

**Table S4.** Enriched pathways associated with saDEGs, and therefore cDEGs, filtered by FDR < 0.05 found in the set analysis. Among the upregulated cDEGs, 91 genes had major roles in immunological pathways. For instance, 34 genes such as *CYBB* (p-value =  $1.758 \times 10^{-20}$ , logfc = 3.1303), *CD3E* (p value =  $2.421 \times 10^{-15}$ , logfc = 2.6583), *CD8A* (p value = 3.734, logfc = 2.2508), *CD19* (p value =  $2.485 \times 10^{-30}$ , logfc = 5.5543) were associated with adaptive immune response and their cellular signaling networks, while 44 genes, including Matrix Metalloproteinases (MMPs) family genes, *DEFB4* (p value =  $2.278 \times 10^{-58}$ , logfc = 7.6490), *TLR8* (p value =  $3,003 \times 10^{-19}$ , logfc = 2.8510), *BIN2* (p value =  $2.563 \times 10^{-13}$ , logfc = 2.4414), were linked with innate immune system. In other important pathways such as extracellular matrix organization, 23 genes like *ADAM12* (p value =  $1.492 \times 10^{-22}$ , logfc = 4.1200), *ADAMTS2* (p value = 2.6091, logfc =  $1.111 \times 10^{-14}$ ) and *COL3A1* (p value =  $1.433 \times 10^{-17}$ , logfc = 2.7178), were found. On the other hand, down-regulated cDEGs such as *FA2H* (p value =  $5.394 \times 10^{-20}$ , logfc = -3.7949), *FADS2* (p value =  $1.073 \times 10^{-24}$ , logfc = -4.61), *GUCY2EP* (p value = 5.673, logfc = -1.9362), *HSD3B1* (p value =  $4.861 \times 10^{-30}$ , logfc = -5.2634), *IYD* (p value =  $1.337 \times 10^{-20}$ , logfc = -2.4972), *MOGAT2* (p value =  $1.59 \times 10^{-23}$ , logfc = -3.7538), *MPPED1* (p value =  $1.519 \times 10^{-25}$ , logfc = -3.1882), *PNPLA5* (p value =  $3.314 \times 10^{-29}$ , logfc = -4.2126), *SOX9-AS1* (p value =  $8.702 \times 10^{-17}$ , logfc = -2,3383), *THRSP* (p value =  $4.101 \times 10^{-48}$ , logfc = -5.4498), play a crucial role in metabolic pathways. In particular, *FA2H*, *FADS2*, *MOGAT2*, *HSD3B1*, *THRSP*, *PNPLA5* are important for the metabolism of lipids while *IYD* participates in thyroxine biosynthesis and metabolism of amine-derived hormones.

Pathway identifier	Pathway name	Pathway also found in the meta-analysis	Entities found	saDEGs	FDR
R-HSA-168256	Immune System	No	91	Up	$7.37 \times 10^{-09}$
R-HSA-380108	Chemokine receptors bind chemokines	Yes	13	Up	$7.37 \times 10^{-09}$
R-HSA-198933	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	Yes	25	Up	$5.48 \times 10^{-08}$
R-HSA-1474244	Extracellular matrix organization	Yes	23	Up	$2.01 \times 10^{-06}$
R-HSA-8949275	RUNX3 Regulates Immune Response and Cell Migration	No	6	Up	$2.12 \times 10^{-06}$
R-HSA-6783783	Interleukin-10 signaling	Yes	11	Up	$2.57 \times 10^{-05}$

R-HSA-375276	Peptide ligand-binding receptors	Yes	16	Up	3.60x10 <sup>-05</sup>
R-HSA-1474228	Degradation of the extracellular matrix	Yes	13	Up	1.10x10 <sup>-04</sup>
R-HSA-1442490	Collagen degradation	Yes	9	Up	1.64x10 <sup>-04</sup>
R-HSA-449147	Signaling by Interleukins	Yes	28	Up	3.11x10 <sup>-04</sup>
R-HSA-1474290	Collagen formation	Yes	10	Up	5.49x10 <sup>-04</sup>
R-HSA-2022090	Assembly of collagen fibrils and other multimeric structures	Yes	8	Up	7.33x10 <sup>-04</sup>
R-HSA-168249	Innate Immune System	No	44	Up	7.33x10 <sup>-04</sup>
R-HSA-1592389	Activation of Matrix Metalloproteinases	Yes	6	Up	9.57x10 <sup>-04</sup>
R-HSA-6798695	Neutrophil degranulation	Yes	21	Up	0.00260791
R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	Yes	19	Up	0.00272173
R-HSA-216083	Integrin cell surface interactions	Yes	8	Up	0.00306491
R-HSA-1280218	Adaptive Immune System	No	34	Up	0.00306491
R-HSA-8939245	RUNX1 regulates transcription of genes involved in BCR signaling	No	3	Up	0.00487645
R-HSA-1280215	Cytokine Signaling in Immune system	No	34	Up	0.01218292
R-HSA-556833	Metabolism of lipids	No	6	Down	0.00202704
R-HSA-8979227	Triglyceride metabolism	No	2	Down	0.0087015
R-HSA-1430728	Metabolism	No	7	Down	0.01607597

R-HSA-193993	Mineralocorticoid biosynthesis	No	1	Down	0.01607597
R-HSA-2046105	Linoleic acid (LA) metabolism	No	1	Down	0.01607597
R-HSA-194002	Glucocorticoid biosynthesis	No	1	Down	0.01607597
R-HSA-209968	Thyroxine biosynthesis	No	1	Down	0.01607597
R-HSA-193048	Androgen biosynthesis	No	1	Down	0.01607597
R-HSA-2046104	alpha-linolenic (omega3) and linoleic (omega6) acid metabolism	No	1	Down	0.01607597
R-HSA-2046106	alpha-linolenic acid (ALA) metabolism	No	1	Down	0.01607597
R-HSA-200425	Carnitine metabolism	No	1	Down	0.01607597
R-HSA-75109	Triglyceride biosynthesis	No	1	Down	0.01607597
R-HSA-8978868	Fatty acid metabolism	Yes	2	Down	0.01761335
R-HSA-209776	Metabolism of amine-derived hormones	Yes	1	Down	0.02062509
R-HSA-163560	Triglyceride catabolism	No	1	Down	0.02741238
R-HSA-196071	Metabolism of steroid hormones	No	1	Down	0.0397431