G: profiler scoring results:

Results for all 55 genes in our list:

ID	Source	Term ID	Term Name	p_{adj} (query_1)
1	GO:MF	GO:0005102	signaling receptor binding	9.900×10^{-23}
2	GO:MF	GO:0001530	lipopolysaccharide binding	4.677×10^{-7}
3	GO:MF	GO:0140375	immune receptor activity	2.179×10^{-6}
4	GO:MF	GO:0019955	cytokine binding	5.408×10^{-5}
5	GO:MF	GO:0001875	lipopolysaccharide immune receptor activity	1.711×10^{-4}
6	GO:BP	GO:0006954	inflammatory response	4.259×10^{-45}
7	GO:BP	GO:0007159	leukocyte cell–cell adhesion	1.199×10^{-25}
8	GO:BP	GO:0060559	positive regulation of calcidiol 1-monooxygena...	3.207×10^{-5}
9	GO:BP	GO:0043388	positive regulation of DNA binding	1.138×10^{-4}
10	GO:BP	GO:0006509	membrane protein ectodomain proteolysis	2.618×10^{-4}
11	GO:BP	GO:0032963	collagen metabolic process	4.818×10^{-4}
12	GO:BP	GO:0045944	positive regulation of transcription by RNA pol...	8.146×10^{-4}
13	GO:BP	GO:0003158	endothelium development	2.412×10^{-3}
14	GO:BP	GO:0019233	sensory perception of pain	4.350×10^{-3}
15	GO:BP	GO:0061844	antimicrobial humoral immune response media...	4.620×10^{-3}
16	GO:CC	GO:0005576	extracellular region	8.200×10^{-15}
17	GO:CC	GO:0030141	secretory granule	1.011×10^{-14}
18	GO:CC	GO:0009986	cell surface	1.190×10^{-14}
19	GO:CC	GO:1990660	calprotectin complex	1.400×10^{-3}

ID	SOURCE	Term ID	Term Name	Padg	relevance
1	GO:MF	GO:0005102	Signaling receptor binding	9.900×10^{-23}	0.5
2	GO:MF	GO:0001530	Lipopolysaccharide binding	4.677×10^{-7}	1
3	GO:MF	GO:0140375	Immune receptor activity	2.179×10^{-6}	1
4	GO:MF	GO:0019955	Cytokine binding	5.048×10^{-6}	1
5	GO:MF	GO:0001875	Lipopolysaccharide immune receptor activity	1.711×10^{-4}	1
6	GO:BD	GO:0006954	Inflammatory response	4.259×10^{-45}	1
7	GO:BD	GO:0007159	Leukocyte cell-cell adhesion	1.199×10^{-25}	1
8	GO:BD	GO:0060559	Positive regulation of calcidiol 1-monooxygenase activity	2.418×10^{-5}	-1
9	GO:BD	GO:0043388	Positive regulation of DNA binding	8.210×10^{-5}	0.5
10	GO:BD	GO:0006509	Membrane protein ectodomain proteolysis	3.140×10^{-6}	0.5
11	GO:BD	GO:0032963	Collagen metabolic process	3.750×10^{-4}	-1
12	GO:BD	GO:0045944	Positive regulation of transcription by RNA polymerase II	3.184×10^{-6}	0.5
13	GO:BD	GO:0003158	Endothelium development	2.412×10^{-3}	1

14	GO:BD	GO:0019233	Sensory perception of pain	4.350x10^-3	-1
15	GO:BD	GO:0061844	Antimicrobial humoral immune response mediated by antimicrobial peptide	1.846x10^-7	1
16	GO:CC	GO:0005576	Extracellular region	1.101x10^-15	0.5
17	GO:CC	GO:0030141	Secretory granule	1.190x10^-14	0.5
18	GO:CC	GO:0009986	Cell surface	1.190x10^-14	0.5
19	GO:CC	GO:1990660	Calprotectin complex	1.400x10^-3	1
19	-	-	-	-	**9.5**

The results is 9.5/19 -> 50 %

✔ 1 for sepsis-relevant processes (e.g., immune response, inflammation, endotoxin recognition).
✔ 0.5 for general biological processes (e.g., receptor binding, transcription regulation).
✔ -1 for unrelated functions (e.g., sensory perception, vitamin metabolism).

