

Table S1: *P*-values for the data obtained by the multiple probability simulation in glioma patients' compared to a healthy volunteer group.

| | <i>p</i> -value | | |
|----------------------|---------------------|------------------------|-------------------------|
| | Classical Monocytes | Intermediate Monocytes | Non-classical monocytes |
| PD-1 [%] | - | <0.0001 | - |
| PD-L1 [%] | <0.0001 | <0.0001 | <0.0001 |
| PD-L1 MFI | 0.8822 | <0.0001 | <0.0001 |
| SIRPalpha [%] | <0.0001 | <0.0001 | 0.0842 |
| SIRPalpha MFI | <0.0001 | 0.0001 | <0.0001 |
| IL-12 [%] | 0.8706 | 0.0014 | <0.0001 |
| TNF [%] | 0.0554 | 0.003 | <0.0001 |
| IL-10 [%] | 0.4675 | <0.0001 | 0.6493 |
| TGF-beta [%] | 0.0008 | <0.0001 | 0.0005 |

To confirm the significance of the obtained results, the Monte Carlo Method was used to simulate the data (n=100) based on the results (n=24) which showed statistical significance in comparison between the expression of immune checkpoint and cytokine molecules expression in glioma patients' compared to a healthy volunteer group. '-' symbolize the absence of statistical significance when comparing 24 original results to the control.

PD-1, programmed cell death 1 protein; PD-L1, programmed cell death 1 ligand, MFI, mean fluorescence intensity; SIRPalpha, signal-regulatory protein alpha; TNF, tumor necrosis factor; TGF-beta, transforming growth factor beta