Inflammation in osteoarthritis – a focus on the role of interleukin-17



Jolet Yvette Mimpen

Green Templeton College

University of Oxford

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Volume 2: Appendices

Contents

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Contents: Volume 2		A-i
List of figures		A-iii
List of tables		A-vii
Appendix A		A-1
Chapter 2: Cellular and molecular characterisation of end-stage osteoarthritis synovium		
A1	Overview of cell surface markers	A-2
A2	Overview of antibodies	A-3
A3	Run details	A-6
A4	Gating strategy	A-7
A4.1	T cells markers	A-7
A4.2	B cells marker	A-8
A4.3	Monocyte(-derived) cell markers and granulocyte markers	A-9
A4.4	Fibroblast markers	A-10
A5	Immunofluorescence negative controls	A-11
A6	High-resolution confocal images Chapter 2	A-12
A7	Additional correlation tests	A-14
A7.1	Correlations of fibroblast subsets with KL-grade and OKS	A-14
A7.2	Correlations of age with KL-grade	A-15
A7.3	Correlations of cytotoxic T cells	A-15
A7.4	Correlations of CD68+CD206+ macrophages with age and OKS	A-16
A8	Proteomics	A-17
A8.1	Subgroups based on flow cytometry results	A-17
A8.2	Full list of protein intensities for each synovial fluid sample	A-19
Appendix B		A-43
Chapter 3: IL-17RA and macrophage markers are increased in OA patients with synovial inflammation		
B1	Negative controls for immunohistochemistry	A-44
B2	Analysis pipeline for immunohistochemistry images	A-45
B3	High-resolution confocal images Chapter 3	A-51

Appendix C A-57

Chapter 4: IL-17 treatment increases expression of OA-related inflammatory and matrix genes in end-stage OA chondrocytes and synovial fibroblasts

C1	Overview of RNA-Seq samples	A-58
C2	Mapping and FastQC for RNA-Seq samples	A-61
C2.1	Bowtie 2 for alignment	A-61
C2.2	FastQ screen	A-64
C3	Differentially expressed genes due to IL-17A/F treatment	A-66
C3.1	Differentially expressed genes in end-stage OA chondrocytes	A-66
C3.2	Differentially expressed genes in end-stage OA synovial fibroblasts	A-87
C4	Results from pathway analyses	A-96
C4.1	Pathway analysis results from chondrocyte samples	A-96
C4.1.1	Hallmark pathways	A-96
C4.1.2	Immune pathways	A-99
C4.1.3	Cytokine/chemokine pathways	A-102
C4.1.4	Matrix pathways	A-104
C4.2	Overview of pathway analyses results: synovial fibroblasts	A-107
C4.2.1	Hallmark pathways	A-107
C4.2.2	Immune pathways	A-110
C4.2.3	Cytokine/chemokine pathways	A-113
C4.2.4	Matrix and cytoskeleton pathways	A-115
C4.3	Volcano plots	A-118
C5	Western blots	A-137

List of figures

Figure A4-1. Gating of T cell markers in CD45+ small cells A-7

Figure A4-2. Gating of B-cell marker CD19. A-8

Figure A4.3. Gating of granulocyte markers in CD45+ large cells A-9

Figure A4.4. Gating of fibroblast activation markers in CD45- cells A-10

Figure A5-1. Immunofluorescent staining with (A-D) universal mouse negative control or (E-G) rabbit negative control. A-11

Figure A6.1. High-resolution confocal images of Figure 2-11A-E. A-12

Figure A6.2. High-resolution confocal images of Figure 2-11F-J. A-13

Figure A7-1. Correlation between fibroblast subsets and clinical markers of disease in synovium from patients with end-stage knee OA (as a percentage of CD45-PDPN+ viable cells). A-14

Figure A7-2. Correlation between the age and Kellgren Lawrence (KL)-grade of patients with end-stage knee OA. A-15

Figure A7-3. Correlations regarding CD8+ T cells (as % of CD45+ cells) in synovium from patients with end-stage knee OA. A-15

Figure A7-4. Correlations regarding CD68+CD206+ macrophages (as % of CD45+ cells) in synovium from patients with end-stage knee OA A-16

Figure A8-1. Principle component analysis (PCA) plots for proteomic results of synovial fluid samples separated into subgroups. A-18

Figure B1-1. Immunohistochemistry DAB staining with (A) universal mouse negative control or (B) rabbit negative control. A-44

Figure B2-1. CellProfiler pipeline “DAB and nuclei measurements”, input step 1. A-45

Figure B2-2. CellProfiler pipeline “DAB and nuclei measurements”, input step 2. A-45

Figure B2-3. CellProfiler pipeline “DAB and nuclei measurements”, input step 3. A-46

Figure B2-4. CellProfiler pipeline “DAB and nuclei measurements”, input step 4. A-46

Figure B2-5. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 1 A-47

Figure B2-6. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 2. A-47

Figure B2-7. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 3. A-48

Figure B2-8. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 4. A-48

Figure B2-9. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 5. A-49

Figure B2-10. CellProfiler pipeline “DAB and nuclei measurements”, analysis step 6. A-50

Figure B3-1. High-resolution confocal images of Figure 3-8A-E. A-51

Figure B3-2. High-resolution confocal images of Figure 3-8F-J. A-52

Figure B3-3. High-resolution confocal images of Figure 3-16A-E. A-53

Figure B3-4. High-resolution confocal images of Figure 3-16F-J. A-54

Figure B3-5. High-resolution confocal images of Figure 3-17A-E. A-55

Figure B3-6. High-resolution confocal images of Figure 3-17F-J. A-56

Figure C2-1. Bowtie2 plot with paired-end (PE) alignment scores for chondrocytes (HAC) samples. A-62

Figure C2-2. Bowtie2 plot with paired-end (PE) alignment scores for synovial fibroblast (SF) samples. A-63

Figure C2-3. Results of the FastQ screen for each chondrocyte sample including the genomes that the aligned sequence match with, showing that most sequences align with the human genome. A-64

Figure C2-4. Results of the FastQ screen for each chondrocyte sample including the genomes that the aligned sequence match with, showing that most sequences align with the human genome. A-65

Figure C4-1. Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots. A-119

Figure C4-2. Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots. A-120

Figure C4-3. Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots. A-121

Figure C4-4. Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots. A-122

Figure C4-5. Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots. A-123

Figure C4-6. Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots. A-124

Figure C4-7. Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots. A-125

Figure C4-8. Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots. A-126

Figure C4-9. Volcano plot representing genes changed by IL-17A treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-127

Figure C4-10. Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-128

Figure C4-11. Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-129

Figure C4-12. Volcano plot representing genes changed by IL-17A treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-130

Figure C4-13. Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-131

Figure C4-14. Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots. A-132

Figure C4-15. Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots. A-133

Figure C4-16. Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots. A-134

Figure C4-17. Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots. A-135

Figure C4-18. Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots. A-136

Figure C5.1. Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, of medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p38, and total p38, and visualised with an enhanced chemiluminescent reagent. A-137

Figure C5.2. Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent. A-137

Figure C5.3. Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies A-138

against vinculin, phosphorylated ERK1/2, and total ERK1/2, and visualised with an enhanced chemiluminescent reagent.

Figure C5.4. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained with antibodies against vinculin, phosphorylated p38, and total p38, and visualised with an enhanced chemiluminescent reagent. A-138

Figure C5.5. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent. A-139

Figure C5.6. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17F or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent. A-139

Figure C5.7. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated ERK1/2, and total ERK1/2, and visualised with an enhanced chemiluminescent reagent. A-140

List of tables

Table A1.1. Overview of cells surface proteins used in this study, including the main cell type that expresses this protein and other cells these proteins can be present on. A-2

Table A2.1. Antibodies used for extracellular staining of cells. If concentrations of the antibody were unknown, recommended concentrations for isotype control antibodies were used A-3

Table A2.2. Antibodies used for intracellular staining of cells. A-5

Table A3.1. Voltages used for each individual flow cytometry run. A-6

Table A8-1. Patient subgroups used for proteomics analysis based on the presence or absence of CCR6+ T cells, and most prominent immune cell type. A-17

Table A8-2. Protein intensities of proteins detected in synovial fluid by mass spectrometry. A-19

Table C1-1. Overview of chondrocytes samples used for RNA Sequencing. A-59

Table C1-2. Overview of synovial fibroblast samples used for RNA Sequencing. A-60

Table C2-1. Percentage alignment of each chondrocyte sample with reference sequences. A-62

Table C2-2. Percentage of each synovial fibroblast sample that aligned with reference sequences. A-63

Table C3-1. Overview of differentially expressed genes in chondrocytes between control or IL-17 treated samples with an adjusted p-value of <0.05 A-66

Table C3-2. Overview of differentially expressed genes in synovial fibroblasts between control or IL-17 treated samples with an adjusted p-value of <0.05. A-87

Table C4-1. Genes that contribute to the changes in hallmark pathways after treatment with IL-17A compared to control. A-96

Table C4-2. Genes that contribute to the changes in hallmark pathways after treatment with IL-17F compared to control. A-98

Table C4-3. Genes that contribute to the changes in hallmark pathways after treatment with IL-17AF compared to control. A-98

Table C4-4. Genes that contribute to the changes in immune pathways after treatment with IL-17A compared to control. A-99

Table C4-5. Genes that contribute to the changes in immune pathways after treatment with IL-17F compared to control. A-100

Table C4-6. Genes that contribute to the changes in immune pathways after treatment with IL-17AF compared to control. A-101

Table C4-7. Genes that contribute to the changes in cytokine/chemokine pathways after treatment with IL-17A compared to control. A-102

Table C4-8. Genes that contribute to the changes in cytokine/chemokine pathways after treatment with IL-17AF compared to control. A-103

Table C4-9. Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17A compared to control. A-104

Table C4-10. Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17AF compared to control. A-106

Table C4-11. Genes that contribute to the changes in hallmark pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. A-107

Table C4-12. Genes that contribute to the changes in hallmark pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. A-108

Table C4-13. Genes that contribute to the changes in hallmark pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. A-109

Table C4-14. Genes that contribute to the changes in immune pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. A-110

Table C4-15. Genes that contribute to the changes in immune pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. A-112

Table C4-16. Genes that contribute to the changes in immune pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. A-112

Table C4-17. Genes that contribute to the changes in cytokine and chemokine pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. A-113

Table C4-18. Genes that contribute to the changes in cytokine and chemokine pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. A-114

Table C4-19. Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. A-115

Table C4-20. Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. A-117

Table C4-21. Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. A-117

Appendix A

Chapter 2: Cellular and molecular characterisation of end-stage osteoarthritis synovium

A1 Overview of cell surface markers

Table A1.1. *Overview of cells surface proteins used in this study, including the main cell type that expresses this protein and other cells these proteins can be present on.*

Cell surface marker	Used as marker for:	Also present on:
CD106 (VCAM)	Fibroblasts	Endothelial cells
CD117	Mast cells	Hematopoietic stem cells, ILC3
CD11c	Dendritic cells	Monocytes, macrophages, neutrophils, and some B cells
CD14	Monocytes and monocyte-derived cells	-
CD15	Neutrophils	Monocytes and granulocytes
CD161	T cell subset	NK cells
CD19	B cells	-
CD196 (CCR6)	T cell subset	T helper cells, regulatory T cells
CD206	M2 macrophages	Macrophages
CD248	Fibroblasts	Pericytes
CD3	T cells	-
CD34	Fibroblasts	Endothelial cells,
CD4	T helper cells	-
CD40	M1 macrophages	Dendritic cells, B cells, endothelial cells, and fibroblasts
CD45	Hematopoietic cells	All differentiated hematopoietic cells except for red blood cells and plasma cells
CD56	Natural killer cells	γδ T cells, CD8+ T cells, dendritic cells
CD68	Macrophages	-
CD8	Cytotoxic T cells	-
CD90	Fibroblasts	NK cells, endothelial cells, follicular dendritic cells
FAP	Fibroblasts	Fibroblast activation marker
GDTCR	γδ T cells	-
PDPN	Fibroblasts	Endothelial cells

A2 Overview of antibodies

***Table A2.1**. Antibodies used for extracellular staining of cells. If concentrations of the antibody were unknown, recommended concentrations for isotype control antibodies were used. *For the viability stain, no matching isotype control was used. For compensation control, CD4 APC-Cy7 antibody (BioLegend, cat# 100526) was used.*

Antibodies							**Matching isotype controls**					
Cell surface marker	**Company**	**Fluo-chrome**	**Isotype**	**Clone**	**Cat number**	**Amount used (uL/ug)**	**Company**	**Fluo-chrome**	**Isotype**	**Clone**	**Cat number**	**Amount used (uL/ug)**
CD106 (VCAM)	BD	PerCP/Cy5.5	Mouse IgG1, kappa	51-10C9	563525	5 / 0.5	BD	PerCP/Cy5.5	Mouse IgG1, kappa	MOPC-21	552834	10 / 0.5
CD117	BD	PerCP/Cy5.5	Mouse IgG1, kappa	YB5.B8	562094	5 / 0.125	BD	PerCP/Cy5.5	Mouse IgG1, kappa	MOPC-21	552834	2.5 / 0.125
CD11c	Miltenyi Biotech	PE	Mouse IgG2b, kappa	MJ4-27G12	130-099-212	2 / unknown	Miltenyi Biotech	PE	Mouse IgG2b, kappa	IS6-11E5.11	130-098-875	2 / unknown
CD14	BioLegend	AlexaFluor 700	Mouse IgG2a, kappa	M5E2	301822	4 / 2	BioLegend	AlexaFluor 700	Mouse IgG2a, kappa	MOPC-173	400247	4 / 2
CD15	BD	BV650	Mouse IgM, kappa	HI98	564232	5 / 0.125	BD	BV650	Mouse IgM, kappa	G155-228	564367	0.625 / 0.125
CD161	BD	BV711	Mouse C3H (C3H/Bi) IgG1, kappa	CX12	563865	5 / 0.5	BD	BV711	Mouse BALB/c IgG1, kappa	X40	563044	2.5 / 0.5
CD19	BD	PE-CF594	Mouse IgG1, kappa	HIB19	562321	5 / 0.25	BD	PE-CF594	Mouse IgG1, kappa	X40	562292	1.25 / 0.25
CD196 (CCR6)	BD	BV650	Mouse IgG1, kappa	11A9	563922	5 / 0.25	BD	BV650	Mouse IgG1, kappa	X40	563231	1.25 / 0.25
CD206	BioLegend	APC	Mouse IgG1, kappa	15-2	321109	5 / 1	BioLegend	APC	Mouse IgG1, kappa	MOPC-21	400119	5 / 1
CD248	BD	AF647	Mouse IgG1, kappa	B1/35	564994	5 / 0.5	BD	AF647	Mouse IgG1, kappa	MOPC-21	557714	5 / 0.5
CD3	BioLegend	PE-Cy7	Mouse IgG1, kappa	SK7	344816	5 / 2	BioLegend	PE-Cy7	Mouse IgG1, kappa	MOPC-21	400125	5 / 0.5

CD34	BioLegend	BV785	Mouse IgG2a, kappa	561	343625	5 / 0.25	BioLegend	BV785	Mouse IgG2a, kappa	MOPC-173	400273	2.5 / 0.25
CD40	BioLegend	BV785	Mouse IgG1, kappa	5C3	334339	5 / 0.25	BioLegend	BV785	Mouse IgG1, kappa	MOPC-21	400169	2.5 / 0.25
CD45	BioLegend	AlexaFluor 700	Mouse IgG1, kappa	HI30	304023	2 / 1	BioLegend	AlexaFluor 700	Mouse IgG1, kappa	MOPC-21	400143	2 / 1
CD45	BioLegend	BV711	Mouse IgG1, kappa	HI30	304050	2 / 0.1	BioLegend	BV711	Mouse IgG1, kappa	MOPC-21	400167	1 / 0.1
CD56	BD	BV786	Mouse BALB/c IgG2b, kappa	NCAM16.2	564058	5 / 0.25	BD	BV786	Mouse C.SW IgG2b	27-35	564090	1.25 / 0.25
CD8	BD	APC	Mouse IgG1, kappa	RPA-T8	561952/555369	8 / 0.096	BD	APC	Mouse IgG1, kappa	MOPC-21	560167	0.48 / 0.096
CD90	BioLegend	PE-Cy7	Mouse IgG1, kappa	5E10	328123	5 / 0.5	BioLegend	PE-Cy7	Mouse IgG1, kappa	MOPC-21	400125	5 / 0.5
FAP	R&D	PE	Mouse IgG1, kappa	427819	FAB3715P-100	10 / unknown	R&D	PE	Mouse IgG1, kappa	11711	IC002P	10 / unknown
GDTCR	BioLegend	PE	Mouse IgG1, kappa	B1	331209	5 / 2	BioLegend	PE	Mouse IgG1, kappa	MOPC-21	400113	10 / 2
IL-17RA	Miltenyi Biotech	PE	Recombinant human IgG1	REA290	130-104-768	9 / unknown	Miltenyi Biotech	PE	Recombinant human IgG1	REA293	130-113-438	2 / unknown
IL-17RC	Miltenyi Biotech	FITC	Recombinant human IgG1	REA571	130-109-196	9 / unknown	Miltenyi Biotech	FITC	Recombinant human IgG1	REA293	130-104-610	2 / unknown
PDPN	BD	BV711	Mouse BALB/c IgG1, kappa	LpMab-17	747632	5 / 1	BD	BV711	Mouse BALB/c IgG1, kappa	X40	563044	5 / 1
Viability*	eBioScience	BV780	-	-	65-0865-14	0.4	-	-	-	-	-	-

***Table A2.2**. Antibodies used for intracellular staining of cells.*

Antibodies							**Matching isotype controls**					
Extra- or intracellular marker	**Company**	**Fluo-chrome**	**Isotype**	**Clone**	**Cat number**	**Amount used (uL/ug)**	**Company**	**Fluo-chrome**	**Isotype**	**Clone**	**Cat number**	**Amount used (uL / ug)**
CD4	BioLegend	PerCP/Cy5.5	Mouse IgG1, kappa	RPA-T4	300530	5 / 0.5	BioLegend	PerCP/Cy5.5	Mouse IgG1, kappa	MOPC-21	400149	2.5 / 0.5
CD68	BioLegend	PE-Cy7	Mouse IgG2b, kappa	Y1/82A	333815	5 / 0.06	BioLegend	PE-Cy7	Mouse IgG2b, kappa	MPC-11	400325	0.3 / 0.06
IL-17A	eBioScience	FITC	Mouse IgG1, kappa	eBio64DEC17	11-7179-42	5 / 0.125	eBioScience	FITC	Mouse IgG1, kappa	P3.6.2.8.1	11-4714-81	0.25 / 0.125
IL-17AF	eBioScience	eF450	Mouse IgG1, kappa	20LJS09	48-9179-42	5 / 0.5	eBioScience	eFluor 450	Mouse IgG1, kappa	P3.6.2.8.1	48-4714-82	2.5 / 0.5
IL-17F	BD	PE-CF594	Mouse IgG1, kappa	O33-782	564263	5 / 0.25	BD	PE-CF594	Mouse IgG1, kappa	X40	562292	1.25 / 0.25

A3 Run details

Table A3.1. *Voltages used for each individual flow cytometry run.*

Patient #	1	2	3	4	5	6	7	8	9	10
Date run	14/12/18		14/02/19	21/02/19	01/03/19		22/03/19	05/04/19	27/04/19	
FSC	240		240	240	240		240	240	240	
SSC	280		280	280	280		270	270	280	
BV421	430		430	430	430		430	430	437	
BV650	580		580	580	580		580	580	580	
BV711	470		470	470	470		470	470	480	
BV786	430		430	420	420		420	420	420	
FITC	494		494	494	494		494	494	494	
PE	505		505	505	505		505	505	495	
PE-CF594	620		620	620	620		620	620	610	
PerCP-Cy5.5	590		590	590	590		590	590	590	
PE-Cy7	580		580	580	580		580	580	580	
APC	600		600	600	600		600	600	600	
AF700	550		550	550	550		550	550	560	
BV780	590		590	554	590		590	590	590	

A4 Gating strategy

A4.1 T cells markers

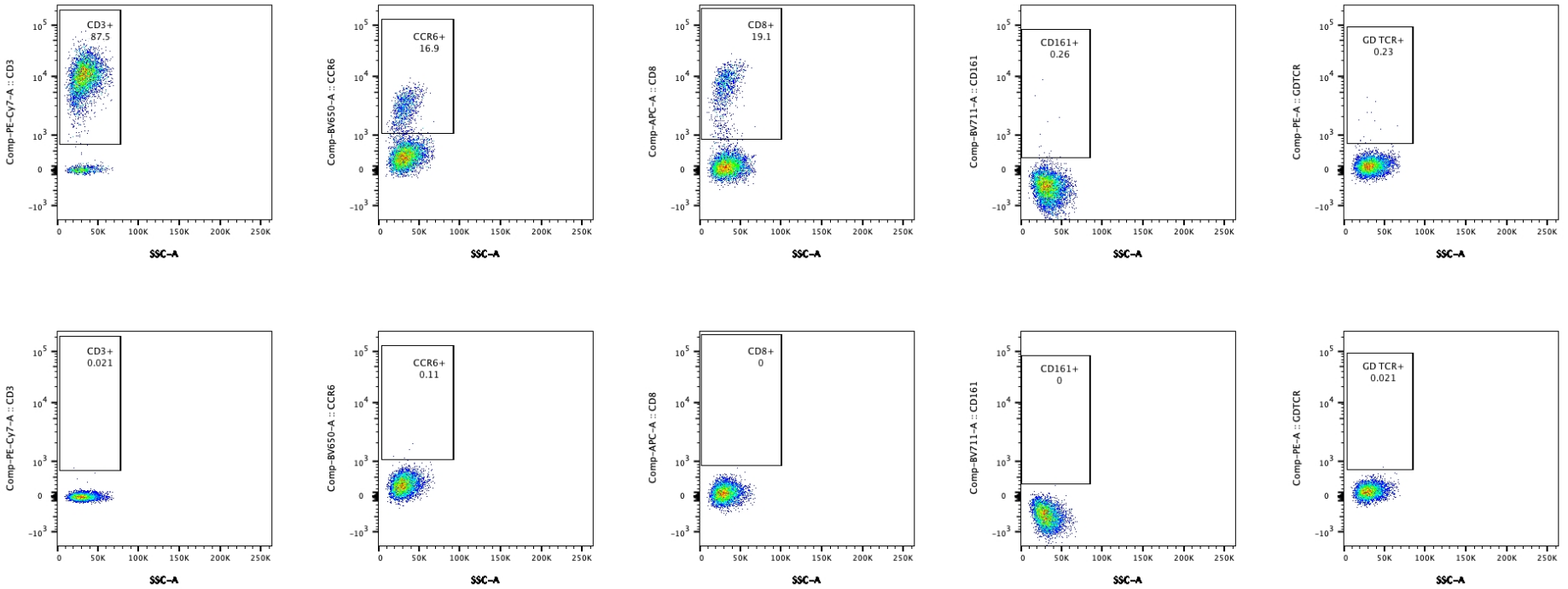

Figure A4-1. *Gating of T cell markers in CD45+ small cells. T cell markers include CD3 (A, F), CCR6 (B, G), CD8 (C, H), CD161 (D, I), and GD TCR (E, J). (A-E) Antibody-stained unstimulated cells, (F-J) isotype-stained stimulated cells. Patient 9.*

A4.2 B cells marker

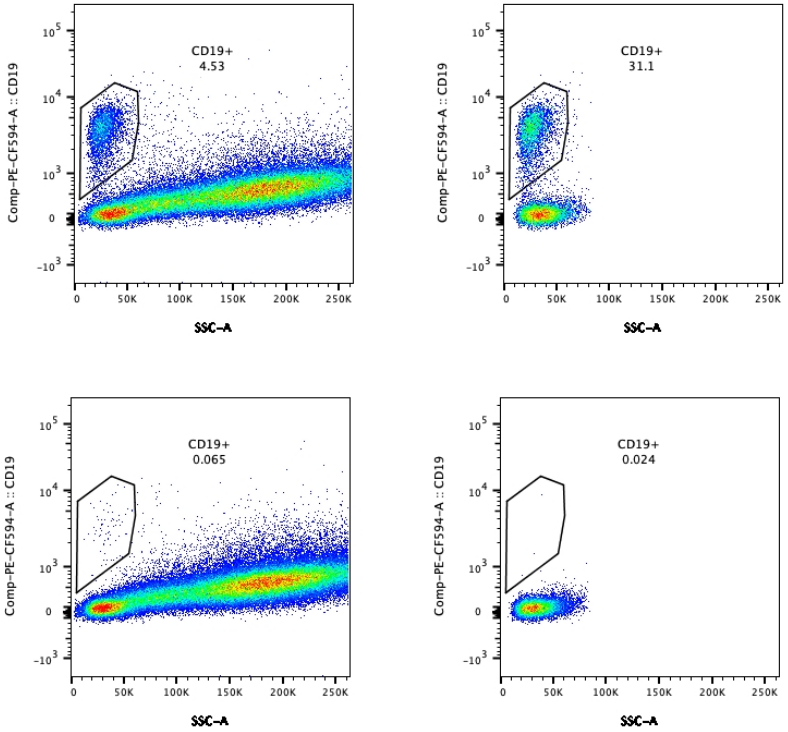

Figure A4-2. *Gating of B-cell marker CD19. B cell marker CD19 as a percentage of all viable cells (A, C), and as a percentage of CD45+ small cells (B, D). (A, B) Antibody-stained unstimulated cells, (C, D) isotype-stained stimulated cells. Patient 5.*

A4.3 Monocyte(-derived) cell markers and granulocyte markers

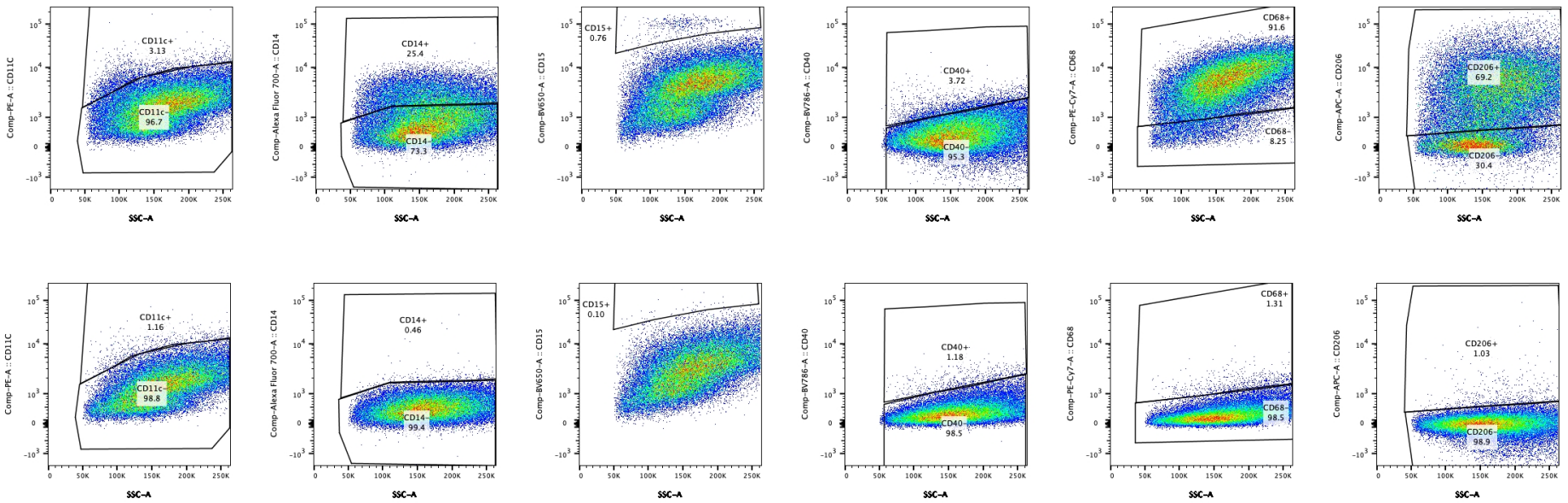

Figure A4.3. *Gating of granulocyte markers in CD45+ large cells. Granulocyte markers include CD11c (A, G), CD14 (B, H), CD15 (C, I), CD40 (D, J), CD68 (E, K), and CD206 (F, L). (A-F) Antibody-stained unstimulated cells, (G-L) isotype-stained stimulated cells. Patient 3.*

A4.4 Fibroblast markers

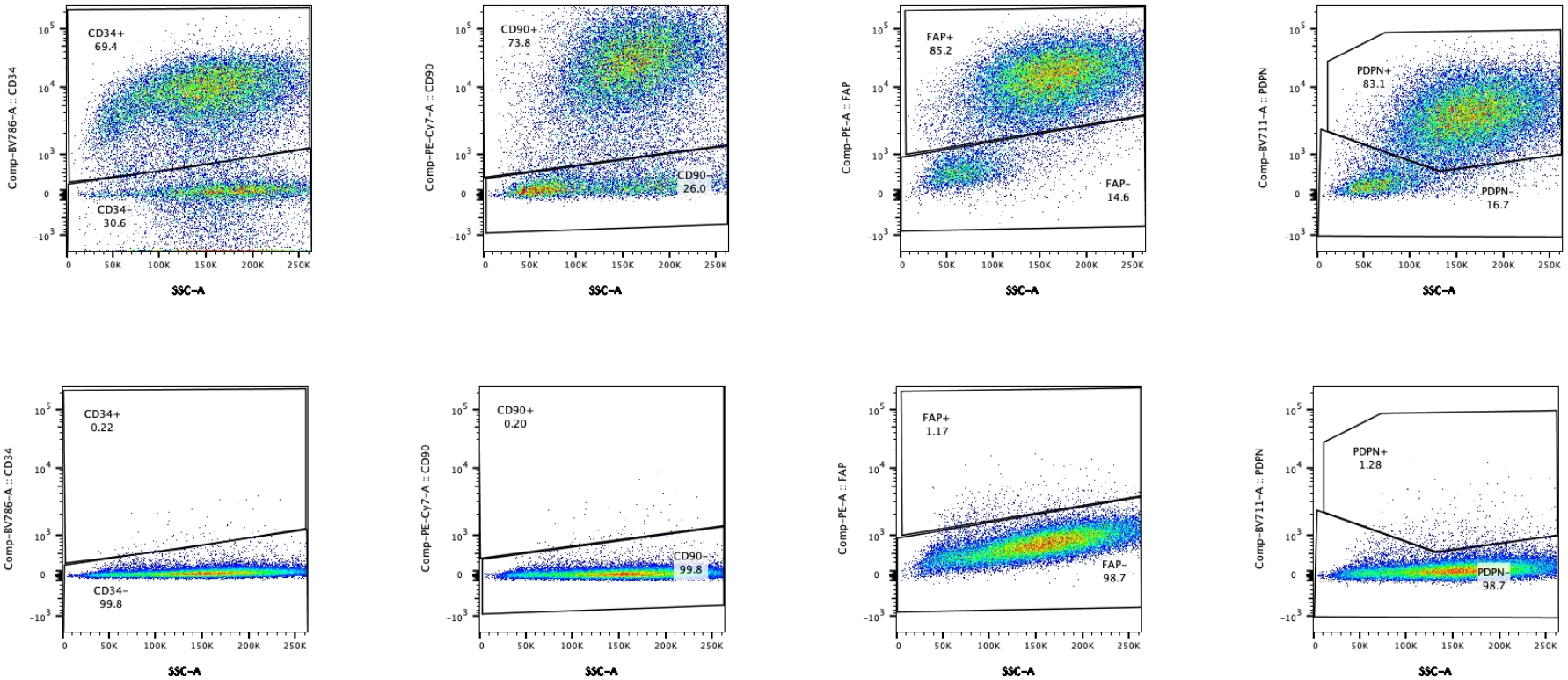

Figure A4.4. *Gating of fibroblast activation markers in CD45- cells. Fibroblast activation markers include CD34 (A, E), CD90 (B, F), FAP (C, G), and PDPN (D, I). (A-D) Antibody-stained unstimulated cells, (E-I) isotype-stained stimulated cells. Patient 9.*

A5 Immunofluorescence negative controls

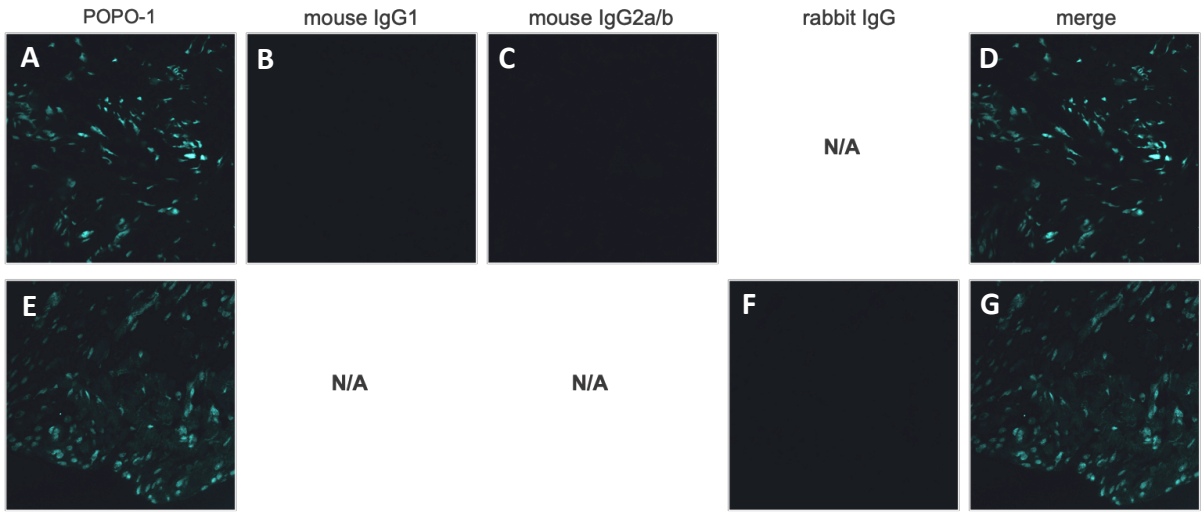

***Figure A5-1**. Immunofluorescent staining with (A-D) universal mouse negative control or (E-G) rabbit negative control.*

A6 High-resolution confocal images Chapter 2

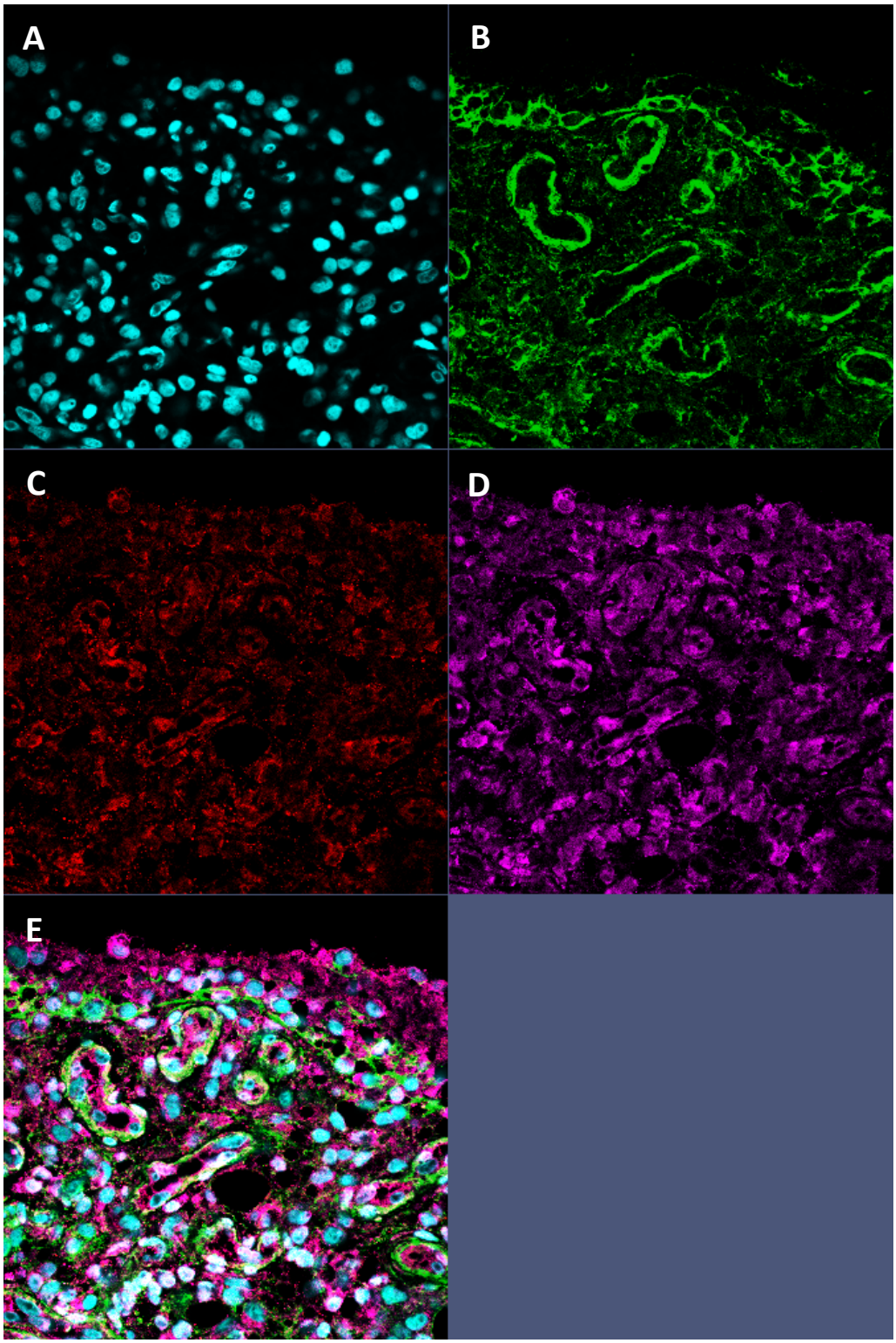

***Figure A6.1**. High-resolution confocal images of Figure 2-11A-E. Expression of fibroblast activation markers CD90, PDPN, and FAP in a synovial section of a patient with high risk of developing OA. Confocal images show expression of CD90 (**green**), PDPN (**red**), and FAP (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

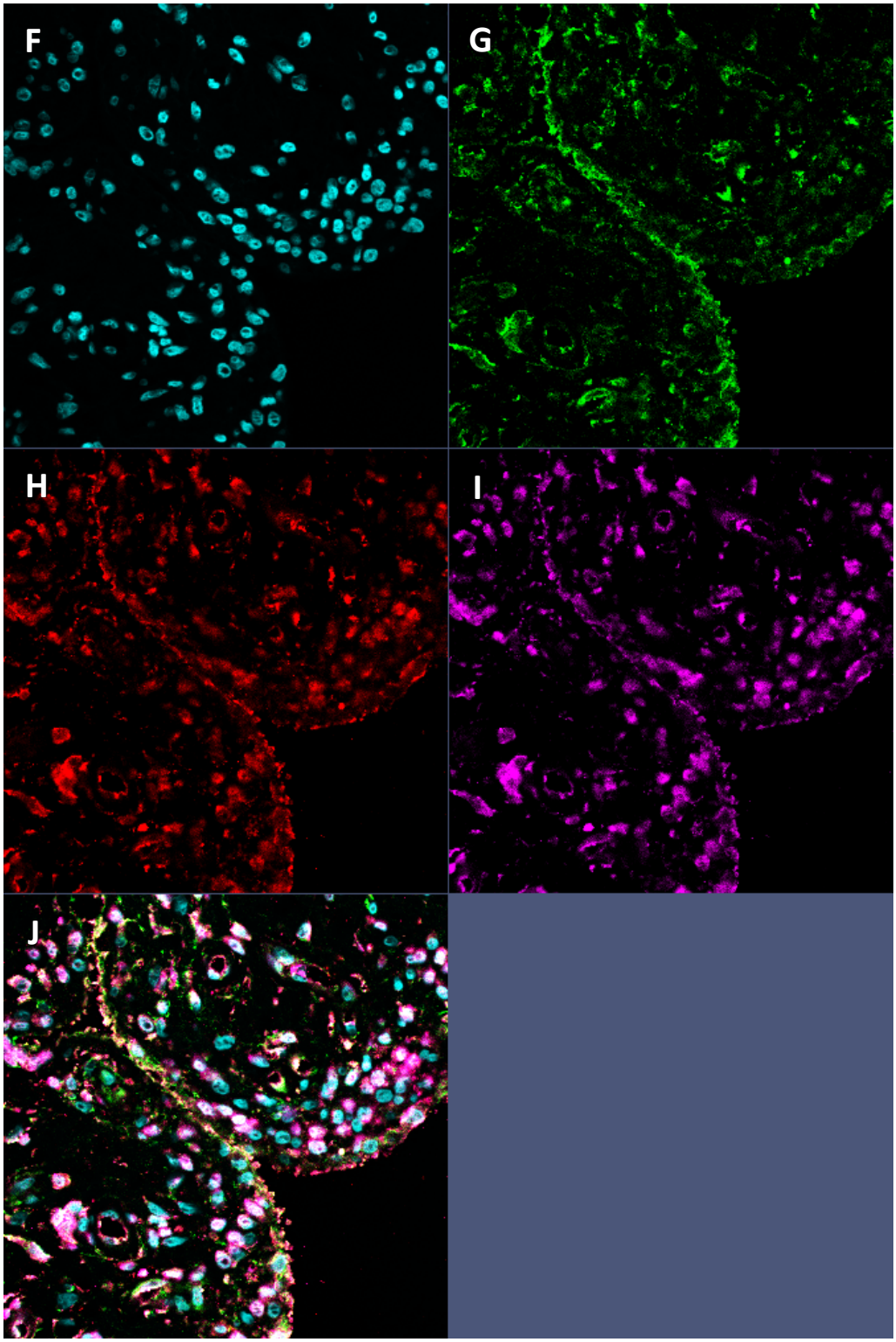

***Figure A6.2**. High-resolution confocal images of Figure 2-11F-J. Expression of fibroblast activation markers CD90, PDPN, and FAP in a synovial section of a patient with high risk of developing OA. Confocal images show expression of CD90 (**green**), PDPN (**red**), and FAP (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

A7 Additional correlation tests

A7.1 Correlations of fibroblast subsets with KL-grade and OKS

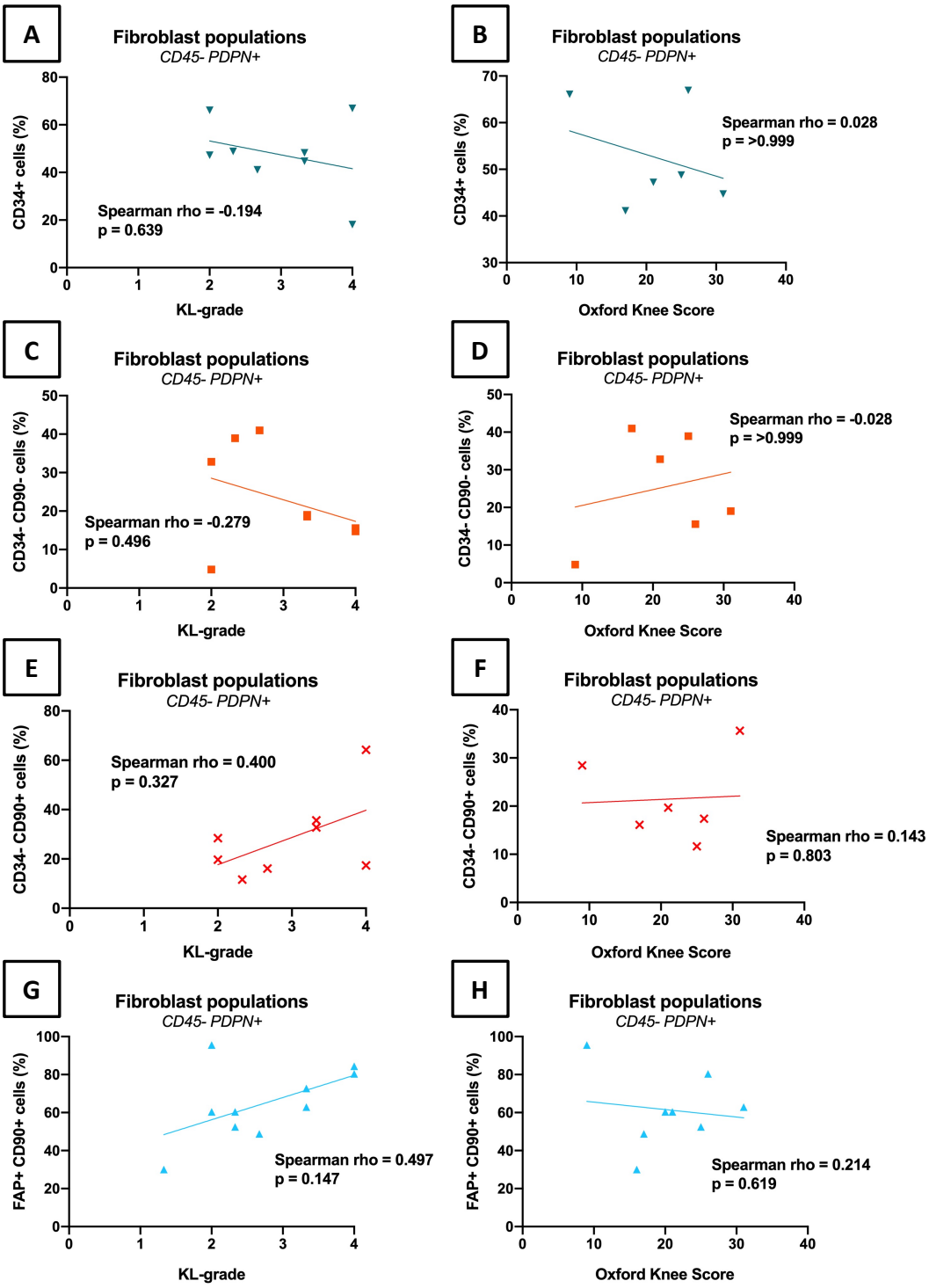

Figure A7-1. *Correlation between fibroblast subsets and clinical markers of disease in synovium from patients with end-stage knee OA (as a percentage of CD45-PDPN+ viable cells). Correlations were calculated between (A,B) CD34+ cells, (C,D) CD34-CD90- cells, (E,F) CD34-CD90+ cells, (G,H) FAP+CD90+ cells and the clinical markers (A,C,E,G) Kellgren-Lawrence (KL)-grade (B,D,F,H) Oxford Knee Score. Non-parametric Spearman correlation. (A-F,H) n=8, (G) n=10.*

A7.2 Correlations of age with KL-grade

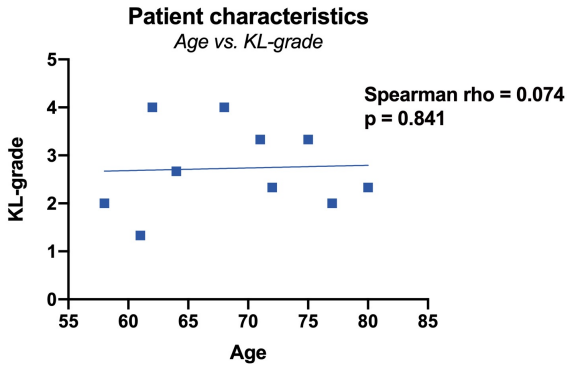

Figure A7-2. *Correlation between the age and Kellgren Lawrence (KL)-grade of patients with end-stage knee OA. Non-parametric Spearman correlation. n=10.*

A7.3 Correlations of cytotoxic T cells

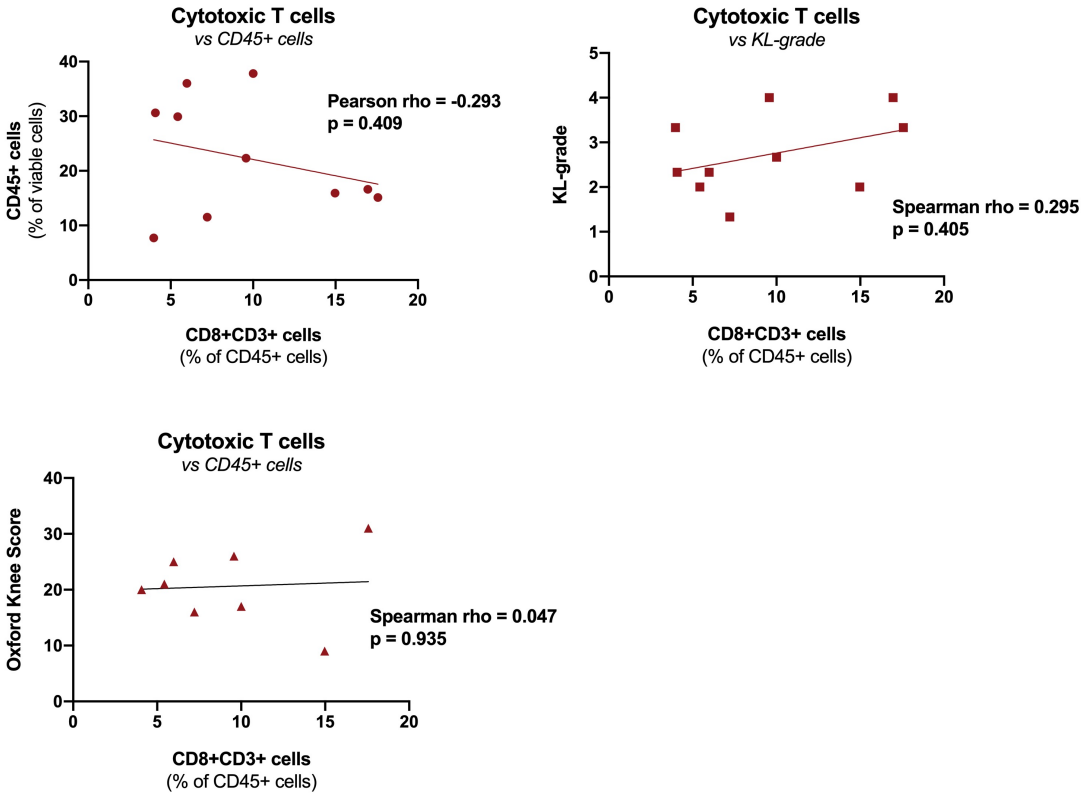

Figure A7-3. *Correlations regarding CD8+ T cells (as % of CD45+ cells) in synovium from patients with end-stage knee OA. Correlations were calculated with (A) CD45+ cells, (B) Kellgren Lawrence (KL)-grade, and (C) Oxford Knee Score. (A) Parametric Pearson correlation, (B,C) Non-parametric Spearman correlation. (A-B) n=10, (B) n=8.*

A7.4 Correlations of CD68+CD206+ macrophages with age and OKS

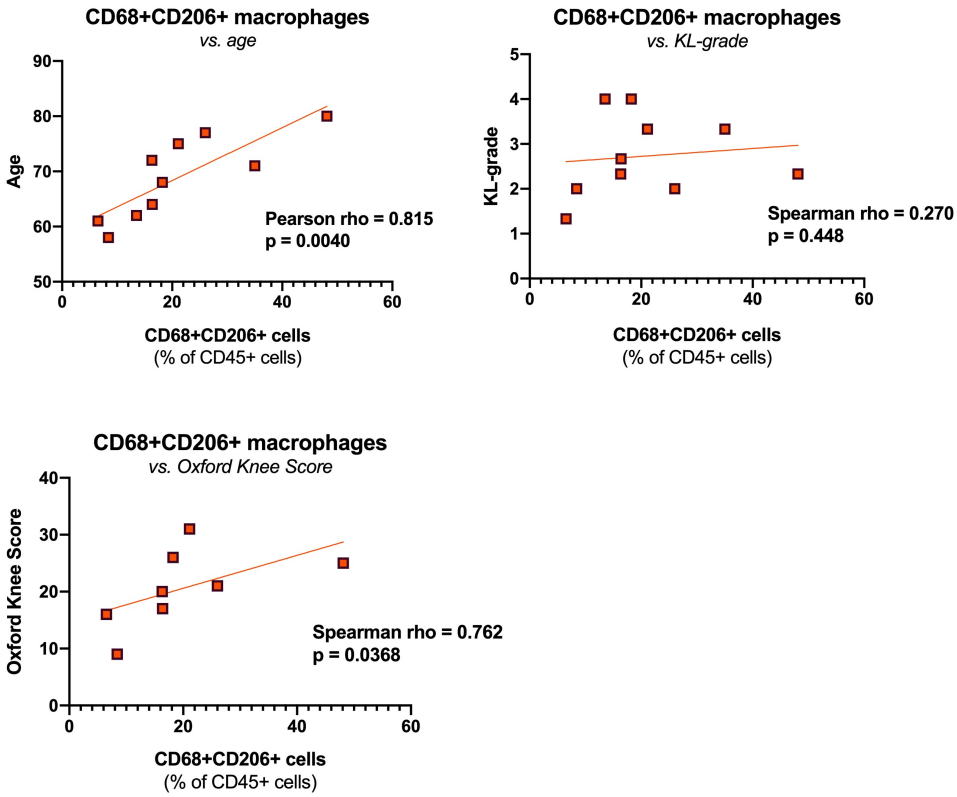

Figure A7-4. *Correlations regarding CD68+CD206+ macrophages (as % of CD45+ cells) in synovium from patients with end-stage knee OA. Correlations were calculated with (A) age, (B) Kellgren Lawrence (KL)-grade, and (C) Oxford Knee Score. (A) Parametric Pearson correlation, (B,C) Non-parametric Spearman correlation. (A-B) n=10, (B) n=8.*

A8 Proteomics

A8.1 Subgroups based on flow cytometry results

The subgroups that were found based on flow cytometry results (CCR6+/- or macrophage/T cell dominant) were used to see if these subgroups predict or correlate with protein signatures of synovial fluid (Table A8-1). Prediction ellipses were calculated with a 95% probability that a new observation of the same group will fall into the ellipse (Figure A8-1). However, none of the flow cytometry-identified subgroups showed an obvious separation in any of the first four principle components, suggesting that these are not predictive of a specific protein signature.