Results for our top genes in Random forests and Mann-w-u tests:
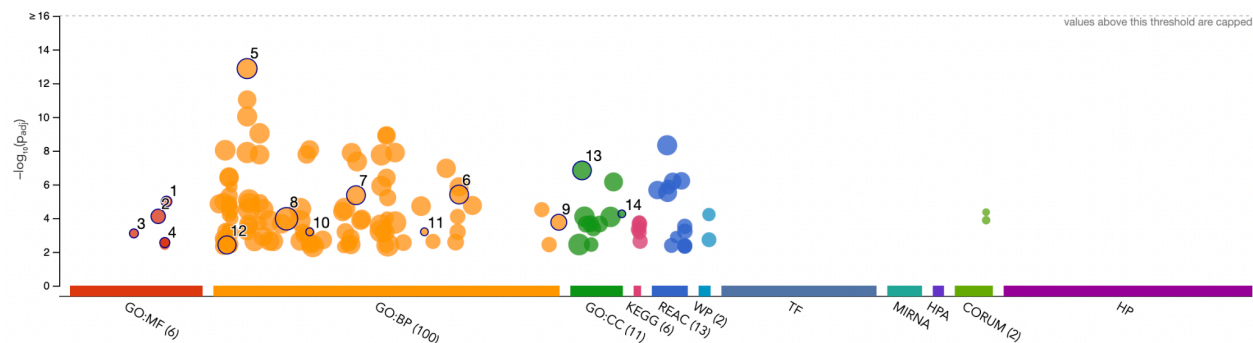
ID	Source	Term ID	Term Name	P_{adj} (query_1)
1	GO:MF	GO:0050786	RAGE receptor binding	$1.027×10^{-5}$
2	GO:MF	GO:0048306	calcium-dependent protein binding	$7.808×10^{-5}$
3	GO:MF	GO:0035662	Toll-like receptor 4 binding	$7.997×10^{-4}$
4	GO:MF	GO:0050544	arachidonate binding	$2.795×10^{-3}$
5	GO:BP	GO:0006952	defense response	$1.351×10^{-13}$
6	GO:BP	GO:0098609	cell-cell adhesion	$3.941×10^{-6}$
7	GO:BP	GO:0044093	positive regulation of molecular function	$4.361×10^{-6}$
8	GO:BP	GO:0019222	regulation of metabolic process	$1.083×10^{-4}$
9	GO:BP	GO:2001242	regulation of intrinsic apoptotic signaling path...	$1.743×10^{-4}$
10	GO:BP	GO:0032119	sequestering of zinc ion	$6.425×10^{-4}$
11	GO:BP	GO:0070488	neutrophil aggregation	$6.425×10^{-4}$
12	GO:BP	GO:0002521	leukocyte differentiation	$3.874×10^{-3}$
13	GO:CC	GO:0030141	secretory granule	$1.471×10^{-7}$
14	GO:CC	GO:1990660	calprotectin complex	$5.505×10^{-5}$

ID	SOURCE	Term ID	Term Name	Padg	relevance
1	GO:MF	GO:0050786	RAGE receptor binding	1.027×10^{-5}	1
2	GO:MF	GO:0048306	Calcium-dependent protein binding	7.808×10^{-5}	0.5
3	GO:MF	GO:0035662	Toll-like receptor 4 binding	7.997×10^{-4}	1
4	GO:MF	GO:0050544	Arachidonate binding	2.795×10^{-3}	0.5
5	GO:MF	GO:0006952	Defense response	1.365×10^{-5}	1
6	GO:BD	GO:0098609	Cell-cell adhesion	3.941×10^{-6}	1
7	GO:BD	GO:0044093	Positive regulation of molecular function	4.361×10^{-6}	0.5
8	GO:BD	GO:0019222	Regulation of metabolic process	1.083×10^{-4}	0.5
9	GO:BD	GO:2001242	Regulation of intrinsic apoptotic signaling pathway	1.024×10^{-4}	1
10	GO:BD	GO:0032119	Sequestering of zinc ion	6.425×10^{-4}	-1
11	GO:BD	GO:0070488	Neutrophil aggregation	8.476×10^{-4}	1
12	GO:BD	GO:0002521	Leukocyte differentiation	2.813×10^{-7}	1
13	GO:BD	GO:0003158	Secretory granule	1.417×10^{-7}	0.5
14	GO:BD	GO:0019233	Calprotectin complex	5.505×10^{-5}	1
14	-	-	-	-	9.5

The results is 9.5/14 -> 68 %

The higher relevance score suggests that the RF and MWU approaches successfully prioritize genes involved in immune response, apoptosis, and inflammatory signaling.

Comparison of Sepsis Relevance Scores