checkpoint therapies requires an understanding of the host immune response within the tumor microenvironment. Clariant Diagnostics Service Inc., has developed a multiplexed Tumor Infiltrating Lymphocyte (TIL) panel consisting of 12 key cancer immune markers: CD3, CD4, CD8, CD20, CD45RO, CD56, CD68, CTLA4, FOXP3, PD1, PD-L1 and Pan-CK. MultiOmyx (MO) TIL panel identifies algorithmically individual T<sub>helper</sub> (CD3+CD4+), T<sub>cytotoxic</sub> (CD3+CD8+), T<sub>regulatory</sub> (CD3+CD4+FoxP3), memory T-cells (CD3+CD4+CD45RO), anergic T-cells (PD1+CD8+), natural killer cells (CD3-CD56+), macrophages (CD68+) and B-cells (CD20+) within the tumor and the stromal regions and differentiate PD-L1 expression in tumor (PanCK+PD-L1+) and macrophages (CD68+PD-L1+). Utilizing the MO TIL panel, immune responses in the tumor microenvironment were profiled in melanoma, lung, colorectal, prostate, and breast cancer.

Overview of MultiOmyx™ Technology Workflow

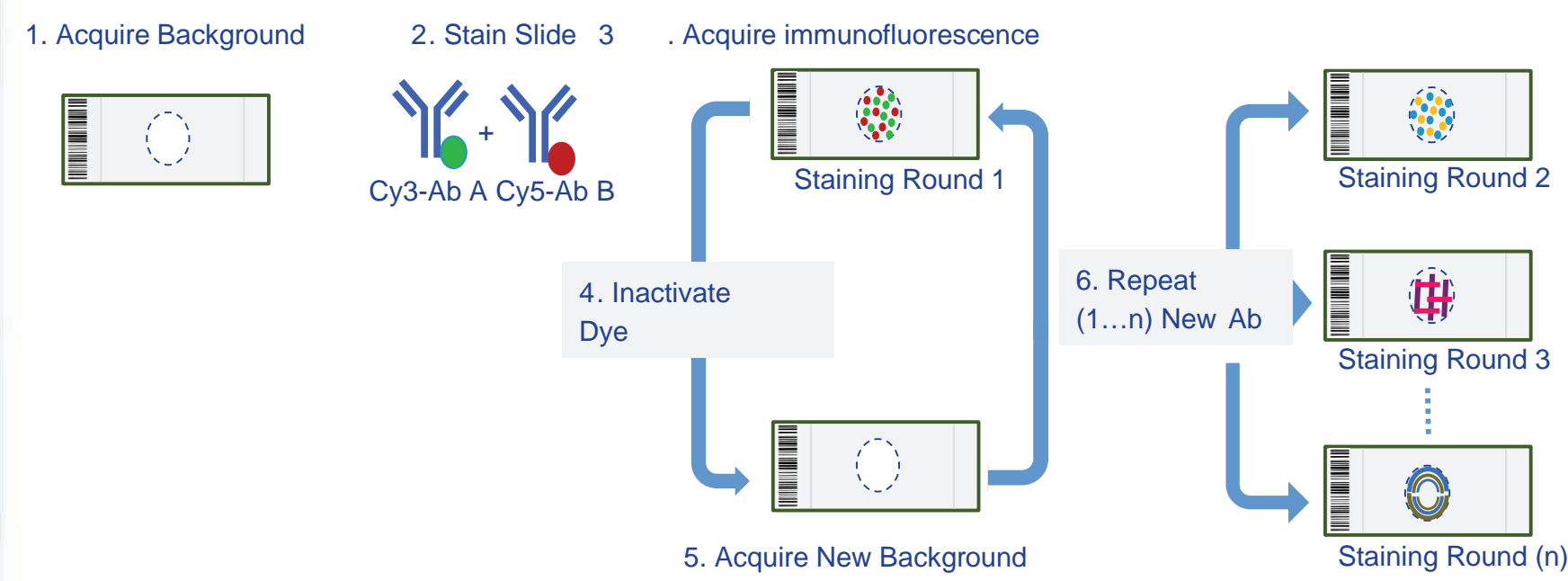


Figure 1. MultiOmyx IF multiplexing scheme from a single tissue section. Conjugated fluorescent antibodies were applied to a slide, followed by whole slide imaging. The dye was chemically inactivated, enabling a second round of staining with another fluorescent antibody. The process is repeated multiple times from a single slide until all biomarkers of interest are multiplexed.