Table A8-1. *Patient subgroups used for proteomics analysis based on the presence or absence of CCR6+ T cells, and most prominent immune cell type. CCR6+ T cells:* ***absent*** *or* ***present****; macrophage/T cell ratio: most prominent cell type is* ***T cells*** *or* ***macrophages****.*

Patient #	CCR6+ T cells	Macrophage/T cell ratio
1	N/A	N/A
2	Absent	T cells
3	Present	Macrophages
4	Present	T cells
5	Absent	Macrophages
6	N/A	N/A
7	Present	Macrophages
8	Present	T cells
9	Present	T cells
10	Present	Macrophages

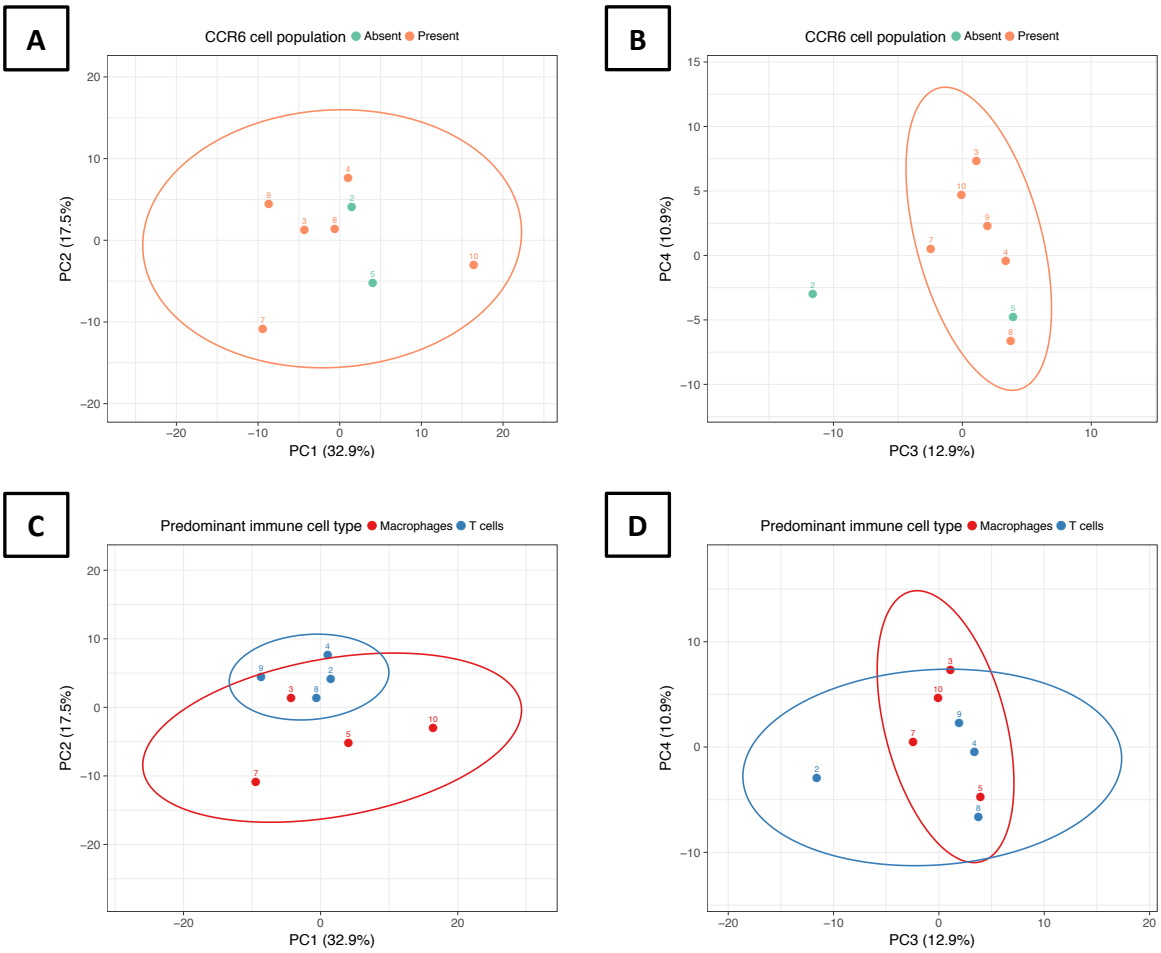

Figure A8-1. *Principle component analysis (PCA) plots for proteomic results of synovial fluid samples separated into subgroups. Principle components (PCs) were calculated using SVD with imputation. (A,C) PCA plot of PC1 and PC2. (B,D) PCA plot of PC3 and PC4. Samples were separated based on (A,B) absence or presence of CCR6+ T cells, and (C,D) ratio of macrophages to T cells. Prediction ellipses are based on a 0.95 probability that a new observation will fall inside the ellipse. n=8*

A8.2 Full list of protein intensities for each synovial fluid sample

Table A8-2. *Protein intensities of proteins detected in synovial fluid by mass spectrometry.*

UniProtKB name	Protein	Protein intensity (per patient)							
		2	3	4	5	7	8	9	10
LV861_HUMAN	Immunoglobulin lambda variable 8-61	NaN	NaN	21.523	22.052	NaN	21.350	NaN	23.908
LV743_HUMAN	Immunoglobulin lambda variable 7-43 (Ig lambda chain V region 4A)	NaN	NaN	21.636	NaN	NaN	NaN	NaN	23.527
LV537_HUMAN	Immunoglobulin lambda variable 5-37	NaN	NaN	NaN	NaN	NaN	NaN	NaN	19.108
LV310_HUMAN	Immunoglobulin lambda variable 3-10	NaN	NaN	20.681	22.064	NaN	NaN	NaN	22.280
KVD28_HUMAN	Immunoglobulin kappa variable 2D-28 (Ig kappa chain V-II region FR) (Ig kappa chain V-II region GM607) (Ig kappa chain V-II region MIL) (Ig kappa chain V-II region TEW)	23.493	24.489	24.976	25.943	NaN	25.615	NaN	26.206
HV364_HUMAN	Immunoglobulin heavy variable 3-64	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.410
KVD29_HUMAN	Immunoglobulin kappa variable 2D-29	NaN	NaN	NaN	NaN	NaN	22.160	NaN	NaN
KV127_HUMAN	Immunoglobulin kappa variable 1-27	24.345	25.467	24.369	25.786	NaN	25.427	NaN	26.269
KVD15_HUMAN	Immunoglobulin kappa variable 3D-15	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.996
KV311_HUMAN	Immunoglobulin kappa variable 3-11 (Ig kappa chain V-III region VG)	NaN	NaN	NaN	26.303	NaN	26.159	NaN	25.840
HV349_HUMAN	Immunoglobulin heavy variable 3-49	24.103	23.940	NaN	23.761	24.186	23.885	22.822	24.290
LV136_HUMAN	Immunoglobulin lambda variable 1-36	NaN	NaN	NaN	NaN	NaN	NaN	20.597	NaN
HV601_HUMAN	Immunoglobulin heavy variable 6-1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.019
HV315_HUMAN	Immunoglobulin heavy variable 3-15	NaN	24.725	NaN	24.879	24.653	24.245	NaN	24.792
HV226_HUMAN	Immunoglobulin heavy variable 2-26	22.483	22.353	20.925	22.914	22.964	23.073	21.339	22.717
HV374_HUMAN	Immunoglobulin heavy variable 3-74	NaN	NaN	NaN	22.238	NaN	NaN	NaN	22.773
HV372_HUMAN	Immunoglobulin heavy variable 3-72	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.927
KV113_HUMAN	Immunoglobulin kappa variable 1-13	NaN	NaN	NaN	18.685	NaN	NaN	NaN	NaN
HV69D_HUMAN	Immunoglobulin heavy variable 1-69D	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.753
KV621_HUMAN	Immunoglobulin kappa variable 6-21	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.470
KVD20_HUMAN	Immunoglobulin kappa variable 3D-20	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.528
HV103_HUMAN	Immunoglobulin heavy variable 1-3	NaN	NaN	NaN	23.697	NaN	NaN	NaN	24.383

HV118_HUMAN	Immunoglobulin heavy variable 1-18	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.393
HV124_HUMAN	Immunoglobulin heavy variable 1-24	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.841
HV428_HUMAN	Immunoglobulin heavy variable 4-28	NaN	NaN	NaN	21.190	NaN	NaN	NaN	21.867
HV551_HUMAN	Immunoglobulin heavy variable 5-51	26.189	25.540	26.037	25.782	26.088	25.664	25.101	25.448
HV459_HUMAN	Immunoglobulin heavy variable 4-59 (Ig heavy chain V-II region NEWM)	23.651	23.883	23.505	23.994	24.233	24.153	23.523	25.419
KV224_HUMAN	Immunoglobulin kappa variable 2-24	25.237	24.880	25.416	25.810	24.735	25.982	24.250	25.282
KV106_HUMAN	Immunoglobulin kappa variable 1-6	NaN	NaN	NaN	NaN	NaN	NaN	NaN	25.108
HV64D_HUMAN	Immunoglobulin heavy variable 3-64D	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.986
HV5X1_HUMAN	Immunoglobulin heavy variable 5-10-1	NaN	NaN	NaN	23.102	NaN	NaN	NaN	21.826
SIG16_HUMAN	Sialic acid-binding Ig-like lectin 16 (Siglec-16) (Siglec-P16)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.640
WDR64_HUMAN	WD repeat-containing protein 64	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.055
IGL1_HUMAN	Immunoglobulin lambda-1 light chain (Immunoglobulin lambda-1 light chain MCG)	30.974	29.941	30.598	30.649	30.915	30.557	29.992	31.594
NACAM_HUMAN	Nascent polypeptide-associated complex subunit alpha, muscle-specific form (Alpha-NAC, muscle-specific form) (skNAC)	NaN	23.099	22.630	23.176	23.238	22.957	22.953	22.279
QSOX1_HUMAN	Sulfhydryl oxidase 1 (hQSOX) (EC 1.8.3.2) (Quiescin Q6)	20.770	NaN	NaN	21.075	NaN	21.626	21.127	NaN
APOL1_HUMAN	Apolipoprotein L1 (Apolipoprotein L) (Apo-L) (ApoL) (Apolipoprotein L-I) (ApoL-I)	24.892	24.712	24.527	24.516	24.449	24.662	24.173	24.337
STX7_HUMAN	Syntaxin-7	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.768
TXNL1_HUMAN	Thioredoxin-like protein 1 (32 kDa thioredoxin-related protein)	23.997	24.378	NaN	23.580	23.900	23.639	23.790	24.100
CD5L_HUMAN	CD5 antigen-like (Apoptosis inhibitor expressed by macrophages) (hAIM) (CT-2) (IgM-associated peptide) (SP-alpha)	22.876	22.478	NaN	23.240	NaN	21.673	NaN	24.330
MAST3_HUMAN	Microtubule-associated serine/threonine-protein kinase 3 (EC 2.7.11.1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	25.741
NMT1_HUMAN	Glycylpeptide N-tetradecanoyltransferase 1 (EC 2.3.1.97) (Myristoyl-CoA:protein N-myristoyltransferase 1) (NMT 1) (Type I N-myristoyltransferase) (Peptide N-myristoyltransferase 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.461
H2B1L_HUMAN	Histone H2B type 1-L (Histone H2B.c) (H2B/c)	NaN	NaN	NaN	NaN	24.374	22.806	NaN	NaN
EDF1_HUMAN	Endothelial differentiation-related factor 1 (EDF-1) (Multiprotein-bridging factor 1) (MBF1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.120

BRE1B_HUMAN	E3 ubiquitin-protein ligase BRE1B (BRE1-B) (EC 2.3.2.27) (95 kDa retinoblastoma-associated protein) (RBP95) (RING finger protein 40) (RING-type E3 ubiquitin transferase BRE1B)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	26.090
GGCT_HUMAN	Gamma-glutamylcyclotransferase (EC 4.3.2.9) (Cytochrome c-releasing factor 21)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.195
SH3L1_HUMAN	SH3 domain-binding glutamic acid-rich-like protein	24.992	25.717	25.028	24.861	25.728	25.175	25.365	24.515
FCN3_HUMAN	Ficolin-3 (Collagen/fibrinogen domain-containing lectin 3 p35) (Collagen/fibrinogen domain-containing protein 3) (Hakata antigen)	24.079	NaN	NaN	21.713	NaN	24.307	22.909	23.246
SPB8_HUMAN	Serpin B8 (Cytoplasmic antiproteinase 2) (CAP-2) (CAP2) (Peptidase inhibitor 8) (PI-8)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.870
ATRN_HUMAN	Attractin (DPPT-L) (Mahogany homolog)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.107
UBP1_HUMAN	Ubiquitin carboxyl-terminal hydrolase 1 (EC 3.4.19.12) (Deubiquitinating enzyme 1) (hUBP) (Ubiquitin thioesterase 1) (Ubiquitin-specific-processing protease 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	19.673
SODC_HUMAN	Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Superoxide dismutase 1) (hSod1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.681
CERU_HUMAN	Ceruloplasmin (EC 1.16.3.1) (Ferroxidase)	28.150	28.429	27.849	28.712	27.831	27.560	27.866	28.260
THRB_HUMAN	Prothrombin (EC 3.4.21.5) (Coagulation factor II) [Cleaved into: Activation peptide fragment 1; Activation peptide fragment 2; Thrombin light chain; Thrombin heavy chain]	26.284	26.073	26.257	26.534	26.520	26.151	25.996	26.527
C1R_HUMAN	Complement C1r subcomponent (EC 3.4.21.41) (Complement component 1 subcomponent r) [Cleaved into: Complement C1r subcomponent heavy chain; Complement C1r subcomponent light chain]	25.518	25.026	25.341	25.166	25.050	25.260	25.218	25.863
HPT_HUMAN	Haptoglobin (Zonulin) [Cleaved into: Haptoglobin alpha chain; Haptoglobin beta chain]	29.908	31.046	30.186	30.014	29.605	29.502	29.175	30.832
HPTR_HUMAN	Haptoglobin-related protein	24.774	24.525	24.531	23.360	23.224	24.570	23.730	23.898
FA10_HUMAN	Coagulation factor X (EC 3.4.21.6) (Stuart factor) (Stuart-Prower factor) [Cleaved into: Factor X light chain; Factor X heavy chain; Activated factor Xa heavy chain]	23.417	23.371	23.258	23.167	NaN	23.661	NaN	23.134
CFAD_HUMAN	Complement factor D (EC 3.4.21.46) (Adipsin) (C3 convertase activator) (Properdin factor D)	24.741	24.966	25.226	25.368	24.985	24.948	24.712	24.382

PLMN_HUMAN	Plasminogen (EC 3.4.21.7) [Cleaved into: Plasmin heavy chain A; Activation peptide; Angiostatin; Plasmin heavy chain A, short form; Plasmin light chain B]	26.930	27.289	27.291	26.936	26.989	27.489	26.913	27.141
FA12_HUMAN	Coagulation factor XII (EC 3.4.21.38) (Hageman factor) (HAF) [Cleaved into: Coagulation factor XIIa heavy chain; Beta-factor XIIa part 1; Coagulation factor XIIa light chain (Beta-factor XIIa part 2)]	24.636	23.214	24.505	23.385	22.976	24.416	23.647	23.386
CFAB_HUMAN	Complement factor B (EC 3.4.21.47) (C3/C5 convertase) (Glycine-rich beta glycoprotein) (GBG) (PBF2) (Properdin factor B) [Cleaved into: Complement factor B Ba fragment; Complement factor B Bb fragment]	28.713	29.349	28.899	29.063	28.539	28.730	28.953	28.412
CAH1_HUMAN	Carbonic anhydrase 1 (EC 4.2.1.1) (Carbonate dehydratase I) (Carbonic anhydrase B) (CAB) (Carbonic anhydrase I) (CA-I)	24.639	NaN	NaN	24.160	25.293	NaN	NaN	20.380
ANT3_HUMAN	Antithrombin-III (ATIII) (Serpin C1)	29.483	29.574	29.749	29.499	29.548	29.364	29.542	29.251
A1AT_HUMAN	Alpha-1-antitrypsin (Alpha-1 protease inhibitor) (Alpha-1-antiproteinase) (Serpin A1) [Cleaved into: Short peptide from AAT (SPAAT)]	33.272	34.229	34.046	33.903	33.126	33.678	33.505	33.962
AACT_HUMAN	Alpha-1-antichymotrypsin (ACT) (Cell growth-inhibiting gene 24/25 protein) (Serpin A3) [Cleaved into: Alpha-1-antichymotrypsin His-Pro-less]	30.157	31.098	30.627	30.248	30.392	30.331	30.328	30.652
ANGT_HUMAN	Angiotensinogen (Serpin A8) [Cleaved into: Angiotensin-1 (Angiotensin 1-10) (Angiotensin I) (Ang I); Angiotensin-2 (Angiotensin 1-8) (Angiotensin II) (Ang II); Angiotensin-3 (Angiotensin 2-8) (Angiotensin III) (Ang III) (Des-Asp[1]-angiotensin II); Angiotensin-4 (Angiotensin 3-8) (Angiotensin IV) (Ang IV); Angiotensin 1-9; Angiotensin 1-7; Angiotensin 1-5; Angiotensin 1-4]	28.317	28.324	28.217	27.578	28.454	28.269	28.780	27.657
A2MG_HUMAN	Alpha-2-macroglobulin (Alpha-2-M) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 5)	30.993	31.079	31.417	31.655	30.906	32.859	30.877	32.291
CO3_HUMAN	Complement C3 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 1) [Cleaved into: Complement C3 beta chain; C3-beta-c (C3bc); Complement C3 alpha chain; C3a anaphylatoxin; Acylation stimulating protein (ASP) (C3adesArg); Complement C3b alpha' chain; Complement C3c alpha' chain fragment 1; Complement C3dg fragment; Complement C3g	32.544	32.622	32.140	32.700	32.306	31.568	32.358	32.566

	fragment; Complement C3d fragment; Complement C3f fragment; Complement C3c alpha' chain fragment 2]								
CO5_HUMAN	Complement C5 (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 4) [Cleaved into: Complement C5 beta chain; Complement C5 alpha chain; C5a anaphylatoxin; Complement C5 alpha' chain]	27.310	27.542	27.052	27.185	27.260	27.274	27.381	27.379
TIMP1_HUMAN	Metalloproteinase inhibitor 1 (Erythroid-potentiating activity) (EPA) (Fibroblast collagenase inhibitor) (Collagenase inhibitor) (Tissue inhibitor of metalloproteinases 1) (TIMP-1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.575
CYTC_HUMAN	Cystatin-C (Cystatin-3) (Gamma-trace) (Neuroendocrine basic polypeptide) (Post-gamma-globulin)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.365
KNG1_HUMAN	Kininogen-1 (Alpha-2-thiol proteinase inhibitor) (Fitzgerald factor) (High molecular weight kininogen) (HMWK) (Williams-Fitzgerald-Flaujeac factor) [Cleaved into: Kininogen-1 heavy chain; T-kinin (Ile-Ser-Bradykinin); Bradykinin (Kallidin I); Lysyl-bradykinin (Kallidin II); Kininogen-1 light chain; Low molecular weight growth-promoting factor]	28.647	28.813	28.819	28.661	28.489	28.755	28.545	28.878
IGJ_HUMAN	Immunoglobulin J chain (Joining chain of multimeric IgA and IgM)	24.218	20.670	21.521	NaN	22.009	NaN	NaN	24.565
KV133_HUMAN	Immunoglobulin kappa variable 1-33 (Ig kappa chain V-I region AU) (Ig kappa chain V-I region Ka)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	25.441
KVD39_HUMAN	Immunoglobulin kappa variable 1D-39 (Ig kappa chain V-I region Daudi)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.258
KV117_HUMAN	Immunoglobulin kappa variable 1-17 (Ig kappa chain V-I region Gal) (Ig kappa chain V-I region WEA)	24.606	22.942	22.847	25.124	23.550	24.326	21.991	28.487
KV105_HUMAN	Immunoglobulin kappa variable 1-5 (Ig kappa chain V-I region CAR) (Ig kappa chain V-I region EU) (Ig kappa chain V-I region HK102) (Ig kappa chain V-I region Kue)	23.921	NaN	23.629	25.292	23.942	25.405	NaN	24.011
KV320_HUMAN	Immunoglobulin kappa variable 3-20 (Ig kappa chain V-III region B6) (Ig kappa chain V-III region GOL) (Ig kappa chain V-III region HAH) (Ig kappa chain V-III region HIC) (Ig kappa chain V-III region IARC/BL41) (Ig kappa chain V-III region NG9) (Ig kappa chain V-III region SIE) (Ig kappa chain V-III region Ti) (Ig kappa chain V-III region WOL)	28.055	28.222	27.882	29.667	28.512	28.090	27.495	29.790
KV315_HUMAN	Immunoglobulin kappa variable 3-15 (Ig kappa chain V-III region CLL) (Ig kappa chain V-III region POM)	26.184	26.183	25.770	26.942	26.613	26.609	24.835	27.537

LV147_HUMAN	Immunoglobulin lambda variable 1-47 (Ig lambda chain V-I region HA) (Ig lambda chain V-I region WAH)	26.188	24.915	25.657	26.708	26.442	26.341	24.827	27.685
LV151_HUMAN	Immunoglobulin lambda variable 1-51 (Ig lambda chain V-I region BL2) (Ig lambda chain V-I region EPS) (Ig lambda chain V-I region NEW) (Ig lambda chain V-I region NIG-64)	23.838	23.222	23.893	25.088	23.401	23.728	22.806	25.252
LV140_HUMAN	Immunoglobulin lambda variable 1-40 (Ig lambda chain V-I region NEWM)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.424
LV214_HUMAN	Immunoglobulin lambda variable 2-14 (Ig lambda chain V-II region NIG-84) (Ig lambda chain V-II region TOG) (Ig lambda chain V-II region VIL)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.231
LV325_HUMAN	Immunoglobulin lambda variable 3-25 (Ig lambda chain V-IV region Hil)	21.766	21.596	22.034	21.716	21.437	22.227	NaN	22.823
LV657_HUMAN	Immunoglobulin lambda variable 6-57 (Ig lambda chain V-VI region AR) (Ig lambda chain V-VI region EB4) (Ig lambda chain V-VI region NIG-48) (Ig lambda chain V-VI region SUT) (Ig lambda chain V-VI region WLT)	25.107	23.042	NaN	NaN	NaN	NaN	NaN	22.870
HV169_HUMAN	Immunoglobulin heavy variable 1-69 (Ig heavy chain V-I region EU) (Ig heavy chain V-I region SIE) (Ig heavy chain V-I region WOL)	NaN	NaN	NaN	23.132	NaN	NaN	NaN	NaN
HV146_HUMAN	Immunoglobulin heavy variable 1-46 (Ig heavy chain V-I region DOT) (Ig heavy chain V-I region HG3) (Ig heavy chain V-I region Mot)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.955
HV323_HUMAN	Immunoglobulin heavy variable 3-23 (Ig heavy chain V-III region LAY) (Ig heavy chain V-III region POM) (Ig heavy chain V-III region TEI) (Ig heavy chain V-III region TIL) (Ig heavy chain V-III region TUR) (Ig heavy chain V-III region VH26) (Ig heavy chain V-III region WAS) (Ig heavy chain V-III region ZAP)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.442
HVC05_HUMAN	Immunoglobulin heavy variable 3-30-5	NaN	26.958	25.949	27.258	26.989	26.402	26.531	27.405
HV307_HUMAN	Immunoglobulin heavy variable 3-7 (Ig heavy chain V-III region GAL) (Ig heavy chain V-III region GAR) (Ig heavy chain V-III region JON)	26.677	26.153	26.467	26.592	26.579	26.099	25.956	26.856
HV270_HUMAN	Immunoglobulin heavy variable 2-70 (Ig heavy chain V-II region COR) (Ig heavy chain V-II region DAW) (Ig heavy chain V-II region OU) (Ig heavy chain V-II region SESS)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.971

HV205_HUMAN	Immunoglobulin heavy variable 2-5 (Ig heavy chain V-II region HE) (Ig heavy chain V-II region MCE)	21.745	21.726	NaN	22.276	22.203	21.700	21.875	24.012
IGKC_HUMAN	Immunoglobulin kappa constant (Ig kappa chain C region) (Ig kappa chain C region AG) (Ig kappa chain C region CUM) (Ig kappa chain C region EU) (Ig kappa chain C region OU) (Ig kappa chain C region ROY) (Ig kappa chain C region TI)	30.268	30.081	30.089	30.652	30.970	30.401	29.405	30.368
IGHG1_HUMAN	Immunoglobulin heavy constant gamma 1 (Ig gamma-1 chain C region) (Ig gamma-1 chain C region EU) (Ig gamma-1 chain C region KOL) (Ig gamma-1 chain C region NIE)	33.900	33.229	33.050	33.924	33.974	34.109	33.013	33.395
IGHG2_HUMAN	Immunoglobulin heavy constant gamma 2 (Ig gamma-2 chain C region) (Ig gamma-2 chain C region DOT) (Ig gamma-2 chain C region TIL) (Ig gamma-2 chain C region ZIE)	30.748	30.110	30.499	30.788	30.961	30.213	29.022	31.915
IGHG3_HUMAN	Immunoglobulin heavy constant gamma 3 (HDC) (Heavy chain disease protein) (Ig gamma-3 chain C region)	26.124	26.378	26.270	25.738	26.670	26.068	24.677	27.256
IGHG4_HUMAN	Immunoglobulin heavy constant gamma 4 (Ig gamma-4 chain C region)	25.817	24.118	25.416	24.809	25.759	24.996	23.255	25.842
IGHM_HUMAN	Immunoglobulin heavy constant mu (Ig mu chain C region) (Ig mu chain C region BOT) (Ig mu chain C region GAL) (Ig mu chain C region OU)	29.569	28.901	27.615	29.492	28.627	27.462	27.575	31.162
IGHA1_HUMAN	Immunoglobulin heavy constant alpha 1 (Ig alpha-1 chain C region) (Ig alpha-1 chain C region BUR) (Ig alpha-1 chain C region TRO)	28.826	29.202	28.954	29.730	30.289	29.548	28.718	31.103
HBD_HUMAN	Hemoglobin subunit delta (Delta-globin) (Hemoglobin delta chain)	24.912	NaN	NaN	24.997	25.552	NaN	NaN	NaN
LMNA_HUMAN	Prelamin-A/C [Cleaved into: Lamin-A/C (70 kDa lamin) (Renal carcinoma antigen NY-REN-32)]	24.098	24.500	24.453	24.554	24.749	24.388	24.362	24.300
APOA1_HUMAN	Apolipoprotein A-I (Apo-AI) (ApoA-I) (Apolipoprotein A1) [Cleaved into: Proapolipoprotein A-I (ProapoA-I); Truncated apolipoprotein A-I (Apolipoprotein A-I(1-242))]	33.247	33.761	33.888	33.833	33.405	33.603	33.591	33.985
APOE_HUMAN	Apolipoprotein E (Apo-E)	27.817	27.538	26.995	27.573	27.651	26.355	25.922	27.999
APOA2_HUMAN	Apolipoprotein A-II (Apo-AII) (ApoA-II) (Apolipoprotein A2) [Cleaved into: Proapolipoprotein A-II (ProapoA-II); Truncated apolipoprotein A-II (Apolipoprotein A-II(1-76))]	28.284	27.792	28.027	27.319	27.706	27.838	28.260	28.969
APOC1_HUMAN	Apolipoprotein C-I (Apo-CI) (ApoC-I) (Apolipoprotein C1) [Cleaved into: Truncated apolipoprotein C-I]	27.815	26.897	27.531	26.974	27.036	27.352	26.728	26.796

APOC2_HUMAN	Apolipoprotein C-II (Apo-CII) (ApoC-II) (Apolipoprotein C2) [Cleaved into: Proapolipoprotein C-II (ProapoC-II)]	23.905	22.100	22.097	22.640	22.393	21.921	21.767	24.032
APOC3_HUMAN	Apolipoprotein C-III (Apo-CIII) (ApoC-III) (Apolipoprotein C3)	25.822	23.946	24.232	24.963	24.374	24.637	24.703	24.583
FIBA_HUMAN	Fibrinogen alpha chain [Cleaved into: Fibrinopeptide A; Fibrinogen alpha chain]	27.872	27.852	28.402	27.322	26.580	27.605	27.671	29.229
FIBB_HUMAN	Fibrinogen beta chain [Cleaved into: Fibrinopeptide B; Fibrinogen beta chain]	28.619	28.795	29.005	28.861	27.129	28.719	28.354	30.150
FIBG_HUMAN	Fibrinogen gamma chain	28.832	28.948	28.928	28.687	27.190	28.623	28.586	29.739
MYP2_HUMAN	Myelin P2 protein (Peripheral myelin protein 2)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.863
CRP_HUMAN	C-reactive protein [Cleaved into: C-reactive protein(1-205)]	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.022
SAMP_HUMAN	Serum amyloid P-component (SAP) (9.5S alpha-1-glycoprotein) [Cleaved into: Serum amyloid P-component(1-203)]	24.287	22.082	22.051	21.738	21.749	22.082	21.787	22.430
C1QA_HUMAN	Complement C1q subcomponent subunit A	NaN	24.133	24.834	22.360	22.255	23.080	NaN	23.090
C1QB_HUMAN	Complement C1q subcomponent subunit B	24.477	25.169	24.917	24.898	24.321	24.986	24.401	25.566
C1QC_HUMAN	Complement C1q subcomponent subunit C	24.347	24.296	24.160	24.098	23.846	24.216	23.847	25.024
CO9_HUMAN	Complement component C9 [Cleaved into: Complement component C9a; Complement component C9b]	27.495	28.156	27.572	27.485	27.017	26.971	27.272	27.478
APOH_HUMAN	Beta-2-glycoprotein 1 (APC inhibitor) (Activated protein C-binding protein) (Anticardiolipin cofactor) (Apolipoprotein H) (Apo-H) (Beta-2-glycoprotein I) (B2GPI) (Beta(2)GPI)	24.984	25.527	25.449	25.721	25.462	26.050	25.421	NaN
A2GL_HUMAN	Leucine-rich alpha-2-glycoprotein (LRG)	27.956	28.561	27.468	27.938	27.532	27.413	27.310	28.102
FINC_HUMAN	Fibronectin (FN) (Cold-insoluble globulin) (CIG) [Cleaved into: Anastellin; Ugl-Y1; Ugl-Y2; Ugl-Y3]	31.431	31.567	32.186	31.123	31.987	31.734	31.815	31.740
RET4_HUMAN	Retinol-binding protein 4 (Plasma retinol-binding protein) (PRBP) (RBP) [Cleaved into: Plasma retinol-binding protein(1-182); Plasma retinol-binding protein(1-181); Plasma retinol-binding protein(1-179); Plasma retinol-binding protein(1-176)]	26.259	25.707	26.405	25.915	26.240	26.639	26.558	25.542
AMBP_HUMAN	Protein AMBP [Cleaved into: Alpha-1-microglobulin (Protein HC) (Alpha-1 microglycoprotein) (Complex-forming glycoprotein heterogeneous in charge); Inter-alpha-trypsin inhibitor light chain (ITI-LC) (Bikunin) (EDC1) (HI-30) (Uronic-acid-rich protein); Trypstatin]	25.287	24.951	25.487	25.174	24.867	25.708	25.515	24.640
A1AG1_HUMAN	Alpha-1-acid glycoprotein 1 (AGP 1) (Orosomucoid-1) (OMD 1)	25.297	23.957	24.586	22.041	22.681	22.859	22.836	23.616

FETUA_HUMAN	Alpha-2-HS-glycoprotein (Alpha-2-Z-globulin) (Ba-alpha-2-glycoprotein) (Fetuin-A) [Cleaved into: Alpha-2-HS-glycoprotein chain A; Alpha-2-HS-glycoprotein chain B]	27.630	27.663	27.970	27.769	28.209	28.140	27.285	27.016
TTHY_HUMAN	Transthyretin (ATTR) (Prealbumin) (TBPA)	31.344	31.251	31.907	31.126	31.313	31.682	31.826	31.421
VTDB_HUMAN	Vitamin D-binding protein (DBP) (VDB) (Gc protein-derived macrophage activating factor) (Gc-MAF) (GcMAF) (Gc-globulin) (Group-specific component) (Gc) (Vitamin D-binding protein-macrophage activating factor) (DBP-maf)	28.694	28.928	28.833	28.621	28.688	28.299	28.590	28.249
TRFE_HUMAN	Serotransferrin (Transferrin) (Beta-1 metal-binding globulin) (Siderophilin)	31.659	32.109	32.179	33.226	31.859	31.883	32.275	31.666
HEMO_HUMAN	Hemopexin (Beta-1B-glycoprotein)	30.805	31.008	30.931	30.441	30.716	30.624	30.764	30.283
KLKB1_HUMAN	Plasma kallikrein (EC 3.4.21.34) (Fletcher factor) (Kininogenin) (Plasma prekallikrein) (PKK) [Cleaved into: Plasma kallikrein heavy chain; Plasma kallikrein light chain]	24.197	23.922	24.167	23.642	23.922	24.014	24.097	23.852
C4BPA_HUMAN	C4b-binding protein alpha chain (C4bp) (Proline-rich protein) (PRP)	25.805	25.075	24.542	24.469	24.073	25.506	24.740	24.260
VTNC_HUMAN	Vitronectin (VN) (S-protein) (Serum-spreading factor) (V75) [Cleaved into: Vitronectin V65 subunit; Vitronectin V10 subunit; Somatomedin-B]	27.083	26.456	26.535	26.605	26.363	26.755	26.306	26.483
ALDOA_HUMAN	Fructose-bisphosphate aldolase A (EC 4.1.2.13) (Lung cancer antigen NY-LU-1) (Muscle-type aldolase)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.592
ANXA1_HUMAN	Annexin A1 (Annexin I) (Annexin-1) (Calpactin II) (Calpactin-2) (Chromobindin-9) (Lipocortin I) (Phospholipase A2 inhibitory protein) (p35)	24.293	24.854	24.192	24.301	24.973	24.593	24.715	23.786
APOB_HUMAN	Apolipoprotein B-100 (Apo B-100) [Cleaved into: Apolipoprotein B-48 (Apo B-48)]	31.339	29.747	30.817	30.315	30.363	30.737	30.944	30.884
LCAT_HUMAN	Phosphatidylcholine-sterol acyltransferase (EC 2.3.1.43) (Lecithin-cholesterol acyltransferase) (Phospholipid-cholesterol acyltransferase)	NaN	NaN	NaN	NaN	NaN	21.239	NaN	NaN
HRG_HUMAN	Histidine-rich glycoprotein (Histidine-proline-rich glycoprotein) (HPRG)	27.683	27.885	27.340	27.432	26.950	27.731	27.169	26.713
A1BG_HUMAN	Alpha-1B-glycoprotein (Alpha-1-B glycoprotein)	29.288	29.632	29.563	29.588	28.766	29.263	29.101	29.771
SHBG_HUMAN	Sex hormone-binding globulin (SHBG) (Sex steroid-binding protein) (SBP) (Testis-specific androgen-binding protein) (ABP)	24.052	23.260	24.183	22.890	22.706	24.104	23.771	24.447

	(Testosterone-estradiol-binding globulin) (TeBG) (Testosterone-estrogen-binding globulin)								
G3P_HUMAN	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) (EC 1.2.1.12) (Peptidyl-cysteine S-nitrosylase GAPDH) (EC 2.6.99.-)	NaN	NaN	NaN	NaN	NaN	NaN	20.009	NaN
KV116_HUMAN	Immunoglobulin kappa variable 1-16 (Ig kappa chain V-I region BAN)	22.300	22.323	23.436	22.401	NaN	23.917	22.776	22.704
H2A1J_HUMAN	Histone H2A type 1-J (Histone H2A/e)	26.200	26.669	26.128	26.169	26.563	26.403	27.340	25.411
IPSP_HUMAN	Plasma serine protease inhibitor (Acrosomal serine protease inhibitor) (Plasminogen activator inhibitor 3) (PAI-3) (PAI3) (Protein C inhibitor) (PCI) (Serpin A5)	23.506	23.959	24.322	22.681	23.872	24.029	24.289	22.747
IC1_HUMAN	Plasma protease C1 inhibitor (C1 Inh) (C1Inh) (C1 esterase inhibitor) (C1-inhibiting factor) (Serpin G1)	28.633	28.709	28.621	28.301	28.384	28.639	28.525	28.605
CFAI_HUMAN	Complement factor I (EC 3.4.21.45) (C3B/C4B inactivator) [Cleaved into: Complement factor I heavy chain; Complement factor I light chain]	26.492	26.737	26.647	25.992	26.111	26.206	26.827	25.787
F13B_HUMAN	Coagulation factor XIII B chain (Fibrin-stabilizing factor B subunit) (Protein-glutamine gamma-glutamyltransferase B chain) (Transglutaminase B chain)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.945
FABPH_HUMAN	Fatty acid-binding protein, heart (Fatty acid-binding protein 3) (Heart-type fatty acid-binding protein) (H-FABP) (Mammary-derived growth inhibitor) (MDGI) (Muscle fatty acid-binding protein) (M-FABP)	24.435	24.666	24.485	24.632	24.986	24.580	24.452	24.300
THBG_HUMAN	Thyroxine-binding globulin (Serpin A7) (T4-binding globulin)	26.087	26.662	26.409	26.587	26.202	26.714	26.408	26.309
HEP2_HUMAN	Heparin cofactor 2 (Heparin cofactor II) (HC-II) (Protease inhibitor leuserpin-2) (HLS2) (Serpin D1)	26.713	26.620	26.826	26.556	26.337	26.853	26.710	26.477
KV230_HUMAN	Immunoglobulin kappa variable 2-30 (Ig kappa chain V-II region RPMI 6410)	NaN	26.421	26.902	27.935	26.650	27.969	NaN	28.102
KV401_HUMAN	Immunoglobulin kappa variable 4-1 (Ig kappa chain V-IV region B17) (Ig kappa chain V-IV region JI) (Ig kappa chain V-IV region Len) (Ig kappa chain V-IV region STH)	26.956	26.445	26.371	26.699	26.856	26.883	25.828	26.553
GELS_HUMAN	Gelsolin (AGEL) (Actin-depolymerizing factor) (ADF) (Brevin)	29.433	29.189	29.454	29.199	29.419	29.350	29.572	28.761
CO2_HUMAN	Complement C2 (EC 3.4.21.43) (C3/C5 convertase) [Cleaved into: Complement C2b fragment; Complement C2a fragment]	25.598	25.532	24.622	25.314	25.135	24.800	24.986	25.204
APOA4_HUMAN	Apolipoprotein A-IV (Apo-AIV) (ApoA-IV) (Apolipoprotein A4)	29.480	29.182	30.376	29.937	29.432	30.182	29.691	29.738

ENOA_HUMAN	Alpha-enolase (EC 4.2.1.11) (2-phospho-D-glycerate hydro-lyase) (C-myc promoter-binding protein) (Enolase 1) (MBP-1) (MPB-1) (Non-neural enolase) (NNE) (Phosphopyruvate hydratase) (Plasminogen-binding protein)	NaN	NaN	NaN	23.039	23.570	NaN	NaN	NaN
NFL_HUMAN	Neurofilament light polypeptide (NF-L) (68 kDa neurofilament protein) (Neurofilament triplet L protein)	23.367	23.905	23.204	22.486	23.137	22.466	23.179	NaN
NFM_HUMAN	Neurofilament medium polypeptide (NF-M) (160 kDa neurofilament protein) (Neurofilament 3) (Neurofilament triplet M protein)	24.499	24.210	23.027	23.112	23.584	NaN	23.447	NaN
PROS_HUMAN	Vitamin K-dependent protein S	25.707	25.242	24.820	25.409	25.235	25.308	24.908	25.456
ACYP1_HUMAN	Acylphosphatase-1 (EC 3.6.1.7) (Acylphosphatase, erythrocyte isozyme) (Acylphosphatase, organ-common type isozyme) (Acylphosphate phosphohydrolase 1)	NaN	25.447	25.688	25.680	25.058	25.909	25.315	27.572
CATD_HUMAN	Cathepsin D (EC 3.4.23.5) [Cleaved into: Cathepsin D light chain; Cathepsin D heavy chain]	27.306	27.296	27.140	27.170	27.993	26.999	27.721	26.405
ANXA2_HUMAN	Annexin A2 (Annexin II) (Annexin-2) (Calpactin I heavy chain) (Calpactin-1 heavy chain) (Chromobindin-8) (Lipocortin II) (Placental anticoagulant protein IV) (PAP-IV) (Protein I) (p36)	30.162	30.528	30.200	30.327	30.720	30.453	30.565	30.175
CO8A_HUMAN	Complement component C8 alpha chain (Complement component 8 subunit alpha)	24.803	25.423	25.698	24.323	24.579	24.771	25.184	24.746
CO8B_HUMAN	Complement component C8 beta chain (Complement component 8 subunit beta)	24.145	25.009	24.582	24.345	24.699	24.672	24.950	24.480
CO8G_HUMAN	Complement component C8 gamma chain	24.514	25.278	24.545	24.340	25.196	24.654	24.899	24.449
PGS2_HUMAN	Decorin (Bone proteoglycan II) (PG-S2) (PG40)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.066
PROF1_HUMAN	Profilin-1 (Epididymis tissue protein Li 184a) (Profilin I)	NaN	NaN	NaN	NaN	22.209	NaN	NaN	NaN
HNRPC_HUMAN	Heterogeneous nuclear ribonucleoproteins C1/C2 (hnRNP C1/C2)	NaN	NaN	NaN	NaN	22.225	NaN	NaN	NaN
CBG_HUMAN	Corticosteroid-binding globulin (CBG) (Serpin A6) (Transcortin)	27.329	27.981	27.457	27.246	27.490	27.332	28.017	27.048
MMP2_HUMAN	72 kDa type IV collagenase (EC 3.4.24.24) (72 kDa gelatinase) (Gelatinase A) (Matrix metalloproteinase-2) (MMP-2) (TBE-1) [Cleaved into: PEX]	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.549
MMP3_HUMAN	Stromelysin-1 (SL-1) (EC 3.4.24.17) (Matrix metalloproteinase-3) (MMP-3) (Transin-1)	24.512	23.078	23.697	24.051	23.487	NaN	NaN	24.777
APOA_HUMAN	Apolipoprotein(a) (Apo(a)) (Lp(a)) (EC 3.4.21.-)	23.009	NaN	NaN	NaN	NaN	NaN	22.600	22.895

CD14_HUMAN	Monocyte differentiation antigen CD14 (Myeloid cell-specific leucine-rich glycoprotein) (CD antigen CD14) [Cleaved into: Monocyte differentiation antigen CD14, urinary form; Monocyte differentiation antigen CD14, membrane-bound form]	23.901	23.935	23.791	23.259	23.587	23.779	23.639	23.815
CFAH_HUMAN	Complement factor H (H factor 1)	28.337	28.470	28.216	28.255	28.157	28.324	27.748	28.121
VIME_HUMAN	Vimentin	23.626	22.738	NaN	22.355	23.234	21.634	22.323	NaN
A2AP_HUMAN	Alpha-2-antiplasmin (Alpha-2-AP) (Alpha-2-plasmin inhibitor) (Alpha-2-PI) (Serpin F2)	28.028	27.650	28.188	27.861	27.635	27.738	27.990	27.380
ANXA5_HUMAN	Annexin A5 (Anchorin CII) (Annexin V) (Annexin-5) (Calphobindin I) (CBP-I) (Endonexin II) (Lipocortin V) (Placental anticoagulant protein 4) (PP4) (Placental anticoagulant protein I) (PAP-I) (Thromboplastin inhibitor) (Vascular anticoagulant-alpha) (VAC-alpha)	22.889	23.775	23.618	23.967	23.377	23.768	23.737	23.638
SNRPA_HUMAN	U1 small nuclear ribonucleoprotein A (U1 snRNP A) (U1-A) (U1A)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.443
GSTP1_HUMAN	Glutathione S-transferase P (EC 2.5.1.18) (GST class-pi) (GSTP1-1)	24.988	24.686	24.152	24.221	24.808	24.177	25.139	24.145
GSTM1_HUMAN	Glutathione S-transferase Mu 1 (EC 2.5.1.18) (GST HB subunit 4) (GST class-mu 1) (GSTM1-1) (GSTM1a-1a) (GSTM1b-1b) (GTH4)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.769
C1S_HUMAN	Complement C1s subcomponent (EC 3.4.21.42) (C1 esterase) (Complement component 1 subcomponent s) [Cleaved into: Complement C1s subcomponent heavy chain; Complement C1s subcomponent light chain]	25.693	25.610	25.575	25.309	25.392	25.350	25.849	25.323
CO4A_HUMAN	Complement C4-A (Acidic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 2) [Cleaved into: Complement C4 beta chain; Complement C4-A alpha chain; C4a anaphylatoxin; C4b-A; C4d-A; Complement C4 gamma chain]	25.548	25.668	25.328	26.142	25.151	25.367	26.637	24.969
CO4B_HUMAN	Complement C4-B (Basic complement C4) (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 3) [Cleaved into: Complement C4 beta chain; Complement C4-B alpha chain; C4a anaphylatoxin; C4b-B; C4d-B; Complement C4 gamma chain]	30.825	31.285	30.259	30.893	29.793	30.632	30.976	30.015
RL40_HUMAN	Ubiquitin-60S ribosomal protein L40 (CEP52) (Ubiquitin A-52 residue ribosomal protein fusion product 1) [Cleaved into:	26.176	25.919	25.541	25.728	26.640	26.130	26.602	25.228

	Ubiquitin; 60S ribosomal protein L40 (Large ribosomal subunit protein eL40)]								
SAA1_HUMAN	Serum amyloid A-1 protein (SAA) [Cleaved into: Amyloid protein A (Amyloid fibril protein AA); Serum amyloid protein A(2-104); Serum amyloid protein A(3-104); Serum amyloid protein A(2-103); Serum amyloid protein A(2-102); Serum amyloid protein A(4-101)]	21.324	22.825	NaN	21.393	21.961	21.859	21.849	22.109
IGA2_HUMAN	Immunoglobulin alpha-2 heavy chain (Immunoglobulin alpha-2 heavy chain BUT)	28.828	29.145	29.005	29.396	30.173	29.821	28.591	31.152
IGD_HUMAN	Immunoglobulin delta heavy chain (Immunoglobulin delta heavy chain WAH)	NaN	23.294	NaN	22.890	24.509	25.225	23.497	24.576
IGM_HUMAN	Immunoglobulin mu heavy chain (Immunoglobulin mu heavy chain OU)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.117
IGK_HUMAN	Immunoglobulin kappa light chain (Immunoglobulin kappa light chain EU)	31.269	31.603	31.012	31.955	31.844	31.794	30.871	31.922
IGLC3_HUMAN	Immunoglobulin lambda constant 3 (Ig lambda chain C region DOT) (Ig lambda chain C region NEWM) (Ig lambda-3 chain C regions)	28.945	28.231	27.927	29.030	29.400	28.549	28.629	29.261
HV108_HUMAN	Immunoglobulin heavy variable 1-8	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.561
H14_HUMAN	Histone H1.4 (Histone H1b) (Histone H1s-4)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.416
THIO_HUMAN	Thioredoxin (Trx) (ATL-derived factor) (ADF) (Surface-associated sulphydryl protein) (SASP)	22.956	23.114	22.809	22.748	23.203	22.977	23.153	22.411
CO7_HUMAN	Complement component C7	25.136	25.382	26.001	25.612	25.759	25.975	24.925	24.744
CLUS_HUMAN	Clusterin (Aging-associated gene 4 protein) (Apolipoprotein J) (Apo-J) (Complement cytolysis inhibitor) (CLI) (Complement-associated protein SP-40,40) (Ku70-binding protein 1) (NA1/NA2) (Sulfated glycoprotein 2) (SGP-2) (Testosterone-repressed prostate message 2) (TRPM-2) [Cleaved into: Clusterin beta chain (ApoJalpha) (Complement cytolysis inhibitor a chain); Clusterin alpha chain (ApoJbeta) (Complement cytolysis inhibitor b chain)]	28.566	28.664	28.911	28.575	29.416	29.009	29.129	28.958
BIP_HUMAN	Endoplasmic reticulum chaperone BiP (EC 3.6.4.10) (78 kDa glucose-regulated protein) (GRP-78) (Binding-immunoglobulin protein) (BiP) (Heat shock protein 70 family protein 5) (HSP70	25.205	25.179	24.973	25.164	25.528	25.070	25.468	25.030

	family protein 5) (Heat shock protein family A member 5) (Immunoglobulin heavy chain-binding protein)								
HSP7C_HUMAN	Heat shock cognate 71 kDa protein (Heat shock 70 kDa protein 8) (Lipopolysaccharide-associated protein 1) (LAP-1) (LPS-associated protein 1)	24.723	25.873	25.601	25.334	25.724	25.112	25.906	24.945
NFH_HUMAN	Neurofilament heavy polypeptide (NF-H) (200 kDa neurofilament protein) (Neurofilament triplet H protein)	NaN	NaN	20.583	NaN	NaN	NaN	NaN	NaN
CO6A1_HUMAN	Collagen alpha-1(VI) chain	NaN	NaN	NaN	NaN	NaN	NaN	21.671	NaN
CO6A3_HUMAN	Collagen alpha-3(VI) chain	23.231	22.783	22.304	22.459	23.151	22.590	23.240	22.791
ANXA3_HUMAN	Annexin A3 (35-alpha calcimedin) (Annexin III) (Annexin-3) (Inositol 1,2-cyclic phosphate 2-phosphohydrolase) (Lipocortin III) (Placental anticoagulant protein III) (PAP-III)	23.266	23.840	23.617	23.570	23.941	23.800	23.543	23.150
CSPG2_HUMAN	Versican core protein (Chondroitin sulfate proteoglycan core protein 2) (Chondroitin sulfate proteoglycan 2) (Glial hyaluronate-binding protein) (GHAP) (Large fibroblast proteoglycan) (PG-M)	22.444	21.189	21.502	NaN	21.814	21.256	NaN	21.575
CO6_HUMAN	Complement component C6	26.223	25.922	25.378	25.033	25.588	25.401	25.749	24.842
PLSL_HUMAN	Plastin-2 (L-plastin) (LC64P) (Lymphocyte cytosolic protein 1) (LCP-1)	24.111	24.477	24.130	23.975	24.589	23.775	24.442	23.580
PLST_HUMAN	Plastin-3 (T-plastin)	22.323	22.298	21.895	21.844	23.282	21.880	22.635	NaN
KPYM_HUMAN	Pyruvate kinase PKM (EC 2.7.1.40) (Cytosolic thyroid hormone-binding protein) (CTHBP) (Opa-interacting protein 3) (OIP-3) (Pyruvate kinase 2/3) (Pyruvate kinase muscle isozyme) (Thyroid hormone-binding protein 1) (THBP1) (Tumor M2-PK) (p58)	NaN	21.763	NaN	21.352	23.225	NaN	22.114	21.493
CBPN_HUMAN	Carboxypeptidase N catalytic chain (CPN) (EC 3.4.17.3) (Anaphylatoxin inactivator) (Arginine carboxypeptidase) (Carboxypeptidase N polypeptide 1) (Carboxypeptidase N small subunit) (Kininase-1) (Lysine carboxypeptidase) (Plasma carboxypeptidase B) (Serum carboxypeptidase N) (SCPN)	21.838	22.279	22.506	22.387	22.357	22.493	22.346	22.005
NDKA_HUMAN	Nucleoside diphosphate kinase A (NDK A) (NDP kinase A) (EC 2.7.4.6) (Granzyme A-activated DNase) (GAAD) (Metastasis inhibition factor nm23) (NM23-H1) (Tumor metastatic process-associated protein)	22.371	22.635	22.329	22.702	22.878	22.674	22.240	22.667
GNS_HUMAN	N-acetylglucosamine-6-sulfatase (EC 3.1.6.14) (Glucosamine-6-sulfatase) (G6S)	24.963	25.402	24.952	25.075	25.683	25.040	25.037	24.479

IGLL1_HUMAN	Immunoglobulin lambda-like polypeptide 1 (CD179 antigen-like family member B) (Ig lambda-5) (Immunoglobulin omega polypeptide) (Immunoglobulin-related protein 14.1) (CD antigen CD179b)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.885
ARSB_HUMAN	Arylsulfatase B (ASB) (EC 3.1.6.12) (N-acetylgalactosamine-4-sulfatase) (G4S)	22.967	22.985	22.548	22.548	23.525	22.815	23.244	21.986
CD44_HUMAN	CD44 antigen (CDw44) (Epican) (Extracellular matrix receptor III) (ECMR-III) (GP90 lymphocyte homing/adhesion receptor) (HUTCH-I) (Heparan sulfate proteoglycan) (Hermes antigen) (Hyaluronate receptor) (Phagocytic glycoprotein 1) (PGP-1) (Phagocytic glycoprotein I) (PGP-I) (CD antigen CD44)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.085
PGCA_HUMAN	Aggrecan core protein (Cartilage-specific proteoglycan core protein) (CSPCP) (Chondroitin sulfate proteoglycan core protein 1) (Chondroitin sulfate proteoglycan 1) [Cleaved into: Aggrecan core protein 2]	24.580	23.618	23.062	23.282	24.153	23.753	24.466	22.616
H12_HUMAN	Histone H1.2 (Histone H1c) (Histone H1d) (Histone H1s-1)	NaN	NaN	NaN	NaN	NaN	NaN	20.918	NaN
LBP_HUMAN	Lipopolysaccharide-binding protein (LBP)	23.182	22.604	23.066	23.211	22.982	23.710	23.483	23.145
ITIH2_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H2 (ITI heavy chain H2) (ITI-HC2) (Inter-alpha-inhibitor heavy chain 2) (Inter-alpha-trypsin inhibitor complex component II) (Serum-derived hyaluronan-associated protein) (SHAP)	29.596	29.192	29.450	29.451	28.691	29.367	29.044	29.376
ITIH1_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H1 (ITI heavy chain H1) (ITI-HC1) (Inter-alpha-inhibitor heavy chain 1) (Inter-alpha-trypsin inhibitor complex component III) (Serum-derived hyaluronan-associated protein) (SHAP)	29.248	29.380	29.340	29.185	28.880	29.317	29.897	28.883
PZP_HUMAN	Pregnancy zone protein (C3 and PZP-like alpha-2-macroglobulin domain-containing protein 6)	24.144	23.290	NaN	23.092	23.985	NaN	NaN	25.281
MIME_HUMAN	Mimecan (Osteoglycin) (Osteoinductive factor) (OIF)	21.864	21.629	21.948	23.306	22.181	22.056	22.735	NaN
C4BPB_HUMAN	C4b-binding protein beta chain	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.494
FLNA_HUMAN	Filamin-A (FLN-A) (Actin-binding protein 280) (ABP-280) (Alpha-filamin) (Endothelial actin-binding protein) (Filamin-1) (Non-muscle filamin)	NaN	NaN	NaN	22.707	NaN	22.955	NaN	22.143
GPX3_HUMAN	Glutathione peroxidase 3 (GPx-3) (GSHPx-3) (EC 1.11.1.9) (Extracellular glutathione peroxidase) (Plasma glutathione peroxidase) (GPx-P) (GSHPx-P)	21.626	22.328	22.642	21.668	22.306	22.450	NaN	21.974

CPN2_HUMAN	Carboxypeptidase N subunit 2 (Carboxypeptidase N 83 kDa chain) (Carboxypeptidase N large subunit) (Carboxypeptidase N polypeptide 2) (Carboxypeptidase N regulatory subunit)	24.863	24.962	24.518	24.864	24.572	24.985	24.925	23.951
HV102_HUMAN	Immunoglobulin heavy variable 1-2 (Ig heavy chain V-I region ND) (Ig heavy chain V-I region V35)	NaN	NaN	22.478	23.786	22.540	NaN	NaN	22.275
TCEA1_HUMAN	Transcription elongation factor A protein 1 (Transcription elongation factor S-II protein 1) (Transcription elongation factor TFIIS.o)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.268
PPAC_HUMAN	Low molecular weight phosphotyrosine protein phosphatase (LMW-PTP) (LMW-PTPase) (EC 3.1.3.48) (Adipocyte acid phosphatase) (Low molecular weight cytosolic acid phosphatase) (EC 3.1.3.2) (Red cell acid phosphatase 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.718
ZA2G_HUMAN	Zinc-alpha-2-glycoprotein (Zn-alpha-2-GP) (Zn-alpha-2-glycoprotein)	24.991	24.682	24.757	23.908	24.249	24.154	24.552	23.694
PON1_HUMAN	Serum paraoxonase/arylesterase 1 (PON 1) (EC 3.1.1.2) (EC 3.1.1.81) (EC 3.1.8.1) (Aromatic esterase 1) (A-esterase 1) (K-45) (Serum aryldialkylphosphatase 1)	26.603	26.395	26.690	26.482	26.296	26.109	27.072	26.682
GSTM2_HUMAN	Glutathione S-transferase Mu 2 (EC 2.5.1.18) (GST class-mu 2) (GSTM2-2)	24.697	24.941	24.966	24.014	24.703	24.546	24.691	23.818
KAIN_HUMAN	Kallistatin (Kallikrein inhibitor) (Peptidase inhibitor 4) (PI-4) (Serpin A4)	26.174	25.805	25.821	26.407	25.961	26.344	26.572	25.444
GFRP_HUMAN	GTP cyclohydrolase 1 feedback regulatory protein (GFRP) (GTP cyclohydrolase I feedback regulatory protein) (p35)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.052
PEBP1_HUMAN	Phosphatidylethanolamine-binding protein 1 (PEBP-1) (HCNPpp) (Neuropolypeptide h3) (Prostatic-binding protein) (Raf kinase inhibitor protein) (RKIP) [Cleaved into: Hippocampal cholinergic neurostimulating peptide (HCNP)]	27.348	27.997	27.485	27.640	28.125	27.901	27.927	27.634
PDIA3_HUMAN	Protein disulfide-isomerase A3 (EC 5.3.4.1) (58 kDa glucose-regulated protein) (58 kDa microsomal protein) (p58) (Disulfide isomerase ER-60) (Endoplasmic reticulum resident protein 57) (ER protein 57) (ERp57) (Endoplasmic reticulum resident protein 60) (ER protein 60) (ERp60)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.041
DNJA1_HUMAN	DnaJ homolog subfamily A member 1 (DnaJ protein homolog 2) (HSDJ) (Heat shock 40 kDa protein 4) (Heat shock protein J2) (HSJ-2) (Human DnaJ protein 2) (hDj-2)	23.485	23.700	23.589	23.192	23.455	23.838	23.344	23.378

