

Table S2. GO terms in tissue clusters of PD-L1-negative and PD-L1-positive triple-negative breast cancer

Cluster number	PD-L1-negative cases			PD-L1-positive cases		
	1	2	3	4	5	6
1	<p>cell migration involved in sprouting angiogenesis (GO:0002042) p = 0.024</p> <p>negative regulation of cell cycle (GO:0045786) p = 0.047</p> <p>positive regulation of apoptotic process (GO:0043065) p = 0.047</p>		<p>neutrophil activation involved in immune response (GO:0002283) p = 3.62E-4</p>		<p>extracellular matrix organization (GO:0030198) p = 3.54E-7</p> <p>positive regulation of cell motility (GO:2000147) p = 1.63E-4</p>	
2	-		<p>negative regulation of angiogenesis (GO:0016525) p = 2.61E-5</p> <p>regulation of cell migration (GO:0030334) p = 0.0012</p>	<p>regulation of cell population proliferation (GO:0042127) p = 0.024</p> <p>negative regulation of cell motility (GO:2000146) p = 0.024</p>	<p>B cell activation (GO:0042113) p = 2.37E-7</p> <p>lymphocyte differentiation (GO:0030098) p = 2.73E-6</p> <p>T-helper cell lineage commitment (GO:0002295) p = 0.009</p>	
3	<p>antigen processing and presentation of exogenous peptide antigen (GO:0002478) p = 1.44E-10</p> <p>positive regulation of cytokine production (GO:0001819) p = 1.399E-7</p>		<p>cytokine-mediated signaling pathway (GO:0019221) p = 4.54E-10</p> <p>negative regulation of programmed cell death (GO:0043069) p = 5.20E-4</p> <p>antigen processing and presentation of peptide</p>		<p>extracellular matrix organization (GO:0030198) p = 3.16E-4</p> <p>regulation of insulin-like growth factor receptor signaling pathway (GO:0043567) p = 0.0024</p>	<p>cellular response to type I interferon (GO:0071357) p = 3.15E-10</p> <p>positive regulation of</p>

			antigen via MHC class I (GO:0002474) p = 0.011		positive regulation of cell motility (GO:2000147) p = 0.004	fibroblast proliferation (GO:0048146) ) p = 7.29E-4
4	extracellular matrix organization (GO:0030198) p = 1.31E-29 negative regulation of cell migration (GO:0030336) p = 4.12E-4	extracellular matrix organization (GO:0030198) ) p = 1.95E-26 negative regulation of angiogenesis (GO:0016525) ) p = 6.30E-8 cytokine- mediated signaling pathway (GO:0019221) ) p = 4.846E-4 antigen processing and presentation of exogenous peptide antigen via MHC class II (GO:0019886) ) p = 4.03E-4	extracellular structure organization (GO:0043062) p = 0.0033 regulation of cell migration (GO:0030334) p = 0.013	defense response to virus (GO:0051607) p = 9.63E-6	positive regulation of cell population proliferation (GO:0008284) p = 2.23E-6 negative regulation of apoptotic process (GO:0043066) p = 8.15E-4 negative regulation of epithelial to mesenchymal transition (GO:0010719) p = 0.0016 positive regulation of cell motility (GO:2000147) p = 0.0018	cytokine- mediated signaling pathway (GO:0019221) ) p = 3.958E- 11 positive regulation of T cell activation (GO:0050870) ) p = 3.400E-5 interferon- gamma- mediated signaling pathway (GO:0060333) ) p = 0.0013 regulation of T-helper 1 cell differentiation (GO:0045625) )

						p = 0.0101
5			<p>extracellular matrix organization (GO:0030198) p = 4.624E-22</p> <p>neutrophil activation involved in immune response (GO:0002283) p = 8.09E-10</p> <p>cytokine-mediated signaling pathway (GO:0019221) p = 1.743E-7</p> <p>antigen processing and presentation of exogenous peptide antigen (GO:0002478) p = 4.448E-4</p>	<p>extracellular structure organization (GO:0043062) p = 1.03E-16</p> <p>cytokine-mediated signaling pathway (GO:0019221) p = 0.0052</p> <p>neutrophil activation involved in immune response (GO:0002283) p = 0.025</p> <p>cellular response to transforming growth factor beta stimulus (GO:0071560) p = 0.0390</p>	<p>cellular response to type I interferon (GO:0071357) p = 3.70E-4</p> <p>negative regulation of transforming growth factor beta production (GO:0071635) p = 0.0020</p> <p>regulation of cell population proliferation (GO:0042127) p = 0.0093</p>	<p>extracellular matrix organization (GO:0030198) ) p = 4.65E-11</p> <p>cellular response to cytokine stimulus (GO:0071345) ) p = 0.0060</p>
6	<p>fatty acid beta-oxidation (GO:0006635) p = 5.31E-4</p>		<p>extracellular matrix organization (GO:0030198) p = 2.92E-8</p> <p>neutrophil activation involved in immune response (GO:0002283) p = 5.32E-7</p> <p>negative regulation of cell migration (GO:0030336) p = 5.32E-7</p> <p>cytokine-mediated signaling pathway (GO:0019221) p = 3.76E-5</p>	<p>extracellular matrix organization (GO:0030198) p = 1.874E-9</p>	<p>extracellular matrix organization (GO:0030198) p = 3.03E-12</p> <p>cellular response to cytokine stimulus (GO:0071345) p = 6.760E-11</p> <p>antigen receptor-mediated signaling pathway (GO:0050851) p = 2.788E-6</p>	<p>epithelium development (GO:0060429) ) p = 0.011</p> <p>negative regulation of programmed cell death (GO:0043069) ) p = 0.035</p>

7	fatty acid beta-oxidation (GO:0006635) p = 7.634E-6		cytokine-mediated signaling pathway (GO:0019221) p = 9.42E-7 negative regulation of intrinsic apoptotic signaling pathway (GO:2001243) p = 4.011E-6 neutrophil activation involved in immune response (GO:0002283) p = 4.011E-6	extracellular matrix organization (GO:0030198) p = 2.42E-15 positive regulation of cytokine production (GO:0001819) p = 4.38E-7 regulation of angiogenesis (GO:0045765) p = 1.267E-5	extracellular matrix organization (GO:0030198) p = 2.44E-15 neutrophil mediated immunity (GO:0002446) p = 6.69E-9 positive regulation of cell migration (GO:0030335) p = 9.175E-5	
8			negative regulation of RNA polymerase II regulatory region sequence-specific DNA binding (GO:1903026) p = 0.0151		positive regulation of wound healing (GO:0090303) p = 0.0225 regulation of cell migration (GO:0030334) p = 0.0491	
9			regulation of immune effector process (GO:0002697) p = 0.0030 positive regulation of immune response (GO:0050778) p = 0.0042 adipose tissue development (GO:0060612) p = 0.0044		extracellular matrix organization (GO:0030198) p = 1.269E-6 endothelium development (GO:0003158) p = 0.00270	