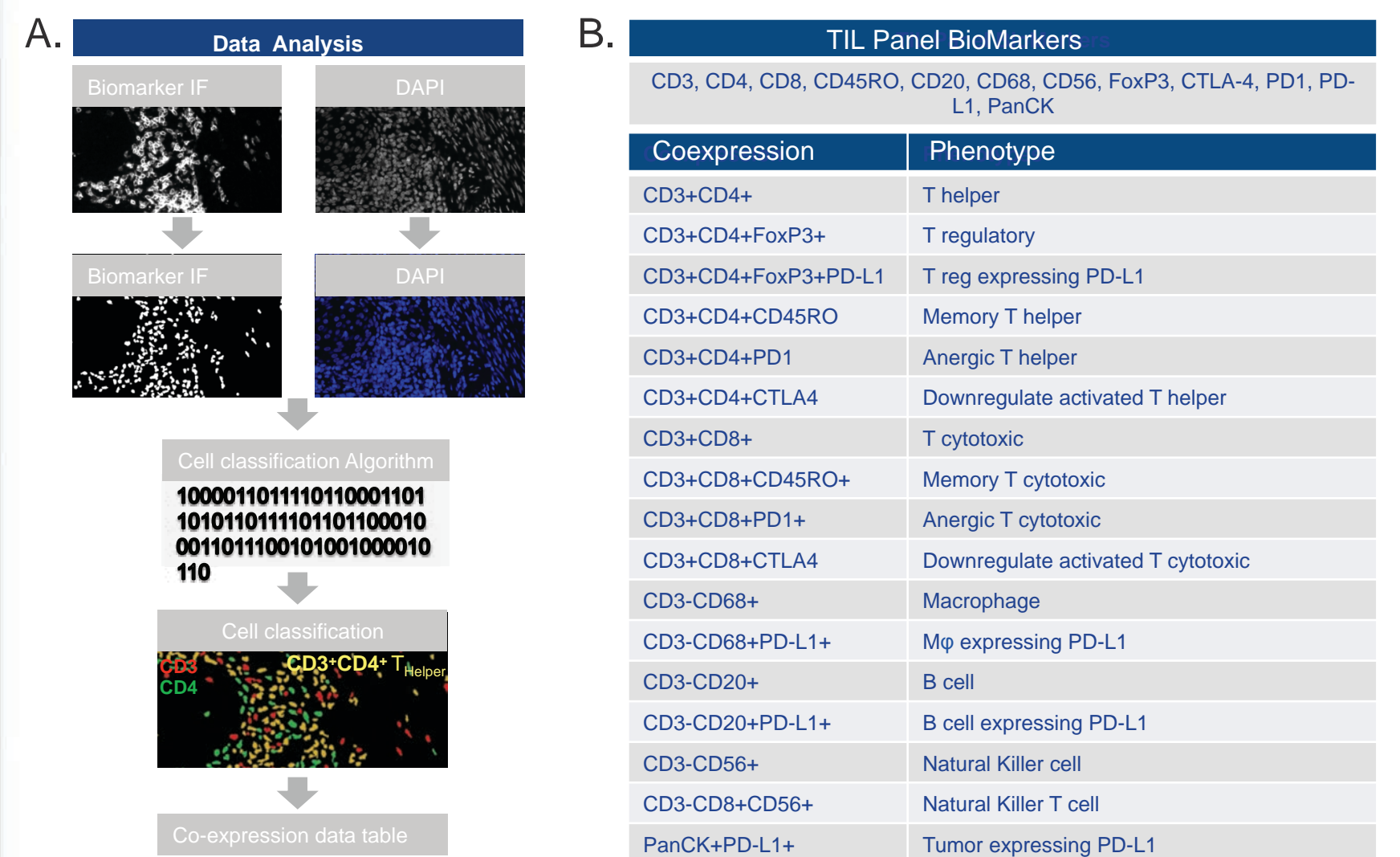


Figure 2. MultiOmyx data analysis workflow and TIL panel coexpression phenotypes. A. For each biomarker, the AF-removed immunofluorescence image is transformed into a biomarker segmentation map via proprietary algorithms that take into account staining pattern for each specific biomarker. Nuclear segmentation algorithms are applied to the DAPI image to identify location of nuclei. The biomarker segmentation map and the nuclear segmentation image are superimposed digitally, and proprietary algorithms compared areas of overlap and determined whether to call a given cell positive or negative. The result of this process is a classification label map and biomarkers coexpressions were obtained by overlapping individual classification label maps. B. Coexpression phenotypes algorithmically classified.

Conclusion

MultiOmyx TIL Panel was utilized to profile immune response in the tumor microenvironment within solid tumors including breast cancer, lung cancer, colorectal cancer, esophageal cancer, prostate cancer, and melanoma. The results shown in figure 4 revealed two distinct immunologic phenotypes, high TIL (Prostate & Breast), and Low TIL (Colorectal). The high TIL samples showed enhanced T cell population within the tumor and in the peritumoral stroma including CD8+ cytotoxic T cells, CD4+ helper T cells and CD45RO+ memory T cells. The low TIL sample showed reduced population of T cells and cells co-expressing different immune phenotypes. In the lung sample shown, PD-L1 is expressed primarily in the macrophages. Immunophenotyping analysis offered by the MultiOmyx TIL panel enabled unambiguous identification of T<sub>cytotoxic</sub>, T<sub>helper</sub>, T<sub>regulatory</sub>, macrophages, B cells, PD-L1 expressing cells and concise spatial relationship between immune cells and immune cells to the tumor.