PRDX2_HUMAN	Peroxiredoxin-2 (EC 1.11.1.15) (Natural killer cell-enhancing factor B) (NKEF-B) (PRP) (Thiol-specific antioxidant protein) (TSA) (Thioredoxin peroxidase 1) (Thioredoxin-dependent peroxide reductase 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	17.987
HS71L_HUMAN	Heat shock 70 kDa protein 1-like (Heat shock 70 kDa protein 1L) (Heat shock 70 kDa protein 1-Hom) (HSP70-Hom)	23.580	23.964	23.722	23.420	24.431	23.773	23.930	22.938
SPB6_HUMAN	Serpin B6 (Cytoplasmic antiproteinase) (CAP) (Peptidase inhibitor 6) (PI-6) (Placental thrombin inhibitor)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.254
TSP4_HUMAN	Thrombospondin-4	NaN	NaN	NaN	NaN	NaN	NaN	NaN	19.915
SAA4_HUMAN	Serum amyloid A-4 protein (Constitutively expressed serum amyloid A protein) (C-SAA)	27.015	26.701	26.296	26.428	25.550	26.455	25.848	27.273
ALS_HUMAN	Insulin-like growth factor-binding protein complex acid labile subunit (ALS)	24.376	24.474	23.292	24.442	25.121	23.684	24.384	23.579
CH3L1_HUMAN	Chitinase-3-like protein 1 (39 kDa synovial protein) (Cartilage glycoprotein 39) (CGP-39) (GP-39) (hCGP-39) (YKL-40)	23.311	22.711	22.483	22.453	23.436	22.222	22.334	23.130
PEDF_HUMAN	Pigment epithelium-derived factor (PEDF) (Cell proliferation-inducing gene 35 protein) (EPC-1) (Serpin F1)	26.984	26.811	26.944	27.060	27.260	26.976	26.927	26.775
TAGL2_HUMAN	Transgelin-2 (Epididymis tissue protein Li 7e) (SM22-alpha homolog)	21.724	22.166	21.388	21.747	22.377	21.877	21.890	21.469
TALDO_HUMAN	Transaldolase (EC 2.2.1.2)	24.931	25.081	24.980	25.245	25.499	24.979	25.309	24.585
GRP75_HUMAN	Stress-70 protein, mitochondrial (75 kDa glucose-regulated protein) (GRP-75) (Heat shock 70 kDa protein 9) (Mortalin) (MOT) (Peptide-binding protein 74) (PBP74)	24.585	25.235	24.980	24.380	25.542	24.857	25.226	24.204
CUX1_HUMAN	Homeobox protein cut-like 1 (CCAAT displacement protein) (CDP) (Homeobox protein cux-1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.041
MDHM_HUMAN	Malate dehydrogenase, mitochondrial (EC 1.1.1.37)	24.894	25.337	25.298	25.187	25.865	25.488	25.448	24.708
PERI_HUMAN	Peripherin (Neurofilament 4)	30.842	31.007	29.886	29.649	30.972	29.038	30.851	27.492
PTGDS_HUMAN	Prostaglandin-H2 D-isomerase (EC 5.3.99.2) (Beta-trace protein) (Cerebrin-28) (Glutathione-independent PGD synthase) (Lipocalin-type prostaglandin-D synthase) (Prostaglandin-D2 synthase) (PGD2 synthase) (PGDS) (PGDS2)	22.423	NaN	NaN	23.344	22.971	22.763	NaN	23.348
PCP_HUMAN	Lysosomal Pro-X carboxypeptidase (EC 3.4.16.2) (Angiotensinase C) (Lysosomal carboxypeptidase C) (Proline carboxypeptidase) (Prolylcarboxypeptidase) (PRCP)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.745
BTD_HUMAN	Biotinidase (Biotinase) (EC 3.5.1.12)	22.722	22.467	22.305	21.790	22.094	21.853	22.417	21.919

AFAM_HUMAN	Afamin (Alpha-albumin) (Alpha-Alb)	25.433	24.595	24.852	24.490	24.708	24.673	25.621	24.166
PPT1_HUMAN	Palmitoyl-protein thioesterase 1 (PPT-1) (EC 3.1.2.22) (Palmitoyl-protein hydrolase 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.129
MMP16_HUMAN	Matrix metalloproteinase-16 (MMP-16) (EC 3.4.24.-) (MMP-X2) (Membrane-type matrix metalloproteinase 3) (MT-MMP 3) (MTMMP3) (Membrane-type-3 matrix metalloproteinase) (MT3-MMP) (MT3MMP)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.669
LUM_HUMAN	Lumican (Keratan sulfate proteoglycan lumican) (KSPG lumican)	27.341	27.312	27.208	27.315	28.006	27.172	27.543	27.753
PRELP_HUMAN	Prolargin (Proline-arginine-rich end leucine-rich repeat protein)	NaN	NaN	NaN	21.577	21.869	NaN	21.941	NaN
GDIR1_HUMAN	Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha)	25.492	25.325	24.862	24.447	25.460	25.025	24.800	25.446
RIDA_HUMAN	2-iminobutanoate/2-iminopropanoate deaminase (EC 3.5.99.10) (14.5 kDa translational inhibitor protein) (hp14.5) (p14.5) (Heat-responsive protein 12) (Reactive intermediate imine deaminase A homolog) (Translation inhibitor L-PSP ribonuclease) (UK114 antigen homolog)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.283
TCP4_HUMAN	Activated RNA polymerase II transcriptional coactivator p15 (Positive cofactor 4) (PC4) (SUB1 homolog) (p14)	25.309	25.029	24.966	25.026	25.559	25.331	25.188	24.208
UBP14_HUMAN	Ubiquitin carboxyl-terminal hydrolase 14 (EC 3.4.19.12) (Deubiquitinating enzyme 14) (Ubiquitin thioesterase 14) (Ubiquitin-specific-processing protease 14)	22.391	22.646	22.101	22.486	22.930	22.572	22.585	22.282
HSP72_HUMAN	Heat shock-related 70 kDa protein 2 (Heat shock 70 kDa protein 2)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	25.194
RD23B_HUMAN	UV excision repair protein RAD23 homolog B (HR23B) (hHR23B) (XP-C repair-complementing complex 58 kDa protein) (p58)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.760
PLTP_HUMAN	Phospholipid transfer protein (Lipid transfer protein II)	24.396	24.255	24.715	23.761	24.414	24.211	24.266	24.924
MANF_HUMAN	Mesencephalic astrocyte-derived neurotrophic factor (Arginine-rich protein) (Protein ARMET)	23.225	23.453	22.896	23.231	23.708	23.874	23.358	23.112
SUMO4_HUMAN	Small ubiquitin-related modifier 4 (SUMO-4) (Small ubiquitin-like protein 4)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.637
TPPP2_HUMAN	Tubulin polymerization-promoting protein family member 2 (Protein p25-beta) (TPPP/p18)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.005
ACTB_HUMAN	Actin, cytoplasmic 1 (Beta-actin) [Cleaved into: Actin, cytoplasmic 1, N-terminally processed]	26.137	26.549	25.762	26.796	27.514	25.617	26.668	26.222
GMFB_HUMAN	Glia maturation factor beta (GMF-beta)	23.925	24.256	24.010	23.809	24.827	24.016	24.540	22.997

UB2D2_HUMAN	Ubiquitin-conjugating enzyme E2 D2 (EC 2.3.2.23) ((E3-independent) E2 ubiquitin-conjugating enzyme D2) (EC 2.3.2.24) (E2 ubiquitin-conjugating enzyme D2) (Ubiquitin carrier protein D2) (Ubiquitin-conjugating enzyme E2(17)KB 2) (Ubiquitin-conjugating enzyme E2-17 kDa 2) (Ubiquitin-protein ligase D2) (p53-regulated ubiquitin-conjugating enzyme 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.608
CH10_HUMAN	10 kDa heat shock protein, mitochondrial (Hsp10) (10 kDa chaperonin) (Chaperonin 10) (CPN10) (Early-pregnancy factor) (EPF)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.885
LYSC_HUMAN	Lysozyme C (EC 3.2.1.17) (1,4-beta-N-acetylmuramidase C)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.889
RS16_HUMAN	40S ribosomal protein S16 (Small ribosomal subunit protein uS9)	NaN	NaN	NaN	NaN	NaN	NaN	22.604	NaN
H4_HUMAN	Histone H4	23.671	24.184	23.965	23.644	24.895	23.898	25.228	23.644
UBC9_HUMAN	SUMO-conjugating enzyme UBC9 (EC 2.3.2.-) (RING-type E3 SUMO transferase UBC9) (SUMO-protein ligase) (Ubiquitin carrier protein 9) (Ubiquitin carrier protein I) (Ubiquitin-conjugating enzyme E2 I) (Ubiquitin-protein ligase I) (p18)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.971
ACTC_HUMAN	Actin, alpha cardiac muscle 1 (Alpha-cardiac actin) [Cleaved into: Actin, alpha cardiac muscle 1, intermediate form]	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.180
EF1A3_HUMAN	Putative elongation factor 1-alpha-like 3 (EF-1-alpha-like 3) (Eukaryotic elongation factor 1 A-like 3) (eEF1A-like 3) (Eukaryotic translation elongation factor 1 alpha-1 pseudogene 5)	23.347	23.825	23.160	23.454	24.047	23.558	23.854	23.279
TBA1C_HUMAN	Tubulin alpha-1C chain (Alpha-tubulin 6) (Tubulin alpha-6 chain) [Cleaved into: Detyrosinated tubulin alpha-1C chain]	NaN	22.474	NaN	21.216	23.469	NaN	23.181	20.560
HBB_HUMAN	Hemoglobin subunit beta (Beta-globin) (Hemoglobin beta chain) [Cleaved into: LVV-hemorphin-7; Spinorphin]	31.343	25.305	27.352	31.761	32.434	26.970	25.462	27.361
HBA_HUMAN	Hemoglobin subunit alpha (Alpha-globin) (Hemoglobin alpha chain)	30.924	24.698	26.879	31.534	31.877	26.474	25.068	26.969
PHLD_HUMAN	Phosphatidylinositol-glycan-specific phospholipase D (PI-G PLD) (EC 3.1.4.50) (Glycoprotein phospholipase D) (Glycosyl-phosphatidylinositol-specific phospholipase D) (GPI-PLD) (GPI-specific phospholipase D)	22.228	NaN	21.781	21.570	21.392	21.673	NaN	21.553

LV321_HUMAN	Immunoglobulin lambda variable 3-21 (Ig lambda chain V-III region LOI) (Ig lambda chain V-V region DEL) (Ig lambda chain V-VII region MOT)	25.833	25.000	25.452	25.384	25.451	26.942	24.825	26.476
SPTB2_HUMAN	Spectrin beta chain, non-erythrocytic 1 (Beta-II spectrin) (Fodrin beta chain) (Spectrin, non-erythroid beta chain 1)	24.566	24.449	24.011	23.952	24.822	24.593	24.308	24.062
FABP5_HUMAN	Fatty acid-binding protein 5 (Epidermal-type fatty acid-binding protein) (E-FABP) (Fatty acid-binding protein, epidermal) (Psoriasis-associated fatty acid-binding protein homolog) (PA-FABP)	23.185	23.925	23.043	NaN	24.000	23.495	23.725	22.831
TAGL_HUMAN	Transgelin (22 kDa actin-binding protein) (Protein WS3-10) (Smooth muscle protein 22-alpha) (SM22-alpha)	22.528	NaN	22.036	22.013	22.822	22.419	21.629	21.576
COEA1_HUMAN	Collagen alpha-1(XIV) chain (Undulin)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.098
ITIH3_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H3 (ITI heavy chain H3) (ITI-HC3) (Inter-alpha-inhibitor heavy chain 3) (Serum-derived hyaluronan-associated protein) (SHAP)	24.066	24.633	24.283	25.067	23.868	24.772	24.169	24.444
FMOD_HUMAN	Fibromodulin (FM) (Collagen-binding 59 kDa protein) (Keratan sulfate proteoglycan fibromodulin) (KSPG fibromodulin)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	NaN
PRDX1_HUMAN	Peroxiredoxin-1 (EC 1.11.1.15) (Natural killer cell-enhancing factor A) (NKEF-A) (Proliferation-associated gene protein) (PAG) (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	24.326	24.720	24.229	24.577	25.254	24.613	24.775	24.203
LG3BP_HUMAN	Galectin-3-binding protein (Basement membrane autoantigen p105) (Lectin galactoside-binding soluble 3-binding protein) (Mac-2-binding protein) (MAC2BP) (Mac-2 BP) (Tumor-associated antigen 90K)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.112
FBLN3_HUMAN	EGF-containing fibulin-like extracellular matrix protein 1 (Extracellular protein S1-5) (Fibrillin-like protein) (Fibulin-3) (FIBL-3)	NaN	NaN	NaN	21.911	NaN	NaN	NaN	21.530
ILF3_HUMAN	Interleukin enhancer-binding factor 3 (Double-stranded RNA-binding protein 76) (DRBP76) (M-phase phosphoprotein 4) (MPP4) (Nuclear factor associated with dsRNA) (NFAR) (Nuclear factor of activated T-cells 90 kDa) (NF-AT-90) (Translational control protein 80) (TCP80)	21.731	21.989	21.666	21.799	22.379	22.295	21.967	21.663

PRDX4_HUMAN	Peroxiredoxin-4 (EC 1.11.1.15) (Antioxidant enzyme AOE372) (AOE37-2) (Peroxiredoxin IV) (Prx-IV) (Thioredoxin peroxidase AO372) (Thioredoxin-dependent peroxide reductase A0372)	NaN	NaN	NaN	23.124	NaN	23.247	23.529	22.581
COTL1_HUMAN	Coactosin-like protein	22.819	22.840	22.625	22.640	23.289	22.823	23.087	22.344
HABP2_HUMAN	Hyaluronan-binding protein 2 (EC 3.4.21.-) (Factor VII-activating protease) (Factor seven-activating protease) (FSAP) (Hepatocyte growth factor activator-like protein) (Plasma hyaluronan-binding protein) [Cleaved into: Hyaluronan-binding protein 2 50 kDa heavy chain; Hyaluronan-binding protein 2 50 kDa heavy chain alternate form; Hyaluronan-binding protein 2 27 kDa light chain; Hyaluronan-binding protein 2 27 kDa light chain alternate form]	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.907
ITIH4_HUMAN	Inter-alpha-trypsin inhibitor heavy chain H4 (ITI heavy chain H4) (ITI-HC4) (Inter-alpha-inhibitor heavy chain 4) (Inter-alpha-trypsin inhibitor family heavy chain-related protein) (IHRP) (Plasma kallikrein sensitive glycoprotein 120) (Gp120) (PK-120) [Cleaved into: 70 kDa inter-alpha-trypsin inhibitor heavy chain H4; 35 kDa inter-alpha-trypsin inhibitor heavy chain H4]	29.337	29.490	29.441	29.310	28.711	29.256	29.113	29.430
POSTN_HUMAN	Periostin (PN) (Osteoblast-specific factor 2) (OSF-2)	23.951	21.193	21.021	20.608	21.073	21.573	21.573	20.942
PDIA6_HUMAN	Protein disulfide-isomerase A6 (EC 5.3.4.1) (Endoplasmic reticulum protein 5) (ER protein 5) (ERp5) (Protein disulfide isomerase P5) (Thioredoxin domain-containing protein 7)	22.441	23.213	22.460	22.638	23.408	23.043	23.323	22.135
PCOC1_HUMAN	Procollagen C-endopeptidase enhancer 1 (Procollagen COOH-terminal proteinase enhancer 1) (PCPE-1) (Procollagen C-proteinase enhancer 1) (Type 1 procollagen C-proteinase enhancer protein) (Type I procollagen COOH-terminal proteinase enhancer)	23.115	23.337	22.317	22.341	NaN	22.604	NaN	22.860
RGN_HUMAN	Regucalcin (RC) (Gluconolactonase) (GNL) (EC 3.1.1.17) (Senescence marker protein 30) (SMP-30)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	25.073
BGH3_HUMAN	Transforming growth factor-beta-induced protein ig-h3 (Beta ig-h3) (Kerato-epithelin) (RGD-containing collagen-associated protein) (RGD-CAP)	23.190	NaN	21.642	21.824	22.051	21.880	22.781	21.426
MARE1_HUMAN	Microtubule-associated protein RP/EB family member 1 (APC-binding protein EB1) (End-binding protein 1) (EB1)	24.365	24.275	24.514	24.073	24.237	24.302	24.753	23.734

MYLK_HUMAN	Myosin light chain kinase, smooth muscle (MLCK) (smMLCK) (EC 2.7.11.18) (Kinase-related protein) (KRP) (Telokin) [Cleaved into: Myosin light chain kinase, smooth muscle, deglutamylated form]	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.261
AINX_HUMAN	Alpha-internexin (Alpha-Inx) (66 kDa neurofilament protein) (NF-66) (Neurofilament-66) (Neurofilament 5)	NaN	20.357	NaN	NaN	NaN	NaN	NaN	NaN
ECM1_HUMAN	Extracellular matrix protein 1 (Secretory component p85)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	19.136
DECR_HUMAN	2,4-dienoyl-CoA reductase, mitochondrial (EC 1.3.1.34) (2,4-dienoyl-CoA reductase [NADPH]) (4-enoyl-CoA reductase [NADPH]) (Short chain dehydrogenase/reductase family 18C member 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.588
STXB5_HUMAN	Syntaxin-binding protein 5 (Lethal(2) giant larvae protein homolog 3) (Tomosyn-1)	NaN	NaN	NaN	NaN	24.854	NaN	NaN	NaN
GSTA5_HUMAN	Glutathione S-transferase A5 (EC 2.5.1.18) (GST class-alpha member 5) (Glutathione S-transferase A5-5)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.033
STX12_HUMAN	Syntaxin-12	23.038	23.345	22.626	23.041	23.303	23.207	22.857	22.906
PLD3_HUMAN	Phospholipase D3 (PLD 3) (EC 3.1.4.4) (Choline phosphatase 3) (HindIII K4L homolog) (Hu-K4) (Phosphatidylcholine-hydrolyzing phospholipase D3)	24.611	24.673	24.706	24.319	24.851	24.630	24.618	23.476
WDTC1_HUMAN	WD and tetratricopeptide repeats protein 1	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.567
PLBL2_HUMAN	Putative phospholipase B-like 2 (EC 3.1.1.-) (76 kDa protein) (p76) (LAMA-like protein 2) (Lamina ancestor homolog 2) (Phospholipase B domain-containing protein 2) [Cleaved into: Putative phospholipase B-like 2 32 kDa form; Putative phospholipase B-like 2 45 kDa form]	NaN	22.639	NaN	22.036	NaN	22.131	NaN	21.853
HTRA1_HUMAN	Serine protease HTRA1 (EC 3.4.21.-) (High-temperature requirement A serine peptidase 1) (L56) (Serine protease 11)	NaN	22.285	22.545	21.802	23.070	22.927	22.969	22.194
GGH_HUMAN	Gamma-glutamyl hydrolase (EC 3.4.19.9) (Conjugase) (GH) (Gamma-Glu-X carboxypeptidase)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.040
PRG4_HUMAN	Proteoglycan 4 (Lubricin) (Megakaryocyte-stimulating factor) (Superficial zone proteoglycan) [Cleaved into: Proteoglycan 4 C-terminal part]	26.772	27.003	27.841	26.234	27.170	27.671	27.229	27.231
SACA9_HUMAN	Sperm acrosome-associated protein 9	22.229	22.568	23.087	22.139	22.918	22.350	23.636	NaN

GNA1_HUMAN	Glucosamine 6-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine acetylase) (Phosphoglucosamine transacetylase)	23.858	24.590	24.132	24.235	25.040	24.160	24.346	23.500
DYL2_HUMAN	Dynein light chain 2, cytoplasmic (8 kDa dynein light chain b) (DLC8b) (Dynein light chain LC8-type 2)	NaN	22.471	22.661	24.445	22.186	22.767	NaN	23.940
PDLI5_HUMAN	PDZ and LIM domain protein 5 (Enigma homolog) (Enigma-like PDZ and LIM domains protein)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.387
CBPB2_HUMAN	Carboxypeptidase B2 (EC 3.4.17.20) (Carboxypeptidase U) (CPU) (Plasma carboxypeptidase B) (pCPB) (Thrombin-activable fibrinolysis inhibitor) (TAFI)	22.589	NaN	22.200	22.414	22.551	22.709	22.560	22.259
BT3L4_HUMAN	Transcription factor BTF3 homolog 4 (Basic transcription factor 3-like 4)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.183
PGRP2_HUMAN	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) (Peptidoglycan recognition protein 2) (Peptidoglycan recognition protein long) (PGRP-L)	26.095	26.037	26.510	26.230	25.920	26.136	26.161	26.185
YMEL1_HUMAN	ATP-dependent zinc metalloprotease YME1L1 (EC 3.4.24.-) (ATP-dependent metalloprotease FtsH1) (Meg-4) (Presenilin-associated metalloprotease) (PAMP) (YME1-like protein 1)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	22.737
CDC5L_HUMAN	Cell division cycle 5-like protein (Cdc5-like protein) (Pombe cdc5-related protein)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.015
PARK7_HUMAN	Protein/nucleic acid deglycase DJ-1 (EC 3.1.2.-) (EC 3.5.1.-) (EC 3.5.1.124) (Maillard deglycase) (Oncogene DJ1) (Parkinson disease protein 7) (Parkinsonism-associated deglycase) (Protein DJ-1) (DJ-1)	27.487	27.997	27.340	27.681	28.291	27.761	28.231	26.932
NPS3B_HUMAN	Protein NipSnap homolog 3B (NipSnap3B) (SNAP1)	NaN	22.418	NaN	22.931	NaN	22.310	22.446	22.428
TEX12_HUMAN	Testis-expressed protein 12	NaN	NaN	NaN	NaN	NaN	NaN	NaN	23.047
DNAI2_HUMAN	Dynein intermediate chain 2, axonemal (Axonemal dynein intermediate chain 2)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	21.521
SH3L3_HUMAN	SH3 domain-binding glutamic acid-rich-like protein 3 (SH3 domain-binding protein 1) (SH3BP-1)	NaN	25.766	25.013	NaN	NaN	25.023	NaN	25.116
CRAC1_HUMAN	Cartilage acidic protein 1 (68 kDa chondrocyte-expressed protein) (CEP-68) (ASPIC)	26.728	26.984	27.093	26.872	27.750	27.071	27.081	26.855
PRDM5_HUMAN	PR domain zinc finger protein 5 (EC 2.1.1.-) (PR domain-containing protein 5)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	24.152

PDLI7_HUMAN	PDZ and LIM domain protein 7 (LIM mineralization protein) (LMP) (Protein enigma)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.701
C1RL_HUMAN	Complement C1r subcomponent-like protein (C1r-LP) (C1r-like protein) (EC 3.4.21.-) (C1r-like serine protease analog protein) (CLSPa)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.539
VAPA_HUMAN	Vesicle-associated membrane protein-associated protein A (VAMP-A) (VAMP-associated protein A) (VAP-A) (33 kDa VAMP-associated protein) (VAP-33)	24.305	24.625	24.585	24.500	25.428	24.615	24.592	24.297
ENPP5_HUMAN	Ectonucleotide pyrophosphatase/phosphodiesterase family member 5 (E-NPP 5) (NPP-5) (EC 3.1.-.-)	25.406	25.758	25.255	25.215	26.392	25.192	25.646	24.539
ZPI_HUMAN	Protein Z-dependent protease inhibitor (PZ-dependent protease inhibitor) (PZI) (Serpin A10)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	20.370
MARE3_HUMAN	Microtubule-associated protein RP/EB family member 3 (EB1 protein family member 3) (EBF3) (End-binding protein 3) (EB3) (RP3)	NaN	NaN	NaN	NaN	NaN	NaN	21.497	NaN
KAD6_HUMAN	Adenylate kinase isoenzyme 6 (AK6) (EC 2.7.4.3) (Adrenal gland protein AD-004) (Coilin-interacting nuclear ATPase protein) (hCINAP) (Dual activity adenylate kinase/ATPase) (AK/ATPase)	NaN	NaN	NaN	NaN	NaN	NaN	NaN	26.992
CBPQ_HUMAN	Carboxypeptidase Q (EC 3.4.17.-) (Lysosomal dipeptidase) (Plasma glutamate carboxypeptidase)	22.971	23.318	23.151	23.058	23.738	22.943	23.313	22.976

Appendix B

Chapter 3: IL-17RA and macrophage markers are increased in OA patients with synovial inflammation

B1 Negative controls for immunohistochemistry

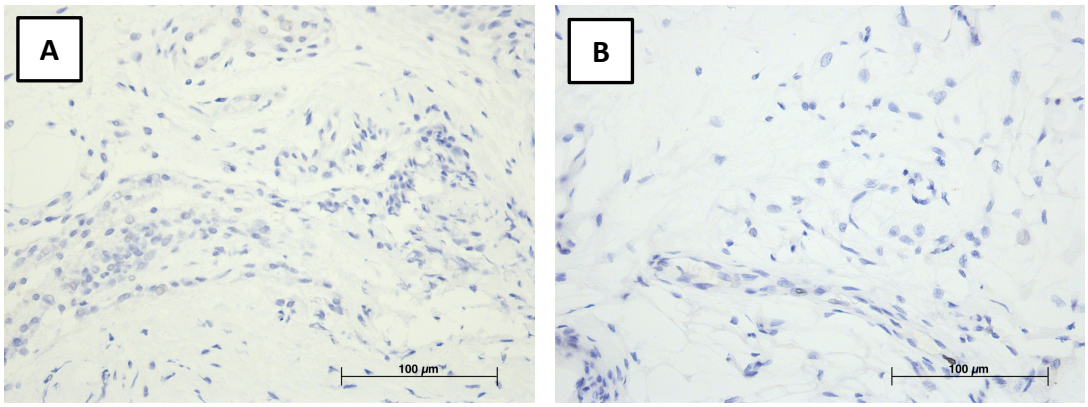

***Figure B1-1**. Immunohistochemistry DAB staining with (A) universal mouse negative control or (B) rabbit negative control. Antibodies were visualised with DAB (brown) and counterstained with haematoxylin (blue). Images were taken at 40x magnification.*

B2 Analysis pipeline for immunohistochemistry images

As described in section 3.5.5, a previously created pipeline was used called “DAB and nuclei measurements”. We have included screenshots of all steps of this pipeline **(Figures B2-1 to S1-12)** with a short description of the steps in each Figure description.

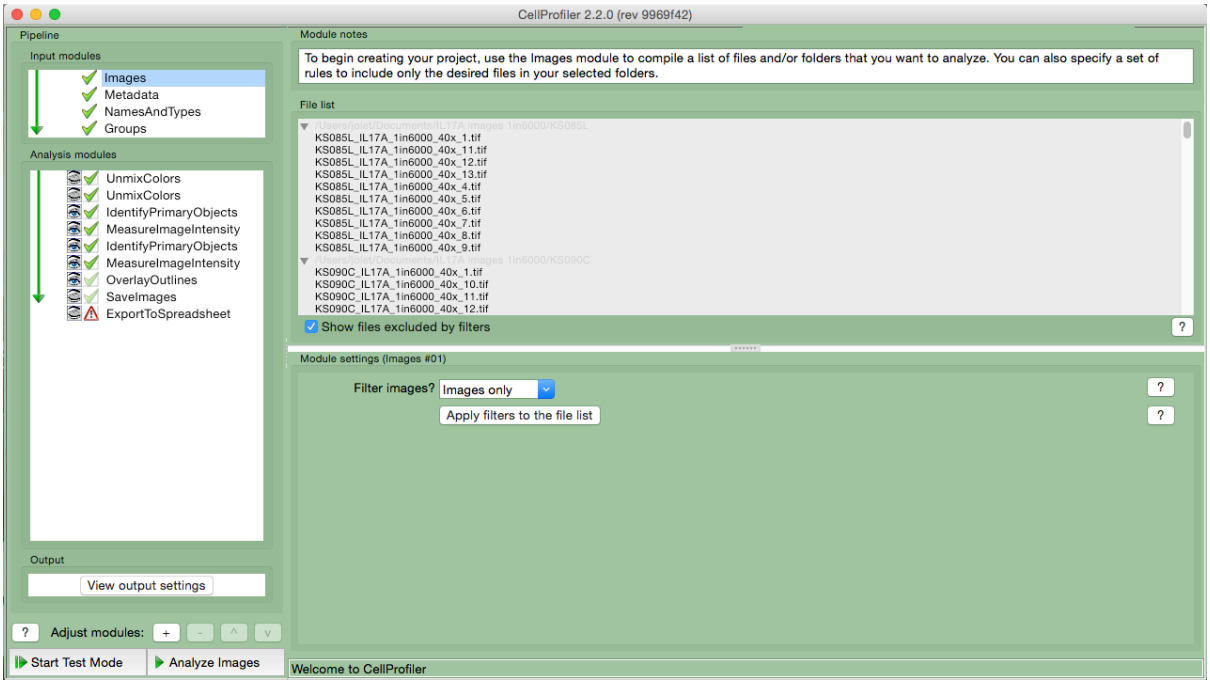

***Figure B2-1**. CellProfiler pipeline “DAB and nuclei measurements”, input step 1. Images to be analysed are added to the File list.*

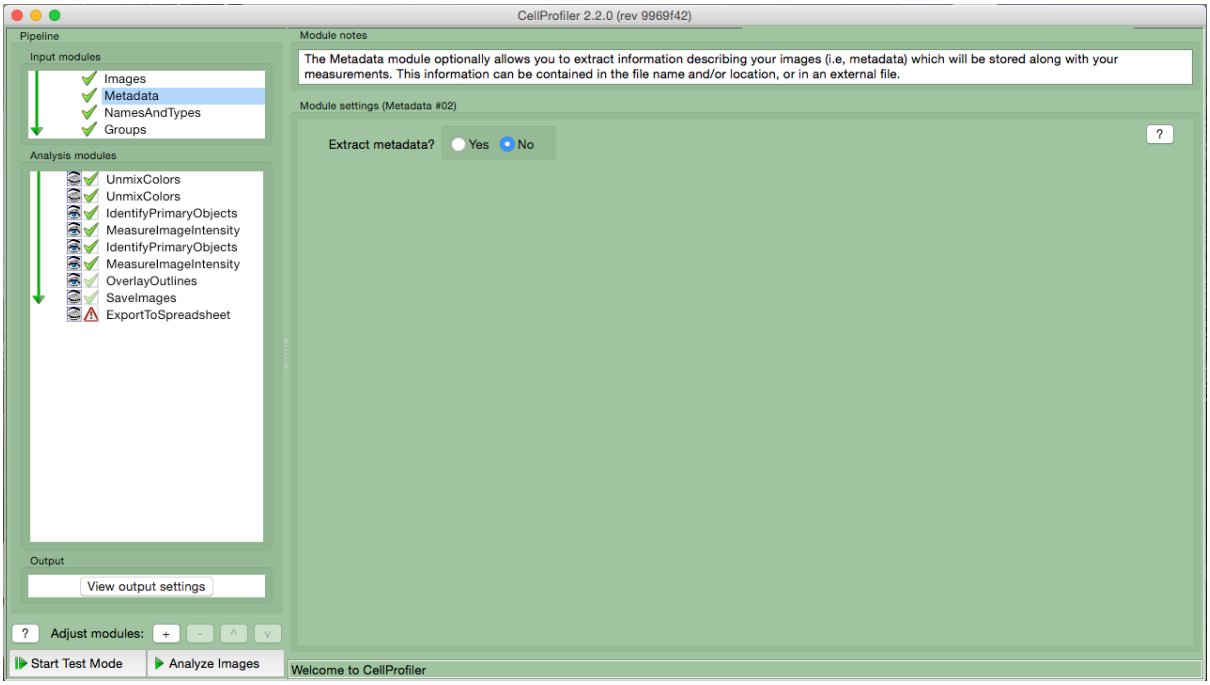

***Figure B2-2**. CellProfiler pipeline “DAB and nuclei measurements”, input step 2. No metadata was extracted from the images.*

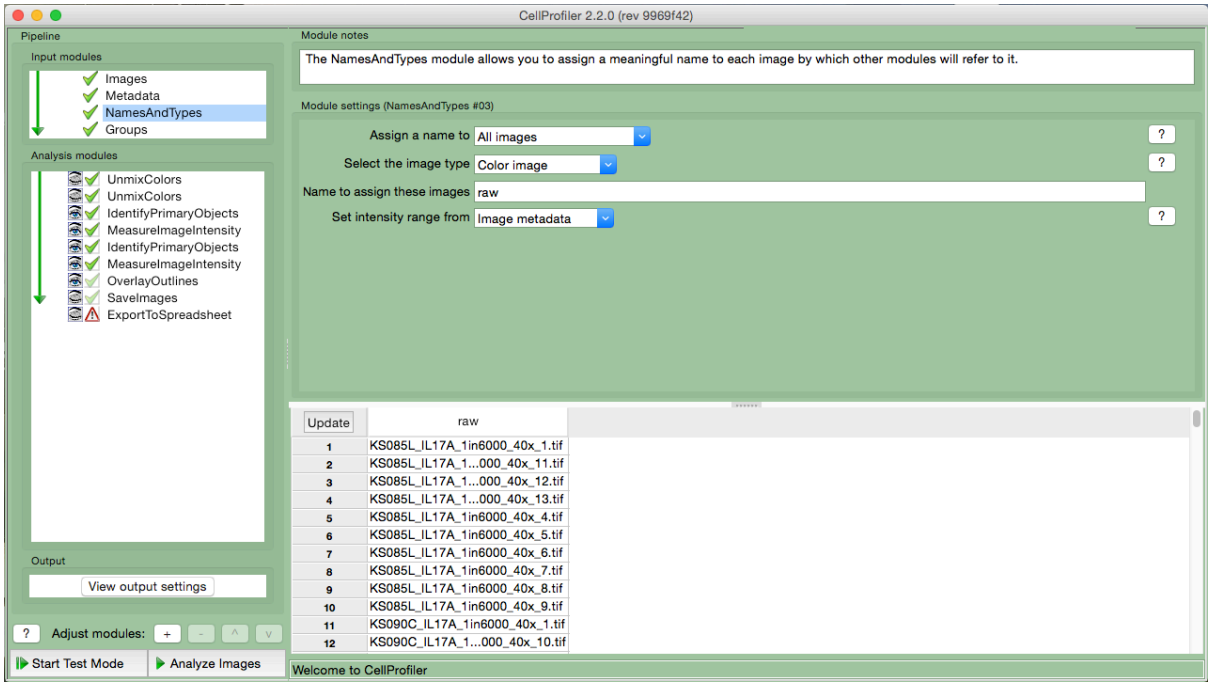

***Figure B2-3**. CellProfiler pipeline "DAB and nuclei measurements", input step 3. All images were names, the full colour images were used, the original images were hereby called "raw" and intensity range was set from image metadata.*

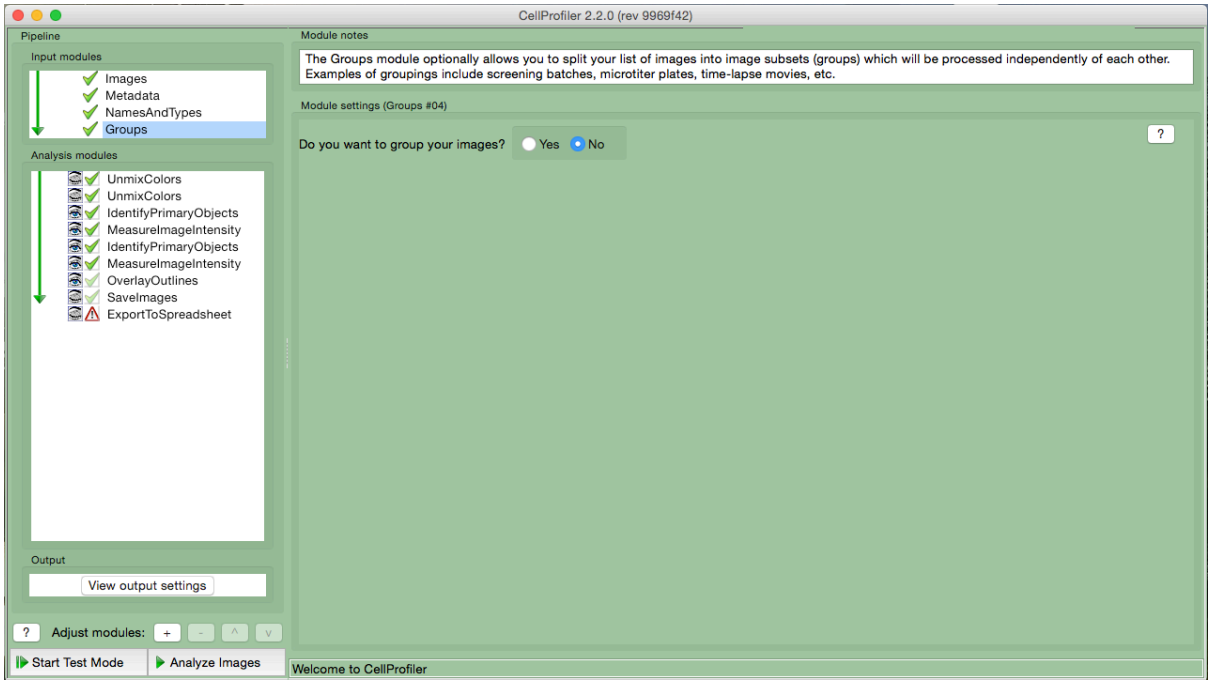

***Figure B2-4**. CellProfiler pipeline "DAB and nuclei measurements", input step 4. Images were not grouped.*

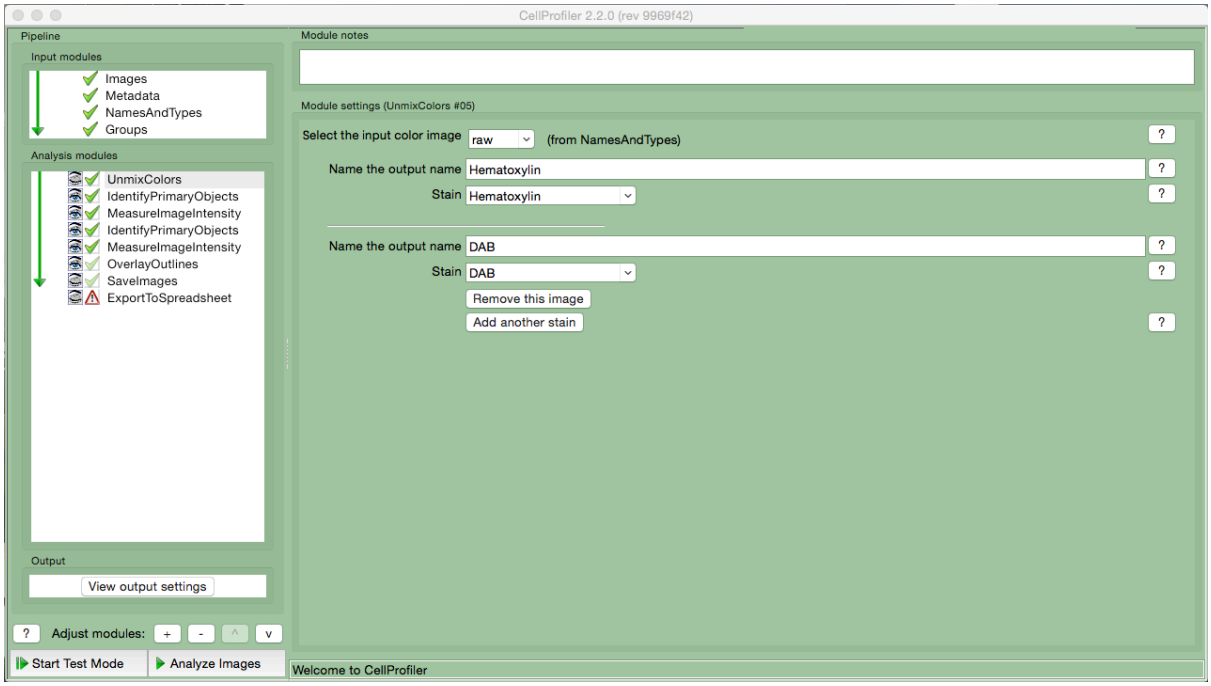

***Figure B2-5**. CellProfiler pipeline "DAB and nuclei measurements", analysis step 1. The colour from the "raw" images was used to unmix two colours: the haematoxylin for the nuclei staining, and the DAB for antibody staining.*

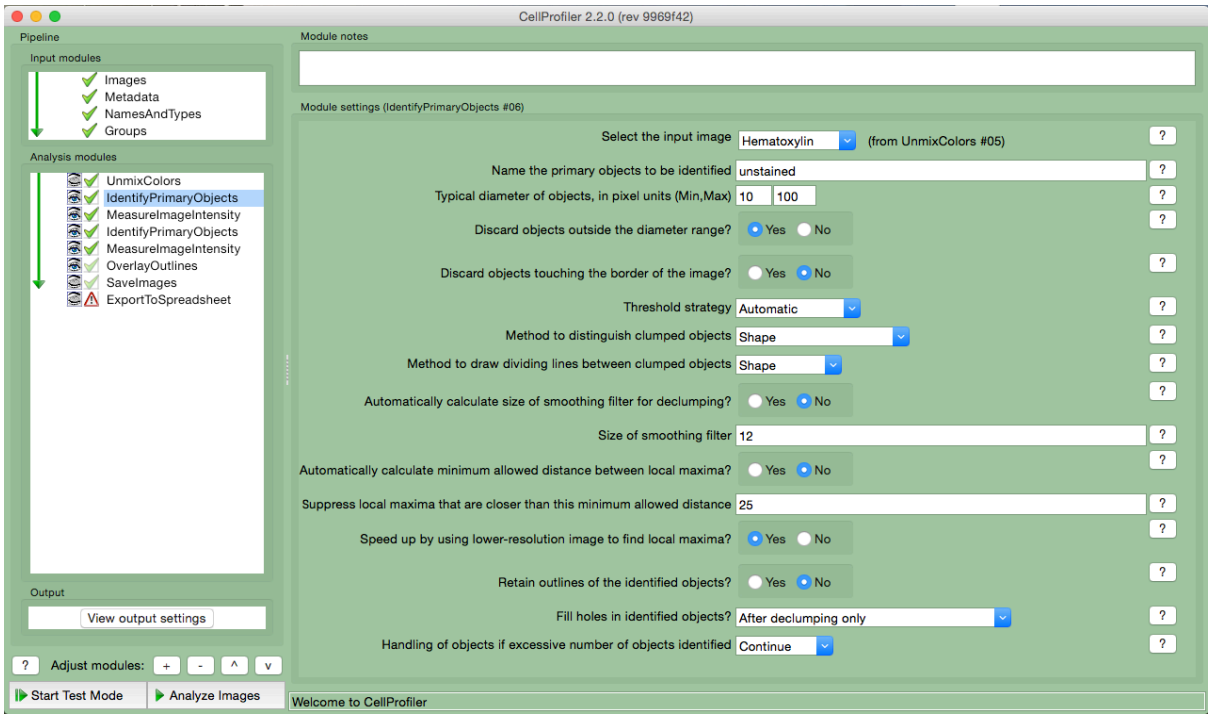

***Figure B2-6**. CellProfiler pipeline "DAB and nuclei measurements", analysis step 2. The image in which the colour haematoxylin was filtered out of the original image was used to identify the nuclei with settings as described.*

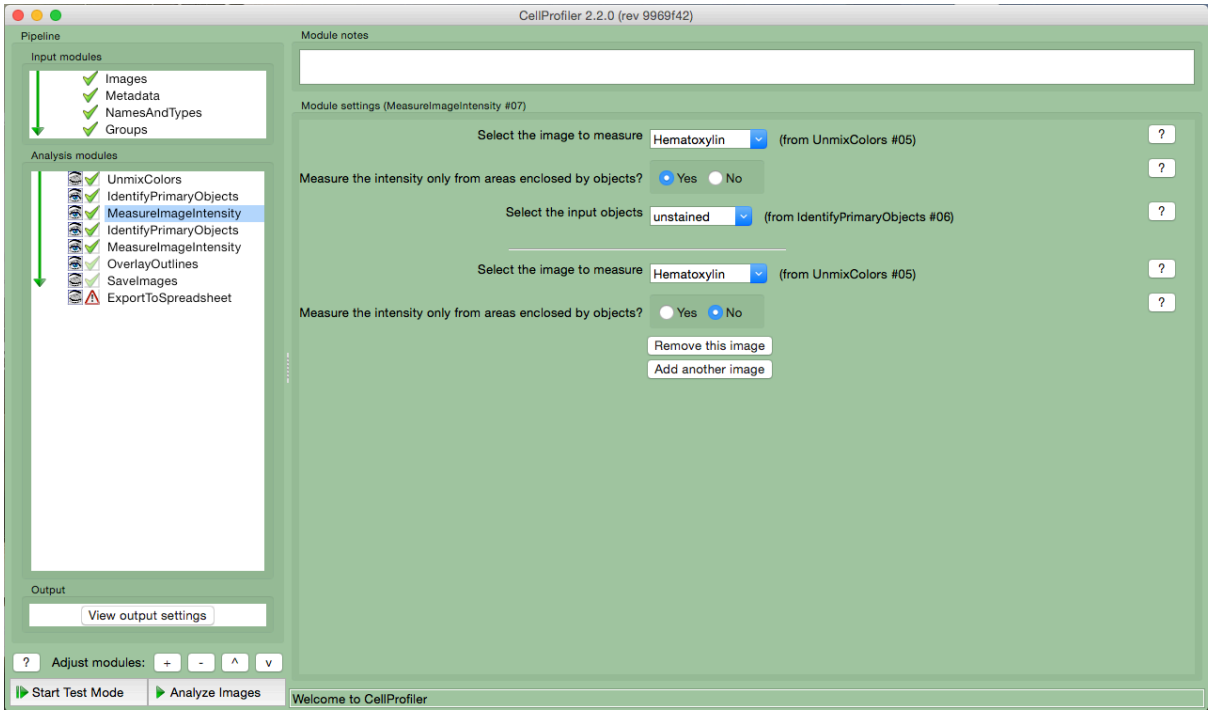

***Figure B2-7**. CellProfiler pipeline "DAB and nuclei measurements", analysis step 3. The image in which the colour haematoxylin was filtered out of the original image was used to measure the intensity of the haematoxylin staining in each image.*

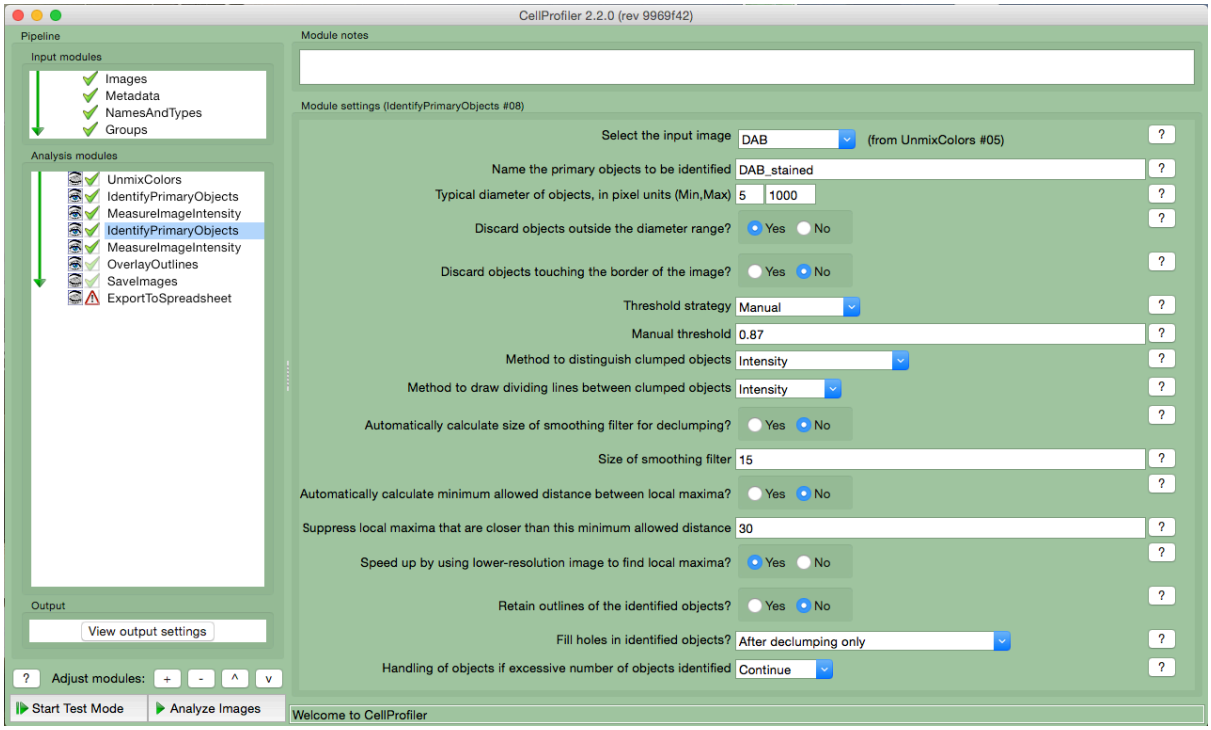

***Figure B2-8**. CellProfiler pipeline "DAB and nuclei measurements", analysis step 4. The image in which the colour DAB was filtered out of the original image was used to identify the DAB staining in the image with setting as described. The manual threshold was tested for each set of DAB staining and changed accordingly.*

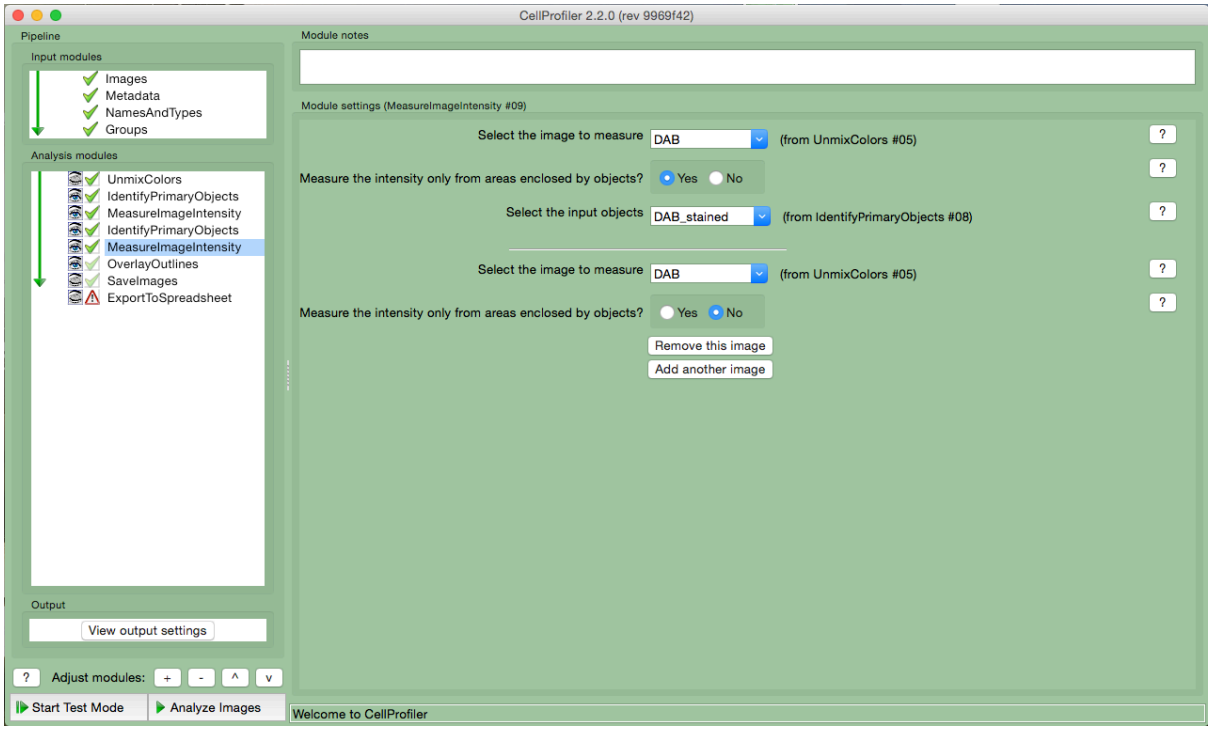

Figure B2-9. *CellProfiler pipeline "DAB and nuclei measurements", analysis step 5. The image in which the colour DAB was filtered out of the original image was used to measure the intensity of the DAB staining in each image.*

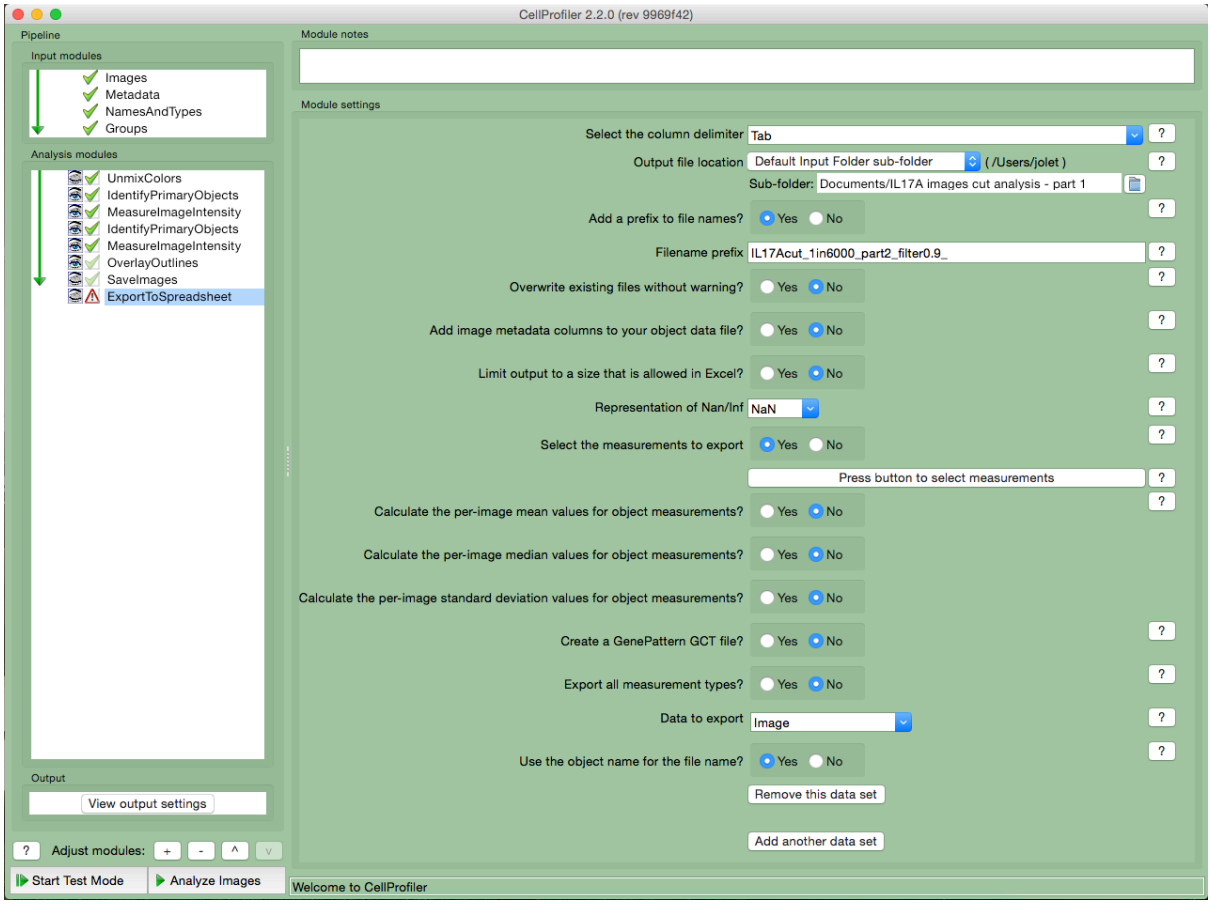

Figure B2-10. *CellProfiler pipeline "DAB and nuclei measurements", analysis step 6. The information gained in each step is automatically exported to an excel sheet with the filename prefix as specified and saved to the sub-folder specified by the user.*

B3 High-resolution confocal images Chapter 3

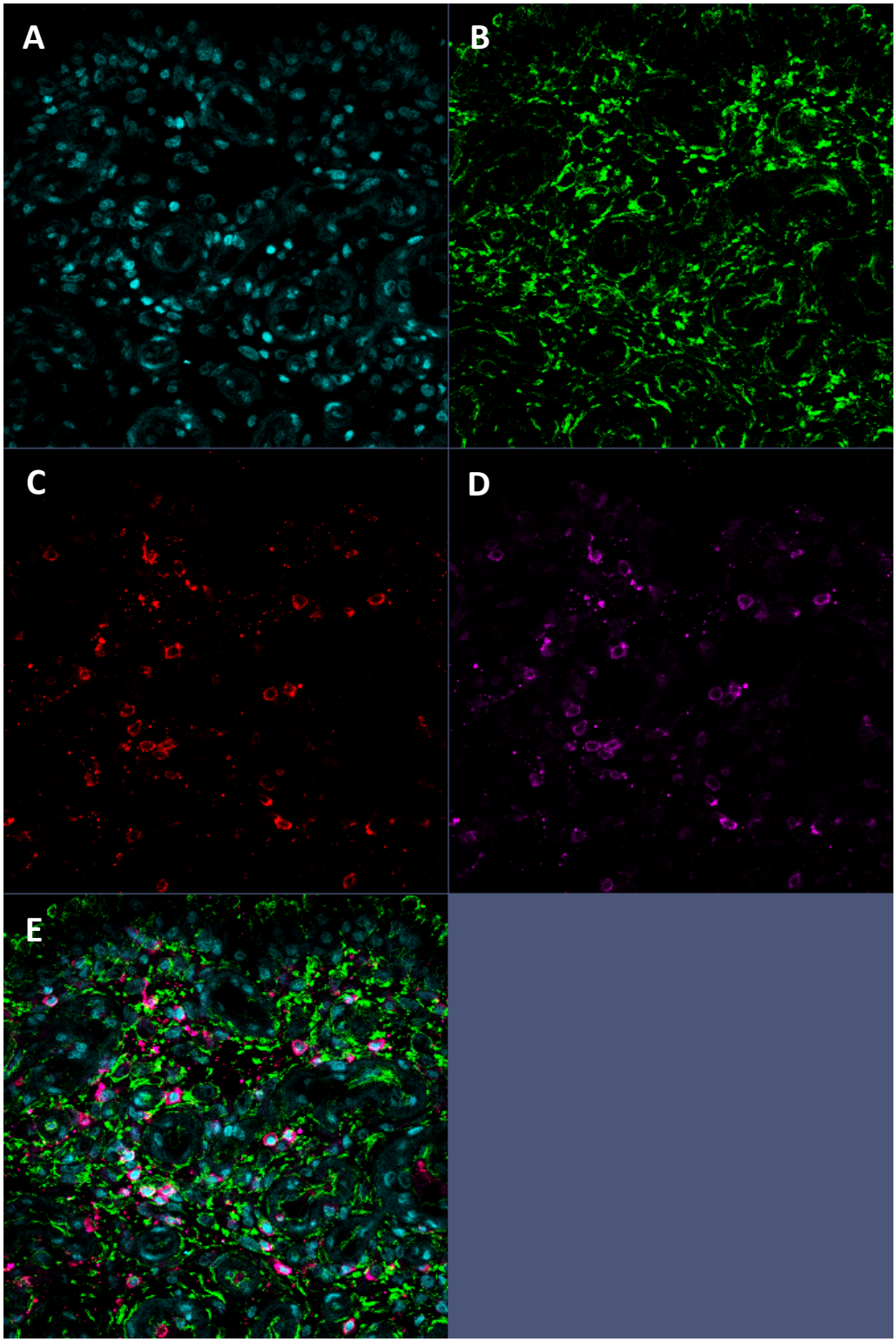

***Figure B3-1**. High-resolution confocal images of Figure 3-8A-E. Expression of cell surface markers CD3 and CD45 and the cytokine IL-17A in two parts of a synovial section of a patient with high risk of developing OA. Confocal images show expression of IL-17A (**green**), CD3 (**red**), and CD45 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

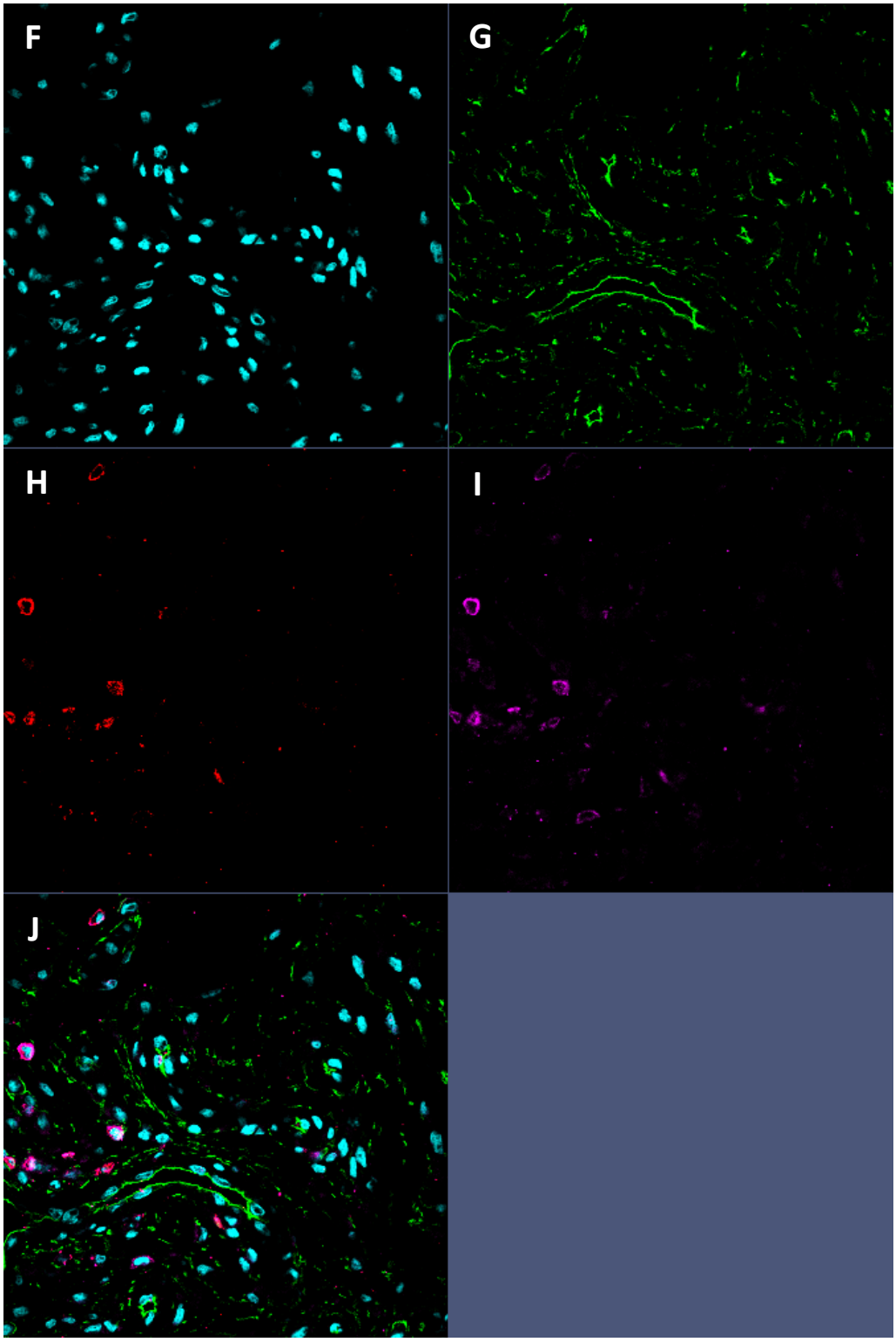

***Figure B3-2**. High-resolution confocal images of Figure 3-8F-J. Expression of cell surface markers CD3 and CD45 and the cytokine IL-17A in two parts of a synovial section of a patient with high risk of developing OA. Confocal images show expression of IL-17A (**green**), CD3 (**red**), and CD45 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

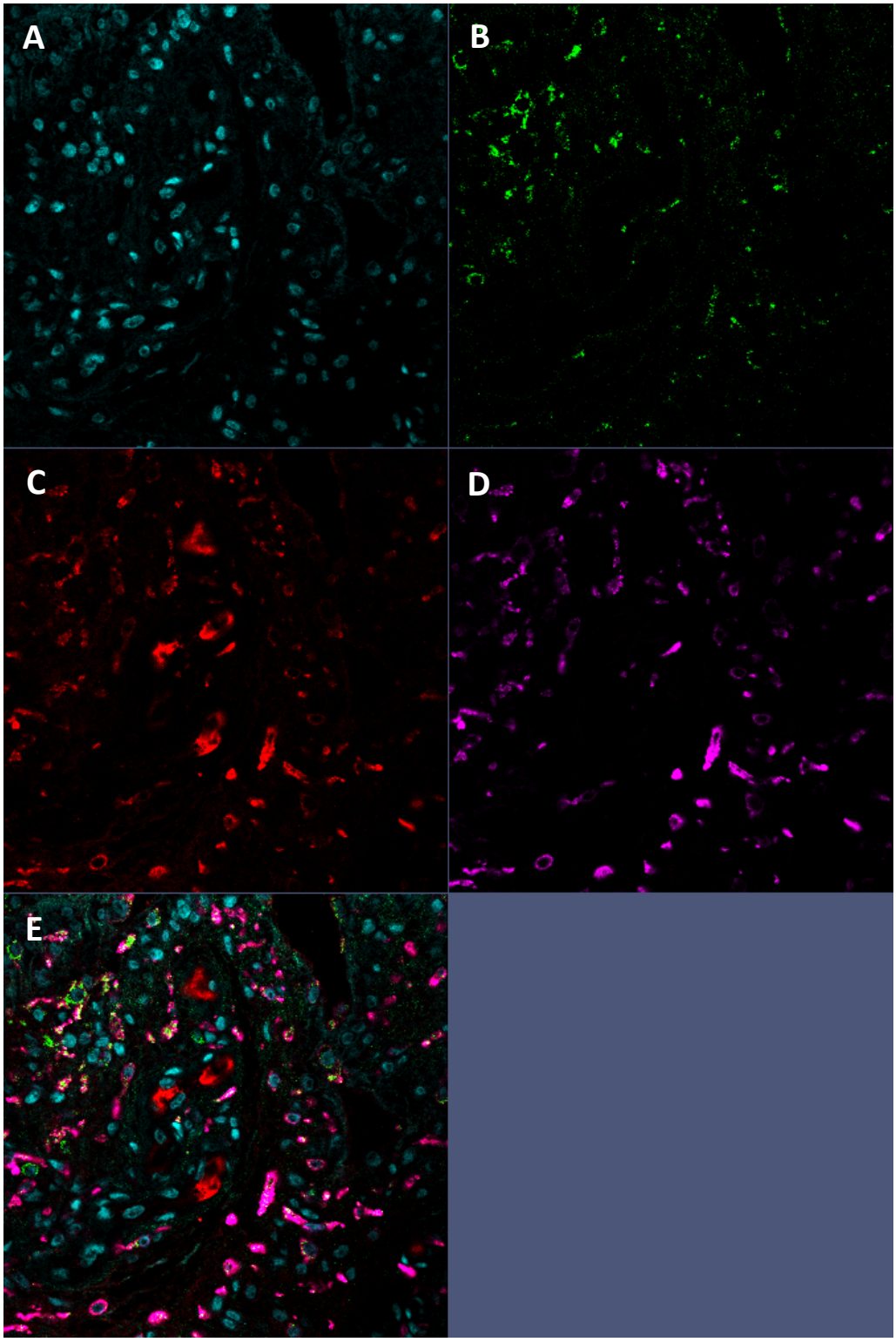

***Figure B3-3**. High-resolution confocal images of Figure 3-16A-E. Expression of macrophage markers and IL-17RA in two parts of a synovial section of a patient with a knee injury who has a high risk of developing post-traumatic OA (synovitis score = 2). Confocal images show expression of CD68 (**green**), IL-17RA (**red**), and CD206 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

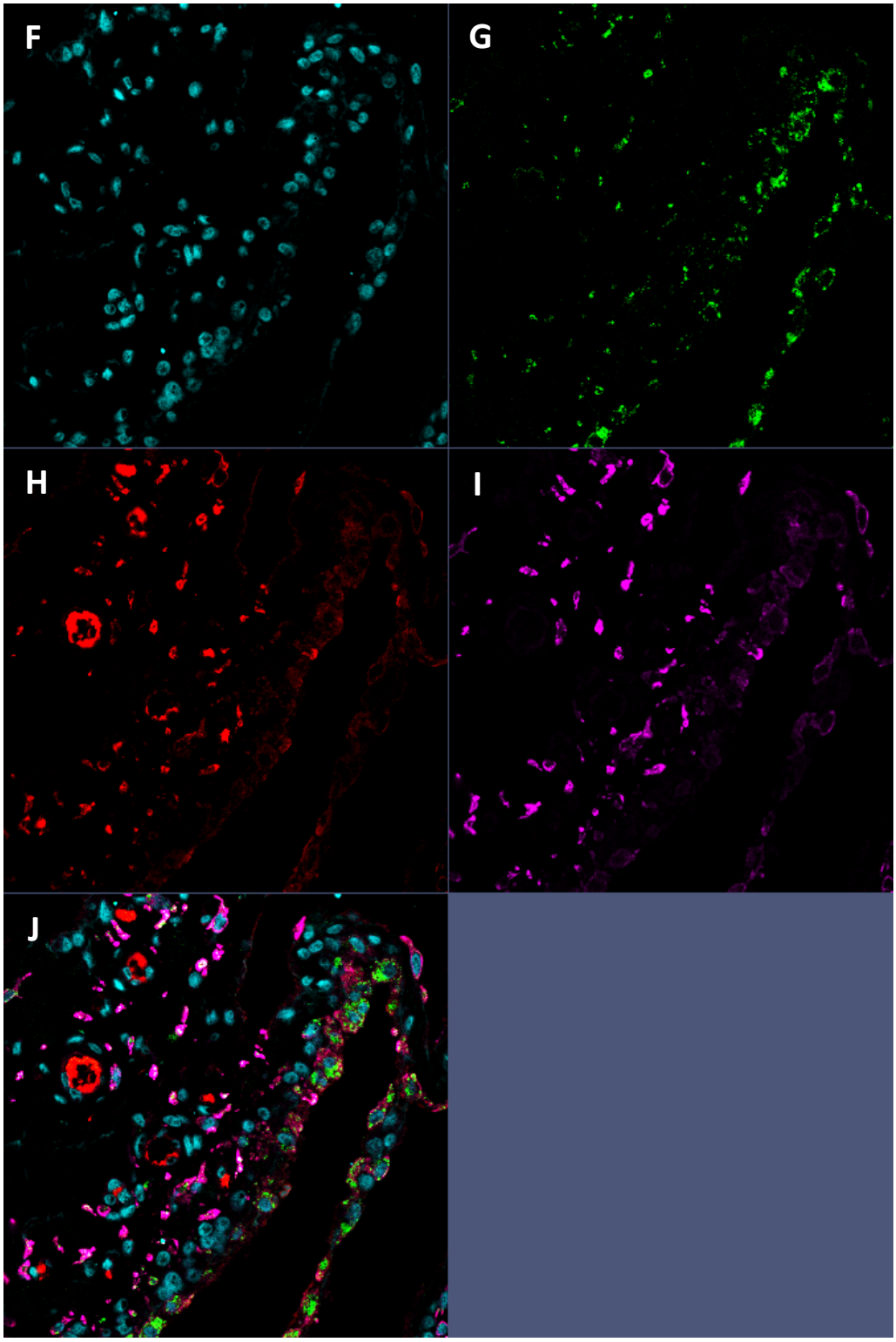

***Figure B3-4**. High-resolution confocal images of Figure 3-16F-J. Expression of macrophage markers and IL-17RA in two parts of a synovial section of a patient with a knee injury who has a high risk of developing post-traumatic OA (synovitis score = 2). Confocal images show expression of CD68 (**green**), IL-17RA (**red**), and CD206 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

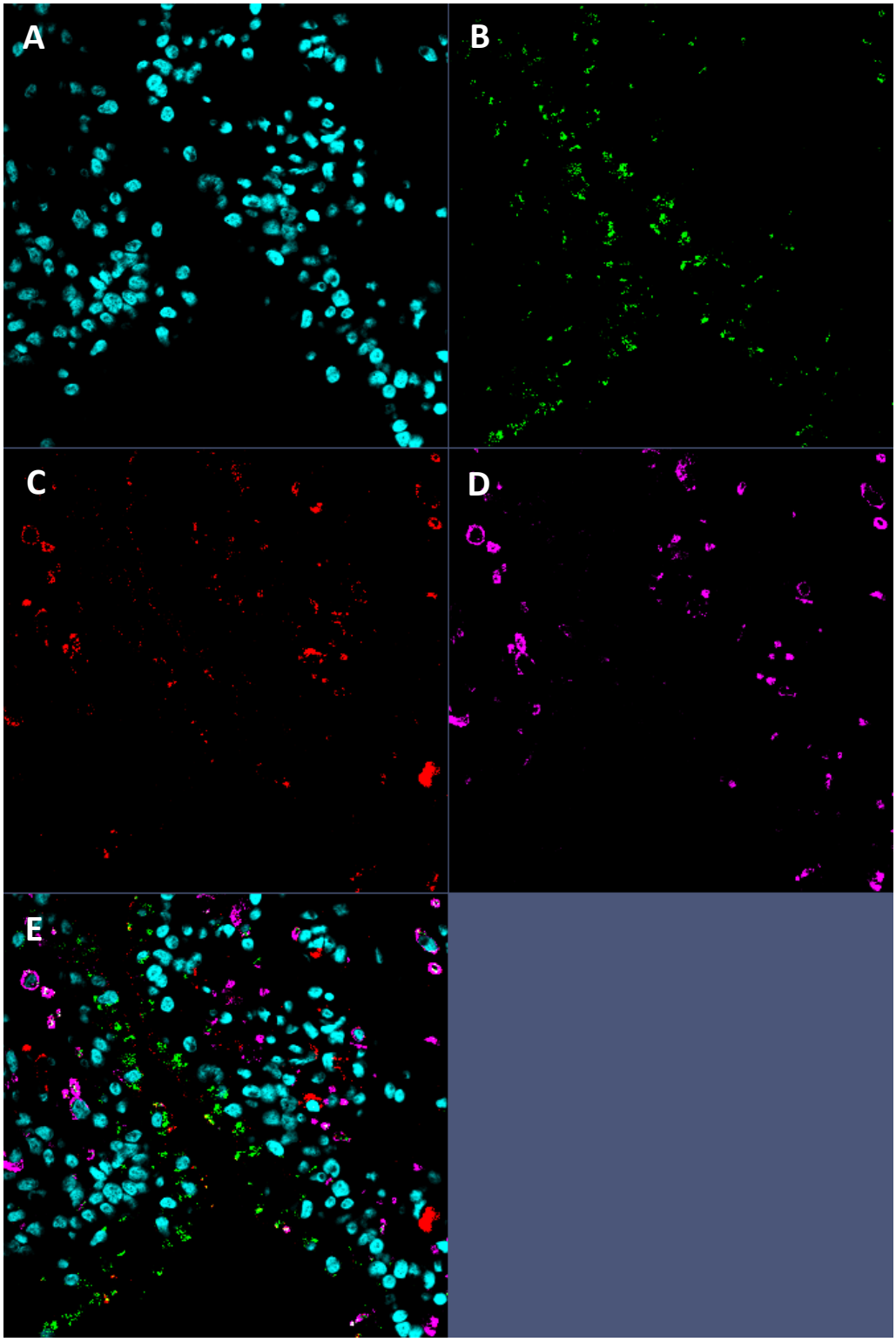

***Figure B3-5**. High-resolution confocal images of Figure 3-17A-E. Expression of macrophage markers and IL-17RC in two parts of a synovial section of a patient with a knee injury who has a high risk of developing post-traumatic OA (synovitis score = 2). Confocal images show expression of CD68 (**green**), IL-17RA (**red**), and CD206 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

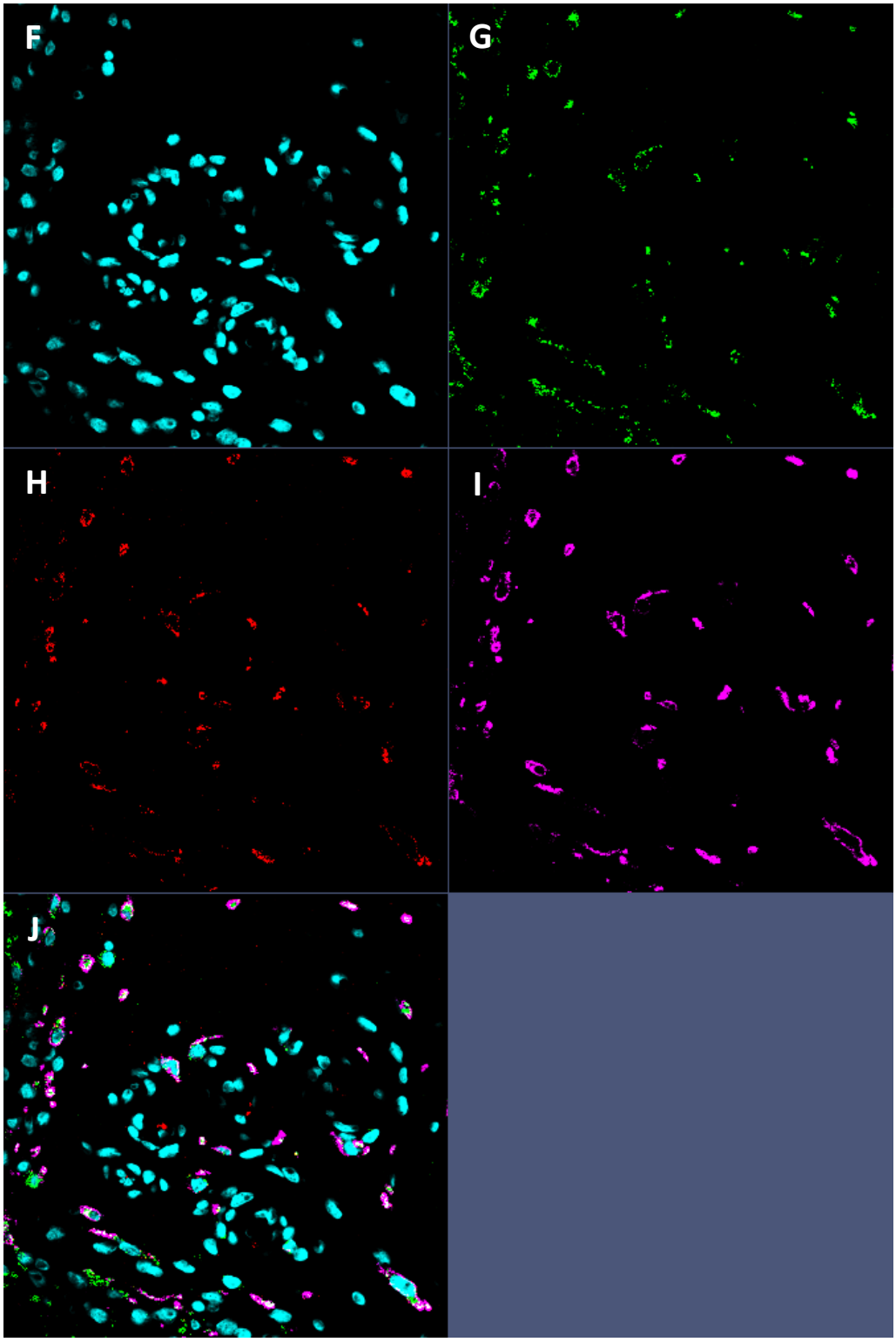

***Figure B3-6**. High-resolution confocal images of Figure 3-17F-J. Expression of macrophage markers and IL-17RC in two parts of a synovial section of a patient with a knee injury who has a high risk of developing post-traumatic OA (synovitis score = 2). Confocal images show expression of CD68 (**green**), IL-17RA (**red**), and CD206 (**purple**), and were counterstained with POPO-1 (**blue**) to visualise nuclei. A merged image is provided to look at the co-expression of markers. Images were taken at 40x magnification with oil.*

Appendix C

Chapter 4: IL-17 treatment increases expression of OA-related inflammatory and matrix genes in end-stage OA chondrocytes and synovial fibroblasts

C1 Overview of RNA-Seq samples

The transcriptome of sets of samples (24 samples of chondrocytes and 24 samples of synovial fibroblasts) were analysed using poly-A tail selected, mRNA sequencing. Samples from each cell type were from 6 different donors and treated for 24 hours with one of the following treatments: control, or IL-17A, IL-17F, or IL-17AF, all at 10 ng/ml. Full overview of the samples can be found in Table C1-1 for chondrocytes and Table C1-2 for synovial fibroblasts.

Table C1-1. *Overview of chondrocytes samples used for RNA Sequencing.*

Sample ID	Species	Project	Nucleic Acid	Sample tag	OMB patient number	Treatment	Day treatment started	Time treatment started	Well number in 12-well plate	Treatment duration
i01_i01_HAC_P33_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i01	P33	Control (C)	02/07/2018	09.38	B2	24h
i02_i02_HAC_P33_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i02	P33	IL-17A (A)	02/07/2018	09.38	B1	24h
i03_i03_HAC_P33_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i03	P33	IL-17F (F)	02/07/2018	09.38	B4	24h
i04_i04_HAC_P33_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i04	P33	IL-17AF (AF)	02/07/2018	09.38	B3	24h
i05_i05_HAC_P332_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i05	P332	Control	02/07/2018	09.44	B2	24h
i06_i06_HAC_P332_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i06	P332	IL-17A	02/07/2018	09.44	B3	24h
i07_i07_HAC_P332_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i07	P332	IL-17F	02/07/2018	09.44	B1	24h
i08_i08_HAC_P332_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i08	P332	IL-17AF	02/07/2018	09.44	B4	24h
i09_i09_HAC_P3_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i09	P3	Control	08/07/2018	09.41	B2	24h
i10_i10_HAC_P3_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i10	P3	IL-17A	08/07/2018	09.41	B1	24h
i11_i11_HAC_P3_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i11	P3	IL-17F	08/07/2018	09.41	B4	24h
i12_i12_HAC_P3_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i12	P3	IL-17AF	08/07/2018	09.41	B3	24h
i13_i13_HAC_P39_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i13	P39	Control	11/06/2018	09.43	B1	24h
i14_i14_HAC_P39_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i14	P39	IL-17A	11/06/2018	09.43	B2	24h
i15_i15_HAC_P39_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i15	P39	IL-17F	11/06/2018	09.43	B3	24h
i16_i16_HAC_P39_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i16	P39	IL-17AF	11/06/2018	09.43	B4	24h
i17_i17_HAC_P226_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i17	P226	Control	20/06/2018	09.44	B4	24h
i18_i18_HAC_P226_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i18	P226	IL-17A	20/06/2018	09.44	B1	24h
i19_i19_HAC_P226_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i19	P226	IL-17F	20/06/2018	09.44	B3	24h
i20_i20_HAC_P226_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i20	P226	IL-17AF	20/06/2018	09.44	B2	24h
i21_i21_HAC_P4_C2	Homo sapiens	Jolet_HAC_pool1	DNA	i21	P4	Control	22/06/2018	09.42	B3	24h
i22_i22_HAC_P4_A2	Homo sapiens	Jolet_HAC_pool1	DNA	i22	P4	IL-17A	22/06/2018	09.42	B4	24h
i23_i23_HAC_P4_F2	Homo sapiens	Jolet_HAC_pool1	DNA	i23	P4	IL-17F	22/06/2018	09.42	B2	24h
i24_i24_HAC_P4_AF2	Homo sapiens	Jolet_HAC_pool1	DNA	i24	P4	IL-17AF	22/06/2018	09.42	B1	24h

Table C1-2. *Overview of synovial fibroblast samples used for RNA Sequencing.*

SampleID	Species	Project	Nucleic Acid	Sample tag	OMB patient number	Treatment	Day treatment started	Time treatment started	Well number in 12-well plate	Treatment duration
i25_SF_P330_C2	Homo sapiens	Jolet_SF_pool2	DNA	i25	P330	Control	08/07/2018	09.53	B2	24h
i26_SF_P330_A2	Homo sapiens	Jolet_SF_pool2	DNA	i26	P330	IL-17A	08/07/2018	09.53	B3	24h
i27_SF_P330_F2	Homo sapiens	Jolet_SF_pool2	DNA	i27	P330	IL-17F	08/07/2018	09.53	B1	24h
i28_SF_P330_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i28	P330	IL-17AF	08/07/2018	09.53	B4	24h
i29_SF_P299_C2	Homo sapiens	Jolet_SF_pool2	DNA	i29	P299	Control	08/07/2018	09.49	B1	24h
i30_SF_P299_A2	Homo sapiens	Jolet_SF_pool2	DNA	i30	P299	IL-17A	08/07/2018	09.49	B3	24h
i31_SF_P299_F2	Homo sapiens	Jolet_SF_pool2	DNA	i31	P299	IL-17F	08/07/2018	09.49	B4	24h
i32_SF_P299_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i32	P299	IL-17AF	08/07/2018	09.49	B2	24h
i33_SF_P368_C2	Homo sapiens	Jolet_SF_pool2	DNA	i33	P368	Control	20/06/2018	09.53	B4	24h
i34_SF_P368_A2	Homo sapiens	Jolet_SF_pool2	DNA	i34	P368	IL-17A	20/06/2018	09.53	B2	24h
i35_SF_P368_F2	Homo sapiens	Jolet_SF_pool2	DNA	i35	P368	IL-17F	20/06/2018	09.53	B3	24h
i36_SF_P368_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i36	P368	IL-17AF	20/06/2018	09.53	B1	24h
i37_SF_P377_C2	Homo sapiens	Jolet_SF_pool2	DNA	i37	P377	Control	15/06/2018	09.49	B1	24h
i38_SF_P377_A2	Homo sapiens	Jolet_SF_pool2	DNA	i38	P377	IL-17A	15/06/2018	09.49	B3	24h
i39_SF_P377_F2	Homo sapiens	Jolet_SF_pool2	DNA	i39	P377	IL-17F	15/06/2018	09.49	B2	24h
i40_SF_P377_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i40	P377	IL-17AF	15/06/2018	09.49	B4	24h
i41_SF_P317_C2	Homo sapiens	Jolet_SF_pool2	DNA	i41	P317	Control	15/06/2018	09.53	B3	24h
i42_SF_P317_A2	Homo sapiens	Jolet_SF_pool2	DNA	i42	P317	IL-17A	15/06/2018	09.53	B4	24h
i43_SF_P317_F2	Homo sapiens	Jolet_SF_pool2	DNA	i43	P317	IL-17F	15/06/2018	09.53	B2	24h
i44_SF_P317_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i44	P317	IL-17AF	15/06/2018	09.53	B1	24h
i45_SF_P310_C2	Homo sapiens	Jolet_SF_pool2	DNA	i45	P310	Control	18/06/2018	09.49	B2	24h
i46_SF_P310_A2	Homo sapiens	Jolet_SF_pool2	DNA	i46	P310	IL-17A	18/06/2018	09.49	B1	24h
i47_SF_P310_F2	Homo sapiens	Jolet_SF_pool2	DNA	i47	P310	IL-17F	18/06/2018	09.49	B4	24h
i48_SF_P310_AF2	Homo sapiens	Jolet_SF_pool2	DNA	i48	P310	IL-17AF	18/06/2018	09.49	B3	24h

C2 Mapping and FastQC for RNA-Seq samples

C2.1 Bowtie 2 for alignment

Bowtie2 is an ultrafast and memory-efficient tool for aligning sequencing reads to long refence sequences. The bowtie2 plots show the number of reads aligning to the reference in different ways (Figure C2-1 and C2-2) and tables give an overview of the percentage of reads that aligned to the reference sequence (Table C2-1 and C2-2).

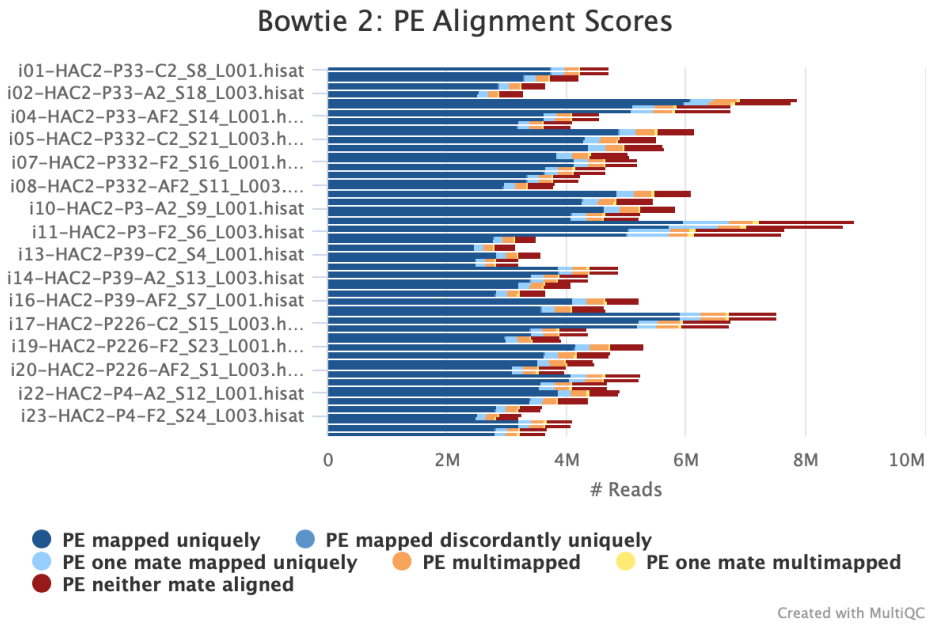

Figure C2-1. *Bowtie2 plot with paired-end (PE) alignment scores for chondrocytes (HAC) samples.*

Table C2-1. *Percentage alignment of each chondrocyte sample with reference sequences.*

Sample Name	% Aligned
i01-HAC2-P33-C2_S8_L001.hisat	89.30%
i02-HAC2-P33-A2_S18_L001.hisat	88.75%
i03-HAC2-P33-F2_S2_L001.hisat	87.35%
i04-HAC2-P33-AF2_S14_L001.hisat	89.35%
i05-HAC2-P332-C2_S21_L001.hisat	89.45%
i06-HAC2-P332-A2_S20_L001.hisat	87.98%
i07-HAC2-P332-F2_S16_L001.hisat	89.53%
i08-HAC2-P332-AF2_S11_L001.hisat	89.10%
i09-HAC2-P3-C2_S17_L001.hisat	89.25%
i10-HAC2-P3-A2_S9_L001.hisat	89.40%
i11-HAC2-P3-F2_S6_L001.hisat	81.25%
i12-HAC2-P3-AF2_S5_L001.hisat	89.45%
i13-HAC2-P39-C2_S4_L001.hisat	89.08%
i14-HAC2-P39-A2_S13_L001.hisat	89.33%
i15-HAC2-P39-F2_S3_L001.hisat	88.73%
i16-HAC2-P39-AF2_S7_L001.hisat	88.95%
i17-HAC2-P226-C2_S15_L001.hisat	88.85%
i18-HAC2-P226-A2_S10_L001.hisat	88.63%
i19-HAC2-P226-F2_S23_L001.hisat	89.08%
i20-HAC2-P226-AF2_S1_L001.hisat	89.43%
i21-HAC2-P4-C2_S22_L001.hisat	88.18%
i22-HAC2-P4-A2_S12_L001.hisat	89.13%
i23-HAC2-P4-F2_S24_L001.hisat	89.30%
i24-HAC2-P4-AF2_S19_L001.hisat	88.75%

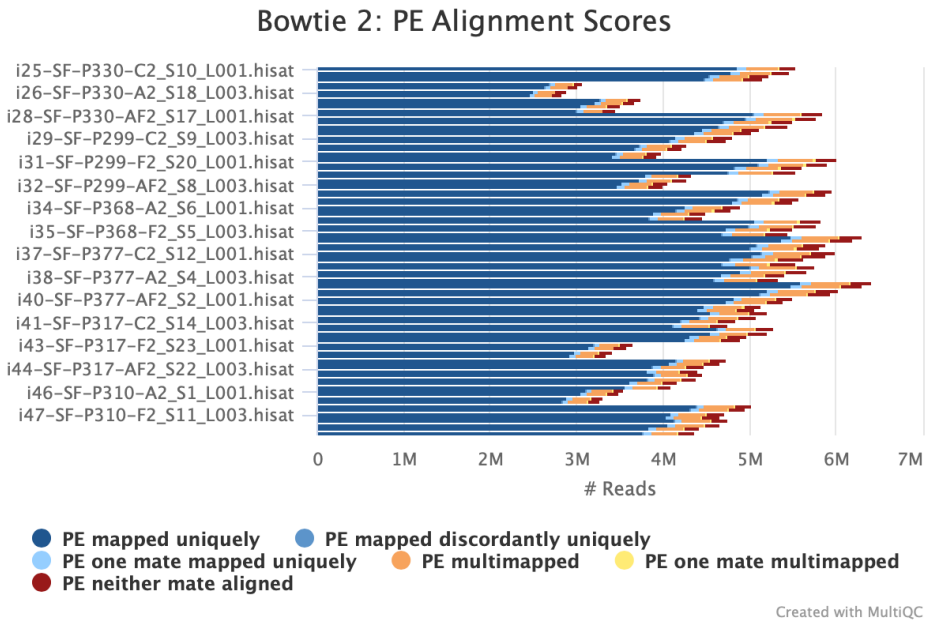

Figure C2-2. *Bowtie2 plot with paired-end (PE) alignment scores for synovial fibroblast (SF) samples.*

Table C2-2. *Percentage of each synovial fibroblast sample that aligned with reference sequences.*

Sample name	% Aligned
i25-SF-P330-C2_S10_L001.hisat	96.18%
i26-SF-P330-A2_S18_L001.hisat	96.23%
i27-SF-P330-F2_S24_L001.hisat	96.03%
i28-SF-P330-AF2_S17_L001.hisat	95.68%
i29-SF-P299-C2_S9_L001.hisat	95.83%
i30-SF-P299-A2_S16_L001.hisat	96.08%
i31-SF-P299-F2_S20_L001.hisat	95.78%
i32-SF-P299-AF2_S8_L001.hisat	96.18%
i33-SF-P368-C2_S15_L001.hisat	96.35%
i34-SF-P368-A2_S6_L001.hisat	95.85%
i35-SF-P368-F2_S5_L001.hisat	95.48%
i36-SF-P368-AF2_S7_L001.hisat	95.78%
i37-SF-P377-C2_S12_L001.hisat	95.03%
i38-SF-P377-A2_S4_L001.hisat	96.05%
i39-SF-P377-F2_S3_L001.hisat	95.98%
i40-SF-P377-AF2_S2_L001.hisat	96.43%
i41-SF-P317-C2_S14_L001.hisat	95.88%
i42-SF-P317-A2_S19_L001.hisat	95.93%
i43-SF-P317-F2_S23_L001.hisat	96.05%
i44-SF-P317-AF2_S22_L001.hisat	95.85%
i45-SF-P310-C2_S21_L001.hisat	96.28%
i46-SF-P310-A2_S1_L001.hisat	96.23%
i47-SF-P310-F2_S11_L001.hisat	96.08%
i48-SF-P310-AF2_S13_L001.hisat	96.15%

C2.2 FastQ screen

FastQ Screen is a tool that allows a researcher to screen a library of sequences in FastQ format against a set of sequence databases to see if the composition of the library matches with the expectations. The FastQ screen for all chondrocyte samples (Figure C2-3) was done on the collected samples, while the FastQ screen for the synovial fibroblast samples (Figure C2-4) were done on the sequences from each lane and each row (from the sequencing run) for each sample.

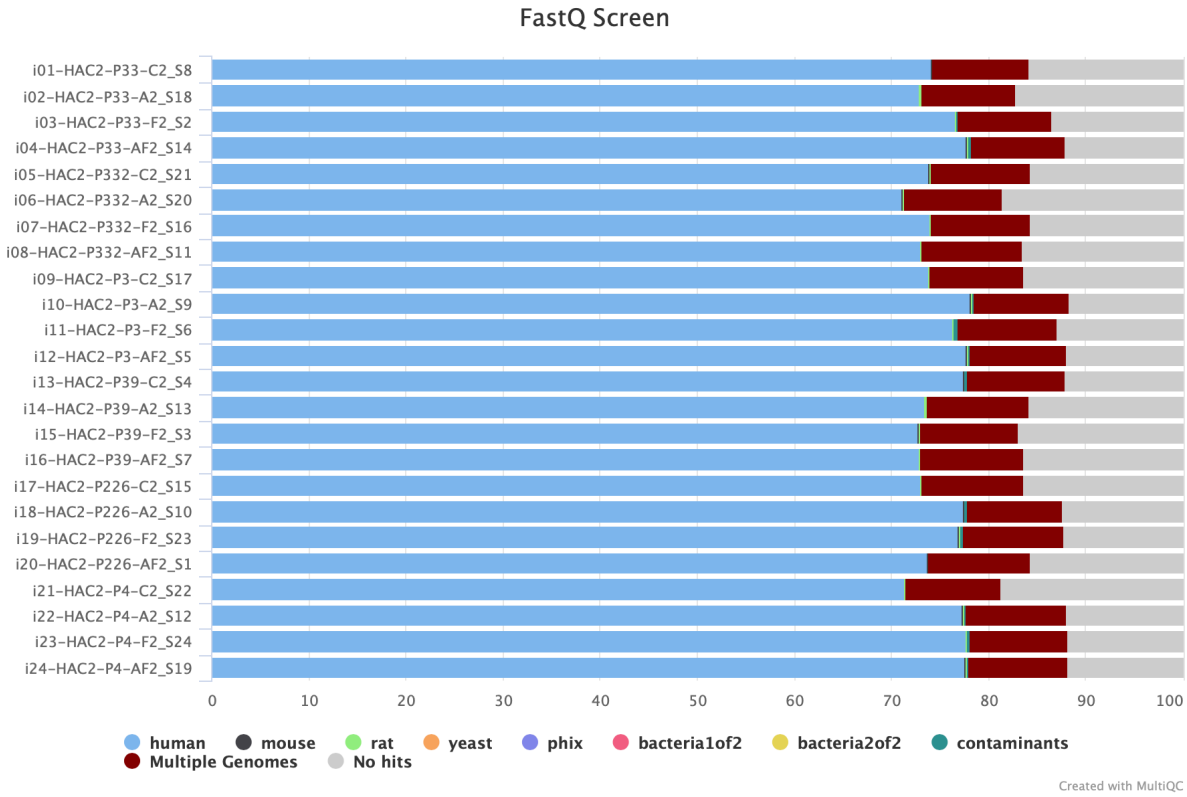

Figure C2-3. *Results of the FastQ screen for each chondrocyte sample including the genomes that the aligned sequence match with, showing that most sequences align with the human genome.*

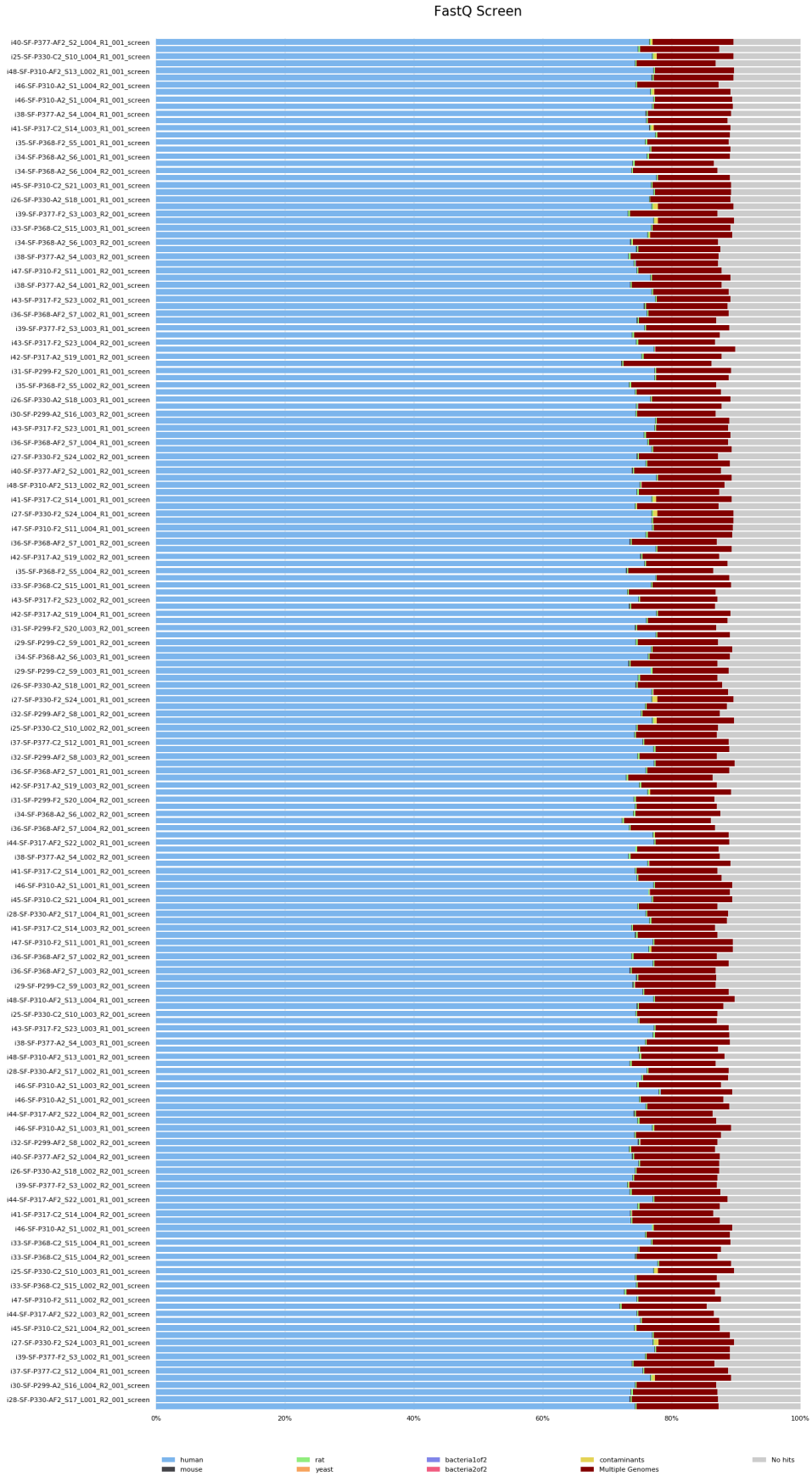

Figure C2-4. *Results of the FastQ screen for each chondrocyte sample including the genomes that the aligned sequence match with, showing that most sequences align with the human genome.*

C3 Differentially expressed genes due to IL-17A/F treatment

IL-17A/F treatment lead to significant (adjusted p-value (padj) < 0.05) changes in ±5400 genes in chondrocytes and ±3000 genes in synovial fibroblasts. When narrowing down the list by only looking at genes that were changes at least +1 or -1 log2 fold change (LFC), this significantly narrowed down the number of genes changed. A full overview of differentially expressed genes between control and IL-17A/F-treated samples for chondrocytes can be found in Table C3-1, and for synovial fibroblasts in Table C3-2 with red boxes indicating a change of <-1 LFC and green boxes indicating changes >1 LFC.

C3.1 Differentially expressed genes in end-stage OA chondrocytes

Table C3-1. *Overview of differentially expressed genes in chondrocytes between control or IL-17 treated samples with an adjusted p-value of <0.05. Green boxes note logarithmic fold changes (LFC) of at least +1 and red boxes note LFC of at least -1, while blank boxes show an LFC -1 and 1. Genes are sorted alphabetically on SYMBOL gene name.*

Ensemble gene name	SYMBOL gene name	Adjusted p-value	Log2 Fold Change (LFC)		
			IL-17A	IL-17F	IL-17AF
ENSG00000183044	*ABAT*	3.74E-11	-1.073	-0.357	-0.744
ENSG00000165029	*ABCA1*	2.28E-17	1.199	0.187	0.450
ENSG00000167972	*ABCA3*	4.89E-10	-1.475	-0.491	-0.923
ENSG00000005471	*ABCB4*	7.13E-09	-1.011	-0.364	-0.989
ENSG00000069431	*ABCC9*	7.20E-05	1.850	0.005	0.053
ENSG00000143994	*ABHD1*	5.23E-03	-1.571	-0.026	-0.177
ENSG00000011198	*ABHD5*	3.70E-11	1.051	0.039	0.405
ENSG00000097007	*ABL1*	1.35E-52	1.128	0.285	0.589
ENSG00000240303	*ACAD11*	3.42E-18	-1.009	-0.309	-0.566
ENSG00000115361	*ACADL*	1.18E-03	-1.519	-0.026	-0.234
ENSG00000144476	*ACKR3*	5.73E-31	2.033	0.645	1.110
ENSG00000129048	*ACKR4*	9.29E-10	-2.812	-0.022	-1.313
ENSG00000122729	*ACO1*	7.38E-16	1.051	0.201	0.425
ENSG00000068366	*ACSL4*	7.02E-18	1.712	0.049	0.521
ENSG00000107796	*ACTA2*	4.53E-08	-1.184	-0.328	-0.727
ENSG00000159251	*ACTC1*	1.80E-17	-2.156	-0.923	-1.205
ENSG00000148848	*ADAM12*	5.00E-18	1.387	0.269	0.642
ENSG00000042980	*ADAM28*	1.27E-14	3.424	0.026	2.038
ENSG00000138316	*ADAMTS14*	2.34E-17	-2.734	-0.926	-1.281
ENSG00000166106	*ADAMTS15*	8.81E-09	-1.549	-0.684	-1.166

ENSG00000049192	*ADAMTS6*	4.16E-04	1.158	0.015	0.109
ENSG00000163638	*ADAMTS9*	2.97E-05	1.616	0.013	0.347
ENSG00000173567	*ADGRF3*	1.50E-02	-1.032	-0.027	-0.256
ENSG00000198099	*ADH4*	1.85E-02	1.357	0.018	0.207
ENSG00000196344	*ADH7*	8.39E-04	-1.117	-0.019	-0.178
ENSG00000128271	*ADORA2A*	5.07E-03	1.074	0.001	0.096
ENSG00000150594	*ADRA2A*	1.96E-09	-2.284	-0.040	-1.134
ENSG00000111863	*ADTRP*	1.73E-06	1.270	0.052	0.545
ENSG00000144218	*AFF3*	8.87E-08	-2.297	-0.025	-0.980
ENSG00000187546	*AGMO*	1.97E-02	-1.307	-0.022	-0.183
ENSG00000026652	*AGPAT4*	1.57E-10	1.227	0.047	0.421
ENSG00000162433	*AK4*	5.46E-09	1.092	0.102	0.484
ENSG00000154027	*AK5*	2.21E-12	-2.558	-0.040	-1.029
ENSG00000131016	*AKAP12*	1.66E-14	-1.242	-0.704	-1.268
ENSG00000151320	*AKAP6*	4.58E-09	-1.153	-0.478	-1.004
ENSG00000227471	*AKR1B15*	2.50E-03	1.352	0.027	0.852
ENSG00000187134	*AKR1C1*	3.14E-07	1.965	0.750	1.276
ENSG00000151632	*AKR1C2*	2.03E-07	1.269	0.644	1.006
ENSG00000144908	*ALDH1L1*	4.75E-02	-1.196	-0.019	-0.063
ENSG00000112294	*ALDH5A1*	6.15E-08	-1.341	-0.070	-0.821
ENSG00000133805	*AMPD3*	4.23E-12	1.453	0.045	0.424
ENSG00000091879	*ANGPT2*	3.13E-10	-1.587	-0.040	-0.828
ENSG00000136859	*ANGPTL2*	7.50E-14	1.008	0.308	0.677
ENSG00000167772	*ANGPTL4*	3.14E-09	1.289	0.360	0.858
ENSG00000165887	*ANKRD2*	1.50E-02	-1.636	-0.019	-0.122
ENSG00000089847	*ANKRD24*	1.18E-03	-1.049	-0.035	-0.838
ENSG00000138772	*ANXA3*	5.96E-03	-1.096	0.001	-0.096
ENSG00000138356	*AOX1*	2.39E-09	1.343	0.033	0.397
ENSG00000154856	*APCDD1*	3.94E-09	1.367	0.395	0.864
ENSG00000171388	*APLN*	3.82E-06	2.090	0.003	0.113
ENSG00000084674	*APOB*	2.51E-02	-1.071	-0.015	-0.210
ENSG00000128284	*APOL3*	4.77E-13	1.100	0.283	0.565
ENSG00000136044	*APPL2*	3.06E-23	-1.084	-0.345	-0.595
ENSG00000165272	*AQP3*	1.33E-14	-1.623	-0.083	-0.400
ENSG00000165269	*AQP7*	2.07E-10	-2.289	-0.602	-1.063
ENSG00000103569	*AQP9*	1.60E-02	3.101	0.005	0.045
ENSG00000169083	*AR*	1.38E-12	-1.150	-0.415	-0.719
ENSG00000146376	*ARHGAP18*	2.83E-05	-1.089	-0.038	-0.614
ENSG00000137727	*ARHGAP20*	1.77E-08	-1.442	-0.053	-0.853
ENSG00000111348	*ARHGDIB*	7.34E-06	-1.345	-0.482	-0.334
ENSG00000183111	*ARHGEF37*	1.34E-07	-1.136	-0.283	-0.733
ENSG00000116017	*ARID3A*	1.49E-19	1.072	0.129	0.485

ENSG00000169126	*ARMC4*	2.72E-03	-1.309	-0.027	-0.391
ENSG00000113369	*ARRDC3*	4.44E-16	1.691	0.060	0.606
ENSG00000099889	*ARVCF*	4.56E-11	-1.192	-0.077	-0.524
ENSG00000110881	*ASIC1*	1.21E-06	-1.006	-0.072	-0.563
ENSG00000108381	*ASPA*	7.01E-03	-1.037	-0.027	-0.359
ENSG00000106819	*ASPN*	1.12E-15	-1.910	-0.606	-1.141
ENSG00000130707	*ASS1*	1.20E-23	1.190	0.346	0.735
ENSG00000148219	*ASTN2*	8.34E-04	-1.119	-0.028	-0.440
ENSG00000162772	*ATF3*	1.50E-08	1.265	0.101	1.044
ENSG00000018625	*ATP1A2*	2.36E-08	-2.275	-0.755	-1.289
ENSG00000070961	*ATP2B1*	7.01E-08	1.003	0.076	0.355
ENSG00000132932	*ATP8A2*	1.27E-02	-0.792	-0.019	-1.255
ENSG00000104043	*ATP8B4*	9.96E-05	1.323	0.023	0.374
ENSG00000107518	*ATRNL1*	9.38E-08	-1.002	-0.285	-0.624
ENSG00000119986	*AVPI1*	9.65E-19	1.141	0.359	0.722
ENSG00000162630	*B3GALT2*	2.98E-10	-3.217	-0.011	-0.179
ENSG00000086062	*B4GALT1*	1.19E-15	1.001	0.105	0.436
ENSG00000164929	*BAALC*	4.05E-04	-1.115	-0.011	-0.211
ENSG00000095739	*BAMBI*	6.21E-10	-1.034	-0.039	-0.270
ENSG00000176788	*BASP1*	1.07E-13	1.150	0.431	0.836
ENSG00000156127	*BATF*	4.55E-04	1.203	0.003	0.105
ENSG00000140379	*BCL2A1*	3.52E-03	2.286	0.001	0.042
ENSG00000069399	*BCL3*	1.74E-46	2.557	1.118	1.713
ENSG00000113916	*BCL6*	9.25E-15	1.181	0.252	0.600
ENSG00000100739	*BDKRB1*	9.95E-74	2.772	1.207	1.764
ENSG00000168398	*BDKRB2*	5.42E-23	1.883	0.723	1.086
ENSG00000176697	*BDNF*	1.35E-04	1.121	0.016	0.198
ENSG00000167995	*BEST1*	7.21E-31	1.871	0.425	0.971
ENSG00000134107	*BHLHE40*	2.26E-08	1.342	0.067	0.742
ENSG00000123095	*BHLHE41*	7.70E-24	1.313	0.123	0.421
ENSG00000015475	*BID*	3.25E-24	1.017	0.288	0.452
ENSG00000023445	*BIRC3*	7.20E-05	1.436	0.007	0.072
ENSG00000104081	*BMF*	6.54E-45	-1.733	-0.574	-0.733
ENSG00000125845	*BMP2*	4.94E-03	1.038	0.010	0.185
ENSG00000153162	*BMP6*	6.62E-13	2.375	0.031	1.093
ENSG00000078725	*BRINP1*	6.40E-05	1.137	0.023	0.207
ENSG00000133639	*BTG1*	1.53E-15	1.059	0.386	0.651
ENSG00000154493	*C10orf90*	6.09E-14	1.446	0.791	1.073
ENSG00000120055	*C10orf95*	1.61E-02	-1.150	-0.016	-0.148
ENSG00000110665	*C11orf21*	1.46E-02	-1.137	-0.004	-0.130
ENSG00000174370	*C11orf45*	4.37E-07	-2.072	-1.161	-1.111
ENSG00000149300	*C11orf52*	3.30E-05	-1.092	-0.380	-0.853

ENSG00000187479	*C11orf96*	1.00E-21	3.216	0.948	1.801
ENSG00000235162	*C12orf75*	1.06E-23	-1.036	-0.370	-0.537
ENSG00000166920	*C15orf48*	4.24E-133	6.492	1.860	3.333
ENSG00000132016	*C19orf57*	1.87E-03	-1.231	-0.032	-0.123
ENSG00000106392	*C1GALT1*	4.18E-37	1.908	0.703	1.091
ENSG00000173918	*C1QTNF1*	6.70E-21	1.844	0.027	0.602
ENSG00000145861	*C1QTNF2*	6.45E-10	-1.790	-0.048	-0.804
ENSG00000163145	*C1QTNF7*	4.42E-10	-2.307	-0.748	-1.415
ENSG00000205863	*C1QTNF9B*	8.86E-03	-1.211	-0.020	-0.088
ENSG00000159403	*C1R*	6.20E-40	1.174	0.413	0.742
ENSG00000139178	*C1RL*	7.07E-35	1.241	0.455	0.750
ENSG00000198535	*C2CD4A*	1.97E-06	4.262	0.015	2.558
ENSG00000205502	*C2CD4B*	1.51E-05	5.453	0.009	0.089
ENSG00000125730	*C3*	4.39E-39	5.653	2.751	3.940
ENSG00000197405	*C5AR1*	5.40E-05	1.264	0.016	0.141
ENSG00000178776	*C5orf46*	4.35E-02	1.714	0.007	0.056
ENSG00000074410	*CA12*	3.53E-35	2.385	0.658	1.177
ENSG00000107159	*CA9*	3.95E-04	1.660	0.024	0.215
ENSG00000183346	*CABCOCO1*	3.51E-08	-1.205	-0.119	-0.604
ENSG00000070808	*CAMK2A*	1.08E-05	-1.522	-0.052	-1.159
ENSG00000058404	*CAMK2B*	4.19E-04	-2.109	-0.023	-0.775
ENSG00000105519	*CAPS*	9.33E-10	-1.012	-0.134	-0.419
ENSG00000204682	*CASC10*	4.69E-08	-1.645	-0.044	-1.292
ENSG00000168497	*CAVIN2*	5.99E-14	-2.012	-0.077	-1.198
ENSG00000150636	*CCDC102B*	1.60E-03	-1.307	-0.018	-0.121
ENSG00000168491	*CCDC110*	1.67E-07	-1.046	-0.402	-0.800
ENSG00000198003	*CCDC151*	2.12E-02	-1.032	-0.024	-0.216
ENSG00000166510	*CCDC68*	1.39E-02	1.033	0.021	0.115
ENSG00000055813	*CCDC85A*	3.05E-12	-1.225	-0.043	-0.536
ENSG00000181374	*CCL13*	4.54E-02	1.739	0.001	0.035
ENSG00000108691	*CCL2*	1.17E-24	4.129	1.530	2.484
ENSG00000115009	*CCL20*	1.03E-21	8.836	0.022	5.726
ENSG00000213927	*CCL27*	1.11E-02	-1.397	-0.011	-0.136
ENSG00000108688	*CCL7*	3.78E-13	4.614	0.022	2.363
ENSG00000108700	*CCL8*	4.55E-28	5.598	0.010	2.603
ENSG00000135083	*CCNJL*	1.29E-02	-1.102	-0.031	-0.175
ENSG00000163823	*CCR1*	1.52E-02	1.585	0.005	0.088
ENSG00000126353	*CCR7*	1.31E-15	2.201	0.785	0.912
ENSG00000158473	*CD1D*	4.79E-19	3.168	1.179	2.009
ENSG00000174807	*CD248*	3.03E-02	-1.244	-0.008	-0.109
ENSG00000004468	*CD38*	7.16E-08	2.508	0.009	1.078
ENSG00000085117	*CD82*	1.69E-15	1.081	0.156	0.464