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MultiOmyx TIL panel immune cells phenotypes

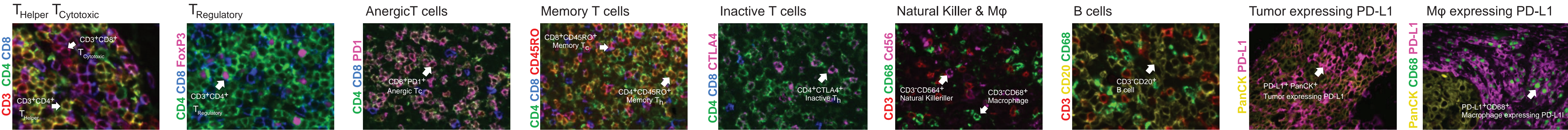


Figure 3. MultiOmyx TIL panel coexpression phenotypes. Autofluorescence removed (AFR) gray scale images of individual biomarkers were color blended based on biomarkers coexpressions to differentiate multiple immune phenotypes. Each phenotype is indicated by an arrow and an individual biomarker color code is indicated above for different combinations of coexpressions.

MultiOmyx TIL panel immuno profiling in solid tumors

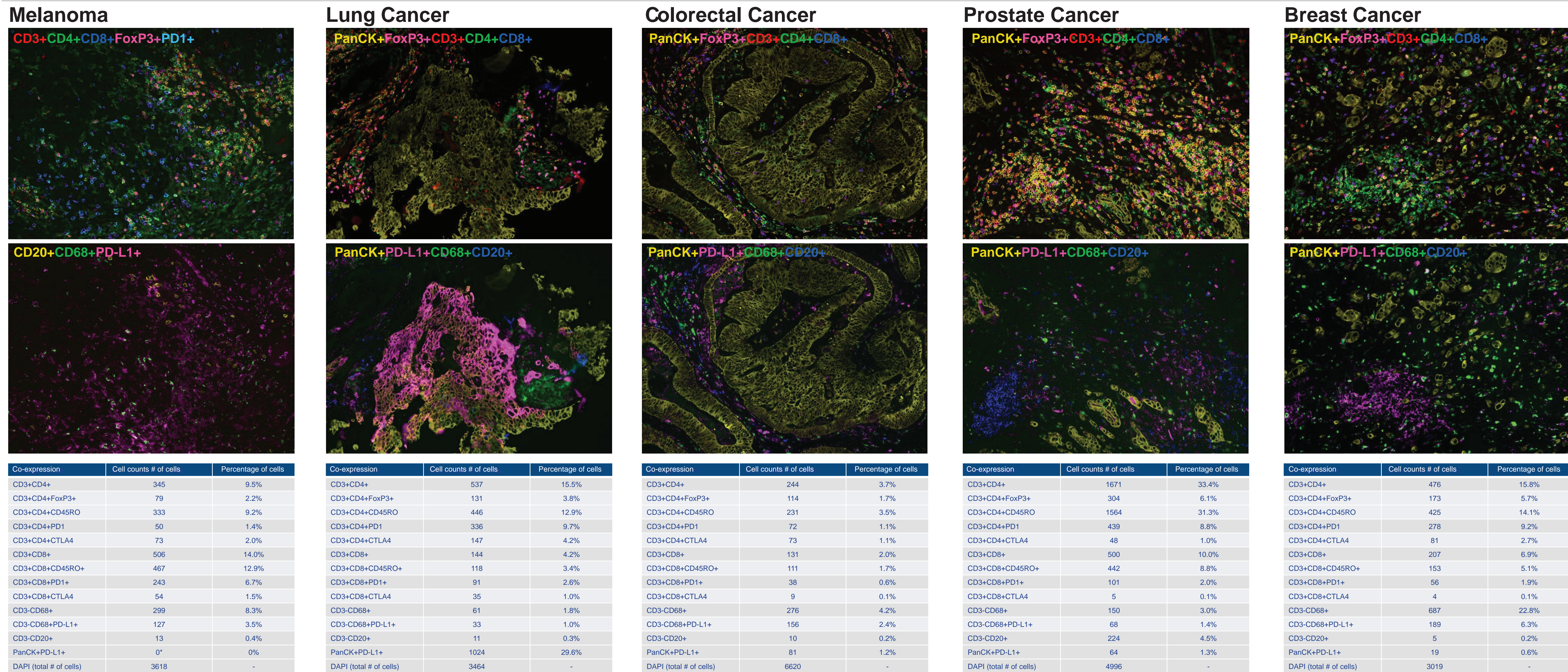


Figure 4. MultiOmyx TIL panel immuno profiling in solid tumors. Representative color blended multiplexed images are shown in melanoma, lung, colorectal cancer, prostate, and breast cancer. All 12 biomarkers were multiplexed on a single slide and displayed as two sets of images to improve visualization. Summary tables list the number of cells classified algorithmically based on co-expression of multiple immune markers. For each phenotype, percentages of cells are calculated using total number of cells based on DAPI staining.