ENSG00000074276	*CDHR2*	4.85E-02	-1.122	-0.020	-0.076
ENSG00000138395	*CDK15*	1.80E-02	-2.317	-0.011	-0.071
ENSG00000138769	*CDKL2*	2.99E-03	-1.391	-0.023	-0.617
ENSG00000129596	*CDO1*	3.01E-11	1.199	0.416	0.669
ENSG00000172216	*CEBPB*	2.40E-32	1.838	0.761	1.227
ENSG00000221869	*CEBPD*	7.11E-44	2.682	1.434	1.985
ENSG00000184524	*CEND1*	2.02E-03	1.365	0.017	0.690
ENSG00000188452	*CERKL*	1.47E-08	-1.523	-0.615	-0.657
ENSG00000105792	*CFAP69*	1.68E-18	1.933	0.051	0.917
ENSG00000243649	*CFB*	1.31E-22	2.906	0.030	0.834
ENSG00000128849	*CGNL1*	2.59E-07	1.058	0.031	0.204
ENSG00000138135	*CH25H*	3.44E-26	2.801	0.030	1.085
ENSG00000100399	*CHADL*	5.07E-07	-1.652	-0.026	-0.516
ENSG00000016391	*CHDH*	1.53E-15	-1.299	-0.283	-0.471
ENSG00000183765	*CHEK2*	1.11E-10	1.379	0.479	0.809
ENSG00000133048	*CHI3L1*	2.71E-44	1.892	0.758	1.273
ENSG00000064886	*CHI3L2*	1.22E-61	3.236	1.137	1.880
ENSG00000255112	*CHMP1B*	4.05E-18	1.514	0.451	0.876
ENSG00000128656	*CHN1*	1.12E-12	-1.419	-0.039	-0.429
ENSG00000054938	*CHRDL2*	6.11E-05	1.706	0.011	0.192
ENSG00000171310	*CHST11*	2.96E-15	1.547	0.042	0.508
ENSG00000163815	*CLEC3B*	2.87E-05	-1.061	-0.063	-0.451
ENSG00000169583	*CLIC3*	2.64E-07	-1.020	-0.330	-0.436
ENSG00000159212	*CLIC6*	4.74E-21	1.064	0.157	0.546
ENSG00000165959	*CLMN*	2.29E-10	1.448	0.354	0.634
ENSG00000149970	*CNKSR2*	3.19E-04	-1.114	-0.029	-0.288
ENSG00000153721	*CNKSR3*	1.78E-17	-1.189	-0.300	-0.547
ENSG00000103647	*CORO2B*	3.84E-07	-1.076	-0.417	-0.594
ENSG00000047457	*CP*	3.73E-35	2.279	0.759	1.220
ENSG00000177685	*CRACR2B*	2.73E-11	-1.369	-0.021	-0.315
ENSG00000213145	*CRIP1*	2.06E-19	-1.028	-0.215	-0.353
ENSG00000121005	*CRISPLD1*	7.42E-26	-1.716	-0.598	-1.002
ENSG00000103196	*CRISPLD2*	5.89E-08	1.684	0.015	0.326
ENSG00000226321	*CROCC2*	8.83E-03	1.235	0.000	0.145
ENSG00000095713	*CRTAC1*	2.18E-13	1.499	0.045	0.664
ENSG00000109943	*CRTAM*	2.23E-03	1.835	0.010	0.113
ENSG00000172346	*CSDC2*	6.74E-05	-1.402	-0.053	-0.553
ENSG00000178662	*CSRNP3*	1.80E-04	-2.323	-0.027	-1.496
ENSG00000118523	*CTGF*	1.27E-14	-1.700	-0.413	-0.908
ENSG00000135047	*CTSL*	1.61E-06	1.024	0.084	0.716
ENSG00000163131	*CTSS*	7.87E-39	1.910	0.366	0.803
ENSG00000006210	*CX3CL1*	2.52E-05	1.445	0.008	0.112

ENSG00000163739	*CXCL1*	1.92E-225	7.081	3.981	4.993
ENSG00000081041	*CXCL2*	5.60E-74	5.839	2.616	3.757
ENSG00000163734	*CXCL3*	4.31E-53	5.404	2.064	3.190
ENSG00000163735	*CXCL5*	2.00E-18	4.569	0.023	2.300
ENSG00000124875	*CXCL6*	1.63E-54	5.656	2.821	3.790
ENSG00000169429	*CXCL8*	2.09E-32	5.969	0.035	2.672
ENSG00000121966	*CXCR4*	3.15E-03	4.545	0.007	0.042
ENSG00000137869	*CYP19A1*	1.41E-02	1.259	0.012	0.161
ENSG00000019186	*CYP24A1*	1.29E-14	4.175	1.879	2.462
ENSG00000146233	*CYP39A1*	1.20E-08	-1.949	-0.535	-0.991
ENSG00000186377	*CYP4X1*	3.75E-04	-1.046	-0.027	-0.310
ENSG00000172817	*CYP7B1*	2.17E-10	1.557	0.501	0.659
ENSG00000205795	*CYS1*	3.28E-13	-1.851	-0.389	-0.888
ENSG00000100592	*DAAM1*	2.96E-20	1.149	0.175	0.420
ENSG00000146122	*DAAM2*	1.98E-07	-1.014	-0.089	-0.593
ENSG00000163331	*DAPL1*	1.26E-06	-2.523	-0.015	-1.630
ENSG00000003249	*DBNDD1*	1.76E-05	-1.215	-0.034	-0.648
ENSG00000105516	*DBP*	2.01E-06	-1.056	-0.053	-0.330
ENSG00000133083	*DCLK1*	7.01E-03	-1.515	-0.018	-0.070
ENSG00000163357	*DCST1*	3.81E-02	-1.075	-0.009	-0.083
ENSG00000153904	*DDAH1*	9.92E-19	-1.398	-0.400	-0.813
ENSG00000168209	*DDIT4*	4.35E-05	1.702	0.018	0.355
ENSG00000145358	*DDIT4L*	5.91E-04	1.253	0.012	0.162
ENSG00000164825	*DEFB1*	3.61E-03	1.231	0.021	0.088
ENSG00000165507	*DEPP1*	3.82E-10	1.926	0.046	0.972
ENSG00000155792	*DEPTOR*	1.63E-15	-2.207	-0.083	-0.908
ENSG00000062282	*DGAT2*	9.04E-12	1.749	0.630	1.305
ENSG00000077044	*DGKD*	1.81E-17	1.152	0.326	0.655
ENSG00000197406	*DIO3*	9.87E-03	2.942	0.008	0.049
ENSG00000140323	*DISP2*	7.79E-04	-1.275	-0.017	-0.984
ENSG00000132837	*DMGDH*	4.38E-07	-1.143	-0.032	-0.200
ENSG00000115423	*DNAH6*	4.98E-02	-1.167	-0.005	-0.103
ENSG00000187957	*DNER*	2.10E-08	1.899	0.014	0.134
ENSG00000149927	*DOC2A*	1.23E-02	-1.316	-0.024	-0.276
ENSG00000128512	*DOCK4*	9.31E-14	1.097	0.049	0.173
ENSG00000136048	*DRAM1*	1.54E-13	1.369	0.399	0.733
ENSG00000136982	*DSCC1*	5.17E-07	-1.138	-0.051	-0.384
ENSG00000134769	*DTNA*	7.01E-06	1.080	0.001	0.265
ENSG00000120129	*DUSP1*	3.91E-16	1.671	0.317	0.870
ENSG00000138166	*DUSP5*	6.11E-12	1.098	0.071	0.579
ENSG00000139318	*DUSP6*	5.52E-17	1.719	0.501	0.919
ENSG00000184545	*DUSP8*	6.49E-21	1.645	0.630	0.957

ENSG00000158560	*DYNC1I1*	2.02E-11	-1.193	-0.150	-0.651
ENSG00000122547	*EEPD1*	1.16E-07	-1.108	-0.292	-0.355
ENSG00000163576	*EFHB*	7.43E-03	-1.231	-0.025	-0.209
ENSG00000115468	*EFHD1*	4.00E-17	-1.699	-0.257	-0.857
ENSG00000129521	*EGLN3*	2.00E-05	1.583	0.022	0.383
ENSG00000013016	*EHD3*	1.27E-05	-1.025	-0.054	-0.676
ENSG00000163435	*ELF3*	4.95E-12	3.004	0.973	1.601
ENSG00000128886	*ELL3*	9.64E-05	-1.023	-0.042	-0.688
ENSG00000197977	*ELOVL2*	1.21E-10	2.657	1.254	2.106
ENSG00000164181	*ELOVL7*	1.08E-03	1.891	0.006	0.054
ENSG00000168913	*ENHO*	1.13E-02	-2.315	-0.003	-0.034
ENSG00000198018	*ENTPD7*	7.13E-20	1.620	0.290	0.682
ENSG00000188833	*ENTPD8*	2.37E-02	-2.824	-0.003	-0.051
ENSG00000082397	*EPB41L3*	7.16E-18	1.390	0.014	0.118
ENSG00000044524	*EPHA3*	3.68E-04	-1.334	-0.028	-0.795
ENSG00000145242	*EPHA5*	3.96E-02	-1.025	-0.009	-0.059
ENSG00000182580	*EPHB3*	1.21E-13	-1.359	-0.224	-0.607
ENSG00000120915	*EPHX2*	6.41E-08	-1.096	-0.242	-0.595
ENSG00000124882	*EREG*	1.59E-02	1.064	0.014	0.172
ENSG00000178752	*ERFE*	8.48E-32	2.633	0.878	1.763
ENSG00000178607	*ERN1*	2.85E-15	1.294	0.067	0.542
ENSG00000116285	*ERRFI1*	7.96E-08	1.221	0.039	0.484
ENSG00000164283	*ESM1*	5.96E-07	1.759	0.037	0.343
ENSG00000157557	*ETS2*	4.64E-13	1.180	0.136	0.569
ENSG00000139083	*ETV6*	9.18E-21	1.194	0.298	0.600
ENSG00000158008	*EXTL1*	4.27E-02	-1.109	-0.016	-0.081
ENSG00000181104	*F2R*	2.26E-16	-1.916	-0.065	-0.713
ENSG00000198734	*F5*	9.27E-04	1.236	0.016	0.368
ENSG00000121769	*FABP3*	1.08E-20	-1.331	-0.307	-0.499
ENSG00000170323	*FABP4*	1.48E-03	-1.263	-0.011	-0.320
ENSG00000169122	*FAM110B*	7.92E-09	1.083	0.069	0.561
ENSG00000135842	*FAM129A*	1.32E-18	-1.874	-0.619	-1.150
ENSG00000179083	*FAM133A*	1.28E-04	-1.181	-0.034	-0.603
ENSG00000109794	*FAM149A*	2.06E-06	-1.280	-0.032	-0.607
ENSG00000154319	*FAM167A*	7.33E-08	1.511	0.046	0.734
ENSG00000185442	*FAM174B*	6.57E-10	1.186	0.113	0.624
ENSG00000197520	*FAM177B*	4.55E-28	4.310	2.489	3.184
ENSG00000108950	*FAM20A*	1.30E-26	2.764	1.197	1.720
ENSG00000177706	*FAM20C*	6.92E-20	1.619	0.427	0.966
ENSG00000185614	*FAM212A*	4.71E-07	-1.540	-0.060	-0.557
ENSG00000157470	*FAM81A*	4.30E-02	-1.023	-0.013	-0.067
ENSG00000162981	*FAM84A*	1.02E-04	-1.271	-0.026	-0.546

ENSG00000165323	*FAT3*	7.84E-09	-1.293	-0.090	-0.837
ENSG00000170271	*FAXDC2*	1.38E-09	-1.342	-0.350	-0.796
ENSG00000165140	*FBP1*	9.42E-12	-1.987	-0.069	-0.856
ENSG00000141665	*FBXO15*	3.04E-03	-1.709	-0.018	-0.176
ENSG00000162894	*FCMR*	1.11E-04	1.898	0.001	0.061
ENSG00000113578	*FGF1*	8.21E-06	1.410	0.013	0.200
ENSG00000070193	*FGF10*	4.31E-24	2.227	0.697	1.249
ENSG00000102466	*FGF14*	7.16E-13	-1.089	-0.236	-0.500
ENSG00000140285	*FGF7*	4.26E-31	1.365	0.505	0.888
ENSG00000137460	*FHDC1*	1.28E-04	1.071	0.016	0.131
ENSG00000022267	*FHL1*	2.13E-21	-1.263	-0.371	-0.648
ENSG00000118407	*FILIP1*	8.06E-17	2.964	0.021	0.363
ENSG00000204131	*FLJ44635*	1.20E-02	-1.523	-0.019	-0.179
ENSG00000075420	*FNDC3B*	1.29E-29	1.237	0.369	0.613
ENSG00000143107	*FNDC7*	2.80E-02	-1.636	-0.015	-0.035
ENSG00000103241	*FOXF1*	7.08E-04	2.075	0.024	1.855
ENSG00000114861	*FOXP1*	3.28E-25	1.069	0.185	0.449
ENSG00000165694	*FRMD7*	1.32E-02	-1.121	-0.026	-0.305
ENSG00000167996	*FTH1*	5.18E-31	1.410	0.322	0.757
ENSG00000010810	*FYN*	4.87E-31	1.242	0.203	0.555
ENSG00000180340	*FZD2*	7.41E-08	-1.184	-0.019	-0.474
ENSG00000123689	*G0S2*	3.45E-30	4.313	1.375	2.400
ENSG00000139112	*GABARAPL1*	4.83E-19	1.177	0.355	0.681
ENSG00000143891	*GALM*	7.21E-09	-1.350	-0.081	-0.552
ENSG00000131386	*GALNT15*	3.92E-28	2.351	0.886	1.441
ENSG00000131979	*GCH1*	1.11E-47	3.628	0.903	1.758
ENSG00000130513	*GDF15*	2.39E-07	1.137	0.528	0.882
ENSG00000125965	*GDF5*	3.78E-19	-1.339	-0.349	-0.615
ENSG00000156466	*GDF6*	3.71E-12	1.012	0.095	0.398
ENSG00000143869	*GDF7*	2.40E-05	-1.355	-0.009	-0.583
ENSG00000158555	*GDPD5*	4.68E-08	-1.045	-0.079	-0.435
ENSG00000131459	*GFPT2*	7.90E-36	1.887	0.514	0.997
ENSG00000168546	*GFRA2*	1.59E-02	1.679	0.004	0.066
ENSG00000179855	*GIPC3*	3.99E-02	-1.063	-0.005	-0.115
ENSG00000198814	*GK*	2.40E-04	1.148	0.035	0.274
ENSG00000074047	*GLI2*	8.46E-09	-1.453	-0.045	-0.931
ENSG00000107249	*GLIS3*	4.98E-18	1.345	0.207	0.594
ENSG00000173221	*GLRX*	1.29E-19	1.729	0.382	0.950
ENSG00000156689	*GLYATL2*	8.77E-03	-1.236	-0.007	-0.217
ENSG00000112312	*GMNN*	2.57E-07	1.101	0.084	0.579
ENSG00000186469	*GNG2*	7.01E-08	-1.149	-0.041	-0.661
ENSG00000176533	*GNG7*	6.70E-05	-1.317	-0.028	-0.213

ENSG00000155265	*GOLGA7B*	6.67E-05	1.299	0.013	0.247
ENSG00000164850	*GPER1*	1.47E-12	-1.042	-0.225	-0.465
ENSG00000112293	*GPLD1*	4.15E-12	-1.010	-0.195	-0.821
ENSG00000180998	*GPR137C*	1.62E-02	-1.281	-0.012	-0.156
ENSG00000158292	*GPR153*	3.62E-15	-1.223	-0.279	-0.611
ENSG00000169508	*GPR183*	2.41E-07	2.841	0.018	0.947
ENSG00000170075	*GPR37L1*	2.68E-09	3.043	0.010	0.106
ENSG00000181656	*GPR88*	2.01E-03	1.175	0.005	0.205
ENSG00000013588	*GPRC5A*	1.99E-19	1.863	0.541	1.080
ENSG00000115290	*GRB14*	4.83E-06	1.441	-0.003	0.094
ENSG00000155511	*GRIA1*	1.73E-08	-1.862	-0.527	-1.065
ENSG00000147697	*GSDMC*	8.53E-03	1.049	0.005	-0.034
ENSG00000169181	*GSG1L*	1.70E-02	-3.352	-0.004	-0.053
ENSG00000134201	*GSTM5*	8.93E-09	-1.463	-0.463	-0.688
ENSG00000164116	*GUCY1A1*	8.76E-06	-1.553	-0.402	-0.745
ENSG00000061918	*GUCY1B1*	3.26E-06	-1.210	-0.022	-0.388
ENSG00000179240	*GVQW3*	7.24E-06	-1.230	-0.334	-0.821
ENSG00000162882	*HAAO*	5.59E-05	-1.156	-0.067	-0.161
ENSG00000188921	*HACD4*	8.18E-21	-1.165	-0.286	-0.705
ENSG00000170961	*HAS2*	1.39E-07	1.691	0.046	0.944
ENSG00000135077	*HAVCR2*	2.96E-04	-1.034	-0.002	-0.301
ENSG00000103145	*HCFC1R1*	9.27E-11	-1.200	-0.343	-0.450
ENSG00000002746	*HECW1*	4.64E-09	-1.226	-0.060	-0.548
ENSG00000135547	*HEY2*	6.04E-05	-1.301	-0.024	-0.563
ENSG00000177374	*HIC1*	7.88E-10	-1.406	-0.061	-0.499
ENSG00000100644	*HIF1A*	1.86E-12	1.171	0.359	0.662
ENSG00000135245	*HILPDA*	8.64E-05	2.547	0.011	0.142
ENSG00000184678	*HIST2H2BE*	4.19E-13	1.125	0.120	0.496
ENSG00000095951	*HIVEP1*	2.00E-18	1.139	0.089	0.336
ENSG00000127124	*HIVEP3*	2.10E-21	1.695	0.575	0.701
ENSG00000159399	*HK2*	1.80E-06	1.444	0.030	0.614
ENSG00000241935	*HOGA1*	5.17E-07	-1.599	0.002	-0.340
ENSG00000196196	*HRCT1*	7.77E-03	-1.700	-0.014	-0.124
ENSG00000117594	*HSD11B1*	4.10E-40	4.420	1.662	2.628
ENSG00000004776	*HSPB6*	1.62E-21	-1.112	-0.435	-0.533
ENSG00000173641	*HSPB7*	1.39E-25	-1.750	-0.719	-1.026
ENSG00000102468	*HTR2A*	6.79E-15	3.417	0.034	1.655
ENSG00000169495	*HTRA4*	4.30E-04	1.547	0.015	0.212
ENSG00000090339	*ICAM1*	7.71E-13	2.080	0.027	0.781
ENSG00000115738	*ID2*	1.16E-26	2.417	0.885	1.336
ENSG00000137331	*IER3*	3.41E-02	1.358	0.011	0.066
ENSG00000185885	*IFITM1*	7.17E-03	1.635	0.014	0.147

ENSG00000142089	*IFITM3*	7.08E-12	1.317	0.359	0.832
ENSG00000017427	*IGF1*	7.44E-11	3.407	0.025	1.588
ENSG00000141753	*IGFBP4*	3.85E-30	1.134	0.232	0.684
ENSG00000164136	*IL15*	3.96E-04	1.093	0.013	0.163
ENSG00000134470	*IL15RA*	9.58E-05	1.052	0.043	0.467
ENSG00000115604	*IL18R1*	4.15E-10	1.238	0.452	0.585
ENSG00000136689	*IL1RN*	2.15E-02	1.394	0.009	0.173
ENSG00000162892	*IL24*	5.89E-05	3.224	0.007	0.037
ENSG00000104998	*IL27RA*	6.73E-04	-1.233	-0.015	-0.188
ENSG00000164509	*IL31RA*	3.25E-12	-1.511	-0.079	-0.912
ENSG00000136696	*IL36B*	4.15E-03	1.027	0.032	0.830
ENSG00000136695	*IL36RN*	3.73E-02	1.626	0.005	0.073
ENSG00000104951	*IL4I1*	7.24E-07	2.266	0.018	0.378
ENSG00000136244	*IL6*	6.73E-32	7.861	0.023	3.915
ENSG00000168685	*IL7R*	8.14E-06	1.089	0.033	0.196
ENSG00000122641	*INHBA*	2.87E-05	1.408	0.019	0.282
ENSG00000188487	*INSC*	3.39E-05	-1.577	-0.048	-1.012
ENSG00000186480	*INSIG1*	2.70E-16	1.471	0.062	0.597
ENSG00000125629	*INSIG2*	4.86E-36	1.206	0.204	0.431
ENSG00000074706	*IPCEF1*	1.22E-03	-1.053	-0.006	-1.443
ENSG00000151151	*IPMK*	7.23E-09	1.161	0.062	0.505
ENSG00000120645	*IQSEC3*	2.90E-03	-1.067	-0.013	-0.188
ENSG00000134070	*IRAK2*	2.59E-27	1.912	0.681	1.117
ENSG00000090376	*IRAK3*	8.60E-17	1.124	0.040	0.266
ENSG00000137265	*IRF4*	1.01E-02	1.761	0.010	0.125
ENSG00000159387	*IRX6*	2.49E-05	-1.550	-0.046	-0.602
ENSG00000101230	*ISM1*	8.74E-05	1.006	0.029	0.330
ENSG00000005961	*ITGA2B*	7.71E-03	-2.161	-0.017	-0.105
ENSG00000115232	*ITGA4*	8.51E-10	-1.026	-0.287	-0.634
ENSG00000105855	*ITGB8*	2.11E-05	1.331	0.023	0.261
ENSG00000150995	*ITPR1*	1.03E-09	1.302	0.047	0.458
ENSG00000148841	*ITPRIP*	3.90E-13	1.375	0.076	0.778
ENSG00000096968	*JAK2*	1.26E-27	1.105	0.115	0.354
ENSG00000188385	*JAKMIP3*	1.32E-04	-1.235	-0.031	-0.255
ENSG00000171223	*JUNB*	3.47E-17	1.836	0.560	1.072
ENSG00000158445	*KCNB1*	6.22E-07	-1.892	-0.031	-1.148
ENSG00000102057	*KCND1*	2.43E-02	-1.019	-0.012	-0.167
ENSG00000152049	*KCNE4*	4.27E-25	1.293	0.509	0.916
ENSG00000143473	*KCNH1*	1.01E-14	1.594	0.047	0.791
ENSG00000055118	*KCNH2*	1.56E-04	-1.158	-0.060	-0.779
ENSG00000157551	*KCNJ15*	2.40E-10	1.409	0.058	0.992
ENSG00000171303	*KCNK3*	6.73E-08	4.271	0.013	3.340

ENSG00000104783	*KCNN4*	1.69E-07	-1.192	-0.037	-0.500
ENSG00000184156	*KCNQ3*	2.03E-21	1.923	0.667	1.085
ENSG00000156486	*KCNS2*	1.06E-02	-1.625	0.002	-0.084
ENSG00000170745	*KCNS3*	2.64E-03	-1.334	-0.011	-0.139
ENSG00000180332	*KCTD4*	1.56E-10	-1.845	-0.057	-0.703
ENSG00000138030	*KHK*	6.01E-03	-1.226	-0.019	-0.067
ENSG00000109265	*KIAA1211*	4.58E-05	-1.109	-0.054	-0.664
ENSG00000162849	*KIF26B*	2.06E-15	-2.017	-0.651	-0.986
ENSG00000155980	*KIF5A*	2.24E-02	-1.404	-0.020	-0.091
ENSG00000157404	*KIT*	3.05E-06	-1.251	-0.710	-0.979
ENSG00000155090	*KLF10*	8.15E-24	1.199	0.390	0.655
ENSG00000171872	*KLF17*	2.34E-08	2.206	0.023	1.025
ENSG00000119138	*KLF9*	2.85E-11	1.064	0.326	0.533
ENSG00000162755	*KLHDC9*	1.02E-04	-1.346	-0.032	-0.303
ENSG00000171345	*KRT19*	1.95E-03	-1.457	-0.023	-0.806
ENSG00000221852	*KRTAP1-5*	2.88E-08	-1.114	-0.311	-0.316
ENSG00000174611	*KY*	2.53E-11	-1.899	-0.774	-0.936
ENSG00000115919	*KYNU*	1.25E-18	3.450	1.416	2.012
ENSG00000101680	*LAMA1*	3.38E-07	1.001	0.156	0.542
ENSG00000129988	*LBP*	1.14E-17	3.270	0.022	1.339
ENSG00000148346	*LCN2*	2.87E-05	2.773	0.020	1.590
ENSG00000136167	*LCP1*	2.22E-02	-1.477	-0.016	-0.053
ENSG00000169744	*LDB2*	1.17E-15	-1.817	-0.449	-0.950
ENSG00000134333	*LDHA*	5.52E-17	1.237	0.421	0.718
ENSG00000166816	*LDHD*	1.08E-07	-1.319	-0.489	-0.798
ENSG00000168675	*LDLRAD4*	1.26E-15	-1.662	-0.704	-1.117
ENSG00000106003	*LFNG*	3.00E-05	-1.194	-0.052	-0.639
ENSG00000153012	*LGI2*	3.69E-08	-1.814	-0.051	-0.935
ENSG00000139292	*LGR5*	3.59E-07	-1.049	-0.295	-0.585
ENSG00000128342	*LIF*	1.03E-07	2.250	0.011	0.180
ENSG00000072163	*LIMS2*	1.03E-11	-1.317	-0.261	-0.608
ENSG00000236882	*LINC01554*	5.61E-06	2.151	0.017	0.194
ENSG00000169783	*LINGO1*	6.64E-05	-1.357	-0.018	-0.699
ENSG00000136153	*LMO7*	3.43E-15	-1.261	-0.189	-0.647
ENSG00000163431	*LMOD1*	2.98E-06	-1.512	-0.040	-0.702
ENSG00000103485	*LOC105369247*	1.49E-03	-2.095	-0.002	-0.063
ENSG00000173535	*LOC254896*	8.92E-04	-1.037	-0.041	-0.189
ENSG00000165379	*LRFN5*	1.30E-02	-1.206	-0.021	-0.354
ENSG00000128606	*LRRC17*	2.49E-09	-2.721	-0.037	-1.610
ENSG00000172731	*LRRC20*	3.28E-08	-1.577	-0.047	-0.690
ENSG00000128594	*LRRC4*	2.20E-06	-2.034	-0.036	-1.102
ENSG00000146006	*LRRTM2*	1.12E-07	-1.450	-0.473	-0.591

ENSG00000130592	*LSP1*	2.67E-14	-1.158	-0.263	-0.473
ENSG00000172264	*MACROD2*	1.49E-05	-1.375	-0.038	-0.533
ENSG00000185022	*MAFF*	2.99E-31	1.474	0.635	0.943
ENSG00000144063	*MALL*	9.59E-08	1.106	0.098	0.610
ENSG00000165072	*MAMDC2*	7.68E-35	-2.104	-0.570	-1.126
ENSG00000196782	*MAML3*	5.86E-04	-1.231	-1.017	-1.138
ENSG00000013619	*MAMLD1*	2.35E-20	-1.770	-0.748	-1.382
ENSG00000176909	*MAMSTR*	3.04E-04	-1.423	-0.035	-0.290
ENSG00000069535	*MAOB*	1.16E-15	1.803	0.052	0.622
ENSG00000197769	*MAP1LC3C*	5.86E-13	-2.132	-1.052	-1.715
ENSG00000108984	*MAP2K6*	5.48E-08	-2.502	-0.827	-1.438
ENSG00000107968	*MAP3K8*	1.85E-188	2.425	1.551	1.929
ENSG00000186868	*MAPT*	1.17E-02	-1.235	-0.019	-0.713
ENSG00000186205	*MARC1*	8.69E-05	-1.215	-0.629	-0.541
ENSG00000173926	*MARCH3*	1.68E-15	2.353	0.014	0.655
ENSG00000144583	*MARCH4*	1.52E-03	-1.606	-0.018	-0.704
ENSG00000172197	*MBOAT1*	1.29E-10	-1.210	-0.092	-0.868
ENSG00000140563	*MCTP2*	1.30E-06	1.065	0.021	0.217
ENSG00000102802	*MEDAG*	4.18E-37	2.175	0.820	1.351
ENSG00000106511	*MEOX2*	2.16E-21	-1.828	-0.423	-1.094
ENSG00000188095	*MESP2*	3.57E-02	-1.320	-0.012	-0.135
ENSG00000170439	*METTL7B*	1.78E-07	-2.638	-0.029	-1.219
ENSG00000168389	*MFSD2A*	7.40E-09	2.118	0.036	1.157
ENSG00000174514	*MFSD4A*	2.24E-02	-1.057	-0.017	-0.783
ENSG00000108960	*MMD*	1.86E-10	1.187	0.689	0.761
ENSG00000196549	*MME*	1.59E-10	1.361	0.047	0.474
ENSG00000196611	*MMP1*	1.83E-39	6.069	1.925	3.486
ENSG00000166670	*MMP10*	1.15E-11	2.147	0.014	0.419
ENSG00000137745	*MMP13*	2.54E-35	3.161	0.037	1.131
ENSG00000149968	*MMP3*	7.44E-59	4.451	0.798	1.889
ENSG00000120162	*MOB3B*	2.94E-04	-0.715	-1.202	-0.217
ENSG00000186732	*MPPED1*	5.45E-03	-1.342	-0.009	-0.945
ENSG00000066382	*MPPED2*	4.07E-05	-1.193	-0.040	-0.469
ENSG00000156968	*MPV17L*	1.06E-07	-1.718	-0.037	-0.998
ENSG00000135324	*MRAP2*	2.12E-15	-1.915	-0.644	-1.070
ENSG00000184350	*MRGPRE*	2.08E-02	-1.190	-0.007	-0.170
ENSG00000072952	*MRVI1*	3.51E-15	-1.650	-0.470	-1.144
ENSG00000178860	*MSC*	8.42E-07	1.032	0.033	0.277
ENSG00000205362	*MT1A*	1.09E-02	1.320	0.017	0.057
ENSG00000169715	*MT1E*	3.11E-14	1.362	0.488	0.934
ENSG00000198417	*MT1F*	2.43E-17	2.308	0.049	1.192
ENSG00000125144	*MT1G*	1.83E-09	3.682	0.024	2.092

ENSG00000205364	*MT1M*	8.46E-08	1.277	0.041	0.518
ENSG00000187193	*MT1X*	1.12E-14	2.105	0.681	1.340
ENSG00000125148	*MT2A*	4.18E-47	2.423	0.980	1.507
ENSG00000242114	*MTFP1*	5.72E-04	1.613	0.027	0.818
ENSG00000185499	*MUC1*	1.09E-06	1.112	0.348	0.610
ENSG00000133055	*MYBPH*	2.52E-10	1.754	0.544	1.003
ENSG00000136449	*MYCBPAP*	2.90E-04	-1.234	-0.052	-0.666
ENSG00000065534	*MYLK*	5.17E-08	-1.189	-0.073	-0.790
ENSG00000128833	*MYO5C*	5.30E-03	-1.058	-0.023	-0.329
ENSG00000034971	*MYOC*	2.57E-14	-1.238	-0.441	-0.734
ENSG00000105835	*NAMPT*	9.42E-20	3.291	0.037	1.523
ENSG00000186462	*NAP1L2*	2.21E-05	-1.184	-0.475	-0.503
ENSG00000186310	*NAP1L3*	4.37E-07	-1.375	-0.038	-0.687
ENSG00000156006	*NAT2*	3.67E-03	-1.105	-0.044	-0.178
ENSG00000067798	*NAV3*	8.35E-05	-1.072	-0.035	-0.567
ENSG00000160796	*NBEAL2*	3.67E-05	-1.076	-0.074	-0.788
ENSG00000104490	*NCALD*	1.84E-05	-1.977	-0.028	-0.519
ENSG00000154654	*NCAM2*	3.37E-11	2.096	0.034	0.896
ENSG00000124479	*NDP*	7.29E-06	1.865	0.014	0.173
ENSG00000104419	*NDRG1*	6.40E-16	1.720	0.073	0.803
ENSG00000165795	*NDRG2*	7.29E-06	-1.302	-0.021	-0.584
ENSG00000165030	*NFIL3*	3.99E-21	1.858	0.438	1.058
ENSG00000077150	*NFKB2*	2.86E-16	1.108	0.037	0.339
ENSG00000100906	*NFKBIA*	1.63E-67	2.447	0.889	1.343
ENSG00000144802	*NFKBIZ*	2.09E-246	3.596	2.648	2.975
ENSG00000257108	*NHLRC4*	2.57E-02	-1.066	-0.019	-0.085
ENSG00000204131	*NHSL2*	1.20E-02	-1.523	-0.019	-0.179
ENSG00000165028	*NIPSNAP3B*	2.75E-06	-1.095	-0.336	-0.463
ENSG00000140807	*NKD1*	4.11E-06	-1.014	-0.043	-0.825
ENSG00000167034	*NKX3-1*	8.92E-18	1.420	0.426	0.511
ENSG00000182261	*NLRP10*	4.17E-05	-2.052	-0.020	-0.847
ENSG00000166741	*NNMT*	1.43E-42	2.245	0.990	1.587
ENSG00000151014	*NOCT*	4.89E-08	1.256	0.031	0.548
ENSG00000167207	*NOD2*	2.53E-24	4.202	0.024	2.032
ENSG00000007171	*NOS2*	7.49E-36	7.417	4.309	5.152
ENSG00000163072	*NOSTRIN*	4.57E-02	-1.134	-0.005	-0.002
ENSG00000136999	*NOV*	4.23E-12	-1.249	-0.062	-0.419
ENSG00000139910	*NOVA1*	5.31E-09	1.037	0.118	0.593
ENSG00000171246	*NPTX1*	1.63E-10	-1.653	-0.607	-0.832
ENSG00000144852	*NR1I2*	3.85E-02	-1.893	-0.012	-0.032
ENSG00000151623	*NR3C2*	7.96E-16	-1.322	-0.309	-0.643
ENSG00000153234	*NR4A2*	2.87E-12	1.755	0.068	0.798

ENSG00000119508	*NR4A3*	2.63E-29	2.536	0.865	1.557
ENSG00000134986	*NREP*	1.58E-15	-1.584	-0.520	-0.995
ENSG00000118257	*NRP2*	9.77E-17	1.388	0.160	0.660
ENSG00000065320	*NTN1*	1.89E-13	1.528	0.386	0.982
ENSG00000148053	*NTRK2*	4.29E-12	-1.044	-0.335	-0.722
ENSG00000186364	*NUDT17*	2.27E-05	-1.084	-0.039	-0.779
ENSG00000182575	*NXPH3*	6.62E-09	-1.428	-0.416	-0.977
ENSG00000205978	*NYNRIN*	3.89E-08	-1.090	-0.192	-0.597
ENSG00000154358	*OBSCN*	1.43E-18	-1.093	-0.384	-0.605
ENSG00000177989	*ODF3B*	2.35E-06	1.401	0.043	0.698
ENSG00000105088	*OLFM2*	8.91E-14	-1.224	-0.255	-0.441
ENSG00000183801	*OLFML1*	2.80E-04	-1.793	-0.035	-0.503
ENSG00000162745	*OLFML2B*	1.45E-13	-1.123	-0.243	-0.460
ENSG00000127083	*OMD*	3.59E-10	-1.017	-0.102	-0.606
ENSG00000183715	*OPCML*	1.39E-02	-1.587	-0.018	-0.102
ENSG00000125510	*OPRL1*	4.77E-05	-1.003	-0.040	-0.518
ENSG00000070882	*OSBPL3*	2.33E-18	-1.226	-0.353	-0.711
ENSG00000006025	*OSBPL7*	2.70E-08	-1.162	-0.125	-0.601
ENSG00000145623	*OSMR*	2.37E-40	2.286	0.869	1.354
ENSG00000180914	*OXTR*	1.12E-03	-1.421	-0.018	-0.105
ENSG00000099957	*P2RX6*	1.85E-06	-1.437	-0.037	-0.787
ENSG00000076641	*PAG1*	2.47E-06	1.096	0.033	0.222
ENSG00000243444	*PALM2*	6.84E-08	1.626	0.064	1.128
ENSG00000157654	*PALM2-AKAP2*	3.63E-03	2.753	0.006	0.068
ENSG00000099260	*PALMD*	8.47E-22	1.838	0.610	1.063
ENSG00000162073	*PAQR4*	1.16E-04	-1.095	-0.013	-0.213
ENSG00000102981	*PARD6A*	3.84E-04	-1.009	-0.055	-0.703
ENSG00000173599	*PC*	1.16E-08	1.102	0.094	0.595
ENSG00000183570	*PCBP3*	2.24E-09	1.408	0.017	0.330
ENSG00000150275	*PCDH15*	9.74E-03	1.621	0.010	0.034
ENSG00000189184	*PCDH18*	1.18E-07	-1.175	-0.370	-0.875
ENSG00000124253	*PCK1*	3.93E-04	4.552	0.006	0.072
ENSG00000175426	*PCSK1*	3.51E-17	1.822	0.362	0.911
ENSG00000172572	*PDE3A*	1.27E-09	1.132	0.010	0.083
ENSG00000184588	*PDE4B*	1.22E-61	2.876	1.289	1.816
ENSG00000113448	*PDE4D*	1.21E-26	2.308	0.456	1.006
ENSG00000138735	*PDE5A*	7.21E-12	-2.086	-0.605	-1.322
ENSG00000170962	*PDGFD*	1.10E-10	-1.129	-0.119	-0.568
ENSG00000152256	*PDK1*	1.17E-15	1.455	0.228	0.679
ENSG00000162493	*PDPN*	2.79E-23	1.576	0.557	1.008
ENSG00000186862	*PDZD7*	6.67E-03	-1.008	-0.018	-0.609
ENSG00000162366	*PDZK1IP1*	4.96E-09	2.736	0.026	1.388

ENSG00000109272	*PF4V1*	1.88E-03	2.203	0.018	1.334
ENSG00000170525	*PFKFB3*	1.36E-09	1.320	0.080	0.711
ENSG00000070087	*PFN2*	4.22E-20	-1.150	-0.289	-0.579
ENSG00000176732	*PFN4*	5.81E-03	-1.269	-0.017	-0.170
ENSG00000119630	*PGF*	5.62E-08	2.104	0.006	0.080
ENSG00000102144	*PGK1*	7.99E-12	1.083	0.245	0.540
ENSG00000153823	*PID1*	4.07E-27	1.845	0.017	0.266
ENSG00000137193	*PIM1*	8.32E-19	1.371	0.588	1.037
ENSG00000198355	*PIM3*	5.24E-13	1.384	0.515	0.885
ENSG00000154217	*PITPNC1*	2.86E-05	1.126	0.027	0.413
ENSG00000166473	*PKD1L2*	6.35E-06	-1.692	-0.017	-1.149
ENSG00000165495	*PKNOX2*	4.56E-37	2.080	0.482	1.166
ENSG00000138193	*PLCE1*	1.01E-16	-1.461	-0.450	-0.944
ENSG00000075651	*PLD1*	7.71E-67	2.041	0.598	1.030
ENSG00000021300	*PLEKHB1*	1.03E-03	-1.057	-0.018	-0.142
ENSG00000171680	*PLEKHG5*	5.12E-08	-1.025	-0.234	-0.379
ENSG00000147872	*PLIN2*	2.19E-03	1.060	0.025	0.435
ENSG00000145632	*PLK2*	1.70E-08	1.122	0.024	0.201
ENSG00000152952	*PLOD2*	2.87E-12	1.370	0.249	0.620
ENSG00000120756	*PLS1*	5.92E-04	-1.200	-0.036	-0.442
ENSG00000188313	*PLSCR1*	3.32E-03	1.213	0.005	0.073
ENSG00000221866	*PLXNA4*	4.69E-09	3.372	1.266	1.980
ENSG00000141682	*PMAIP1*	1.81E-10	1.965	0.979	1.539
ENSG00000182013	*PNMA8A*	6.63E-06	-1.479	-0.030	-0.915
ENSG00000204851	*PNMA8B*	1.14E-04	-1.291	-0.042	-0.446
ENSG00000130653	*PNPLA7*	1.23E-08	-1.385	-0.092	-0.712
ENSG00000146278	*PNRC1*	4.82E-06	1.054	0.025	0.273
ENSG00000028277	*POU2F2*	1.15E-29	2.726	1.458	1.909
ENSG00000109819	*PPARGC1A*	2.83E-03	1.321	0.027	0.644
ENSG00000110841	*PPFIBP1*	2.21E-19	1.046	0.176	0.470
ENSG00000108179	*PPIF*	5.14E-16	1.278	0.395	0.791
ENSG00000156475	*PPP2R2B*	6.70E-11	-2.243	-0.045	-1.067
ENSG00000214140	*PRCD*	1.96E-02	-1.622	-0.013	-0.106
ENSG00000057657	*PRDM1*	2.00E-04	1.887	0.010	0.099
ENSG00000186652	*PRG2*	1.81E-02	1.104	0.032	0.516
ENSG00000139174	*PRICKLE1*	2.64E-10	-1.465	-0.455	-0.998
ENSG00000146143	*PRIM2*	1.14E-08	-1.246	-0.077	-0.616
ENSG00000175785	*PRIMA1*	1.11E-03	-1.537	-0.006	-0.280
ENSG00000005249	*PRKAR2B*	7.90E-23	1.903	0.063	0.994
ENSG00000138669	*PRKG2*	5.05E-04	-1.822	-0.028	-0.314
ENSG00000135406	*PRPH*	1.71E-06	-1.918	-0.037	-0.518
ENSG00000167371	*PRRT2*	1.99E-12	-1.247	-0.409	-0.676

ENSG00000146250	*PRSS35*	1.28E-11	-2.521	-0.046	-1.041
ENSG00000125637	*PSD4*	6.35E-08	1.226	0.065	0.595
ENSG00000117425	*PTCH2*	2.59E-09	-1.434	-0.073	-0.783
ENSG00000148344	*PTGES*	6.11E-14	2.616	0.022	0.466
ENSG00000122420	*PTGFR*	1.91E-45	2.022	0.871	1.315
ENSG00000073756	*PTGS2*	4.17E-12	3.153	0.016	0.546
ENSG00000087494	*PTHLH*	9.10E-07	1.282	0.561	1.080
ENSG00000163629	*PTPN13*	2.79E-14	-1.131	-0.366	-0.767
ENSG00000163661	*PTX3*	4.05E-04	1.148	0.038	0.566
ENSG00000068976	*PYGM*	4.76E-03	-1.517	-0.025	-0.396
ENSG00000103485	*QPRT*	1.49E-03	-2.095	-0.002	-0.063
ENSG00000139832	*RAB20*	2.62E-04	1.252	0.032	0.677
ENSG00000167964	*RAB26*	9.84E-06	-1.505	-0.034	-0.465
ENSG00000041353	*RAB27B*	1.02E-25	2.460	1.060	1.576
ENSG00000172794	*RAB37*	1.75E-04	-1.168	-0.035	-0.530
ENSG00000169750	*RAC3*	5.60E-10	-1.220	-0.057	-0.306
ENSG00000166349	*RAG1*	1.73E-04	-1.221	-0.018	-0.840
ENSG00000164188	*RANBP3L*	2.29E-02	-1.006	0.001	-0.093
ENSG00000108551	*RASD1*	2.39E-10	2.710	0.024	1.313
ENSG00000103710	*RASL12*	1.29E-05	-1.542	-0.038	-0.967
ENSG00000163694	*RBM47*	3.45E-04	1.122	0.037	0.494
ENSG00000159200	*RCAN1*	2.03E-07	1.210	0.024	0.337
ENSG00000172348	*RCAN2*	7.86E-18	-3.059	-0.077	-1.624
ENSG00000167771	*RCOR2*	5.78E-05	-1.537	-0.033	-0.566
ENSG00000104856	*RELB*	2.20E-22	1.716	0.334	0.760
ENSG00000054967	*RELT*	3.67E-06	1.316	0.022	0.982
ENSG00000088320	*REM1*	1.07E-04	-1.040	-0.037	-0.306
ENSG00000174236	*REP15*	1.99E-04	1.104	0.039	0.467
ENSG00000154153	*RETREG1*	1.18E-17	1.586	0.356	0.817
ENSG00000009413	*REV3L*	2.18E-17	1.223	0.154	0.477
ENSG00000178882	*RFLNA*	2.75E-04	-1.472	-0.038	-0.755
ENSG00000131378	*RFTN1*	1.55E-18	-1.043	-0.387	-0.651
ENSG00000143333	*RGS16*	2.21E-13	1.196	0.341	0.625
ENSG00000132554	*RGS22*	1.49E-02	-1.142	-0.024	-0.206
ENSG00000108370	*RGS9*	1.58E-02	-1.429	-0.015	-0.133
ENSG00000072422	*RHOBTB1*	3.65E-17	-1.372	-0.532	-0.866
ENSG00000111913	*RIPOR2*	4.17E-06	1.034	0.020	0.222
ENSG00000042062	*RIPOR3*	6.20E-07	1.573	0.014	0.670
ENSG00000108830	*RND2*	9.52E-04	-1.250	-0.020	-0.157
ENSG00000101695	*RNF125*	1.10E-03	-1.462	-0.019	-0.917
ENSG00000137393	*RNF144B*	2.03E-10	1.068	0.008	0.124
ENSG00000108375	*RNF43*	3.04E-05	-1.388	-0.057	-0.583

ENSG00000185008	*ROBO2*	1.81E-07	-0.969	-0.279	-1.007
ENSG00000169071	*ROR2*	4.34E-06	1.114	0.086	0.511
ENSG00000143365	*RORC*	2.25E-02	-1.433	-0.015	-0.133
ENSG00000156313	*RPGR*	2.81E-09	1.026	0.271	0.686
ENSG00000215853	*RPTN*	1.48E-02	-1.545	-0.016	-0.157
ENSG00000166592	*RRAD*	1.48E-05	1.292	0.033	0.589
ENSG00000146374	*RSPO3*	4.14E-20	1.701	0.633	1.056
ENSG00000179300	*RTL3*	1.32E-04	-1.032	-0.040	-0.438
ENSG00000242732	*RTL5*	3.00E-17	-1.066	-0.425	-0.529
ENSG00000040608	*RTN4R*	4.82E-02	-1.059	0.000	-0.070
ENSG00000186907	*RTN4RL2*	3.21E-09	2.475	0.029	1.593
ENSG00000171509	*RXFP1*	2.70E-03	1.111	0.030	0.109
ENSG00000170989	*S1PR1*	5.56E-11	1.886	0.537	1.197
ENSG00000213694	*S1PR3*	1.23E-05	1.144	0.030	0.454
ENSG00000173432	*SAA1*	2.81E-28	6.628	0.033	4.583
ENSG00000134339	*SAA2*	1.63E-17	6.156	0.030	4.201
ENSG00000177570	*SAMD12*	8.30E-06	-1.894	-0.012	-0.956
ENSG00000203943	*SAMD13*	5.60E-04	-1.538	-0.024	-0.684
ENSG00000164483	*SAMD3*	1.34E-02	-1.185	-0.008	-0.171
ENSG00000203727	*SAMD5*	8.65E-15	-1.299	-0.267	-0.728
ENSG00000123453	*SARDH*	6.98E-05	-1.678	-0.026	-0.550
ENSG00000130066	*SAT1*	1.03E-30	1.594	0.276	0.648
ENSG00000064932	*SBNO2*	7.65E-27	1.791	0.783	1.247
ENSG00000073060	*SCARB1*	3.38E-12	1.087	0.370	0.685
ENSG00000184178	*SCFD2*	2.13E-10	-1.104	-0.409	-0.653
ENSG00000171951	*SCG2*	3.17E-06	1.217	0.428	0.888
ENSG00000161929	*SCIMP*	6.46E-04	-1.006	-0.013	-0.521
ENSG00000006747	*SCIN*	1.97E-06	-1.206	-0.041	-0.542
ENSG00000136531	*SCN2A*	6.29E-03	-1.399	-0.017	-0.340
ENSG00000149575	*SCN2B*	1.97E-08	-1.536	-0.050	-0.568
ENSG00000153253	*SCN3A*	5.28E-03	-1.499	-0.010	-0.838
ENSG00000103184	*SEC14L5*	4.45E-04	-1.255	-0.591	-0.829
ENSG00000120341	*SEC16B*	3.21E-05	-1.076	-0.035	-0.696
ENSG00000174175	*SELP*	3.55E-04	1.944	0.009	0.148
ENSG00000170381	*SEMA3E*	1.31E-14	-1.120	-0.188	-0.596
ENSG00000137872	*SEMA6D*	1.75E-05	1.014	0.018	0.174
ENSG00000108387	*SEPT4*	1.86E-05	-1.468	-0.036	-0.658
ENSG00000135919	*SERPINE2*	4.30E-11	1.381	0.056	0.539
ENSG00000198879	*SFMBT2*	1.84E-08	1.439	0.004	0.195
ENSG00000104332	*SFRP1*	8.13E-11	2.622	0.031	1.204
ENSG00000167037	*SGSM1*	5.88E-04	-1.524	-0.013	-0.112
ENSG00000183918	*SH2D1A*	1.57E-02	-1.499	-0.011	-0.103

ENSG00000169247	*SH3TC2*	4.95E-03	-1.051	-0.020	-0.676
ENSG00000162105	*SHANK2*	1.54E-05	-1.122	-0.057	-0.680
ENSG00000107338	*SHB*	1.68E-17	1.951	0.422	1.116
ENSG00000185634	*SHC4*	7.72E-07	-1.502	-0.477	-0.702
ENSG00000138771	*SHROOM3*	2.40E-13	-1.768	-0.622	-1.255
ENSG00000197046	*SIGLEC15*	4.55E-03	-1.345	-0.019	-0.930
ENSG00000142178	*SIK1*	4.87E-16	2.314	0.038	1.065
ENSG00000198053	*SIRPA*	3.08E-34	1.125	0.116	0.409
ENSG00000101307	*SIRPB1*	1.20E-04	1.119	0.031	0.163
ENSG00000110911	*SLC11A2*	1.21E-34	1.278	0.495	0.731
ENSG00000141469	*SLC14A1*	2.60E-16	-3.065	-1.073	-1.855
ENSG00000112394	*SLC16A10*	9.05E-07	3.011	0.003	0.089
ENSG00000174326	*SLC16A11*	2.40E-02	-1.070	-0.016	0.011
ENSG00000163053	*SLC16A14*	2.86E-06	-1.387	-0.033	-0.592
ENSG00000141526	*SLC16A3*	2.02E-11	1.187	0.253	0.723
ENSG00000108932	*SLC16A6*	4.90E-02	1.236	0.004	0.011
ENSG00000118596	*SLC16A7*	2.84E-12	1.629	0.059	0.591
ENSG00000165449	*SLC16A9*	1.05E-05	-1.593	-0.041	-0.436
ENSG00000146409	*SLC18B1*	1.41E-13	1.132	0.097	0.451
ENSG00000117479	*SLC19A2*	1.26E-12	1.334	0.069	0.654
ENSG00000135917	*SLC19A3*	1.32E-43	3.422	1.244	2.043
ENSG00000112499	*SLC22A2*	7.10E-03	1.944	0.003	0.024
ENSG00000137266	*SLC22A23*	9.23E-20	1.576	0.620	0.964
ENSG00000258708	*SLC25A21-AS1*	6.55E-03	-1.002	-0.031	-0.357
ENSG00000155287	*SLC25A28*	1.62E-21	1.803	0.185	0.818
ENSG00000147454	*SLC25A37*	1.43E-11	1.069	0.040	0.306
ENSG00000091137	*SLC26A4*	3.33E-07	-1.623	-0.046	-0.932
ENSG00000174502	*SLC26A9*	2.87E-05	2.849	0.001	0.067
ENSG00000143554	*SLC27A3*	4.65E-09	-1.113	-0.056	-0.408
ENSG00000117394	*SLC2A1*	2.22E-06	1.119	0.026	0.473
ENSG00000146411	*SLC2A12*	1.70E-09	-1.417	-0.060	-0.882
ENSG00000059804	*SLC2A3*	1.72E-06	1.590	0.033	0.740
ENSG00000142583	*SLC2A5*	1.50E-23	2.401	0.893	1.618
ENSG00000170385	*SLC30A1*	4.90E-27	1.591	0.522	0.818
ENSG00000139209	*SLC38A4*	4.18E-05	-1.631	-0.022	-0.983
ENSG00000104635	*SLC39A14*	3.49E-63	3.314	1.548	2.172
ENSG00000138821	*SLC39A8*	6.20E-40	3.420	0.048	1.223
ENSG00000138449	*SLC40A1*	2.74E-15	-1.888	-0.079	-0.930
ENSG00000167703	*SLC43A2*	6.82E-43	2.283	0.761	1.247
ENSG00000134802	*SLC43A3*	1.38E-27	1.441	0.406	0.840
ENSG00000180638	*SLC47A2*	3.29E-09	-1.426	-0.261	-0.466
ENSG00000131389	*SLC6A6*	5.46E-06	1.261	0.036	0.374

ENSG00000196517	*SLC6A9*	1.99E-06	1.089	0.043	0.550
ENSG00000003989	*SLC7A2*	5.29E-29	3.335	0.804	1.424
ENSG00000103257	*SLC7A5*	4.02E-10	1.743	0.039	0.736
ENSG00000183023	*SLC8A1*	1.00E-17	-1.473	-0.428	-0.946
ENSG00000124107	*SLPI*	4.44E-10	1.593	0.042	0.885
ENSG00000198732	*SMOC1*	2.13E-04	1.385	0.011	0.172
ENSG00000088826	*SMOX*	2.44E-10	1.584	0.449	0.837
ENSG00000124216	*SNAI1*	5.57E-05	1.017	0.057	0.435
ENSG00000065609	*SNAP91*	1.17E-02	-1.169	-0.014	-1.511
ENSG00000023608	*SNAPC1*	1.09E-11	1.102	0.346	0.619
ENSG00000145335	*SNCA*	7.74E-03	-1.663	-0.008	-0.063
ENSG00000064692	*SNCAIP*	1.36E-02	-1.093	-0.030	-0.169
ENSG00000173267	*SNCG*	5.00E-11	-1.374	-0.092	-0.485
ENSG00000184557	*SOCS3*	2.99E-31	1.734	0.544	1.037
ENSG00000112096	*SOD2*	1.02E-44	4.185	1.970	2.777
ENSG00000112096	*SOD2-OT1*	1.02E-44	4.185	1.970	2.777
ENSG00000137642	*SORL1*	2.25E-06	-1.024	-0.244	-0.817
ENSG00000137098	*SPAG8*	1.90E-03	-1.073	-0.029	-0.424
ENSG00000164266	*SPINK1*	2.27E-02	1.480	0.019	1.844
ENSG00000187678	*SPRY4*	1.89E-10	1.449	0.021	0.432
ENSG00000137877	*SPTBN5*	1.88E-03	-1.169	-0.035	-1.017
ENSG00000196542	*SPTSSB*	2.34E-09	-2.019	-0.054	-1.195
ENSG00000122862	*SRGN*	7.70E-23	1.195	0.041	0.298
ENSG00000184343	*SRPK3*	6.40E-05	-1.339	-0.020	-0.545
ENSG00000117155	*SSX2IP*	1.90E-10	-1.174	-0.051	-0.495
ENSG00000144057	*ST6GAL2*	6.48E-03	-1.614	-0.021	-0.095
ENSG00000136840	*ST6GALNAC4*	1.35E-13	1.020	0.371	0.660
ENSG00000141750	*STAC2*	3.87E-08	2.019	0.017	0.660
ENSG00000168610	*STAT3*	5.08E-31	1.279	0.465	0.811
ENSG00000159167	*STC1*	2.29E-40	4.459	1.831	2.826
ENSG00000164647	*STEAP1*	1.18E-45	2.596	0.880	1.521
ENSG00000157214	*STEAP2*	4.31E-24	1.844	0.085	0.719
ENSG00000127954	*STEAP4*	1.34E-12	2.272	0.040	0.895
ENSG00000165209	*STRBP*	7.30E-16	-1.072	-0.271	-0.513
ENSG00000128578	*STRIP2*	2.18E-11	1.818	0.834	1.360
ENSG00000135604	*STX11*	1.05E-03	1.177	0.028	0.541
ENSG00000130540	*SULT4A1*	4.48E-05	1.355	-0.002	0.112
ENSG00000078269	*SYNJ2*	1.68E-23	1.294	0.469	0.747
ENSG00000182253	*SYNM*	1.57E-19	-1.167	-0.318	-0.625
ENSG00000143028	*SYPL2*	2.83E-02	-1.091	-0.006	-0.050
ENSG00000019505	*SYT13*	1.33E-02	-1.629	-0.008	-0.136
ENSG00000137501	*SYTL2*	9.06E-08	-1.076	-0.069	-0.535

ENSG00000165929	*TC2N*	2.56E-09	2.618	0.019	1.394
ENSG00000081059	*TCF7*	2.28E-11	-1.165	-0.069	-0.407
ENSG00000182134	*TDRKH*	1.44E-04	-1.218	-0.027	-0.640
ENSG00000120156	*TEK*	8.87E-08	-1.877	-0.045	-1.082
ENSG00000105825	*TFPI2*	1.65E-07	2.166	0.023	0.842
ENSG00000072274	*TFRC*	3.83E-14	1.188	0.458	0.663
ENSG00000092969	*TGFB2*	9.61E-19	-1.089	-0.409	-0.715
ENSG00000106799	*TGFBR1*	1.02E-22	1.125	0.300	0.561
ENSG00000177426	*TGIF1*	1.38E-11	1.042	0.259	0.596
ENSG00000157150	*TIMP4*	5.58E-07	-1.138	-0.039	-0.482
ENSG00000137462	*TLR2*	4.35E-06	2.375	0.009	0.104
ENSG00000187554	*TLR5*	3.71E-05	-1.362	-0.040	-0.703
ENSG00000166292	*TMEM100*	7.77E-11	2.097	0.771	0.944
ENSG00000183160	*TMEM119*	1.53E-23	-2.257	-0.682	-1.119
ENSG00000166448	*TMEM130*	1.57E-02	-1.677	-0.014	-0.147
ENSG00000157111	*TMEM171*	4.35E-13	-1.651	-0.516	-1.198
ENSG00000172738	*TMEM217*	8.14E-06	1.647	0.025	0.838
ENSG00000196932	*TMEM26*	9.94E-24	-2.393	-0.813	-1.337
ENSG00000126950	*TMEM35A*	1.73E-05	-2.574	-0.020	-0.257
ENSG00000171227	*TMEM37*	2.49E-03	-1.280	-0.033	-0.864
ENSG00000147027	*TMEM47*	1.94E-34	-1.079	-0.395	-0.728
ENSG00000136842	*TMOD1*	7.91E-20	2.336	0.786	1.473
ENSG00000128872	*TMOD2*	2.31E-05	-1.158	-0.042	-0.790
ENSG00000041982	*TNC*	3.92E-14	1.354	0.075	0.616
ENSG00000185215	*TNFAIP2*	1.79E-24	1.668	0.071	0.535
ENSG00000118503	*TNFAIP3*	2.62E-50	1.978	0.262	0.675
ENSG00000123610	*TNFAIP6*	9.68E-38	5.293	1.605	2.813
ENSG00000145779	*TNFAIP8*	6.62E-12	1.202	0.010	0.184
ENSG00000173535	*TNFRSF10C*	8.92E-04	-1.037	-0.041	-0.189
ENSG00000164761	*TNFRSF11B*	2.72E-15	1.711	0.580	0.971
ENSG00000127863	*TNFRSF19*	1.00E-17	-2.323	-0.753	-1.361
ENSG00000028137	*TNFRSF1B*	6.99E-21	2.501	0.464	1.185
ENSG00000049249	*TNFRSF9*	1.70E-04	1.759	0.007	0.062
ENSG00000121858	*TNFSF10*	3.79E-02	1.039	0.010	0.051
ENSG00000120659	*TNFSF11*	5.25E-04	2.614	0.010	0.123
ENSG00000154310	*TNIK*	2.64E-14	1.084	0.219	0.328
ENSG00000131746	*TNS4*	1.18E-05	1.562	0.028	0.695
ENSG00000198846	*TOX*	1.00E-12	-2.133	-0.060	-1.047
ENSG00000078804	*TP53INP2*	3.82E-25	1.166	0.216	0.569
ENSG00000111669	*TPI1*	1.53E-12	1.024	0.260	0.588
ENSG00000056972	*TRAF3IP2*	1.81E-17	1.010	0.325	0.637
ENSG00000124731	*TREM1*	3.71E-09	3.986	0.010	1.826

ENSG00000173334	*TRIB1*	9.21E-19	1.772	0.837	1.302
ENSG00000121060	*TRIM25*	2.96E-06	1.020	0.008	0.157
ENSG00000134253	*TRIM45*	1.69E-07	-1.413	-0.046	-0.880
ENSG00000158022	*TRIM63*	3.45E-02	1.631	0.016	0.133
ENSG00000137672	*TRPC6*	2.99E-06	-1.897	-0.025	-0.760
ENSG00000157514	*TSC22D3*	2.73E-24	-1.014	-0.255	-0.374
ENSG00000099282	*TSPAN15*	1.58E-04	-1.463	-0.032	-0.238
ENSG00000157570	*TSPAN18*	6.47E-07	-1.570	-0.036	-0.681
ENSG00000064201	*TSPAN32*	2.54E-07	-1.578	-0.026	-0.736
ENSG00000122691	*TWIST1*	2.52E-17	1.387	0.456	0.825
ENSG00000025708	*TYMP*	3.81E-11	2.102	0.046	1.054
ENSG00000145040	*UCN2*	5.69E-05	1.270	-0.003	0.000
ENSG00000112715	*VEGFA*	2.62E-08	1.960	0.030	0.796
ENSG00000112299	*VNN1*	1.20E-31	3.323	0.048	1.656
ENSG00000112303	*VNN2*	1.89E-02	1.555	0.003	0.056
ENSG00000093134	*VNN3*	7.11E-26	5.096	0.014	2.715
ENSG00000214376	*VSTM5*	5.62E-04	-2.034	-0.008	-0.722
ENSG00000188730	*VWC2*	4.69E-04	1.596	0.024	1.410
ENSG00000166272	*WBP1L*	5.64E-24	1.051	0.272	0.627
ENSG00000162643	*WDR63*	8.08E-04	-1.140	-0.036	-0.504
ENSG00000187260	*WDR86*	1.46E-06	1.905	0.005	0.236
ENSG00000103175	*WFDC1*	5.21E-07	-1.376	-0.439	-0.887
ENSG00000070540	*WIPI1*	4.81E-26	1.542	0.497	0.888
ENSG00000104415	*WISP1*	4.73E-20	1.562	0.052	0.488
ENSG00000114251	*WNT5A*	1.37E-10	1.138	0.057	0.352
ENSG00000075035	*WSCD2*	8.32E-19	-1.953	-0.649	-1.198
ENSG00000146457	*WTAP*	1.64E-42	2.368	0.830	1.355
ENSG00000047597	*XK*	8.54E-03	-0.855	-0.025	-1.347
ENSG00000103489	*XYLT1*	5.83E-11	1.129	0.055	0.439
ENSG00000166793	*YPEL4*	4.03E-06	-1.011	-0.102	-0.356
ENSG00000163874	*ZC3H12A*	5.33E-56	3.384	1.932	2.424
ENSG00000066185	*ZMYND12*	1.60E-05	-1.369	-0.011	-0.202
ENSG00000168661	*ZNF30*	1.15E-04	-1.093	-0.038	-0.232
ENSG00000161642	*ZNF385A*	7.29E-07	1.101	0.107	0.644
ENSG00000144331	*ZNF385B*	1.09E-04	-1.022	-0.019	-0.233
ENSG00000175322	*ZNF519*	7.13E-05	-1.299	-0.038	-0.375
ENSG00000176472	*ZNF575*	1.39E-05	-1.149	-0.033	-0.439
ENSG00000178882	*ZNF664-RFLNA*	2.75E-04	-1.472	-0.038	-0.755
ENSG00000143067	*ZNF697*	5.77E-09	1.141	0.063	0.670
ENSG00000164684	*ZNF704*	7.74E-11	-1.126	-0.187	-0.626
ENSG00000197385	*ZNF860*	2.75E-07	-1.183	-0.024	-0.839
ENSG00000132003	*ZSWIM4*	9.33E-10	1.152	0.078	0.566

C3.2 Differentially expressed genes in end-stage OA synovial fibroblasts

Table C3-2. *Overview of differentially expressed genes in synovial fibroblasts between control or IL-17 treated samples with an adjusted p-value of <0.05. Green boxes note logarithmic fold changes (LFC) of at least +1 and red boxes note LFC of at least -1, while blank boxes show an LFC between -1 and 1. Genes are sorted alphabetically on SYMBOL gene name.*

Ensemble gene name	SYMBOL gene name	Adjusted p-value	Log2 Fold Change (LFC)		
			IL-17A	IL-17F	IL-17AF
ENSG00000198691	*ABCA4*	1.41E-02	1.608	0.017	0.043
ENSG00000129048	*ACKR4*	5.44E-07	-1.132	-0.024	-0.075
ENSG00000068366	*ACSL4*	9.93E-17	1.072	0.213	0.352
ENSG00000159251	*ACTC1*	1.15E-08	-1.709	-0.823	-0.968
ENSG00000138316	*ADAMTS14*	1.06E-11	-1.173	-0.374	-0.541
ENSG00000158859	*ADAMTS4*	9.61E-03	1.363	0.009	0.040
ENSG00000111452	*ADGRD1*	2.21E-11	1.993	0.041	0.900
ENSG00000150594	*ADRA2A*	6.37E-04	-1.397	-0.017	-0.053
ENSG00000111863	*ADTRP*	5.40E-04	1.027	0.047	0.505
ENSG00000042286	*AIFM2*	2.05E-16	1.192	0.445	0.637
ENSG00000154027	*AK5*	3.95E-03	-1.120	-0.032	-0.074
ENSG00000171819	*ANGPTL7*	2.52E-04	-2.096	-0.020	-0.068
ENSG00000151150	*ANK3*	1.35E-06	-1.430	-0.020	-0.055
ENSG00000154856	*APCDD1*	1.24E-03	1.100	0.023	0.496
ENSG00000171388	*APLN*	6.14E-08	1.679	0.684	1.079
ENSG00000221963	*APOL6*	9.66E-10	1.078	0.555	0.682
ENSG00000165272	*AQP3*	2.16E-10	-1.920	-0.951	-1.104
ENSG00000165269	*AQP7*	8.36E-07	-1.958	-0.030	-0.786
ENSG00000103569	*AQP9*	2.07E-10	3.261	0.018	1.766
ENSG00000106819	*ASPN*	6.59E-05	-1.163	-0.390	-0.592
ENSG00000018625	*ATP1A2*	1.75E-02	-1.055	-0.024	-0.065
ENSG00000104043	*ATP8B4*	3.24E-04	1.082	0.416	0.666
ENSG00000140379	*BCL2A1*	2.38E-09	2.812	0.033	1.549
ENSG00000069399	*BCL3*	1.61E-38	1.728	0.849	1.037
ENSG00000100739	*BDKRB1*	5.09E-05	1.169	0.021	0.066
ENSG00000023445	*BIRC3*	1.25E-08	1.167	0.009	0.048
ENSG00000153162	*BMP6*	1.28E-06	1.711	0.024	0.101
ENSG00000166920	*C15orf48*	2.19E-25	4.851	0.024	2.328
ENSG00000145861	*C1QTNF2*	2.92E-08	-1.767	-0.036	-0.322
ENSG00000163145	*C1QTNF7*	2.41E-03	-1.068	0.006	-0.004
ENSG00000139178	*C1RL*	7.97E-26	1.331	0.943	1.039
ENSG00000198535	*C2CD4A*	8.65E-12	2.015	0.037	0.742
ENSG00000205502	*C2CD4B*	2.47E-13	2.029	0.020	1.095

ENSG00000125730	*C3*	7.08E-08	1.400	0.034	0.514
ENSG00000134830	*C5AR2*	2.21E-02	1.194	0.007	0.030
ENSG00000074410	*CA12*	9.22E-12	1.017	0.324	0.450
ENSG00000204682	*CASC10*	1.13E-03	-1.142	-0.002	-0.076
ENSG00000143318	*CASQ1*	4.27E-03	-1.458	-0.014	0.003
ENSG00000198624	*CCDC69*	4.54E-05	1.282	0.031	0.676
ENSG00000181374	*CCL13*	3.19E-03	2.551	0.004	0.022
ENSG00000108691	*CCL2*	7.03E-09	2.150	0.023	0.769
ENSG00000115009	*CCL20*	3.46E-15	6.252	0.021	0.068
ENSG00000163823	*CCR1*	1.93E-03	1.096	0.016	0.097
ENSG00000126353	*CCR7*	1.97E-05	2.089	0.018	1.022
ENSG00000004468	*CD38*	2.02E-03	1.861	0.001	0.007
ENSG00000121594	*CD80*	2.00E-03	2.310	0.009	0.017
ENSG00000163814	*CDCP1*	9.80E-14	1.655	0.592	0.903
ENSG00000138395	*CDK15*	8.80E-04	-1.863	0.001	-0.034
ENSG00000221869	*CEBPD*	8.01E-19	1.888	0.792	1.063
ENSG00000105792	*CFAP69*	1.38E-18	1.498	0.494	0.605
ENSG00000243649	*CFB*	8.25E-13	1.676	0.035	0.625
ENSG00000138135	*CH25H*	3.82E-03	2.043	0.004	0.030
ENSG00000016391	*CHDH*	1.54E-05	-1.015	-0.376	-0.096
ENSG00000064886	*CHI3L2*	8.97E-24	3.314	0.770	1.760
ENSG00000159212	*CLIC6*	2.02E-06	1.648	0.029	0.866
ENSG00000134326	*CMPK2*	1.93E-02	1.671	0.871	0.039
ENSG00000154529	*CNTNAP3B*	4.06E-03	-1.012	-0.029	-0.604
ENSG00000100473	*COCH*	3.55E-04	1.317	0.026	0.028
ENSG00000204291	*COL15A1*	7.51E-06	1.019	0.382	0.583
ENSG00000081052	*COL4A4*	2.92E-03	1.067	0.019	0.037
ENSG00000047457	*CP*	3.00E-24	1.472	0.475	0.707
ENSG00000108342	*CSF3*	8.69E-18	8.823	0.023	5.969
ENSG00000135047	*CTSL*	3.03E-30	1.443	0.659	0.865
ENSG00000163131	*CTSS*	1.35E-23	1.492	0.261	0.648
ENSG00000163739	*CXCL1*	3.52E-43	7.132	4.338	4.983
ENSG00000081041	*CXCL2*	1.76E-25	4.725	2.923	3.067
ENSG00000163734	*CXCL3*	2.85E-28	4.971	2.435	2.917
ENSG00000163735	*CXCL5*	2.70E-14	3.685	0.018	1.398
ENSG00000124875	*CXCL6*	2.68E-27	6.126	3.437	4.140
ENSG00000169429	*CXCL8*	2.64E-19	3.686	0.918	1.386
ENSG00000137869	*CYP19A1*	2.38E-06	1.844	1.032	1.569
ENSG00000172817	*CYP7B1*	2.19E-03	1.703	0.012	0.045
ENSG00000164488	*DACT2*	1.80E-04	2.179	0.019	1.661
ENSG00000123977	*DAW1*	3.19E-05	2.235	0.023	0.982
ENSG00000164825	*DEFB1*	3.48E-02	1.159	0.009	0.029

ENSG00000165507	*DEPP1*	2.11E-09	1.402	0.468	0.598
ENSG00000062282	*DGAT2*	4.02E-25	2.007	1.117	1.327
ENSG00000211448	*DIO2*	7.23E-07	1.661	0.028	0.603
ENSG00000149927	*DOC2A*	6.79E-03	-1.323	-0.012	-0.051
ENSG00000102385	*DRP2*	8.72E-06	-1.610	-0.046	-0.556
ENSG00000134769	*DTNA*	1.24E-12	1.162	0.430	0.546
ENSG00000139318	*DUSP6*	5.38E-11	1.498	0.509	0.782
ENSG00000136160	*EDNRB*	8.44E-10	1.099	0.420	0.637
ENSG00000164181	*ELOVL7*	9.27E-10	1.698	0.034	0.763
ENSG00000198018	*ENTPD7*	9.37E-09	1.030	0.092	0.282
ENSG00000133106	*EPSTI1*	6.45E-03	1.281	0.926	0.818
ENSG00000124882	*EREG*	3.28E-04	1.095	0.027	0.222
ENSG00000178752	*ERFE*	2.16E-09	1.346	0.331	0.802
ENSG00000139083	*ETV6*	3.02E-11	1.014	0.474	0.633
ENSG00000185862	*EVI2B*	3.69E-10	1.934	0.585	1.265
ENSG00000110723	*EXPH5*	7.62E-13	-1.347	-0.569	-0.886
ENSG00000181104	*F2R*	1.33E-13	-1.213	-0.052	-0.400
ENSG00000121769	*FABP3*	7.39E-12	-1.154	-0.536	-0.697
ENSG00000170323	*FABP4*	1.11E-03	-1.406	-0.028	-0.058
ENSG00000150510	*FAM124A*	2.79E-08	1.299	0.039	0.634
ENSG00000159784	*FAM131B*	1.16E-02	-1.061	-0.015	-0.065
ENSG00000147724	*FAM135B*	1.68E-03	-1.137	-0.031	-0.079
ENSG00000148541	*FAM13C*	1.77E-03	-1.198	-0.021	-0.091
ENSG00000197520	*FAM177B*	1.94E-04	1.496	0.016	0.621
ENSG00000204767	*FAM196B*	4.71E-03	1.046	0.436	0.398
ENSG00000164125	*FAM198B*	4.24E-18	1.249	0.595	0.661
ENSG00000108950	*FAM20A*	8.35E-15	1.680	0.614	0.949
ENSG00000185112	*FAM43A*	1.50E-05	-1.107	-0.041	-0.370
ENSG00000165323	*FAT3*	1.34E-07	-1.146	-0.364	-0.833
ENSG00000146267	*FAXC*	1.07E-02	-1.332	-0.002	-0.015
ENSG00000162894	*FCMR*	2.36E-03	1.275	-0.005	0.020
ENSG00000118407	*FILIP1*	4.84E-02	1.127	0.005	0.020
ENSG00000204131	*FLJ44635*	1.19E-03	-1.201	-0.020	-0.110
ENSG00000125848	*FLRT3*	1.24E-09	2.141	0.026	0.746
ENSG00000138759	*FRAS1*	7.46E-05	1.587	0.019	0.986
ENSG00000131386	*GALNT15*	1.58E-19	1.225	0.569	0.720
ENSG00000162645	*GBP2*	1.19E-05	1.262	0.025	0.618
ENSG00000131979	*GCH1*	4.03E-04	1.401	0.011	0.044
ENSG00000131459	*GFPT2*	3.48E-12	1.017	0.163	0.436
ENSG00000168546	*GFRA2*	3.87E-02	1.130	0.017	0.062
ENSG00000165474	*GJB2*	4.02E-06	1.112	0.017	0.169
ENSG00000107249	*GLIS3*	4.46E-16	1.251	0.353	0.499

ENSG00000173221	*GLRX*	2.16E-13	1.168	0.399	0.589
ENSG00000127920	*GNG11*	5.58E-23	1.276	0.582	0.763
ENSG00000167588	*GPD1*	3.10E-07	-1.705	-0.031	-0.121
ENSG00000164850	*GPER1*	6.99E-09	-1.022	-0.123	-0.132
ENSG00000158292	*GPR153*	4.90E-17	-1.122	-0.413	-0.514
ENSG00000105509	*HAS1*	2.72E-06	1.649	0.016	0.081
ENSG00000188290	*HES4*	2.65E-04	1.072	0.033	1.028
ENSG00000135245	*HILPDA*	4.57E-08	1.764	0.014	0.059
ENSG00000127124	*HIVEP3*	1.30E-07	1.548	0.726	0.538
ENSG00000108924	*HLF*	2.21E-07	-1.564	-0.833	-1.054
ENSG00000164120	*HPGD*	1.14E-05	-3.144	-0.019	-0.049
ENSG00000117594	*HSD11B1*	9.16E-15	1.219	0.466	0.628
ENSG00000169271	*HSPB3*	1.77E-03	-1.657	-0.018	-0.057
ENSG00000173641	*HSPB7*	2.12E-21	-1.279	-0.470	-0.586
ENSG00000102468	*HTR2A*	2.72E-04	1.727	0.017	0.061
ENSG00000169495	*HTRA4*	1.14E-02	1.113	0.013	0.061
ENSG00000090339	*ICAM1*	3.33E-28	1.765	0.528	0.782
ENSG00000160223	*ICOSLG*	5.86E-07	1.466	0.669	0.667
ENSG00000131203	*IDO1*	3.66E-03	2.037	0.014	0.039
ENSG00000068079	*IFI35*	3.00E-04	1.172	0.427	0.544
ENSG00000103742	*IGDCC4*	1.76E-07	-1.160	-0.255	-0.449
ENSG00000146678	*IGFBP1*	7.61E-10	1.294	0.405	0.741
ENSG00000134470	*IL15RA*	2.63E-10	1.622	0.674	0.573
ENSG00000115604	*IL18R1*	9.66E-10	1.346	0.616	0.799
ENSG00000115602	*IL1RL1*	3.15E-08	1.087	0.039	0.597
ENSG00000136689	*IL1RN*	1.69E-03	1.066	0.011	0.016
ENSG00000142677	*IL22RA1*	2.27E-02	-1.101	-0.017	-0.023
ENSG00000008517	*IL32*	3.73E-13	1.719	0.582	1.167
ENSG00000137033	*IL33*	6.84E-20	1.898	0.719	1.047
ENSG00000136696	*IL36B*	1.92E-08	1.541	0.053	1.105
ENSG00000136695	*IL36RN*	1.66E-04	1.555	0.015	0.067
ENSG00000104951	*IL4I1*	2.17E-04	1.627	0.014	1.354
ENSG00000136244	*IL6*	6.10E-23	5.532	2.586	3.071
ENSG00000168685	*IL7R*	4.60E-04	1.031	0.049	0.440
ENSG00000125347	*IRF1*	2.57E-22	1.183	0.537	0.655
ENSG00000137265	*IRF4*	2.31E-03	1.058	0.018	0.048
ENSG00000128604	*IRF5*	5.34E-03	1.522	0.019	0.042
ENSG00000091409	*ITGA6*	1.52E-12	-1.016	-0.498	-0.758
ENSG00000105855	*ITGB8*	1.79E-10	1.019	0.399	0.476
ENSG00000105639	*JAK3*	3.98E-07	1.728	0.758	0.817
ENSG00000158445	*KCNB1*	1.02E-04	-1.076	-0.020	-0.023
ENSG00000143473	*KCNH1*	8.53E-04	1.229	0.025	0.635

ENSG00000184156	*KCNQ3*	2.56E-06	1.361	0.589	0.839
ENSG00000157404	*KIT*	1.25E-05	-1.175	-0.031	-0.502
ENSG00000239474	*KLHL41*	8.44E-18	-1.099	-0.474	-0.639
ENSG00000170454	*KRT75*	9.33E-06	1.836	0.025	0.846
ENSG00000115919	*KYNU*	3.00E-17	1.320	0.632	0.813
ENSG00000179630	*LACC1*	6.12E-09	1.035	0.342	0.523
ENSG00000129988	*LBP*	5.74E-10	4.020	0.014	1.532
ENSG00000169744	*LDB2*	2.01E-22	-1.345	-0.330	-0.280
ENSG00000174697	*LEP*	5.90E-08	3.769	0.013	1.784
ENSG00000128342	*LIF*	3.24E-19	1.799	0.512	0.661
ENSG00000236882	*LINC01554*	7.50E-03	2.247	0.011	0.036
ENSG00000178734	*LMO7DN*	1.99E-04	-1.012	-0.789	-0.667
ENSG00000163431	*LMOD1*	4.54E-26	-2.020	-0.658	-0.847
ENSG00000111684	*LPCAT3*	4.25E-29	1.076	0.548	0.745
ENSG00000165379	*LRFN5*	5.92E-13	-1.251	-0.066	-0.588
ENSG00000173114	*LRRN3*	1.60E-12	-1.017	-0.627	-0.700
ENSG00000162951	*LRRTM1*	3.74E-02	1.511	0.012	0.035
ENSG00000172901	*LVRN*	2.28E-05	1.187	0.023	0.132
ENSG00000165072	*MAMDC2*	1.92E-05	-1.019	-0.032	-0.330
ENSG00000107968	*MAP3K8*	2.92E-45	1.692	1.346	1.484
ENSG00000081189	*MEF2C*	1.32E-09	-1.091	-0.308	-0.611
ENSG00000005102	*MEOX1*	3.34E-03	1.052	-0.004	0.005
ENSG00000106511	*MEOX2*	2.90E-07	-1.495	-0.031	-0.180
ENSG00000106484	*MEST*	5.39E-15	-1.346	-0.503	-0.673
ENSG00000185432	*METTL7A*	2.94E-13	-1.075	-0.401	-0.611
ENSG00000168389	*MFSD2A*	2.74E-04	1.450	0.015	0.069
ENSG00000111341	*MGP*	3.90E-13	-1.158	-0.466	-0.652
ENSG00000108960	*MMD*	2.26E-21	1.029	0.409	0.588
ENSG00000196611	*MMP1*	6.39E-18	3.020	0.876	1.393
ENSG00000166670	*MMP10*	4.41E-06	1.390	0.020	0.753
ENSG00000149968	*MMP3*	3.27E-14	2.020	0.051	0.916
ENSG00000082126	*MPP4*	2.46E-02	-1.057	-0.022	-0.068
ENSG00000072952	*MRVI1*	6.13E-14	-1.613	-0.045	-0.159
ENSG00000178860	*MSC*	1.72E-14	1.255	0.255	0.436
ENSG00000138379	*MSTN*	1.45E-09	-2.534	-0.045	-0.687
ENSG00000120149	*MSX2*	2.74E-09	1.079	0.090	0.580
ENSG00000169715	*MT1E*	1.37E-18	1.151	0.438	0.631
ENSG00000198417	*MT1F*	1.73E-02	1.132	0.007	0.031
ENSG00000125144	*MT1G*	3.17E-06	2.363	0.018	0.047
ENSG00000187193	*MT1X*	9.02E-21	1.646	0.534	0.946
ENSG00000125148	*MT2A*	9.47E-13	1.399	0.390	0.705
ENSG00000183486	*MX2*	6.01E-03	2.070	1.135	0.034

ENSG00000136449	*MYCBPAP*	4.20E-02	-1.452	-0.004	-0.009
ENSG00000034971	*MYOC*	1.07E-20	-1.110	-0.592	-0.780
ENSG00000101605	*MYOM1*	3.38E-05	-1.389	-0.036	-1.203
ENSG00000105835	*NAMPT*	2.76E-13	2.208	0.039	0.758
ENSG00000176771	*NCKAP5*	1.34E-02	-1.281	-0.012	-0.030
ENSG00000124479	*NDP*	1.92E-15	2.278	0.850	1.032
ENSG00000167604	*NFKBID*	3.08E-08	1.137	0.793	1.091
ENSG00000144802	*NFKBIZ*	2.09E-163	3.681	2.950	3.025
ENSG00000204131	*NHSL2*	1.19E-03	-1.201	-0.020	-0.110
ENSG00000166741	*NNMT*	1.46E-29	2.315	1.196	1.540
ENSG00000183691	*NOG*	2.85E-05	1.411	0.037	0.924
ENSG00000171246	*NPTX1*	1.16E-11	-1.203	-0.437	-0.680
ENSG00000182575	*NXPH3*	2.54E-04	-1.157	-0.006	-0.018
ENSG00000177989	*ODF3B*	3.64E-08	1.190	0.042	0.687
ENSG00000125510	*OPRL1*	3.71E-02	-1.259	-0.007	-0.041
ENSG00000145623	*OSMR*	2.03E-19	1.335	0.513	0.710
ENSG00000187950	*OVCH1*	9.50E-03	1.398	0.018	0.035
ENSG00000243444	*PALM2*	7.00E-07	1.195	0.059	0.614
ENSG00000138496	*PARP9*	5.02E-05	1.118	0.752	0.673
ENSG00000175426	*PCSK1*	5.06E-03	1.197	0.014	0.047
ENSG00000115252	*PDE1A*	1.13E-16	-1.013	-0.313	-0.530
ENSG00000113448	*PDE4D*	1.97E-07	2.047	0.024	0.907
ENSG00000138735	*PDE5A*	1.28E-26	-1.500	-0.452	-0.633
ENSG00000162493	*PDPN*	1.10E-32	1.809	0.745	1.046
ENSG00000109272	*PF4V1*	2.61E-02	1.309	0.001	0.031
ENSG00000114268	*PFKFB4*	1.61E-04	1.331	0.014	0.057
ENSG00000119630	*PGF*	3.04E-15	1.985	0.034	1.013
ENSG00000153823	*PID1*	3.84E-08	1.598	0.034	0.528
ENSG00000122861	*PLAU*	2.46E-04	1.060	0.045	0.748
ENSG00000115896	*PLCL1*	1.06E-13	-1.576	-0.846	-0.974
ENSG00000075651	*PLD1*	3.55E-07	1.400	0.025	0.406
ENSG00000147872	*PLIN2*	3.26E-10	1.020	0.064	0.356
ENSG00000188313	*PLSCR1*	4.31E-08	1.150	0.754	0.843
ENSG00000221866	*PLXNA4*	1.04E-03	1.046	0.013	0.099
ENSG00000141682	*PMAIP1*	8.72E-09	1.447	0.065	0.728
ENSG00000028277	*POU2F2*	6.86E-36	2.188	1.344	1.434
ENSG00000158528	*PPP1R9A*	1.64E-03	-1.531	-0.017	-0.045
ENSG00000156475	*PPP2R2B*	4.73E-05	-1.987	-0.028	-0.973
ENSG00000061455	*PRDM6*	1.51E-03	-1.144	-0.022	-0.049
ENSG00000186652	*PRG2*	2.76E-06	1.052	0.052	0.519
ENSG00000146250	*PRSS35*	8.58E-12	-1.544	-0.732	-0.766
ENSG00000140368	*PSTPIP1*	2.99E-02	0.150	0.014	1.586

ENSG00000117425	*PTCH2*	2.14E-03	-1.028	-0.022	-0.119
ENSG00000148344	*PTGES*	2.40E-13	1.121	0.075	0.366
ENSG00000122420	*PTGFR*	6.82E-26	1.698	0.727	0.921
ENSG00000073756	*PTGS2*	4.12E-09	1.958	0.036	0.659
ENSG00000163661	*PTX3*	7.13E-07	1.178	0.563	0.854
ENSG00000041353	*RAB27B*	1.26E-03	1.077	0.020	0.088
ENSG00000108551	*RASD1*	3.87E-06	1.895	0.018	0.645
ENSG00000198774	*RASSF9*	8.29E-09	-1.655	-0.727	-1.054
ENSG00000088320	*REM1*	2.15E-06	-1.622	0.000	-0.078
ENSG00000117152	*RGS4*	1.50E-06	-2.045	-0.678	-1.080
ENSG00000108370	*RGS9*	2.26E-06	-1.121	-0.389	-0.535
ENSG00000143878	*RHOB*	1.75E-07	1.491	0.025	0.503
ENSG00000072422	*RHOBTB1*	5.90E-10	-1.219	-0.297	-0.273
ENSG00000126785	*RHOJ*	2.09E-06	-1.163	-0.039	-0.076
ENSG00000079841	*RIMS1*	4.57E-04	-1.113	-0.032	-0.486
ENSG00000042062	*RIPOR3*	2.99E-14	1.877	0.466	0.738
ENSG00000169071	*ROR2*	2.80E-05	1.070	0.020	0.077
ENSG00000134321	*RSAD2*	1.48E-04	2.810	1.313	0.043
ENSG00000186907	*RTN4RL2*	1.03E-22	1.886	0.670	0.897
ENSG00000102445	*RUBCNL*	7.49E-23	1.805	0.861	1.156
ENSG00000231274	*SBK3*	3.88E-05	1.810	0.020	1.017
ENSG00000064932	*SBNO2*	2.54E-24	1.187	0.443	0.642
ENSG00000170381	*SEMA3E*	9.66E-15	-1.005	-0.325	-0.501
ENSG00000197632	*SERPINB2*	1.26E-26	2.110	0.628	1.076
ENSG00000102683	*SGCG*	3.28E-04	-1.620	-0.018	-0.545
ENSG00000164690	*SHH*	1.80E-06	1.846	0.028	1.085
ENSG00000142178	*SIK1*	1.11E-05	1.118	0.020	0.246
ENSG00000141469	*SLC14A1*	9.79E-05	-1.217	-0.021	-0.072
ENSG00000110446	*SLC15A3*	1.02E-03	1.072	0.026	0.134
ENSG00000118596	*SLC16A7*	1.80E-15	1.335	0.367	0.267
ENSG00000135917	*SLC19A3*	4.07E-17	2.331	0.577	0.831
ENSG00000137266	*SLC22A23*	1.69E-14	1.005	0.350	0.472
ENSG00000185052	*SLC24A3*	3.17E-08	1.601	0.043	0.709
ENSG00000140284	*SLC27A2*	3.29E-02	1.586	0.007	0.039
ENSG00000142583	*SLC2A5*	7.20E-24	1.277	0.506	0.798
ENSG00000169507	*SLC38A11*	2.79E-02	-1.491	-0.006	-0.028
ENSG00000104635	*SLC39A14*	9.59E-05	1.293	0.021	0.076
ENSG00000138821	*SLC39A8*	2.09E-06	2.061	0.014	0.058
ENSG00000138449	*SLC40A1*	4.85E-15	-1.246	-0.520	-0.797
ENSG00000167703	*SLC43A2*	4.18E-14	1.934	0.659	0.931
ENSG00000134802	*SLC43A3*	1.73E-17	1.011	0.307	0.486
ENSG00000003989	*SLC7A2*	3.90E-18	2.875	1.107	1.566

ENSG00000155465	*SLC7A7*	6.15E-06	1.080	0.602	0.574
ENSG00000184557	*SOCS3*	1.48E-19	1.343	0.322	0.631
ENSG00000112096	*SOD2*	6.72E-07	1.756	0.030	0.595
ENSG00000112096	*SOD2-OT1*	6.72E-07	1.756	0.030	0.595
ENSG00000137767	*SQOR*	3.26E-19	1.068	0.536	0.701
ENSG00000122862	*SRGN*	3.45E-17	1.112	0.055	0.352
ENSG00000115415	*STAT1*	3.46E-12	1.004	0.628	0.739
ENSG00000138378	*STAT4*	3.57E-13	1.978	0.967	1.474
ENSG00000159167	*STC1*	1.14E-22	2.934	1.167	1.536
ENSG00000164647	*STEAP1*	4.95E-24	1.721	0.754	0.971
ENSG00000157214	*STEAP2*	1.74E-09	1.548	0.591	0.731
ENSG00000127954	*STEAP4*	1.62E-04	1.337	0.583	0.965
ENSG00000140022	*STON2*	1.76E-04	1.055	0.396	0.331
ENSG00000128578	*STRIP2*	5.19E-16	1.702	0.558	0.844
ENSG00000170921	*TANC2*	2.21E-28	-1.005	-0.482	-0.673
ENSG00000170379	*TCAF2*	2.47E-03	1.055	0.005	0.021
ENSG00000176907	*TCIM*	7.51E-03	1.850	0.008	0.022
ENSG00000197905	*TEAD4*	1.08E-08	1.127	0.069	0.586
ENSG00000105825	*TFPI2*	2.05E-19	2.438	0.907	1.345
ENSG00000038295	*TLL1*	6.70E-07	-1.060	-0.405	-0.485
ENSG00000137462	*TLR2*	8.72E-09	2.258	0.010	0.050
ENSG00000183160	*TMEM119*	2.21E-28	-1.188	-0.414	-0.454
ENSG00000139364	*TMEM132B*	3.37E-05	1.255	0.023	0.076
ENSG00000164124	*TMEM144*	3.53E-03	1.019	0.025	0.051
ENSG00000249992	*TMEM158*	2.35E-08	1.493	0.446	0.865
ENSG00000196932	*TMEM26*	5.87E-04	-1.396	-0.022	-0.079
ENSG00000182107	*TMEM30B*	5.16E-19	-1.018	-0.332	-0.558
ENSG00000133687	*TMTC1*	2.39E-15	1.015	0.325	0.454
ENSG00000185215	*TNFAIP2*	8.69E-18	1.371	0.457	0.602
ENSG00000123610	*TNFAIP6*	4.04E-12	3.429	0.822	1.478
ENSG00000127863	*TNFRSF19*	1.64E-09	-1.236	-0.049	-0.198
ENSG00000028137	*TNFRSF1B*	1.84E-14	1.273	0.460	0.680
ENSG00000125735	*TNFSF14*	3.42E-04	2.187	0.008	0.030
ENSG00000111907	*TPD52L1*	4.27E-17	-1.066	-0.367	-0.469
ENSG00000124731	*TREM1*	3.10E-06	2.256	0.013	0.053
ENSG00000173334	*TRIB1*	2.06E-08	1.277	0.036	0.554
ENSG00000158022	*TRIM63*	1.98E-02	-1.277	-0.020	-0.047
ENSG00000104321	*TRPA1*	1.66E-03	1.046	0.020	0.083
ENSG00000182463	*TSHZ2*	5.00E-10	1.054	0.329	0.499
ENSG00000025708	*TYMP*	7.04E-39	2.023	1.057	1.337
ENSG00000162692	*VCAM1*	8.74E-07	1.198	0.035	0.191
ENSG00000170162	*VGLL2*	6.70E-03	1.047	0.013	0.084

ENSG00000119703	*ZC2HC1C*	6.46E-03	1.671	0.014	0.032
ENSG00000163874	*ZC3H12A*	2.17E-47	3.152	2.226	2.377
ENSG00000144331	*ZNF385B*	1.52E-10	-1.205	-0.315	-0.284

C4 Results from pathway analyses

C4.1 Pathway analysis results from chondrocyte samples

C4.1.1 Hallmark pathways

Table C4-1. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17A compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Allograft Rejection	0.021	1.91	*B2M, BCL3, CCL2, CCL7, CD1D, CTSS, EGFR, EIF5A, ETS1, GBP2, HDAC9, HIF1A, ICAM1, IFNGR1, IFNGR2, IL6, INHBA, JAK2, LIF, LYN, NCK1, NOS2, RIPK2, SRGN, TAPBP, TLR2, TRAF2, WARS*
Angiogenesis	0.024	2.02	*COL3A1, CXCL6, FSTL1, STC1, VEGFA*
Complement	0.001	2.41	*ADAM9, BRPF3, C1R, C1S, C3, CASP3, CD59, CEBPB, CFB, CLU, CP, CTSC, CTSD, CTSL, CTSS, CXCL1, DOCK4, DUSP5, DUSP6, FYN, GPD2, HSPA5, IL6, IRF1, IRF2, JAK2, KYNU, LYN, MAFF, MMP13, MMP14, PIM1, PLA2G4A, PLAUR, PSEN1, RAF1, RCE1, SERPINA1, TFPI2, TNFAIP3*
Estrogen Response Early	0.043	1.68	*B4GALT1, BAG1, BHLHE40, CA12, CD44, ELF3, ELOVL2, FKBP4, FOXC1, IGFBP4, IL6ST, JAK2, KLF10, KLF4, MUC1, MYC, PMAIP1, PPIF, PTGES, RAB31, RETREG1, SCARB1, SLC16A1, SLC19A2, SLC2A1, SLC7A2, SLC7A5, STC2, TGM2, TMEM164, TSKU, UGCG, XBP1*
Glycolysis	0.011	1.94	*AK4, ALDOA, ANGPTL4, B4GALT1, B4GALT4, CD44, COPB2, DDIT4, EGFR, EGLN3, ELF3, ENO1, ENO2, ERO1A, EXT2, FKBP4, GFPT1, GLRX, GNE, HK2, HS2ST1, HSPA5, IL13RA1, ISG20, LDHA, MET, NASP, P4HA1, PC, PGAM1, PGK1, PKM, PLOD2, PMM2, SAP30, SLC16A3, SLC25A13, STC1, STC2, TGFBI, TPI1, TXN, UGP2, VEGFA, VLDLR*
Hypoxia	0.001	2.36	*ACKR3, ADM, AK4, ALDOA, AMPD3, ANGPTL4, ATF3, BHLHE40, BNIP3L, BTG1, CA12, CP, DDIT4, DUSP1, EGFR, ENO1, ERO1A, ERRFI1, ETS1, FOSL2, GBE1, GLRX, GPI, HK2, HSPA5, IL6, JMJD6, KDM3A, KLHL24, LDHA, MAFF, MT1E, MT2A, NDRG1, NEDD4L, NFIL3, NOCT, P4HA1, PDK1, PFKFB3, PGF, PGK1, PGM1, PIM1, PLAUR, PNRC1, RORA, SAP30, SCARB1, SLC2A1, SLC2A3, SLC2A5, SLC6A6, STC1, STC2, TGFBI, TGM2, TNFAIP3, TPI1, UGP2, VEGFA, VLDLR*
Il2 Stat5 Signalling	0.001	2.27	*BHLHE40, CASP3, CD44, CKAP4, DENND5A, FURIN, GABARAPL1, HK2, IFITM3, IFNGR1, IL18R1, LIF, MAFF, MAP3K8, MAPKAPK2, MUC1, MYC, NDRG1, NFIL3, NFKBIZ, P4HA1, PIM1, RGS16, RORA, SLC2A3, SLC39A8, SPRY4, TNFRSF1B, XBP1*
Il6 Jak Stat3 Signalling	0.001	2.46	*ACVR1B, CCL7, CD38, CD44, CXCL1, CXCL3, IFNGR1, IL13RA1, IL18R1, IL1R1, IL6, IL6ST, IRF1, LTBR, MAP3K8, OSMR, PIM1, PLA2G2A, PTPN2, SOCS3, STAT3, TLR2, TNFRSF1A, TNFRSF1B*
Inflammatory Response	0.001	2.74	*ABCA1, ACVR1B, ADM, ATP2A2, ATP2B1, BDKRB1, BEST1, CCL2, CCL20, CCL7, CCR7, CD55, CD82, CXCL6, CXCL8, GCH1, GPR183, HAS2, HIF1A, HRH1, ICAM1, IFNGR2, IL15RA, IL18R1, IL1R1, IL4R, IL6, IL7R, INHBA, IRAK2, IRF1, ITGA5, ITGB8, LIF, LPAR1, LYN, MET, MMP14, MYC, NAMPT, NDP, NFKB1, NFKBIA, NOD2, OSMR, PDE4B, PDPN, PLAUR, PSEN1, PTPRE, RAF1, RELA, RGS16, RIPK2,*

			RNF144B, SELENOS, SLC11A2, SLC31A1, SLC7A2, TAPBP, TLR2, TNFAIP6, TNFRSF1B, TNFSF9
Interferon Alpha Response	0.011	2.16	*B2M, C1S, GBP2, IFI30, IFITM2, IFITM3, IL15, IL4R, IRF1, IRF2, ISG20, NCOA7, NUB1, PROCR, PSME1, PSME2, RIPK2, SLC25A28, TENT5A, TRAFD1, TRIM25, WARS*
Interferon Gamma Response	0.001	2.65	*BTG1, C1R, C1S, CASP3, CCL2, CCL7, CFB, GCH1, HIF1A, ICAM1, IFITM2, IFITM3, IL6, IRF1, IRF2, JAK2, MT2A, NAMPT, NFKB1, NFKBIA, PDE4B, PIM1, PLA2G4A, PTGS2, PTPN2, RIPK2, SLC25A28, SOCS3, SOD2, SPPL2A, STAT3, TNFAIP2, TNFAIP3, TNFAIP6, TRAFD1, WARS*
Kras Signalling Up	0.011	1.97	*ANGPTL4, CCL20, CFB, CTSS, DUSP6, EPB41L3, G0S2, GFPT2, GLRX, HDAC9, HSD11B1, ID2, MALL, MMD, MMP10, PLAUR, PTGS2, RBP4, RGS16, SERPINA3, SLPI, TFPI, TMEM100, TNFAIP3, TNFRSF1B, TRIB1*
Mtorc1 Signalling	0.013	1.82	*ABCF2, AK4, ALDOA, ATP2A2, BHLHE40, CALR, CANX, CTSC, DDIT4, EEF1E1, EGLN3, ENO1, ERO1A, ETF1, FADS1, GBE1, GLRX, GPI, HK2, HSP90B1, HSPA5, HSPA9, HSPD1, HSPE1, IFI30, INSIG1, LDHA, MAP2K3, NAMPT, NFIL3, NFKBIB, NMT1, P4HA1, PDK1, PGK1, PGM1, PITPNB, PLOD2, PSMD12, PSMG1, RAB1A, RPN1, RRP9, SLC2A1, SLC2A3, SLC6A6, SLC7A11, SLC7A5, SLC9A3R1, STC1, TBK1, TFRC, TOMM40, TPI1, UBE2D3, UFM1, VLDLR, WARS, XBP1*
Myc Targets V1	0.043	1.68	*AP3S1, BUB3, C1QBP, CANX, CBX3, CCT2, CCT5, CCT7, CDK2, COX5A, CUL1, CYC1, DDX18, DDX21, DEK, DHX15, EIF2S1, EIF2S2, EIF3B, EIF4A1, ETF1, G3BP1, GNL3, GSPT1, H2AFZ, HDGF, HNRNPA2B1, HNRNPA3, HSPD1, HSPE1, ILF2, KPNA2, LDHA, MYC, NAP1L1, NDUFAB1, NOLC1, NOP16, PCBP1, PGK1, PHB2, PPIA, PRDX3, PRDX4, PSMA1, PSMA6, PSMA7, PSMC4, PSMD3, PSMD7, RNPS1, RRP9, RSL1D1, RUVBL2, SNRPB2, SNRPG, SRPK1, SRSF1, SRSF2, SYNCRIP, TARDBP, TUFM, U2AF1, VDAC1, YWHAE*
Myogenesis	0.023	-1.54	*ACTC1, ADCY9, CKB, CRYAB, DMPK, EPHB3, FABP3, FHL1, FST, GSN, HSPB2, ITGB5, LAMA2, LSP1, MEF2C, MYH9, MYLK, MYO1C, PDLIM7, PTGIS, SIRT2, SPEG, TAGLN, TPM2*
Tnfa Signalling Via Nfkb	0.001	3.14	*ABCA1, ACKR3, ATF3, ATP2B1, B4GALT1, BCL3, BCL6, BHLHE40, BTG1, BTG3, CCL2, CCL20, CCNL1, CD44, CEBPB, CEBPD, CFLAR, CLCF1, CXCL1, CXCL2, CXCL3, CXCL6, DENND5A, DRAM1, DUSP1, DUSP5, ETS2, FOSL2, G0S2, GCH1, GFPT2, GPR183, ICAM1, ID2, IL6, IL6ST, IRF1, JUNB, KLF10, KLF4, KLF9, KYNU, LAMB3, LIF, MAFF, MAP2K3, MAP3K8, MYC, NAMPT, NFE2L2, NFIL3, NFKB1, NFKB2, NFKBIA, NR4A2, NR4A3, PANX1, PDE4B, PFKFB3, PLAUR, PLK2, PTGS2, PTPRE, RCAN1, RELB, RIPK2, SAT1, SERPINB8, SIK1, SLC2A3, SOCS3, SOD2, TANK, TGIF1, TNC, TNFAIP2, TNFAIP3, TNFAIP6, TNFAIP8, TNFSF9, TRIB1, VEGFA, ZC3H12A*
Unfolded Protein Response	0.019	1.95	*ALDH18A1, ATF3, CALR, CCL2, CEBPB, DDIT4, DNAJB9, DNAJC3, EIF4A1, EIF4EBP1, ERN1, ERO1A, HSP90B1, HSPA5, HSPA9, HYOU1, IGFBP1, PREB, RRP9, SHC1, SLC7A5, SRPRA, STC2, TARS, TATDN2, VEGFA, WIPI1, XBP1*

Table C4-2. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17F compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Tnfa Signalling Via Nfkb	0.001	2.37	*ACKR3, BCL3, CCL2, CCL20, CEBPB, CEBPD, CXCL1, CXCL2, CXCL3, CXCL6, G0S2, ID2, KYNU, MAFF, MAP2K3, MAP3K8, NFKBIA, NR4A3, PDE4B, SERPINB8, SOCS3, SOD2, TNFAIP6, TNFSF9, TRIB1, ZC3H12A*

Table C4-3. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17AF compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Complement	0.003	2.56	*C1R, C1S, C3, CEBPB, CLU, CP, CTSD, CTSL, CTSS, CXCL1, DUSP5, DUSP6, FYN, IL6, IRF2, KYNU, MAFF, MMP13, PIM1, PLAUR, TNFAIP3*
Hypoxia	0.005	2.40	*ACKR3, ALDOA, ANGPTL4, ATF3, BHLHE40, BTG1, CA12, CP, DUSP1, ENO1, FOSL2, GBE1, GLRX, GPI, HK1, IL6, LDHA, MAFF, MT1E, MT2A, NDRG1, NFIL3, PDK1, PFKFB3, PGK1, PIM1, PLAUR, SAP30, SCARB1, SLC2A5, STC1, STC2, TNFAIP3, TPI1*
Il2 Stat5 Signaling	0.001	2.69	*GABARAPL1, IFITM3, IFNGR1, MAFF, MAP3K8, MYC, NFIL3, NFKBIZ, PIM1, SLC39A8, TNFRSF1B, XBP1*
Il6 Jak Stat3 Signaling	0.001	2.94	*CXCL1, CXCL3, IFNGR1, IL1R1, IL6, LTBR, MAP3K8, OSMR, PIM1, SOCS3, STAT3, TNFRSF1A, TNFRSF1B*
Inflammatory Response	0.001	2.74	*BDKRB1, BEST1, CCL2, CCL20, CCL7, CXCL6, CXCL8, GCH1, HIF1A, IL1R1, IL6, IRAK2, MYC, NAMPT, NFKBIA, NOD2, OSMR, PDE4B, PDPN, PLAUR, RGS16, SLC11A2, SLC7A2, TNFAIP6, TNFRSF1B, TNFSF9*
Interferon Gamma Response	0.001	2.84	*BTG1, C1R, C1S, CCL2, GCH1, HIF1A, IFITM2, IFITM3, IL6, IRF2, MT2A, NAMPT, NFKBIA, PDE4B, PIM1, SLC25A28, SOCS3, SOD2, STAT3, TNFAIP3, TNFAIP6, TRAFD1*
Tnfa Signalling Via Nfkb	0.001	3.47	*ACKR3, ATF3, B4GALT1, BCL3, BCL6, BHLHE40, BTG1, CCL2, CCL20, CEBPB, CEBPD, CLCF1, CXCL1, CXCL2, CXCL3, CXCL6, DRAM1, DUSP1, DUSP5, ETS2, FOSL2, G0S2, GCH1, GEM, GFPT2, ID2, IL6, JUNB, KLF10, KLF4, KLF9, KYNU, MAFF, MAP2K3, MAP3K8, MYC, NAMPT, NFE2L2, NFIL3, NFKBIA, NR4A2, NR4A3, PANX1, PDE4B, PFKFB3, PLAUR, PLPP3, RELB, SAT1, SERPINB8, SIK1, SOCS3, SOD2, TANK, TGIF1, TNC, TNFAIP3, TNFAIP6, TNFSF9, TRIB1, ZC3H12A*

C4.1.2 Immune pathways

Table C4-4. *Genes that contribute to the changes in immune pathways after treatment with IL-17A compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Cellular Response To Interleukin 1	0.002	2.35	*CCL2, CCL20, CCL7, CCL8, CEBPB, CHI3L1, CXCL8, HAS2, HIF1A, ICAM1, IL1R1, IL6, IRAK2, IRAK3, NFKB1, NKX3-1, RORA, SFRP1, VLDLR, ZC3H12A*
Positive Regulation Of Immune Effector Process	0.027	1.97	*B2M, C3, CCL2, CLCF1, HSPD1, IL6, LBP, LYN, NECTIN2, NOS2, NR4A3, RARA, RBP4, RIPK2, TRAF2, WNT5A, XBP1*
Positive Regulation Of Immune Response	0.002	2.01	*ABL1, B2M, C1R, C1RL, C1S, C3, C5AR1, CCR7, CD1D, CD38, CD55, CFB, CLCF1, CLU, CTSL, CTSS, CUL1, CYLD, ELMO1, FYN, GAB2, HMGB1, HSP90B1, HSPD1, IFI16, IL4R, IL6, IL6ST, IRAK2, IRAK3, LBP, LYN, MAPKAPK2, MMP2, MYO10, NCK1, NECTIN2, NFKB1, NFKBIA, NOD2, NR4A3, PAG1, PDE4B, PDE4D, PLEKHA1, POLR3D, PSEN1, PSMA6, PSMD12, PSMD7, PSME1, PSME2, RAF1, RARA, RELA, RELB, RIPK2, STK11, TAB2, TANK, TBK1, TLR2, TNFAIP3, TNIP1, TRAF2, TRAF3, UBE2D3, WNT5A, XBP1*
Positive Regulation Of Immune System Process	0.002	2.31	*ABL1, ACVR1B, ARNT, ATP11C, BCL6, BDKRB1, C1R, C1RL, C1S, C3, CCL2, CCL20, CCL7, CCL8, CCR7, CD1D, CD38, CD59, CFB, CLCF1, CLU, CTSL, CTSS, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, ELMO1, FGF10, FOXC1, FYN, GPR183, HIF1A, HMGB1, HSP90B1, HSPD1, ICAM1, ID2, IFI16, IGF1, IL6, IL6R, IL6ST, IRAK2, IRAK3, KLF10, LBP, LIF, MAP3K8, MAPKAPK2, MMP14, MMP2, NCK1, NECTIN2, NFKB1, NFKBIA, NOD2, NOS2, NR4A3, PAG1, PDE4B, PDE4D, POLR3D, PRMT1, PSEN1, PSMA6, PSMD12, RAF1, RBP4, RELB, RIPK2, TANK, TLR2, TNFAIP3, TNFSF9, TRAF2, TRAF3, TRIB1, UBE2D3, VEGFA, VNN1, WNT5A, XBP1*
Positive Regulation Of Innate Immune Response	0.005	1.98	*BIRC3, CD1D, CTSL, CTSS, CUL1, CYLD, FYN, HMGB1, HSP90B1, HSPD1, IFI16, IRAK2, IRAK3, LBP, LYN, MAPKAPK2, MMP2, NECTIN2, NFKB1, NFKBIA, NOD1, NOD2, PIK3C3, POLR3D, PSMA1, PSMA6, PSMD12, PSMD3, PSMD7, PSME1, PSME2, RAF1, RELA, RELB, RIPK2, TAB2, TANK, TBK1, TLR2, TNFAIP3, TNIP1, TRAF3, UBE2D3, WNT5A*
Regulation Of Immune Effector Process	0.007	1.89	*ACKR3, BCL6, C3, CCL2, CFB, CLCF1, ELMO1, FGF7, FYN, HMGB1, HSPD1, ICAM1, IL6, IRAK3, LBP, NECTIN2, NOS2, NR4A3, RBM18, RBP4, RIPK2, STOM, TNFAIP3, TNIK, TRAF2, TRAF3, TRAF3IP2, TREM1, WNT5A, XBP1, ZC3H12A*
Regulation Of Immune Response	0.002	1.86	*ABL1, B2M, BCL6, C1R, C1RL, C1S, C3, C5AR1, CCR7, CD1D, CD38, CD55, CD59, CFB, CLCF1, CLU, COL3A1, CTSL, CTSS, CUL1, CYLD, DUSP3, ELMO1, ERAP1, FYN, GAB2, HMGB1, HSP90B1, HSPD1, ICAM1, IFI16, IFNGR1, IFNGR2, IL4R, IL6, IL6ST, IL7R, IRAK2, IRAK3, IRF1, JAK2, LBP, LYN, MAPK8, MAPKAPK2, MMP2, MYO10, NCK1, NECTIN2, NFKB1, NFKBIA, NOD2, NR1H2, NR4A3, PAG1, PDE4B, PDE4D, PLEKHA1, POLR3D, PPP3CA, PSEN1, PSMA6, PSMD12, PSMD7, PSME1, PSME2, PTPN2, RAF1, RARA, RELA, RELB, RIPK2, SELENOS, SHC1, SOCS3, SPPL2A, STK11, TAB2, TANK, TBK1, TLR2, TNFAIP3, TNIP1, TRAF2, TRAF3, TRAFD1, TREM1, UBE2D3, WNT5A, XBP1*

Regulation Of Innate Immune Response	0.005	1.97	*BIRC3, CD1D, CTSL, CTSS, CUL1, CYLD, ERAP1, FYN, HMGB1, HSP90B1, HSPD1, IFI16, IFNGR1, IFNGR2, IRAK2, IRAK3, IRF1, JAK1, JAK2, LBP, LYN, MAPKAPK2, MMP2, NECTIN2, NFKB1, NFKBIA, NOD1, NOD2, NR1H2, PIK3C3, POLR3D, PSMA1, PSMA6, PSMD12, PSMD3, PSMD7, PSME1, PSME2, PTPN1, PTPN2, RAF1, RELA, RELB, RIPK2, SOCS3, TAB2, TANK, TBK1, TLR2, TNFAIP3, TNIP1, TRAF3, TRAFD1, UBE2D3, WNT5A*
Regulation Of Interleukin 1 Beta Production	0.049	1.89	*CCR7, ERRFI1, FOXP1, HMGB1, IFI16, JAK2, NOD2, PANX1, S1PR3, TNFAIP3, WNT5A, ZC3H12A*
Regulation Of Interleukin 1 Production	0.044	1.96	*CCL20, CCR7, ERRFI1, FOXP1, HMGB1, IFI16, JAK2, NOD2, PANX1, S1PR3, SAA1, TNFAIP3, WNT5A, ZC3H12A*
Regulation Of Interleukin 6 Production	0.019	2.06	*ARHGEF2, CEBPB, HMGB1, HSPD1, IL6, IL6R, IRAK3, LBP, MAPKAPK2, NOD2, RIPK2, SELENOS, TBC1D23, TLR2, TNFAIP3, TNFSF9, TWIST1, WNT5A, XBP1, ZC3H12A*
Regulation Of Myeloid Cell Differentiation	0.049	1.78	*ACVR1B, ARNT, CEBPB, CTNNB1, ESRRA, ETS1, FOXP1, HIF1A, HMGB1, ID2, INHBA, KLF10, LIF, LYN, MYC, NFKBIA, PRMT1, PTPN2, RARA, RUNX1, SFRP1, TFE3, TRIB1, ZBTB7A*
Response To Interleukin 1	0.003	2.31	*BYSL, CCL2, CCL20, CCL7, CCL8, CD38, CEBPB, CHI3L1, CXCL8, ETS1, HAS2, HDAC4, HIF1A, HSPA9, ICAM1, IL1R1, IL6, IRAK2, IRAK3, NFKB1, NKX3-1, RELA, RIPK2, RORA, SFRP1, VLDLR, ZC3H12A*

Table C4-5. *Genes that contribute to the changes in immune pathways after treatment with IL-17F compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Positive Regulation Of Immune System Process	0.011	2.18	*ABL1, BDKRB1, C1R, C1RL, C1S, C3, CCL2, CCL20, CXCL1, CXCL2, CXCL3, CXCL6, ID2, IRAK2, MAP3K8, NFKBIA, NOS2, NR4A3, PDE4B, TNFSF9, TRIB1*
Regulation Of Immune System Process	0.012	1.99	*ABL1, ACKR3, BDKRB1, C1R, C1RL, C1S, C3, CCL2, CCL20, CEBPB, CXCL1, CXCL2, CXCL3, CXCL6, FGF7, ID2, IRAK2, MAP3K8, NFKBIA, NFKBID, NOS2, NR4A3, PDE4B, SOCS3, TNFSF9, TRIB1, ZC3H12A*

Table C4-6. *Genes that contribute to the changes in immune pathways after treatment with IL-17AF compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Positive Regulation Of Immune System Process	0.002	2.60	*ABL1, BCL6, BDKRB1, C1R, C1RL, C1S, C3, CCL2, CCL20, CCL7, CD1D, CLCF1, CLU, CTSS, CXCL1, CXCL2, CXCL3, CXCL6, CXCL8, FGF10, FYN, HIF1A, ID2, IL6, IRAK2, KLF10, MAP3K8, MMP2, NECTIN2, NFKBIA, NOD2, NOS2, NR4A3, PDE4B, PDE4D, PSMA6, RBP4, RELB, TNFAIP3, TNFSF9, TRIB1, UBE2D3, VNN1, XBP1*
Regulation Of Immune System Process	0.002	2.41	*ABL1, ACKR3, ADORA1, BCL6, BDKRB1, C1R, C1RL, C1S, C3, CCL2, CCL20, CCL7, CCL8, CCR7, CD1D, CD59, CEBPB, CLCF1, CLU, CTSL, CTSS, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, ESRRA, FGF10, FGF7, FOXF1, FOXP1, FYN, GPX1, HIF1A, ID2, IFNGR1, IGF1, IL6, IRAK2, KLF10, MAP3K8, MAPKAPK2, MMP2, MYC, NECTIN2, NFE2L2, NFKBIA, NFKBID, NOD2, NOS2, NR1H2, NR4A3, PDE4B, PDE4D, PHB2, PHYHIP, PPP3CA, PRMT1, PSMA6, PSMD7, RBP4, RELB, SFRP1, SHC1, SLC7A2, SNRPB, SNRPB2, SOCS3, STK11, STOM, TANK, TEAD4, TFE3, TNFAIP3, TNFSF13B, TNFSF9, TRAF3, TRAF3IP2, TRAFD1, TRIB1, UBE2D3, VNN1, XBP1, ZBTB7A, ZC3H12A*

C4.1.3 Cytokine/chemokine pathways

Table C4-7. *Genes that contribute to the changes in cytokine/chemokine pathways after treatment with IL-17A compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Chemokine Activity	0.001	2.5	*CCL2, CCL20, CCL7, CCL8, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8*
Chemokine Receptor Binding	0.001	2.55	*CCL2, CCL20, CCL7, CCL8, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, STAT3*
Cytokine Activity	0.001	2.32	*BMP1, BMP6, CCL2, CCL20, CCL7, CCL8, CLCF1, CMTM7, CXCL1, CXCL16, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, FGF2, GDF15, GDF6, GPI, HMGB1, IL6, LIF, NAMPT, NDP, SCG2, TNFRSF11B, TNFSF9, VEGFA, WNT5A*
Cytokine Receptor Binding	0.001	2.38	*BID, BMP1, BMP6, CASP3, CCL2, CCL20, CCL7, CCL8, CFLAR, CLCF1, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, ERAP1, GDF15, GDF6, IL1RAP, IL6, IL6ST, JAK2, LIF, LIFR, SHC1, SMAD7, SNX25, STAT3, TGFBR1, TNFSF9, TRAF2, TRAF3, VEGFA*
Positive Regulation Of Cytokine Production	0.001	2.14	*ABL1, ARHGEF2, ARNT, B2M, BCL3, C3, CCL2, CCL20, CCR7, CEBPB, CLU, CTNNB1, CX3CL1, CYP1B1, DDX3X, HIF1A, HILPDA, HMGB1, HSPD1, IFI16, IL17RA, IL18R1, IL4R, IL6, IL6R, IL6ST, IRF1, JAK2, LBP, LUM, MAPKAPK2, NFATC4, NFKB1, NFKB2, NOD2, NR4A3, PANX1, PDE4B, PDE4D, POLR3D, POLR3E, PTGS2, RARA, RELA, RIPK2, RORA, RUNX1, SAA1, TBC1D23, TBK1, TLR2, TMF1, TNFSF9, TRAF2, TWIST1, WNT5A, XBP1*
Regulation Of Cytokine Production	0.001	2.12	*ABL1, ARHGEF2, ARNT, B2M, BCL3, BCL6, C3, CCL2, CCL20, CCR7, CEBPB, CLU, CTNNB1, CYLD, CYP1B1, DDX3X, ERRFI1, FBLN1, FOXP1, FURIN, HIF1A, HILPDA, HMGB1, HSPD1, IFI16, IL18R1, IL4R, IL6, IL6R, IL6ST, INHBA, IRAK3, IRF1, JAK2, KLF4, LBP, LUM, LYN, MAP2K3, MAPKAPK2, NFATC4, NFKB1, NFKB2, NOD2, NOS2, NR4A3, PANX1, PDE4B, PDE4D, POLR3D, POLR3E, PTGS2, RARA, RELA, RELB, RIPK2, RORA, RUNX1, S1PR3, SAA1, SELENOS, SRGN, TBC1D23, TLR2, TMF1, TNFAIP3, TNFSF9, TRAF2, TRAF3, TRIM25, TWIST1, UBE2J1, WNT5A, XBP1, ZC3H12A*
Regulation Of Vascular Endothelial Growth Factor Production	0.037	2.07	*ARNT, C3, CCL2, CYP1B1, HIF1A, IL6, IL6ST, PTGS2, RORA*

Table C4-8. *Genes that contribute to the changes in cytokine/chemokine pathways after treatment with IL-17AF compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Chemokine Receptor Binding	0.004	2.7	*CCL2, CCL20, CXCL1, CXCL2, CXCL3, CXCL6, CXCL8, STAT3*
Cytokine Activity	0.005	2.59	*BMP6, CCL2, CCL20, CCL7, CCL8, CLCF1, CMTM7, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, GDF15, GPI, IL6, NAMPT, SCG2, TNFRSF11B, TNFSF9*
Cytokine Receptor Binding	0.01	2.51	*BID, BMP6, CCL2, CCL20, CCL7, CCL8, CLCF1, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, GDF15, IL6, JAK2, SHC1, SMAD7, SNX25, STAT3, TGFBR1, TNFSF13B, TNFSF9, TRAF3, YARS*

C4.1.4 Matrix pathways

Table C4-9. *Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17A compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Actin Cytoskeleton	0.006	-2.02	*ABLIM3, ACTA2, ACTC1, ACTG1, ACTN4, ADD1, AHNAK, BAIAP2, BFSP1, BMF, CALD1, CAPG, CAPN2, CCDC102A, CFL2, CNN2, CORO1B, CORO1C, CORO2B, CORO6, CROCC, CRYAB, DAPK1, DBN1, DCTN1, DCTN3, DSTN, EPB41, EPB41L2, EZR, FBLIM1, FERMT1, FHL3, FHOD1, FLNA, FMN2, FSCN1, GSN, HFE, HSPB7, ILK, IVNS1ABP, JUP, LASP1, LLGL1, LMOD1, LSP1, MAEA, MAP7D3, MYADM, MYH10, MYH9, MYL12A, MYL9, MYLK, MYO18A, MYO1B, MYO1C, MYO1D, MYO6, MYOM1, NEBL, NFATC2, OPHN1, PAK1, PALLD, PARD6A, PAWR, PDLIM2, PDLIM7, PLEKHH2, PLS1, PPP1R12B, PPP1R9B, PXN, RAC3, RAPGEF3, RFLNA, SCNN1D, SEPTIN11, SPTBN1, TEK, TLN2, TMOD2, TPM2, UTRN, VCL, WIPF1, ZNF185*
Actin Filament	0.038	-1.62	*ACTC1, FLNA, MYO1B, MYO1C, MYO6, PAK1, PALLD, PAWR, RAC3, TEK, WIPF1*
Actin Filament Based Movement	0.008	-1.86	*ACTC1, ACTN4, FNBP1L, GPD1L, KCNH2, MYH10, MYH9, MYO1B, MYO6, SCN1B, SCN2B, SNTA1, TPM2, VIM, WIPF1*
Actin Filament Bundle	0.006	-2.26	*ABLIM3, ACTN4, CNN2, CORO1B, CRYAB, FBLIM1, FHL3, FHOD1, FSCN1, ILK, MYH10, MYH9, MYL9, MYLK, MYO1C, NEBL, PDLIM2, PDLIM7, PXN, RFLNA, SEPTIN11, TEK*
Actin Filament Bundle Organization	0.008	-1.85	*ACTN4, ADD1, ARRB1, BAIAP2, CORO1B, EPS8, EZR, FMN2, FSCN1, ITGB5, MYO1B, PAWR, PTK2B, RFLNA*
Actin Filament Organization	0.048	-1.46	*ACTC1, ACTN4, ADD1, ARRB1, BAIAP2, CFL2, COBLL1, CORO1B, DBN1, DSTN, EPS8, EZR, FHOD3, FLNA, FMN2, FRY, FSCN1, GSN, ITGB5, LMOD1, MICAL1, MYO1B, NEBL, PAWR, PPP1R9B, PTK2B, RFLNA, SCIN, TMOD2, WIPF1*
Cortical Actin Cytoskeleton	0.006	-2.56	*CALD1, CAPN2, DSTN, EPB41, EPB41L2, GSN, HFE, LASP1, LLGL1, MAEA, MYADM, MYH9, PDLIM2, PLEKHH2, RAPGEF3, SPTBN1, UTRN, VCL, WIPF1*
Cortical Cytoskeleton	0.006	-2.07	*ACTN4, CALD1, CAPN2, CLASP2, DSTN, EPB41, EPB41L2, FLNA, GSN, HFE, LASP1, LLGL1, MAEA, MPP1, MYADM, MYH9, PDLIM2, PLEKHH2, RAPGEF3, SPTBN1, UTRN, VCL, WIPF1*
Extracellular Matrix Disassembly	0.048	1.82	*BMP1, CD44, CTSL, CTSS, FBN2, FURIN, LAMB3, MMP1, MMP10, MMP13, MMP14, MMP2, MMP3, SH3PXD2B*
Intermediate Filament Cytoskeleton	0.008	-1.79	*BFSP1, FAAP100, GPER1, HOXA13, IFFO1, JUP, KRTAP1-5, LMNA, MICAL1, MNS1, PLEC, PRPH, SHANK2, SMARCA2, STN1, SYNM, VIM*
Negative Regulation Of Actin Filament Depolymerization	0.023	-1.79	*ADD1, CAPG, EPS8, GSN, LMOD1, PLEKHH2, SCIN, SPTBN1, TMOD2*
Negative Regulation Of Actin Filament Polymerization	0.007	-2.05	*ADD1, CAPG, EPS8, FHOD3, GSN, LMOD1, MYADM, PFN2, PRKCD, SCIN, SPTBN1, TMOD2*

Negative Regulation Of Cytoskeleton Organization	0.021	-1.57	*ADD1, APC, ARHGEF10, C16orf45, CAPG, CEP126, CKAP5, CLASP2, EPS8, FHOD3, FLNA, GPSM2, GSN, HAUS5, LMOD1, MYADM, MYH9, MYOC, PFN2, PLEKHH2, PRKCD, SCIN, SPTBN1, STMN1, TMOD2*
Positive Regulation Of Actin Filament Bundle Assembly	0.023	-1.77	*ARHGEF10, CTGF, FHOD1, MYOC, PAK1, PFN2, RAPGEF3*
Positive Regulation Of Cytoskeleton Organization	0.008	-1.71	*ARHGEF10, BAIAP2, CDC42EP5, CFL2, CTGF, DSTN, FES, FHOD1, GSN, MYOC, PAK1, PFN2, PLXNA3, PTK2B, PYCARD, RAPGEF3, ROCK2, SCIN, SIRT2, TEK, WIPF1*
Regulation Of Actin Filament Based Process	0.009	-1.52	*ADD1, ARHGAP18, ARHGDIB, ARHGEF10, ATP1A2, BAIAP2, CAPG, CDC42EP5, CLASP2, CNN2, CTGF, DIXDC1, DSTN, EPS8, FES, FHOD1, FHOD3, FSCN1, GSN, ILK, LMOD1, MEF2C, MYADM, MYH9, MYOC, PAK1, PFN2, PLEKHH2, PRKCD, PTK2B, PYCARD, RAPGEF3, ROCK2, SCIN, SEMA3E, SH3BGRL3, SPTBN1, SSH3, TEK, TGFB2, TMOD2, TRPM4, WIPF1*
Regulation Of Actin Filament Depolymerization	0.007	-2.04	*ADD1, CAPG, CFL2, DSTN, EPS8, GSN, LMOD1, PLEKHH2, SCIN, SH3BGRL3, SPTBN1, TMOD2*
Regulation Of Actin Filament Length	0.006	-1.86	*ADD1, ARHGAP18, BAIAP2, CAPG, CDC42EP5, CFL2, DSTN, EPS8, FHOD3, GSN, LMOD1, MYADM, PFN2, PLEKHH2, PRKCD, PTK2B, PYCARD, SCIN, SH3BGRL3, SPTBN1, SSH3, TMOD2, WIPF1*
Regulation Of Cytoskeleton Organization	0.006	-1.60	*ADD1, APC, ARHGAP18, ARHGDIB, ARHGEF10, BAIAP2, C16orf45, CAPG, CAPN2, CDC42EP5, CEP126, CKAP5, CLASP2, CTGF, DIXDC1, DSTN, EPS8, FES, FHOD1, FHOD3, FLNA, FSCN1, GPSM2, GSN, HAUS5, ILK, LMOD1, MEF2C, MYADM, MYH9, MYOC, NEXN, PAK1, PFN2, PHLDB1, PLEKHH2, PLXNA3, PRKCD, PTK2B, PYCARD, RAPGEF3, ROCK2, SCIN, SEMA3E, SH3BGRL3, SIRT2, SPTBN1, SSH3, STMN1, STMN3, TEK, TGFB2, TMOD2, WIPF1*

Table C4-10. *Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17AF compared to control. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Actin Based Cell Projection	0.016	-1.97	*ACTA2, ACTC1, ATP8B1, DNALI1, EPS8, EXOC4, FARP1, FAT1, FSCN1, KIF13B, LRRK2, MYO1B, MYO1C, MYO5A, MYO6, NFASC, NLGN1, OSBPL3, RAPGEF3, TEK, UTRN*
Actin Cytoskeleton	0.008	-2.02	*ACTA2, ACTC1, ADD1, AHNAK, BAIAP2, BMF, CALD1, CAPG, CAPN2, CDC42BPA, CORO1C, CORO2B, DBN1, DST, DSTN, EPB41L2, FBLIM1, FER, FERMT1, FHL3, FLNA, FLNB, FSCN1, GSN, HFE, HSPB7, ILK, IPP, IVNS1ABP, KLHL20, LASP1, LMOD1, LSP1, MAP7D3, MYH10, MYH9, MYL12A, MYL9, MYLK, MYO18A, MYO1B, MYO1C, MYO1D, MYO5A, MYO6, NFATC2, NOTCH3, OPHN1, PAK1, PALLD, PARD6A, PAWR, PDLIM5, PEAK1, PLEKHH2, PPP1R12A, PPP1R12B, PXN, RAPGEF3, RFLNA, SEPTIN11, SPTAN1, SPTBN1, SPTBN5, TEK, TMOD2, TRIM32, TTN, UTRN, VCL, WIPF1, ZNF185*
Actin Filament Bundle	0.016	-2.09	*ABLIM1, ABLIM3, CNN2, FBLIM1, FHL3, FHOD1, FLNB, FSCN1, ILK, MYH10, MYH9, MYL9, MYLK, MYO1C, NEBL, PXN, RFLNA, SEPTIN11, TEK*
Cortical Actin Cytoskeleton	0.008	-2.38	*CALD1, CAPN2, DSTN, EPB41L2, GSN, HFE, LASP1, MYH9, PLEKHH2, RAPGEF3, SPTBN1, SPTBN5, UTRN, VCL, WIPF1*
Cortical Cytoskeleton	0.041	-1.82	*CALD1, CAPN2, CLASP2, DSTN, EPB41L2, FLNA, GSN, LASP1, MYH9, PLEKHH2, RAPGEF3, SPTBN1, UTRN, VCL, WIPF1*
Cytoskeleton	0.016	-1.47	*ABCA2, ACTA2, ACTC1, ADD1, AGBL2, AHNAK, AJUBA, AK5, AKAP12, ANK1, APC, ARHGAP26, ARHGEF10, ATM, BMF, C16orf45, C2CD5, CABYR, CALD1, CALM1, CAPG, CAPN2, CC2D2A, CCDC14, CCDC92, CCSER2, CDK6, CEP126, CEP290, CEP68, CKAP5, CLASP2, CORO2B, CRMP1, CUL7, CYS1, DBN1, DIDO1, DNALI1, DNM1, DST, DSTN, DYNC1I1, EML6, EPB41L1, EPB41L2, EVC, FARP1, FARP2, FBLIM1, FER, FGD6, FHOD3, FLNA, FLNB, FLNC, FNBP1L, FRMD4A, FRY, FSCN1, GNAI2, GPER1, GPSM2, GSN, HFE, HIP1, HSPB1, HSPB7, ICK, IPP, IVNS1ABP, KIF13A, KIF13B, KIF26B, KITLG, KLHL3, KLHL41, KY, LASP1, LMOD1, LSP1, MAP1B, MAP1LC3C, MAP2K6, MAPRE2, MBNL1, MICAL1, MTUS1, MYH9, MYL9, MYLK, MYO18A, MYO1B, MYO1C, MYO1D, MYO5A, MYO6, NFATC2, NOTCH3, OPHN1, OSBPL10, PAK1, PALLD, PARD6A, PAWR, PDCD6IP, PDE4DIP, PDLIM5, PEAK1, PFN2, PLEC, PLEKHH2, PPL, PPP1R12A, PPP1R12B, PPP2R2B, PREPL, PTPN13, PTPN21, PXN, RAPGEF3, RMDN1, ROCK2, SEPTIN11, SEPTIN5, SEPTIN6, SEPTIN8, SHANK2, SHROOM3, SIPA1L1, SLC8A1, SMARCA2, SNCG, SPTBN1, SPTBN5, SSH3, SSX2IP, STRBP, SYNM, TEK, TGFB1I1, TMOD2, TRAF5, TTLL3, TTLL7, TTN, UACA, UTRN, VCL, VPS41, WDR19, WIPF1*

C4.2 Overview of pathway analyses results: synovial fibroblasts

C4.2.1 Hallmark pathways

Table C4-11. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Allograft Rejection	0.005	2.18	*BCL3, CCL13, CCL2, CCL7, CCR1, CD80, CTSS, EIF5A, EREG, GBP2, HIF1A, HLA-E, ICAM1, ICOSLG, IFNAR2, IFNGR1, IL4R, IL6, INHBA, IRF4, IRF7, LIF, LYN, PSMB10, SOCS5, SRGN, STAT1, STAT4, TAPBP, TLR2, WARS*
Complement	0.001	2.38	*C1R, C3, CASP4, CEBPB, CFB, CP, CTSL, CTSS, CXCL1, DUSP6, GPD2, IL6, IRF1, KYNU, PLSCR1, SERPINB2, TFPI2*
Glycolysis	0.032	1.84	*AK4, B3GAT3, CHST2, DDIT4, ENO1, ERO1A, FKBP4, GLRX, HK2, HS2ST1, IL13RA1, LDHA, MET, NT5E, PDK3, PGK1, PKM, PLOD2, PMM2, PSMC4, QSOX1, SAP30, SLC16A3, STC1, TPI1, TXN, VCAN, VEGFA*
Hypoxia	0.001	2.24	*ACKR3, AK4, AMPD3, BNIP3L, CA12, CHST2, CP, CSRP2, DDIT4, DTNA, ENO1, ERO1A, FOSL2, GLRX, HAS1, HK1, IGFBP1, IL6, LDHA, MT1E, MT2A, PDK1, PDK3, PFKFB3, PGF, PGK1, PLIN2, SCARB1, SLC2A1, SLC2A3, SLC2A5, STC1, TGM2, TPI1, TPST2, VEGFA*
Il2 Stat5 Signaling	0.002	2.21	*CDCP1, GSTO1, IFITM3, IFNGR1, IL18R1, IL1RL1, LIF, MAP3K8, NFKBIZ, NT5E, PLIN2, PLSCR1, RHOB, SLC2A3, SLC39A8, TGM2, TNFRSF1B*
Il6 Jak Stat3 Signaling	0.001	2.71	*ACVR1B, CXCL1, CXCL3, IFNGR1, IL13RA1, IL15RA, IL18R1, IL6, IRF1, IRF9, ITGB3, LTBR, MAP3K8, OSMR, PTPN1, PTPN2, SOCS3, STAT1, STAT3, TLR2, TNFRSF1B*
Inflammatory Response	0.001	2.96	*ACVR1B, ADRM1, AQP9, ATP2A2, ATP2B1, BDKRB1, BEST1, CCL2, CCL20, CCL7, CCR7, CD82, CHST2, CSF3, CXCL6, CXCL8, EREG, GCH1, HAS2, HIF1A, HRH1, ICAM1, ICOSLG, IL15RA, IL18R1, IL6, IL7R, INHBA, IRAK2, IRF1, IRF7, ITGB3, ITGB8, LDLR, LIF, LPAR1, LYN, NAMPT, NDP, OSMR, PDPN, PSEN1, PTPRE, SEMA4D, SLC11A2, SLC1A2, SLC31A1, SLC7A2, TLR2, TNFAIP6, TNFRSF1B*
Interferon Alpha Response	0.005	2.24	*ADAR, B2M, C1S, CMPK2, CNP, EPSTI1, GBP2, HELZ2, IFI35, IFITM1, IFITM2, IFITM3, IL4R, IRF1, IRF2, IRF7, IRF9, ISG15, LAP3, NMI, NUB1, PARP14, PARP9, PLSCR1, PNPT1, PROCR, PSMA3, PSME1, PSME2, RNF31, RSAD2, SLC25A28, STAT2, TRIM25, UBE2L6, WARS*
Interferon Gamma Response	0.001	2.75	*APOL6, ARID5B, ARL4A, BANK1, C1R, C1S, CASP3, CASP4, CASP7, CCL2, CCL7, CD38, CFB, CMPK2, EPSTI1, FGL2, GCH1, HIF1A, ICAM1, IDO1, IFI35, IFITM2, IFITM3, IFNAR2, IL15RA, IL4R, IL6, IRF1, IRF2, IRF4, IRF5, IRF7, IRF9, ISOC1, MT2A, MX2, MYD88, NAMPT, NFKBIA, NMI, PLA2G4A, PLSCR1, PNP, PNPT1, PSMA3, PSMB10, PSME1, PSME2, PTGS2, PTPN1, PTPN2, RIPK1, RNF31, RSAD2, SLC25A28, SOCS3, SOD2, SPPL2A, STAT1, STAT2, STAT3, STAT4, TAPBP, TNFAIP2, TNFAIP6, TRIM25, UBE2L6, VCAM1, WARS*
Kras Signaling Up	0.002	2.19	*BIRC3, CCL20, CFB, CTSS, DUSP6, EPB41L3, EREG, ERO1A, GFPT2, GLRX, GNG11, GYPC, HSD11B1, IL33, IL7R, INHBA, LIF, MAFB, MMD, MMP10, PLAU, PTGS2, TMEM158, TNFRSF1B, TRIB1*
Mitotic Spindle	0.009	-1.70	*ACTN4, ANLN, ARHGAP10, ARHGAP29, CDC42EP1, CEP57, DST, EPB41, EPB41L2, FLNB, FSCN1, GSN, KIF1B, KIF20B, KIFAP3, MYH10,*

			NEDD9, NUMA1, PDLIM5, PKD2, PRC1, PXN, RANBP9, RAPGEF5, SEPTIN9, SPTBN1, TUBA4A
Mtorc1 Signaling	0.002	2.10	*ABCF2, ACLY, ADIPOR2, AK4, ARPC5L, ATP2A2, ATP5MC1, CCT6A, DDIT4, ENO1, ERO1A, FADS1, GLA, GLRX, HK2, HSPA9, HSPD1, HSPE1, IMMT, INSIG1, LDHA, LDLR, NAMPT, PDK1, PFKL, PGK1, PLOD2, PNO1, PPA1, PSMA3, PSMC4, PSMD12, PSMD14, PSME3, RAB1A, RDH11, SCD, SLC2A1, SLC2A3, SLC7A5, SLC9A3R1, STC1, STIP1, TBK1, TFRC, TOMM40, TPI1, WARS*
Myc Targets V1	0.018	1.92	*AIMP2, AP3S1, C1QBP, CCT2, CCT3, CCT5, CCT7, CDK2, CTPS1, CYC1, DDX18, DDX21, EIF2S1, EIF2S2, EIF3B, EIF3J, EIF4A1, ETF1, FBL, G3BP1, HNRNPR, HNRNPU, HPRT1, HSPD1, HSPE1, KPNA2, KPNB1, LDHA, NCBP2, NME1, NOLC1, NOP16, NOP56, ODC1, PA2G4, PCNA, PGK1, PHB, POLE3, PPM1G, PSMA6, PSMA7, PSMC4, PSMD14, PSMD7, PTGES3, RAN, RANBP1, RSL1D1, SMARCC1, SNRPD1, SRM, SRPK1, SRSF2, SRSF3, SRSF7, SSBP1, TRA2B, U2AF1, XPOT, XRCC6*
Myc Targets V2	0.032	2.00	*AIMP2, BYSL, DDX18, FARSA, GRWD1, HK2, HSPD1, HSPE1, IMP4, IPO4, MRTO4, MYBBP1A, NOLC1, NOP16, NOP2, NOP56, PA2G4, PES1, PHB, PPAN, PUS1, RCL1, RRP12, SRM, TBRG4, TFB2M, UTP20, WDR74*
Myogenesis	0.001	-2.21	*ACTC1, ADCY9, AEBP1, CKB, COL1A1, COL6A2, COL6A3, CRYAB, DMPK, EFS, FABP3, FHL1, FXYD1, GPX3, GSN, HDAC5, HSPB2, IFRD1, ITGB5, LAMA2, LSP1, MAPRE3, MEF2A, MEF2C, MYL6B, MYLK, MYO1C, MYOM1, NCAM1, PLXNB2, SGCG, SIRT2, SMTN, SPARC, SPEG, TAGLN, TPD52L1*
Tnfa Signaling Via Nfkb	0.001	3.23	*ACKR3, ATP2B1, B4GALT5, BCL2A1, BCL3, BIRC3, CCL2, CCL20, CEBPB, CEBPD, CXCL1, CXCL2, CXCL3, CXCL6, ETS2, GFPT2, ICAM1, ICOSLG, IL15RA, IL6, INHBA, IRF1, KLF10, KYNU, LDLR, LIF, MAP3K8, MSC, NAMPT, NFKB2, PANX1, PLK2, PTGS2, PTPRE, PTX3, RELB, RHOB, SERPINB2, SERPINB8, SIK1, SLC2A3, SOCS3, SOD2, SPSB1, TLR2, TNFAIP2, TNFAIP6, TNIP2, TRIB1, VEGFA, ZC3H12A*

Table C4-12. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Il2 Stat5 Signaling	0.006	2.38	*IFITM3, MAP3K8, NFKBIZ, PLSCR1*
Myogenesis	0.002	-2.25	*ACTC1, ADCY9, COL6A2, FABP3, FHL1, HDAC5, HSPB2, IFRD1, LAMA2, TPD52L1*
Tnfa Signaling Via Nfkb	0.001	2.58	*BCL3, CCL20, CEBPD, CXCL1, CXCL2, CXCL3, CXCL6, IL6, IRF1, KYNU, MAP3K8, PANX1, ZC3H12A*

Table C4-13. *Genes that contribute to the changes in hallmark pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Complement	0.026	2.53	*C1R, CASP4, CP, CTSL, CTSS, CXCL1, DUSP6, IL6, IRF1, KYNU, PLSCR1, SERPINB2, TFPI2*
Il2 Stat5 Signaling	0.026	2.49	*CDCP1, IFITM3, IL18R1, MAP3K8, NFKBIZ, NT5E, PLSCR1, TNFRSF1B*
Il6 Jak Stat3 Signaling	0.002	2.84	*ACVR1B, CXCL1, CXCL3, IL18R1, IL6, IRF1, IRF9, LTBR, MAP3K8, MYD88, OSMR, SOCS3, STAT1, STAT3, TNFRSF1A, TNFRSF1B*
Inflammatory Response	0.030	2.40	*ACVR1B, ADRM1, CCL20, CSF3, CXCL6, CXCL8, HIF1A, ICAM1, IL18R1, IL6, IRF1, ITGB8, LIF, NDP, OSMR, PDPN, SLC7A2, TNFAIP6, TNFRSF1B*
Interferon Gamma Response	0.003	2.62	*APOL6, BANK1, C1R, CASP4, HIF1A, ICAM1, IFITM2, IFITM3, IL6, IRF1, IRF9, MT2A, MYD88, PLSCR1, PSMB10, PSME1, PSME2, SOCS3, STAT1, STAT3, STAT4, TNFAIP2, TNFAIP6, WARS*
Myogenesis	0.003	-2.16	*ACTC1, ADCY9, FABP3, FHL1, HDAC5, IFRD1, LAMA2, MEF2A, MEF2C, MYOM1, TPD52L1*
Tnfa Signaling Via Nfkb	0.002	2.98	*BCL3, CCL20, CEBPD, CXCL1, CXCL2, CXCL3, CXCL6, ICAM1, IL6, IRF1, KYNU, MAP3K8, PANX1, PTX3, SERPINB2, SOCS3, TNFAIP2, TNIP2, ZC3H12A*

C4.2.2 Immune pathways

Table C4-14. *Genes that contribute to the changes in immune pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Cellular Response To Interleukin 1	0.021	2.15	*CCL2, CCL20, CCL7, CEBPB, CHI3L1, CXCL8, HAS2, HIF1A, ICAM1, IL6, IRAK2, NKX3-1, RPS6KA4, TNIP2, ZC3H12A*
Negative Regulation Of Lymphocyte Differentiation	0.043	1.81	*ANXA1, HMGB1, IL4R, INHBA, IRF1, JAK3, NFKBID, PTPN2, SFRP1, SHH, SOCS5*
Positive Regulation Of Immune Response	0.001	2.08	*ABL1, ANXA1, BIRC3, C1QBP, C1R, C1RL, C1S, C3, CCR7, CD80, CFB, COCH, COLEC12, CTSB, CTSL, CTSS, EREG, HLA-E, HMGB1, HSPD1, IDO1, IFI16, IL33, IL4R, IL6, IL6ST, IRAK2, IRAK3, IRF7, JAK3, LBP, LYN, MAPKAPK2, NECTIN2, NFKBIA, PAG1, PDE4D, PIK3CD, PLSCR1, PSEN1, PSMA3, PSMA6, PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSMD7, PSME1, PSME2, PSME3, PVR, RELB, RSAD2, SIN3A, SOCS5, TANK, TBK1, TLR2, TNIP1, TNIP2, TRAF3*
Positive Regulation Of Immune System Process	0.001	2.46	*ABL1, ACVR1B, ANXA1, BDKRB1, BIRC3, C1R, C1RL, C1S, C3, CCL2, CCL20, CCL7, CCR7, CFB, COCH, CSF3, CTSB, CTSL, CTSS, CXCL1, CXCL12, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, EREG, FOXC1, HIF1A, ICAM1, ICOSLG, IFI16, IL1RL1, IL33, IL36B, IL6, IL6R, IL7R, INHBA, IRAK2, IRF7, JAK3, KLF10, LBP, LEP, LIF, LYN, MAP3K8, MIA3, NECTIN2, PAG1, PDE4D, PLSCR1, PRMT1, PSEN1, PSMA6, PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSME1, PSME2, PSME3, RELB, RSAD2, RUNX1, SHH, SIN3A, TBK1, TLR2, TNFSF13B, TNFSF14, TNIP2, TRAF3, TRIB1, VCAM1, VEGFA*
Positive Regulation Of Innate Immune Response	0.001	2.41	*BIRC3, COCH, COLEC12, CTSB, CTSL, CTSS, EREG, HLA-E, HMGB1, HSPD1, IFI16, IRAK2, IRAK3, IRF7, LBP, LYN, MAPKAPK2, MYD88, NECTIN2, NFKBIA, PLSCR1, PSMA3, PSMA6, PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSMD7, PSME1, PSME2, PSME3, PVR, RELB, SIN3A, TANK, TBK1, TLR2, TNIP1, TNIP2, TRAF3*
Positive Regulation Of Myeloid Cell Differentiation	0.039	1.97	*ACVR1B, CSF3, HIF1A, INHBA, KLF10, LEP, LIF, PRMT1, RUNX1, TRIB1*
Positive Regulation Of T Cell Proliferation	0.042	1.84	*ANXA1, CD80, HLA-E, HMGB1, ICOSLG, IGF1, IL6, IL6ST, JAK3, LEP, SHH, TNFSF9, VCAM1*
Regulation Of Immune Effector Process	0.039	1.75	*ACKR3, ANXA1, AP1M1, BIRC3, C3, CCL2, CFB, FGF7, HILPDA, ICAM1, IL33, IL6, IL7R, JAK3, LBP, LEP, LMCD1, LYN, NECTIN2, RIPK3, RSAD2, SIN3A, STOM, TEAD4, TRAF3, TRAF3IP2, TREM1, ZC3H12A*
Regulation Of Immune Response	0.004	1.95	*ABL1, ANXA1, BIRC3, C1QBP, C1R, C1RL, C1S, C3, CCR7, CD80, CFB, COCH, COLEC12, CTSB, CTSL, CTSS, ERAP1, EREG, GPX1, HLA-E, HMGB1, HSPD1, ICAM1, IDO1, IFI16, IFNAR1, IFNAR2, IFNGR1, IL1RL1, IL33, IL4R, IL6, IL6ST, IL7R, IRAK2, IRAK3, IRF1, IRF4, IRF7, JAK3, LBP, LEP, LYN, MAPKAPK2, MYD88, NECTIN2, NFKBIA, NMI, PAG1, PARP9, PDE4D, PIK3CD, PLSCR1, PSEN1, PSMA3, PSMA6,*

			PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSMD7, PSME1, PSME2, PSME3, PTPN1, PTPN2, PVR, RELB, RIPK3, RSAD2, SHC1, SIN3A, SOCS3, SOCS5, SPPL2A, STAT1, STAT2, TANK, TBK1, TLR2, TNIP1, TNIP2, TRAF3, TREM1, VCAM1
Regulation Of Immune System Process	0.001	2.22	*ABL1, ACKR3, ACVR1B, ANXA1, AP1M1, BDKRB1, BIRC3, C1R, C1RL, C1S, C3, CCL2, CCL20, CCL7, CCR7, CEBPB, CFB, COCH, CSF3, CTNNB1, CTSB, CTSL, CTSS, CXCL1, CXCL12, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, CYP19A1, EREG, FGF7, FOXC1, FOXP1, GPX1, HIF1A, HILPDA, ICAM1, ICOSLG, IFI16, IFNAR2, IFNGR1, IL1RL1, IL33, IL36B, IL6, IL6R, IL7R, INHBA, IRAK2, IRF1, IRF7, JAK3, KLF10, LBP, LEP, LIF, LMCD1, LYN, MAFB, MAP3K8, MIA3, NECTIN2, NFKBID, PAG1, PARP9, PDE4D, PLSCR1, PRMT1, PSEN1, PSMA6, PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSME1, PSME2, PSME3, PTPN1, PTPN2, PTPRE, RELB, RIPK3, RSAD2, RUNX1, SHH, SIN3A, SLC7A2, SOCS3, STAT1, STOM, TBK1, TEAD4, TJP2, TLR2, TNFSF13B, TNFSF14, TNIP2, TRAF3, TRAF3IP2, TREM1, TRIB1, VCAM1, VEGFA, ZC3H12A*
Regulation Of Innate Immune Response	0.001	2.53	*BIRC3, C1QBP, COCH, COLEC12, CTSB, CTSL, CTSS, ERAP1, EREG, HLA-E, HMGB1, HSPD1, IFI16, IFNAR1, IFNAR2, IFNGR1, IRAK2, IRAK3, IRF1, IRF4, IRF7, LBP, LEP, LYN, MAPKAPK2, MYD88, NECTIN2, NFKBIA, NMI, PARP9, PLSCR1, PSMA3, PSMA6, PSMB10, PSMC4, PSMD12, PSMD14, PSMD2, PSMD7, PSME1, PSME2, PSME3, PTPN1, PTPN2, PVR, RELB, RSAD2, SIN3A, SOCS3, STAT1, STAT2, TANK, TBK1, TLR2, TNIP1, TNIP2, TRAF3*
Regulation Of Interleukin 1 Production	0.042	1.86	*ANXA1, CCL20, CCR7, FOXP1, IFI16, PANX1, ZC3H12A*
Regulation Of Interleukin 12 Production	0.039	1.94	*BANK1, CEBPB, EREG, HMGB1, HSPD1, IL33, IL36B, IL36RN, IL6, IL6R, IRAK3, LBP, MAPKAPK2, MYD88, NCL, SOCS5, TLR2, TNFSF9, ZC3H12A*
Regulation Of Interleukin 6 Production	0.043	1.85	*C1QBP, CCR7, FOXP1, HMGB1, HSPD1, IDO1, IRAK3, IRF1, IRF5, JAK3, TLR2, TNFSF9*
Regulation Of T Cell Differentiation	0.044	1.79	*ANXA1, CD80, HMGB1, IL36B, IL4R, IL6, IL7R, IRF1, IRF4, JAK3, NFKBID, PTPN2, SHH, SOCS5, TNFSF9*
Response To Interleukin 1	0.033	2.02	*ANXA1, CCL2, CCL20, CCL7, CEBPB, CHI3L1, CXCL8, HAS2, HIF1A, ICAM1, IL6, IRAK2, NKX3-1, RPS6KA4, TNIP2, ZC3H12A*
Toll Like Receptor Signaling Pathway	0.033	2.15	*BIRC3, COLEC12, CTSB, CTSL, CTSS, HSPD1, IRAK2, IRAK3, IRF7, LBP, MAPKAPK2, MYD88, NFKBIA, TANK, TBK1, TLR2, TNIP1, TNIP2, TRAF3*

Table C4-15. *Genes that contribute to the changes in immune pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Positive Regulation Of Immune System Process	0.019	2.27	*ACVR1B, C1RL, CCL20, CSF3, CTSL, CXCL1, CXCL2, CXCL3, CXCL6, ICAM1, IFI16, IL33, IL6, MAP3K8, PLSCR1, PSME2*
Regulation Of Immune System Process	0.016	2.19	*ACVR1B, C1RL, CCL20, CSF3, CTSL, CXCL1, CXCL2, CXCL3, CXCL6, ICAM1, IFI16, IL33, IL6, IRF1, MAP3K8, NFKBID, PARP9, PLSCR1, PSME2, SLC7A2, STAT1, ZC3H12A*

Table C4-16. *Genes that contribute to the changes in immune pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Positive Regulation Of Immune System Process	0.002	2.41	*ACVR1B, ANXA1, BANK1, C12orf4, C1R, C1RL, CCL20, CFB, CSF3, CTSB, CTSL, CTSS, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, CYP19A1, FGF7, GPX1, HIF1A, ICAM1, IFI16, IFNGR1, IL1RL1, IL33, IL36B, IL6, IRF1, LBP, LEP, LIF, LMCD1, MAP3K8, MYD88, NECTIN2, NFKBID, PARP9, PHB, PLSCR1, PSMA3, PSMB10, PSMC4, PSME1, PSME2, RELB, RIPK3, RUNX1, SHH, SLC7A2, SNRPD1, SOCS3, STAT1, STOM, TARBP2, TEAD4, TNIP2, ZC3H12A*
Regulation Of Immune System Process	0.004	2.18	*ACVR1B, ANXA1, C12orf4, C1R, C1RL, CCL20, CCR7, CFB, CSF3, CTSB, CTSL, CTSS, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, HIF1A, ICAM1, ICOSLG, IFI16, IL1RL1, IL33, IL36B, IL6, JAK3, LBP, LEP, LIF, MAP3K8, MYD88, NECTIN2, PDE4D, PHB, PLSCR1, PSMA3, PSMB10, PSMC4, PSMD13, PSMD14, PSME1, PSME2, RELB, RUNX1, SHH, TNIP2, TRAF3, TRIB1*

C4.2.3 Cytokine/chemokine pathways

Table C4-17. *Genes that contribute to the changes in cytokine and chemokine pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Chemokine Receptor Binding	0.001	2.57	*CCL2, CCL20, CXCL1, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, STAT3*
Cytokine Activity	0.001	2.64	*BMP6, CCL2, CCL20, CSF3, CXCL1, CXCL12, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, IL32, IL33, IL36B, IL6, INHBA, LIF, NAMPT, NDP, TSLP, VEGFA*
Cytokine Receptor Activity	0.036	1.83	*ACKR3, CCR1, CCR7, IFNAR1, IFNAR2, IFNGR1, IL13RA1, IL15RA, IL18R1, IL1RL1, IL4R, IL6R, IL6ST, IL7R, OSMR*
Cytokine Receptor Binding	0.001	2.42	*BID, BMP6, CCL2, CCL20, CCL7, CSF3, CXCL1, CXCL12, CXCL2, CXCL3, CXCL5, CXCL6, CXCL8, ENG, IL36B, IL36RN, IL6, IL6R, INHBA, ITGB3, LIF, STAT1, STAT3, TGFBR1, TNFSF13B, TNFSF14, TRAF3, VEGFA*
Growth Factor Activity	0.022	2.14	*BMP6, CSF3, CXCL1, CXCL12, FGF7, IL6, INHBA, LEP, LIF, NDP, PGF, TYMP, VEGFA*
Negative Regulation Of Cytokine Production	0.034	1.94	*ANXA1, BCL3, IL1RL1, IL33, IL36RN, IL6, IL6R, INHBA, JAK3, LBP, PRG2, RELB, RPS6KA4, SRGN, TRAF3, TRIM25, ZC3H12A*
Positive Regulation Of Chemokine Production	0.036	1.91	*HIF1A, IL1RL1, IL33, IL6, IL6R, LBP, TLR2*
Positive Regulation Of Cytokine Biosynthetic Process	0.036	1.84	*BCL3, CCL20, CD80, CEBPG, EREG, IRF1, IRF4, LBP, MAPKAPK2, TBK1*
Positive Regulation Of Cytokine Production	0.004	2.12	*ABL1, ANXA1, BCL3, C3, CCL2, CCL20, CCR7, CEBPB, CYP1B1, HIF1A, HILPDA, IFI16, IL18R1, IL1RL1, IL33, IL36B, IL6, IRF1, LBP, LEP, LUM, NFKB2, PANX1, PDE4D, PRG2, PTGS2, RSAD2, RUNX1, TLR2*
Regulation Of Chemokine Production	0.036	1.82	*HIF1A, IL1RL1, IL33, IL6, IL6R, LBP, TLR2*
Regulation Of Cytokine Biosynthetic Process	0.035	2.02	*BCL3, CCL20, CD80, CEBPB, CEBPG, EREG, IL6, INHBA, IRF1, IRF4, LBP, MAPKAPK2, NMI, PRG2, TBK1*
Regulation Of Cytokine Production	0.001	2.07	*ABL1, ANXA1, BCL3, BIRC3, C1QBP, C3, CCL2, CCL20, CCR7, CD80, CEBPB, CEBPG, CTNNB1, CYP1B1, DHX9, EREG, FOXP1, FURIN, GSDMD, HIF1A, HILPDA, HMGB1, HSPD1, IDO1, IFI16, IFNAR1, IL18R1, IL1RL1, IL33, IL36B, IL36RN, IL4R, IL6, IL6R, IL6ST, INHBA, IRAK3, IRF1, IRF4, IRF5, IRF7, JAK3, LBP, LEP, LUM, LYN, MAPKAPK2, NFKB2, NMI, PANX1, PDE4D, PRG2, PTGS2, RELB, RIPK3, RPS6KA4,*

			RSAD2, RUNX1, SOCS5, SRGN, TBK1, TLR2, TNFSF9, TRAF3, TRIM25, UBE2L6, ZC3H12A
Regulation Of Cytokine Secretion	0.036	1.91	*ABL1, ANXA1, CCR7, FOXP1, IL1RL1, IL33, IL6, LYN, PANX1, SRGN, TLR2, ZC3H12A*

Table C4-18. *Genes that contribute to the changes in cytokine and chemokine pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Cytokine Activity	0.004	2.72	*CCL20, CSF3, CXCL1, CXCL2, CXCL3, CXCL6, CXCL8, IL32, IL33, IL36B, IL6, LIF, NDP*
Cytokine Receptor Binding	0.005	2.67	*BID, CCL20, CSF3, CXCL1, CXCL2, CXCL3, CXCL6, CXCL8, ENG, IL36B, IL6, LIF, MYD88, STAT1, STAT3*

C4.2.4 Matrix and cytoskeleton pathways

Table C4-19. *Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17A compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant.* ***Blue*** *= significant increase in normalised enrichment score (NES),* ***red*** *= significant decrease in NES.*

Pathway	padj	NES	Genes
Actin Cytoskeleton	0.001	-2.00	*ACTA2, ACTC1, ACTG1, ACTN4, ACTR1B, ADD1, AHNAK, ANLN, ARHGAP35, ARPC1B, CAPG, CAPN2, CARMIL1, CCDC102A, CDC42EP1, CFL2, CORO2B, CORO6, CRYAB, DAPK1, DBN1, DCTN1, DCTN3, DLC1, DST, DSTN, EPB41, EPB41L2, FHOD1, FLNB, FMN2, FSCN1, GSN, HFE, HSPB7, IVNS1ABP, KRT19, LASP1, LMOD1, LSP1, MPRIP, MYADM, MYH10, MYL6B, MYL9, MYLK, MYO18A, MYO1C, MYO1D, MYOM1, MYRIP, PDLIM2, PDLIM5, PKD2, PLEKHH2, PPP1R12A, PPP1R12B, PPP1R9A, PPP1R9B, PXN, SEPTIN9, SMTN, SPTBN1, SRC, TEK, TMOD2, TPM1, UTRN, WIPF1, ZYX*
Actin Filament Based Process	0.001	-1.78	*ACTC1, ACTG1, ACTN4, ADRA2A, ARHGEF17, BCL2, CACNA2D1, CFL2, COBLL1, CORO2B, CORO6, DAAM2, DBN1, DSTN, EHD2, EMP2, EPB41, EPB41L1, EPB41L2, FLNB, FNBP1L, FRY, GSN, INPPL1, IQSEC1, ITGB5, KIT, KLHL41, KRT19, LIMCH1, LMOD1, MEF2A, MINK1, MYH10, MYO18A, MYPN, NEDD9, PDGFRA, PDGFRB, PFN2, PPP1R9A, PPP1R9B, PTK7, RHOJ, SCN1B, SIPA1L1, SNTA1, SYNE2, TPM1, WIPF1, ZYX*
Actin Filament Bundle	0.012	-1.83	*ACTN4, CRYAB, FHOD1, FLNB, FSCN1, MYH10, MYL9, MYLK, MYO1C, PDLIM2, PXN, SEPTIN9, TPM1, ZYX*
Actin Filament Organization	0.033	-1.59	*ACTC1, ACTN4, ADD1, ARPC1B, BCL2, CARMIL1, CFL2, COBLL1, DBN1, DSTN, EMP2, FMN2, FRY, FSCN1, GSN, INPPL1, ITGB5, LMOD1, NEDD9, PPP1R9A, PPP1R9B, SPIRE1, SRC, TMOD2, WIPF1, ZYX*
Cortical Actin Cytoskeleton	0.001	-2.30	*ANLN, CAPN2, DSTN, EPB41, EPB41L2, GSN, KRT19, LASP1, MYADM, PDLIM2, PLEKHH2, PPP1R9A, SPTBN1, UTRN, WIPF1*
Cortical Cytoskeleton	0.001	-2.13	*ACTN4, ANLN, CAPN2, DSTN, EPB41, EPB41L2, GSN, KRT19, LASP1, MYADM, PDLIM2, PLEKHH2, PPP1R9A, SPTBN1, UTRN, WIPF1*
Cytoskeleton	0.002	-1.53	*ABCA2, ACTC1, ACTG1, ACTN4, AHNAK, AJUBA, AK5, AKAP12, ANK3, ANLN, ANXA11, ARHGAP24, ARHGAP35, ARL2, ARL2BP, ARL6IP5, ARPC1B, ASPM, C2CD5, CAPG, CAPN2, CC2D2A, CCDC102A, CCDC6, CDK6, CEP68, CFL2, CORO2B, CORO6, CRYAB, DAPK1, DBN1, DCTN1, DCTN3, DNM1, DST, DSTN, DVL1, EFHC1, EPB41, EPB41L1, EPB41L2, FHOD1, FIGN, FLNB, FNBP1L, FRMD5, FRY, GNAI2, GPER1, GPSM2, GSN, HIP1, HIP1R, HSPB1, HSPB7, HTT, IFFO1, INPPL1, IVNS1ABP, KIF13A, KIF1B, KIF20B, KIFAP3, KLHL41, KRT19, LASP1, LCA5, LMNA, LMOD1, LSP1, MAP1A, MAP1B, MAP2K2, MAPRE2, MARVELD1, MBNL1, MPRIP, MTCL1, MYADM, MYH10, MYL6B, MYL9, MYLIP, MYLK, MYO18A, MYO1D, MYOM1, NEDD9, NES, NEXN, NUAK1, NUMA1, PBXIP1, PDLIM2, PDLIM5, PFN2, PKD2, PLEC, PLEKHH2, PPP1R12A, PPP1R9A, PPP1R9B, PPP2R2B, PRC1, PTPN13, PTPN14, PXN, SEPTIN5, SEPTIN9, SGCB, SGCE, SGCG, SIPA1L1, SIRT2, SLC8A1, SMTN, SNTA1, SPIRE1, SPTBN1, STARD9, STK39, SYNE1, SYNE2, SYNM, TGFB1I1, TPM1, TPPP3, TRIP6, TTLL3, TTLL7, TUBA4A, TUBG2, UTRN, VIM, WIPF1, XRN1, ZYX*

Cytoskeleton Organization	0.001	-1.68	*ACTC1, ACTG1, ACTN4, ADRA2A, ANK3, ANLN, ARHGAP10, ARHGEF17, ARL2, ARPC1B, ASPM, BCL2, CAV1, CC2D2A, CEP68, CFL2, COBLL1, CORO2B, CORO6, CRYAB, DAAM2, DBN1, DIAPH3, DST, DSTN, DVL1, EHD2, EMP2, EPB41, EPB41L1, EPB41L2, FIGN, FITM2, FLNB, FRY, GPSM2, GSN, HTT, INPPL1, IQSEC1, ITGB5, KIT, KLHL41, KRT19, LIMCH1, LMNA, LMOD1, MAP1A, MAP1B, MAST4, MEF2A, MINK1, MTCL1, MYH10, MYO18A, MYPN, NEDD9, NUMA1, PALM, PDGFRA, PDGFRB, PFN2, PKD2, PPP1R12A, PPP1R9A, PPP1R9B, PRC1, PTK7, RHOJ, SH3D19, SIPA1L1, SPIRE1, STARD9, SUN1, SYNE1, SYNE2, SYNE3, SYNM, TPM1, TPPP3, TTLL3, TUBG2, VIM, WIPF1, WTIP, ZYX*
Extracellular Matrix	0.001	-1.74	*ACAN, ADAMTS10, ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, AEBP1, ASPN, BMP4, CCBE1, CD248, COL14A1, COL1A1, COL1A2, COL5A3, COL6A1, COL6A2, COL6A3, COL8A2, CRIP2, CRTAP, CTGF, CTHRC1, CYR61, FBLN2, FGF1, GPC1, HMCN1, ITGA6, KAZALD1, LAMA2, LAMA4, LAMB2, LOXL1, LTBP3, LTBP4, MAMDC2, MFAP2, MGP, MMP16, MMRN2, MYOC, NOV, OLFML2A, OMD, PODN, POSTN, SLIT3, SPARC, SPON2, SSC5D, TGFB1I1, TIMP2, VIT, WISP2*
Extracellular Matrix Component	0.033	-1.59	*ADAMTS10, COL14A1, COL1A1, COL1A2, COL5A3, COL6A1, COL6A3, COL8A2, HMCN1, ITGA6, LAMA2, LAMA4, LAMB2, LOXL1, MFAP2, MMRN2, SPARC*
Negative Regulation Of Cytoskeleton Organization	0.015	-1.68	*CAPG, GPSM2, GSN, LMOD1, MAP1A, MYOC, PFN2, PLEKHH2, SPTBN1, STMN2, TMEFF2*
Proteinaceous Extracellular Matrix	0.001	-1.86	*ACAN, ADAMTS10, ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, ASPN, BMP4, CCBE1, CD248, COL14A1, COL1A1, COL1A2, COL5A3, COL6A1, COL6A2, COL6A3, COL8A2, CRTAP, CTGF, CTHRC1, CYR61, FBLN2, FGF1, GPC1, HMCN1, ITGA6, KAZALD1, LAMA2, LAMA4, LAMB2, LOXL1, LTBP4, MAMDC2, MFAP2, MGP, MMP16, MMRN2, MYOC, NOV, OLFML2A, OMD, PODN, POSTN, SLIT3, SPARC, SPON2, TIMP2, VIT, WISP2*
Regulation Of Actin Filament Depolymerization	0.002	-2.16	*CAPG, CFL2, DSTN, GSN, LMOD1, PLEKHH2, SH3BGRL3, SPTBN1*
Regulation Of Cytoskeleton Organization	0.017	-1.52	*ARHGAP18, ARL2, CAPG, CAPN2, CAV1, CDKN1B, CFL2, CLIP3, CTGF, DIXDC1, DSTN, FHOD1, GPSM2, GSN, JAM3, LMOD1, MAP1A, MEF2C, MYADM, MYOC, NES, NEXN, PDGFRA, PDGFRB, PFN2, PHLDB1, PLEKHH2, PLXNA3, PPP1R9A, PYCARD, SEMA3E, SH3BGRL3, SIRT2, SPIRE1, SPTBN1, STARD9, STMN2, TMEFF2, TPM1, WIPF1*

Table C4-20. *Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17F compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant. **Blue** = significant increase in normalised enrichment score (NES), **red** = significant decrease in NES.*

Pathway	padj	NES	Genes
Extracellular Matrix	0.015	-1.98	*ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, COL14A1, COL6A1, COL6A2, FBLN2, GLG1, HMCN1, ITGA6, KAZALD1, LAMA2, LOXL1, LTBP3, LTBP4, MGP, MMP16, MYOC, TIMP2, VIT*
Proteinaceous Extracellular Matrix	0.007	-2.23	*ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, COL14A1, COL6A1, COL6A2, FBLN2, GLG1, HMCN1, ITGA6, KAZALD1, LAMA2, LOXL1, LTBP4, MGP, MMP16, MYOC, TIMP2, VIT*

Table C4-21. *Genes that contribute to the changes in matrix and cytoskeleton pathways after treatment with IL-17AF compared to control in end-stage OA synovial fibroblasts. An adjusted p-value (padj) < 0.05 is considered significant. **Blue** = significant increase in normalised enrichment score (NES), **red** = significant decrease in NES.*

Pathway	padj	NES	Genes
Actin Cytoskeleton	0.017	-1.89	*ACTC1, ACTN4, AHNAK, ARHGAP35, CAPG, CDC42BPA, CFL2, CORO6, CRYAB, DAPK1, DST, EPB41, EPB41L2, FER, FLNB, HSPB7, IVNS1ABP, KRT19, LMOD1, LSP1, MPRIP, MYO18A, MYOM1, PDLIM5, PHC3, PKD2, PLEKHH2, PPP1R12A, PXN, RFLNB, SPTBN1, STAG2, WIPF1*
Extracellular Matrix	0.035	-1.71	*ADAMTS1, ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, ADAMTSL4, ASPN, CCBE1, COL14A1, COL1A1, COL1A2, COL3A1, COL5A3, COL6A1, COL6A2, COL6A3, COL8A2, CRIP2, CRTAP, CYR61, DLG1, DST, FBLN2, FBN1, GLG1, HMCN1, HSPG2, ITGA6, KAZALD1, LAMA2, LAMB2, LAMC1, LOX, LOXL1, LTBP2, LTBP3, LTBP4, MFAP2, MGP, MMP16, MMRN2, MYOC, NID1, NOV, OGN, PODN, POSTN, RELN, SLIT3, SPARC, SSC5D, TIMP2, TINAGL1, VIT, WISP2*
Extracellular Matrix Component	0.047	-1.75	*ADAMTS1, COL14A1, COL1A1, COL1A2, COL3A1, COL5A3, COL6A1, COL6A3, COL8A2, DLG1, DST, FBN1, HMCN1, HSPG2, ITGA6, LAMA2, LAMB2, LAMC1, LOXL1, MFAP2, MMRN2, NID1, SPARC*
Negative Regulation Of Cytoskeleton Organization	0.017	-2.04	*GPSM2, LMOD1, MAP1A, MYOC, PLEKHH2, STARD9*
Proteinaceous Extracellular Matrix	0.017	-1.86	*ADAMTS1, ADAMTS14, ADAMTS5, ADAMTS7, ADAMTSL1, ADAMTSL4, ASPN, CCBE1, COL14A1, COL1A1, COL1A2, COL3A1, COL5A3, COL6A1, COL6A2, COL6A3, COL8A2, CRTAP, CYR61, DLG1, DST, FBLN2, FBN1, GLG1, HMCN1, HSPG2, ITGA6, KAZALD1, LAMA2, LAMB2, LAMC1, LOX, LOXL1, LTBP2, LTBP4, MFAP2, MGP, MMP16, MMRN2, MYOC, NID1, NOV, OGN, PODN, POSTN, RELN, SLIT3, SPARC, TIMP2, VIT, WISP2*
Regulation Of Cytoskeleton Organization	0.047	-1.70	*CDKN1B, CFL2, GPSM2, JAM3, LMOD1, MAP1A, MEF2C, MYOC, NCKAP1, PDGFRB, PKD1, PLEKHH2, SDC4, SEMA3E, SPIRE1, SPTBN1, STARD9, STMN2*

C4.3 Volcano plots

Chapter 5 mainly focussed on the effect of IL-17A on gene expression, as this cytokine lead to the largest changes in gene expression and the affected the most pathways in enrichment analyses of hallmark, immune, and matrix pathways. Here, the volcano plots for the hallmark, immune, and matrix/cytoskeleton enrichment analysis will be presented for the changes due to IL-17F or IL-17AF treatment and changes in cytokine/chemokine pathways due to IL-17A, IL-17F, or IL-17AF treatment in chondrocytes and synovial fibroblasts, including an information box of significantly changed pathways including their normalised enrichment score and p-value.

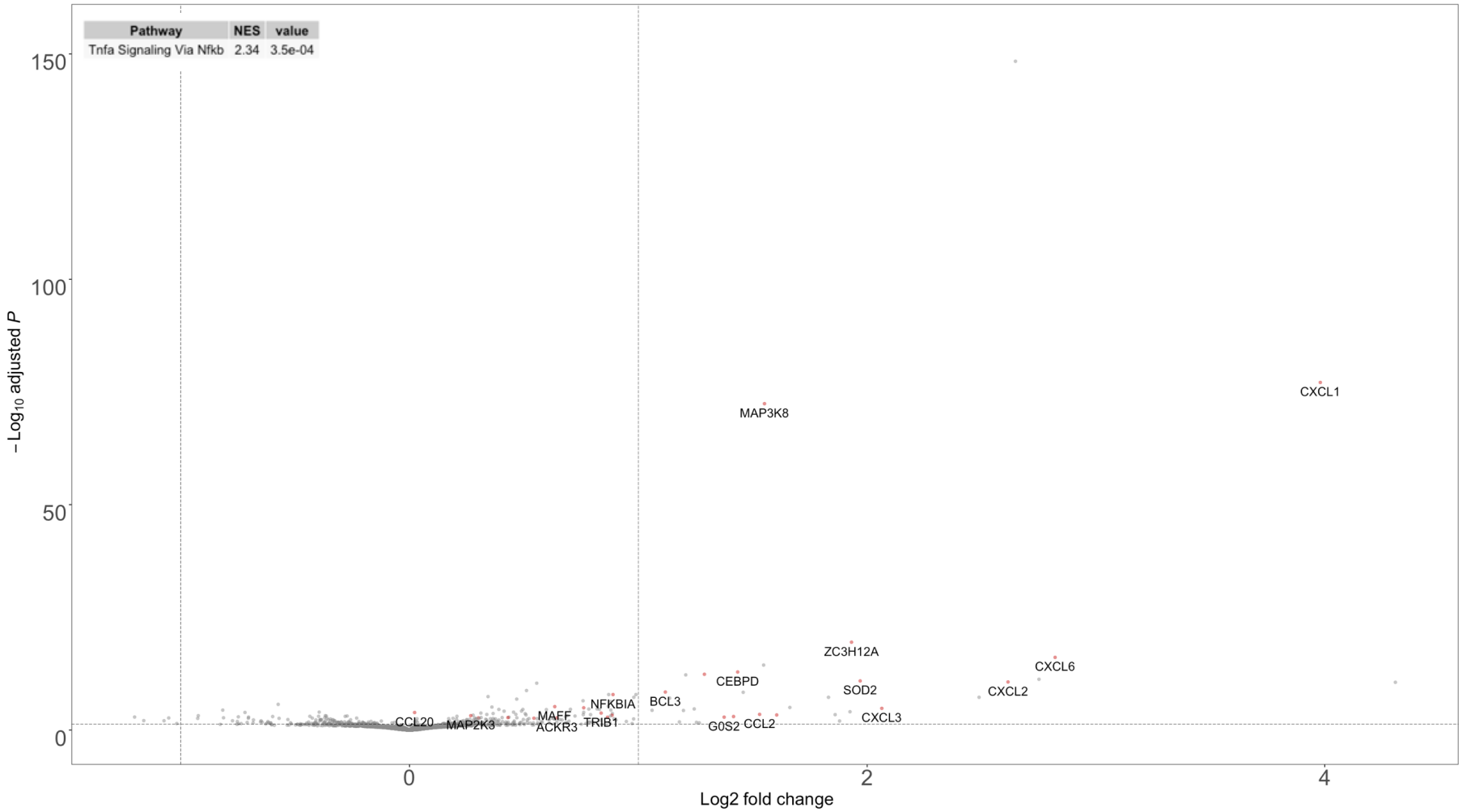

Figure C4-1. *Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots*.

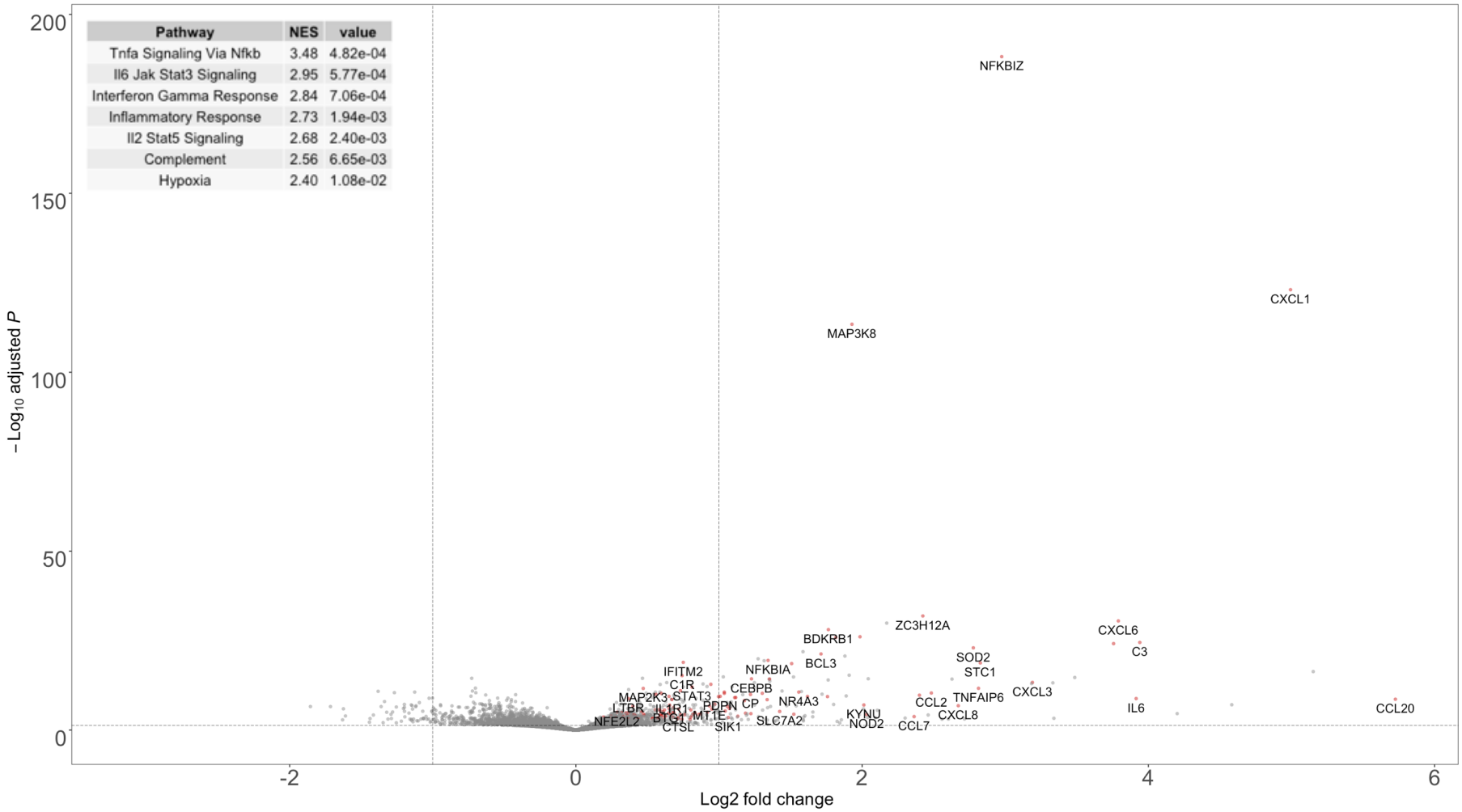

Figure C4-2. *Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots.*

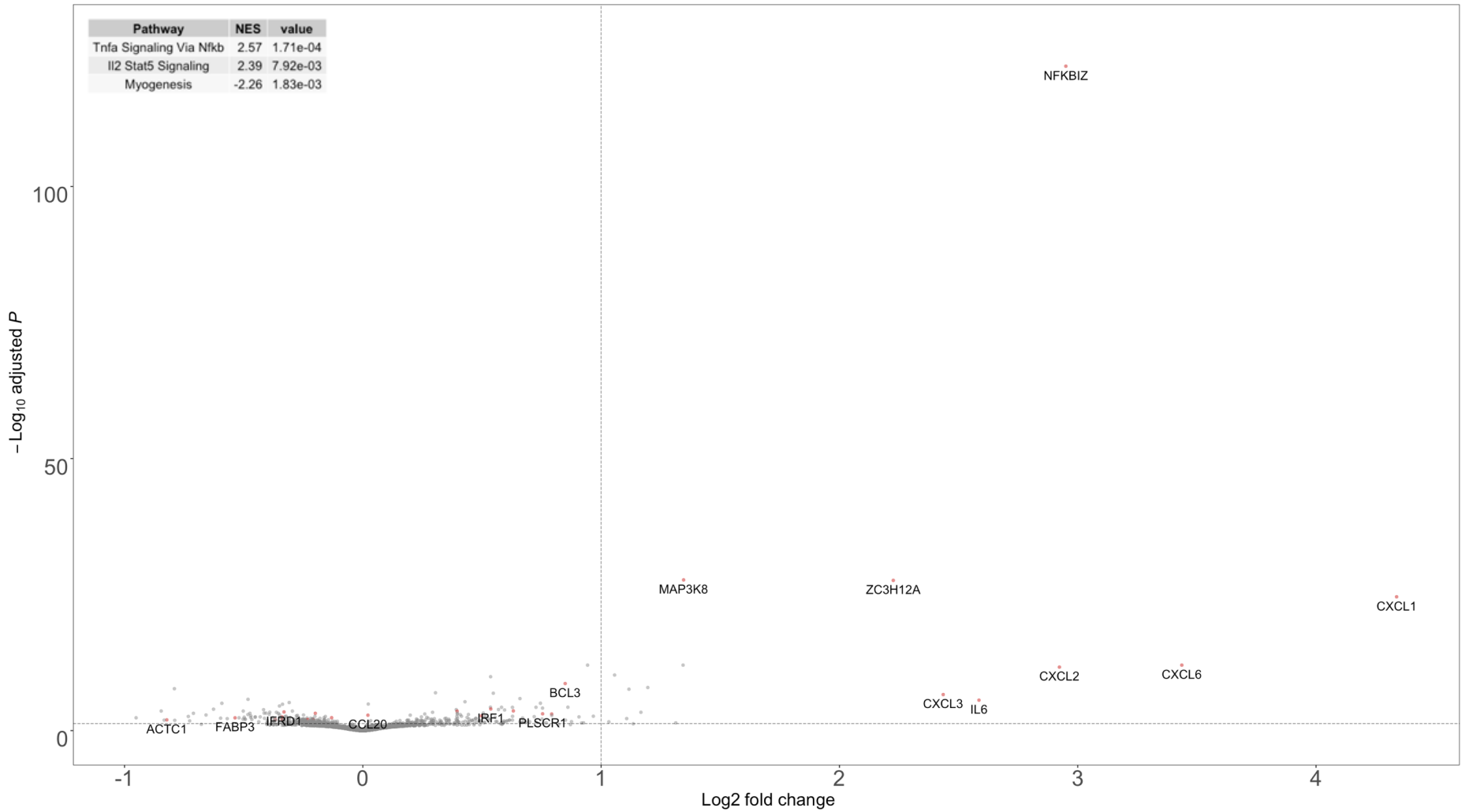

Figure C4-3. *Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots.*

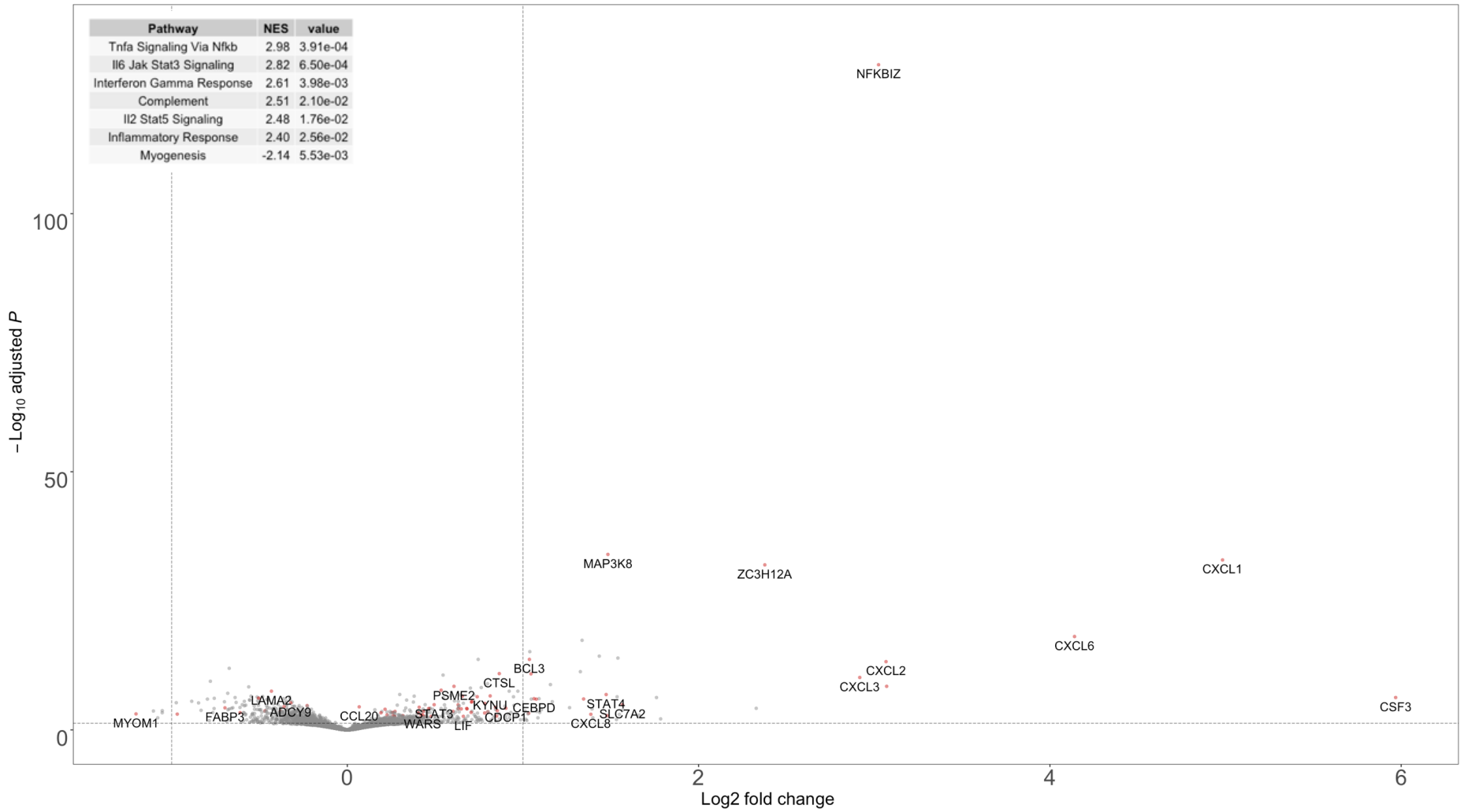

Figure C4-4. *Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in hallmark pathways highlighted by name and red dots.*

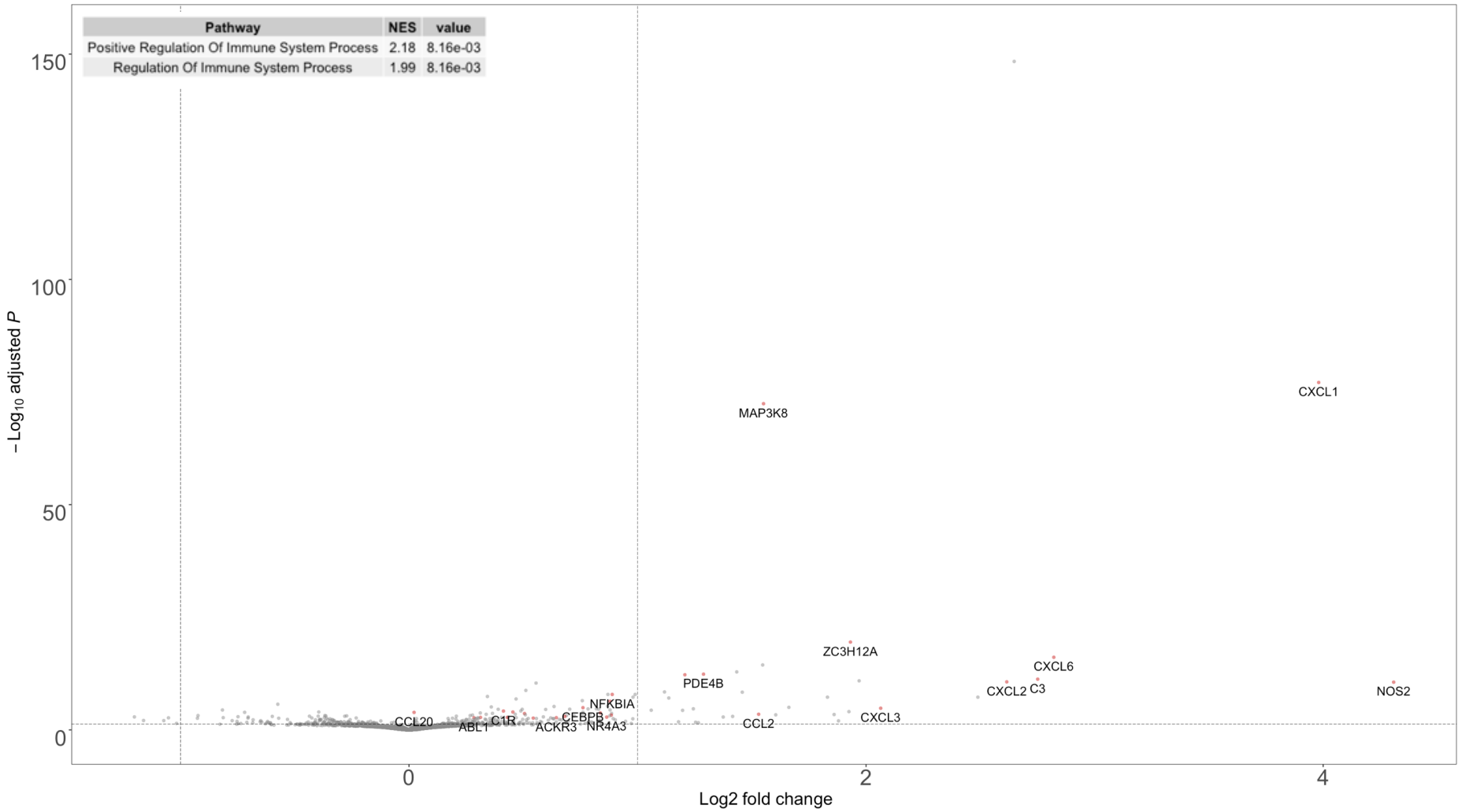

Figure C4-5. *Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots.*

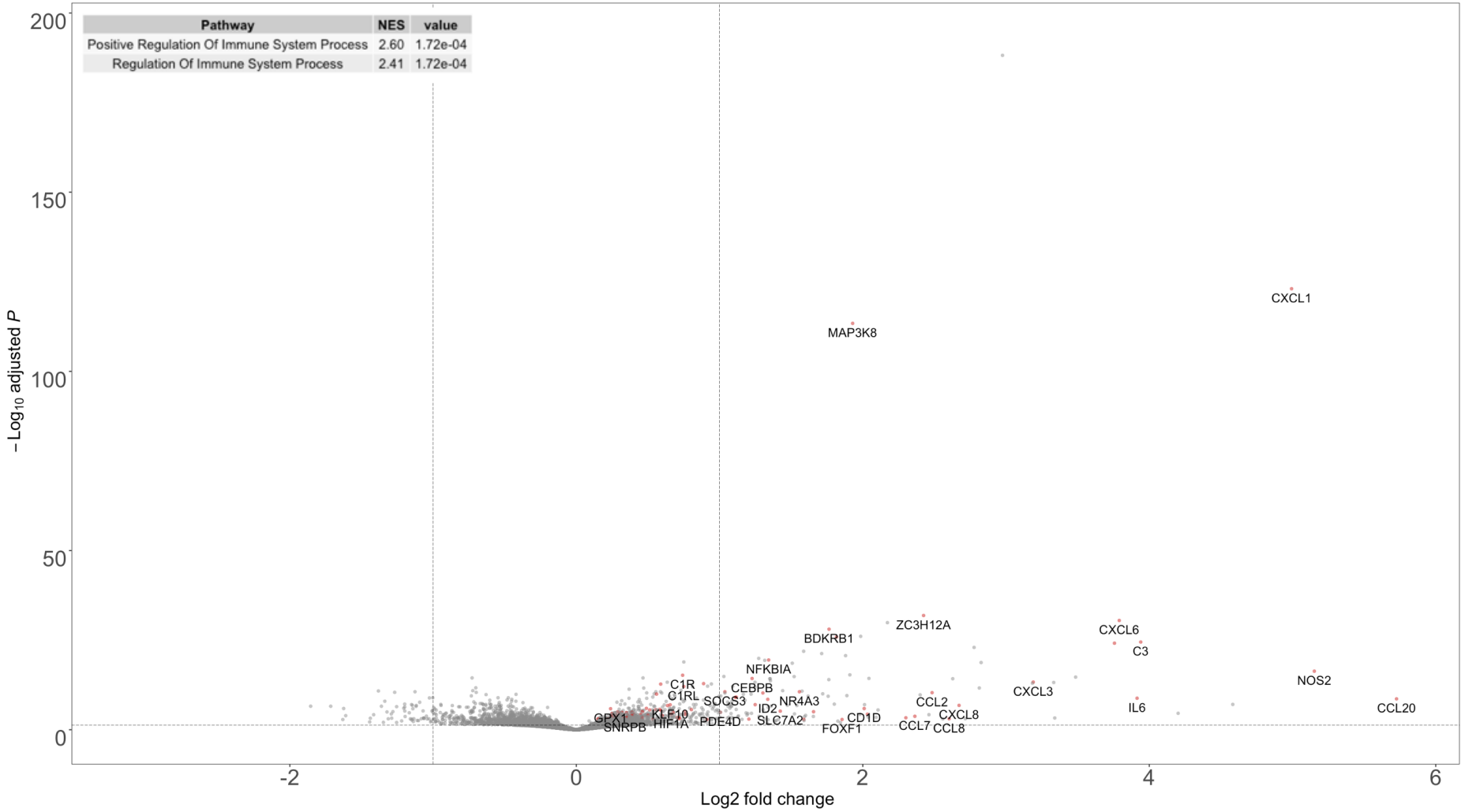

Figure C4-6. *Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots.*

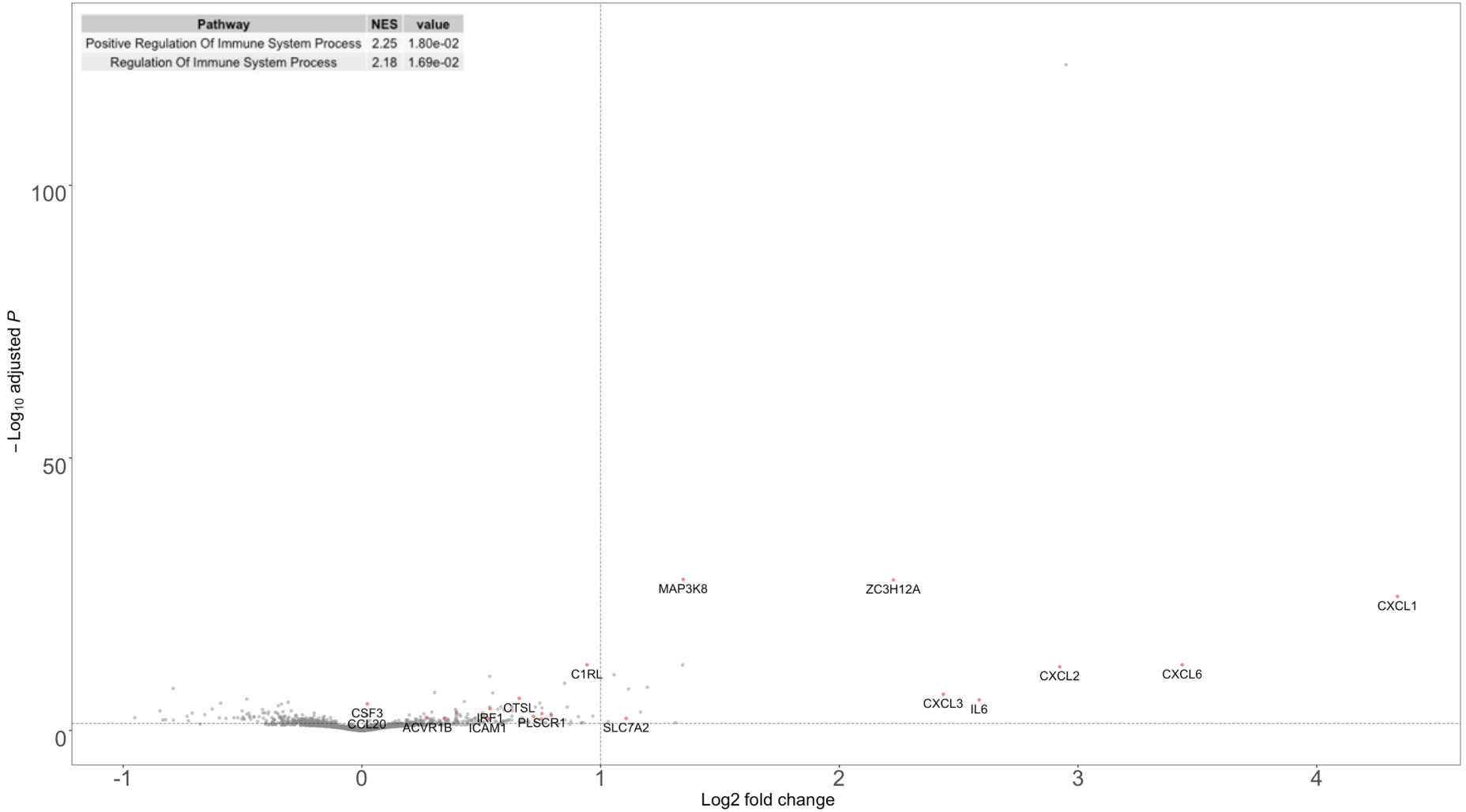

Figure C4-7. *Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots.*

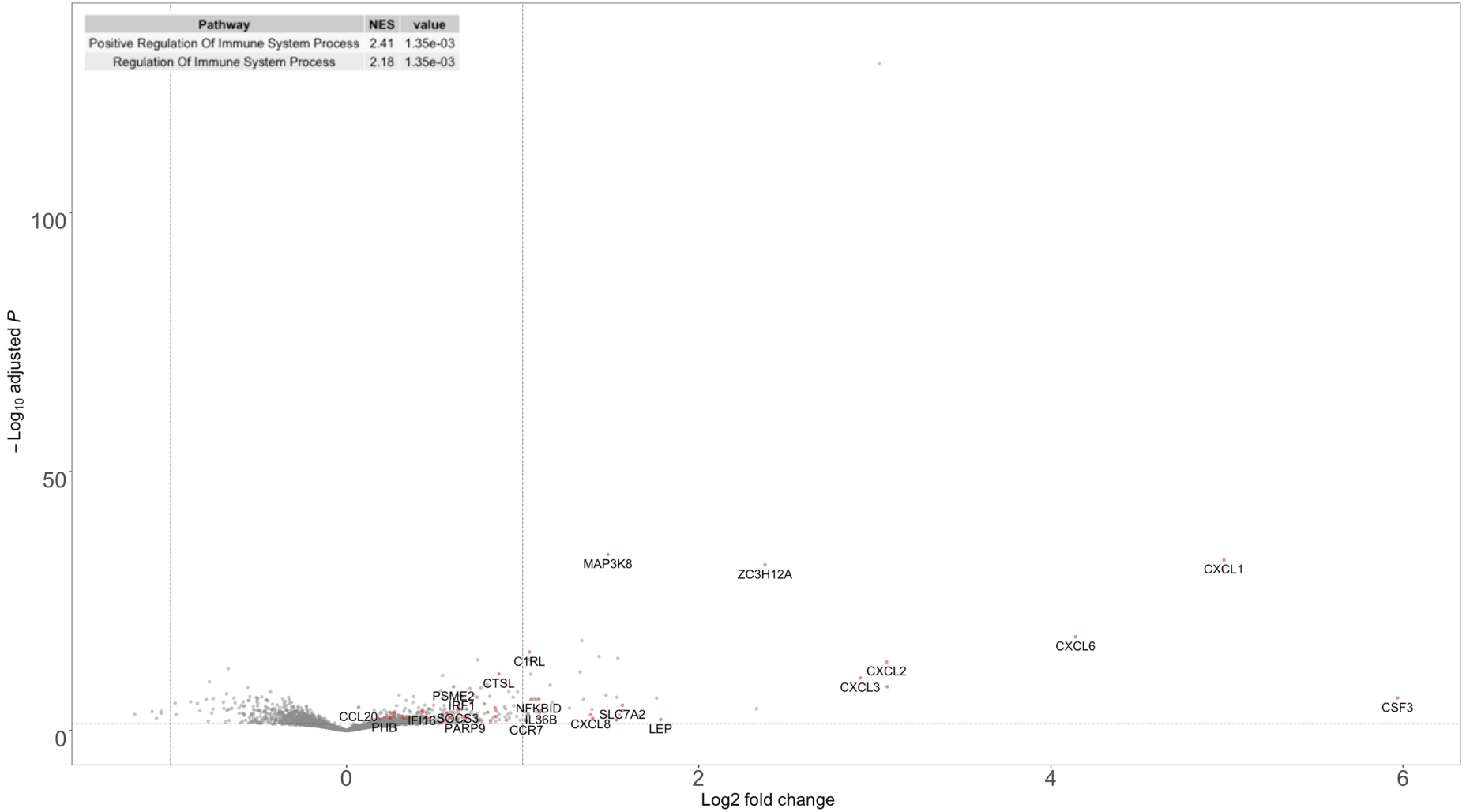

Figure C4-8. *Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in immune pathways highlighted by name and red dots.*

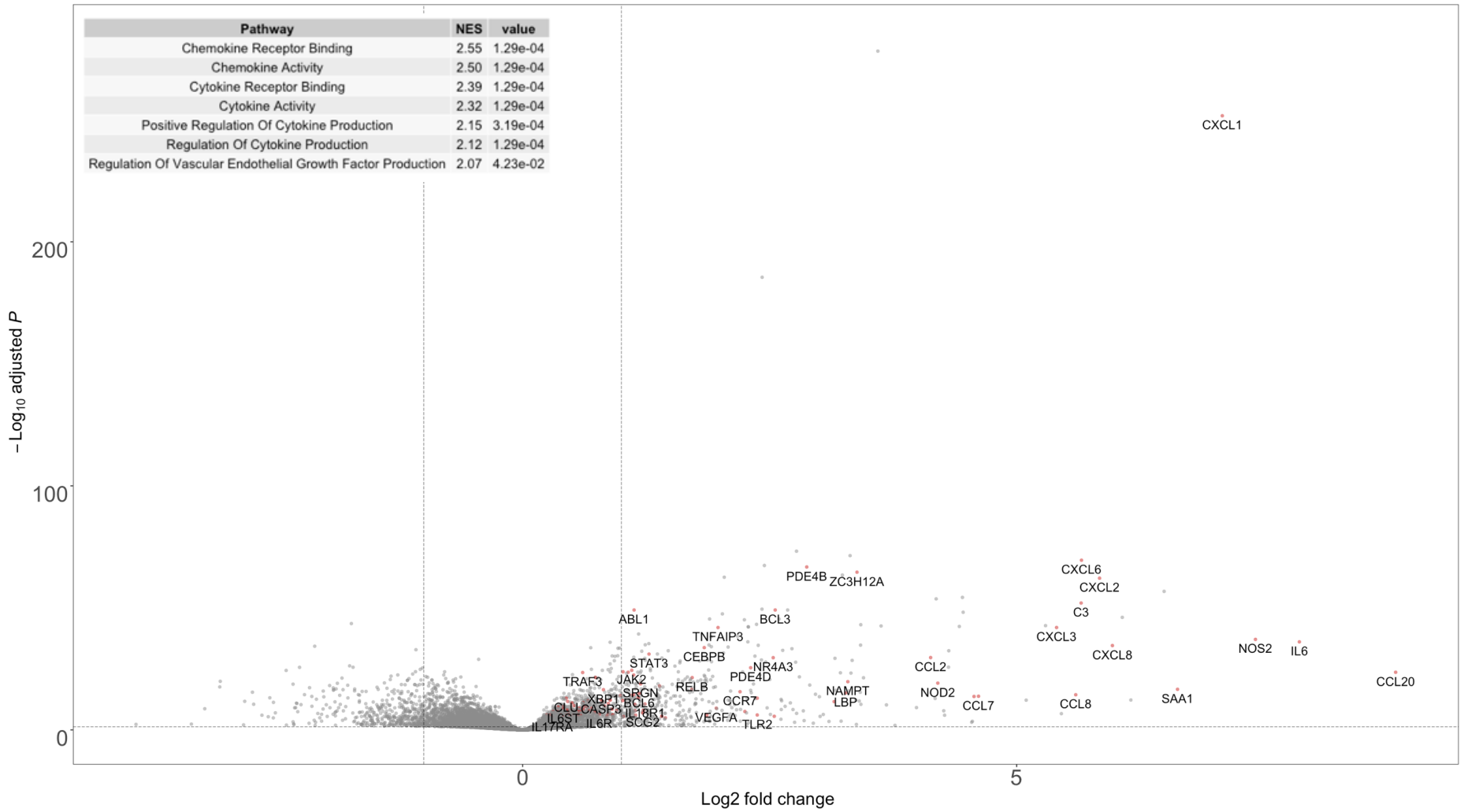

Figure C4-9. *Volcano plot representing genes changed by IL-17A treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots*.

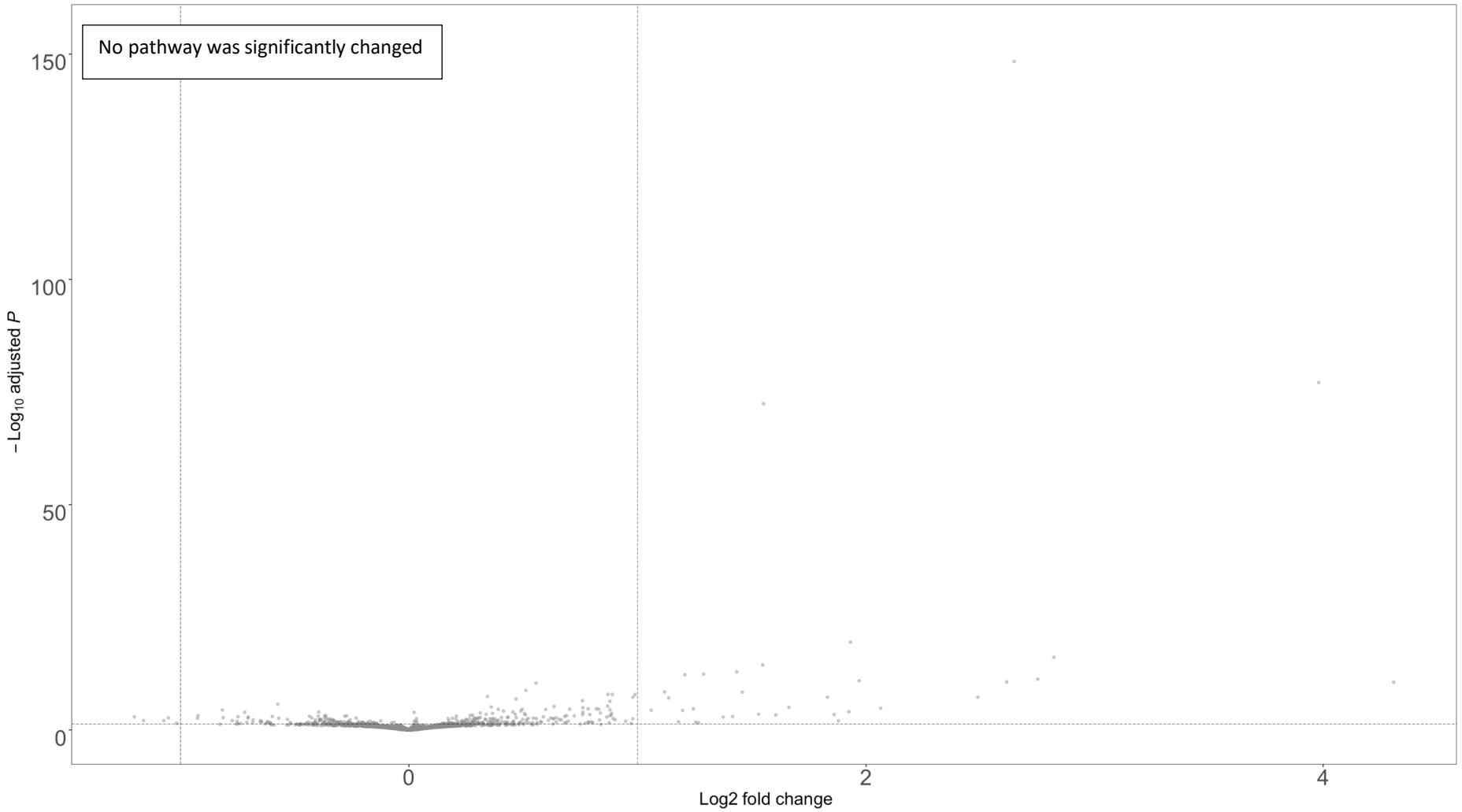

Figure C4-10. *Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots.*

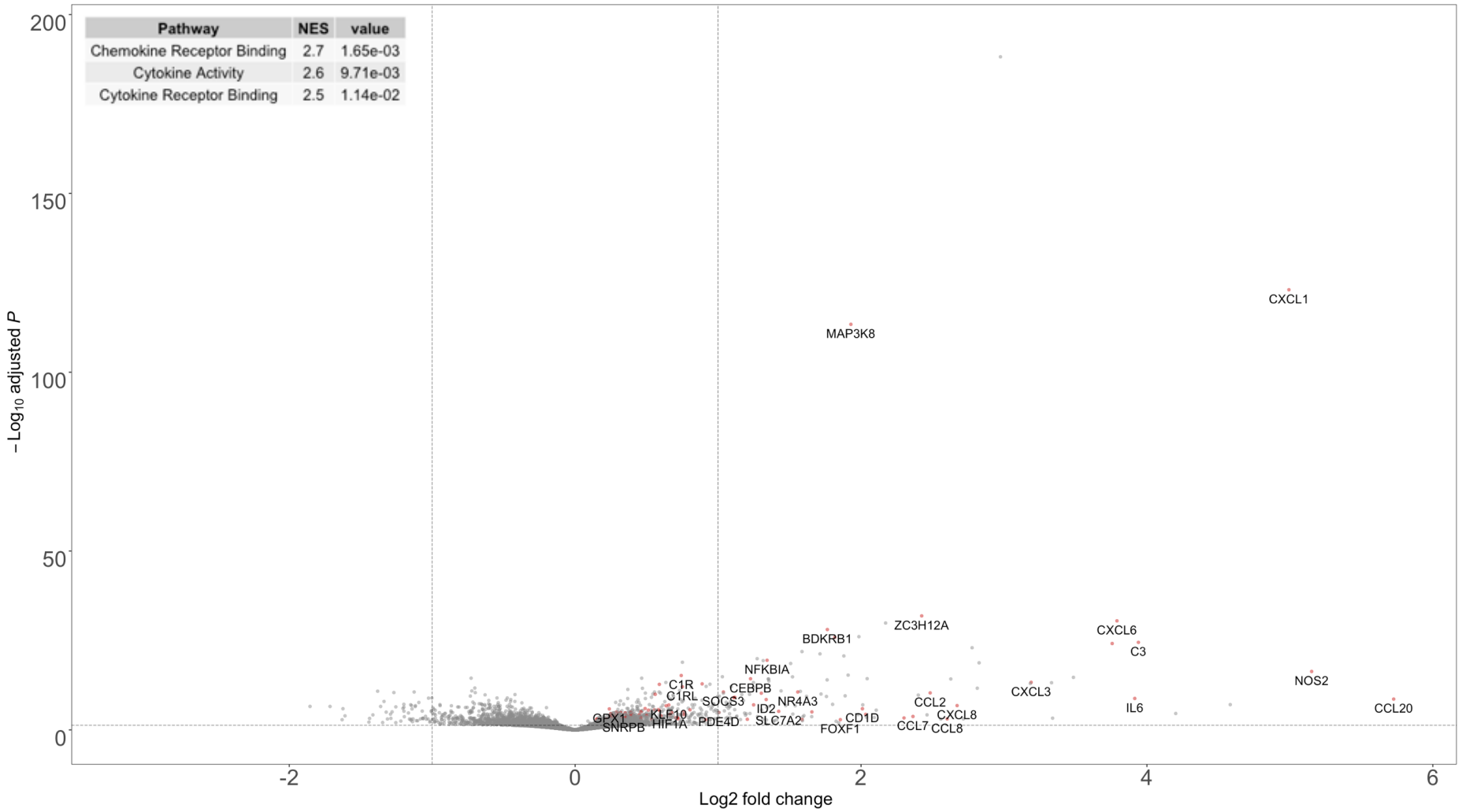

Figure C4-11. *Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots.*

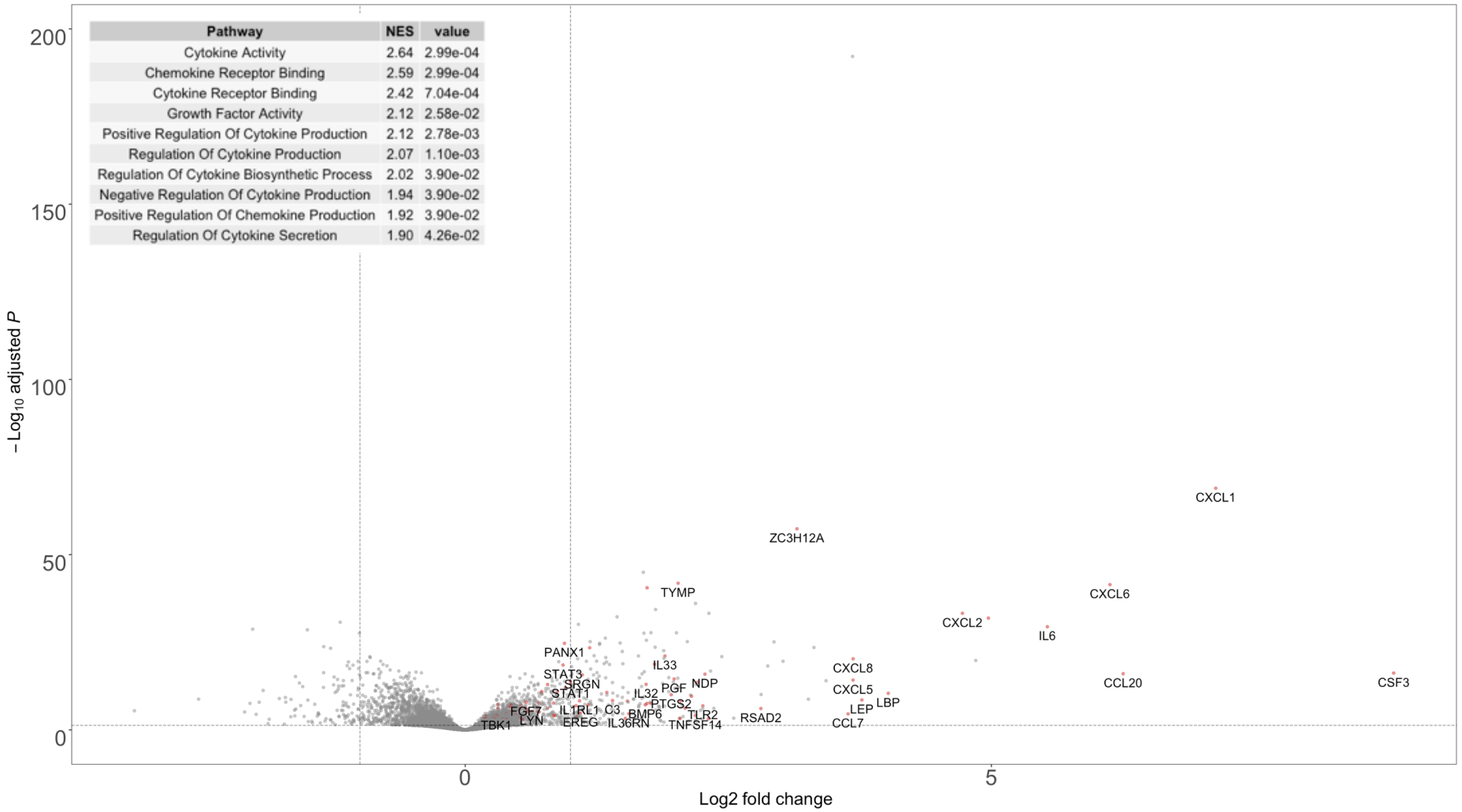

Figure C4-12. *Volcano plot representing genes changed by IL-17A treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots*.

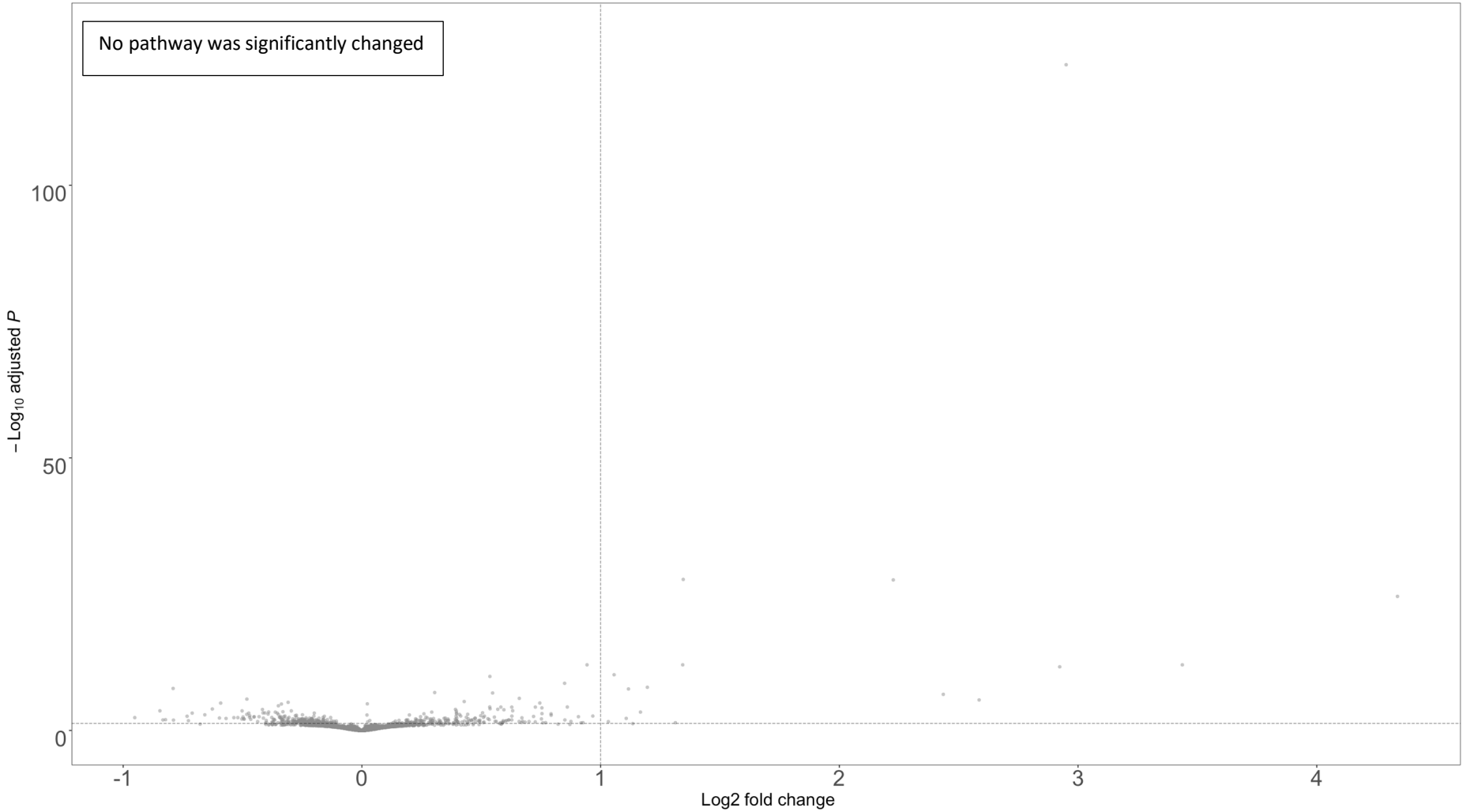

Figure C4-13. *Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots*.

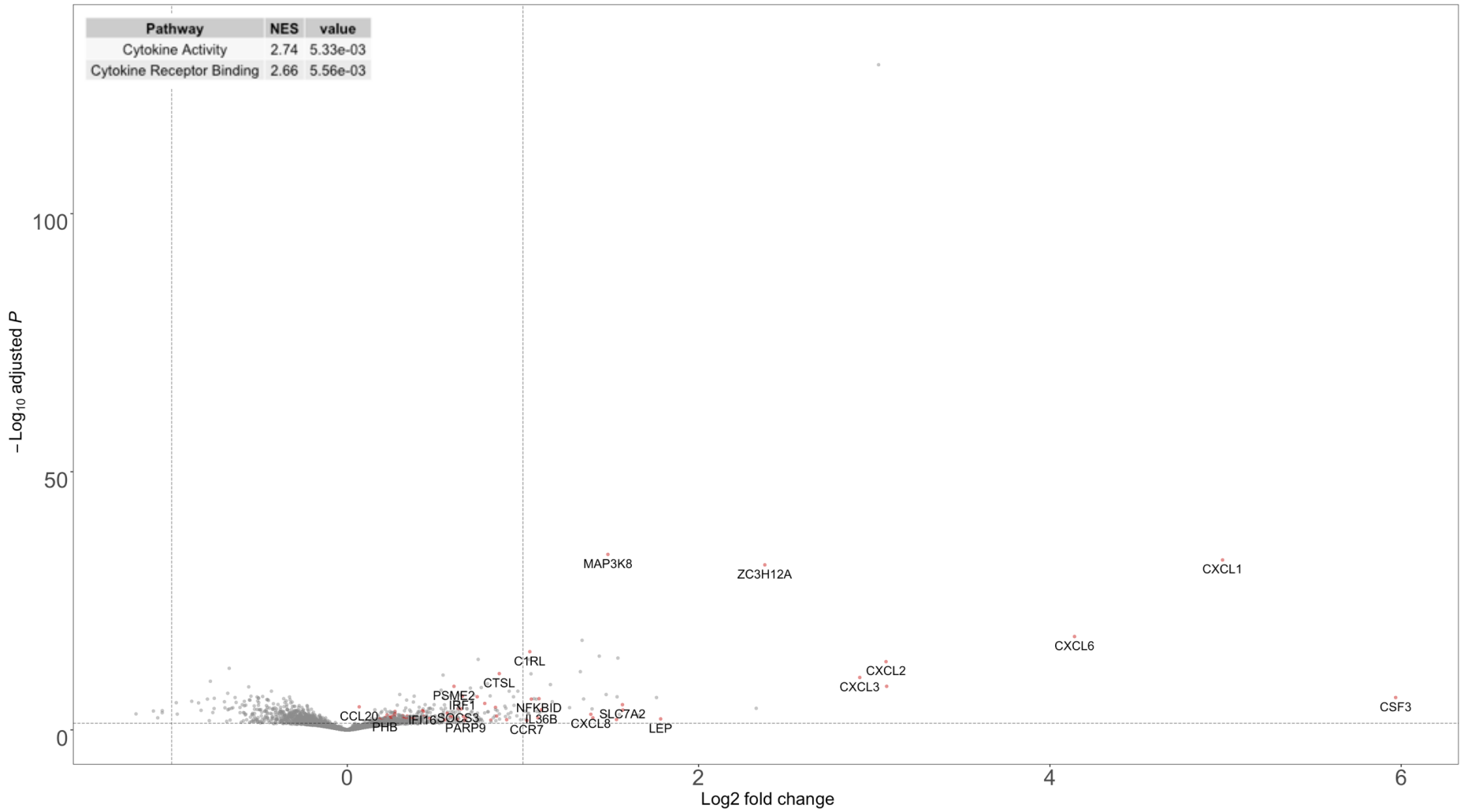

Figure C4-14. *Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in cytokine/chemokine regulation pathways highlighted by name and red dots*.

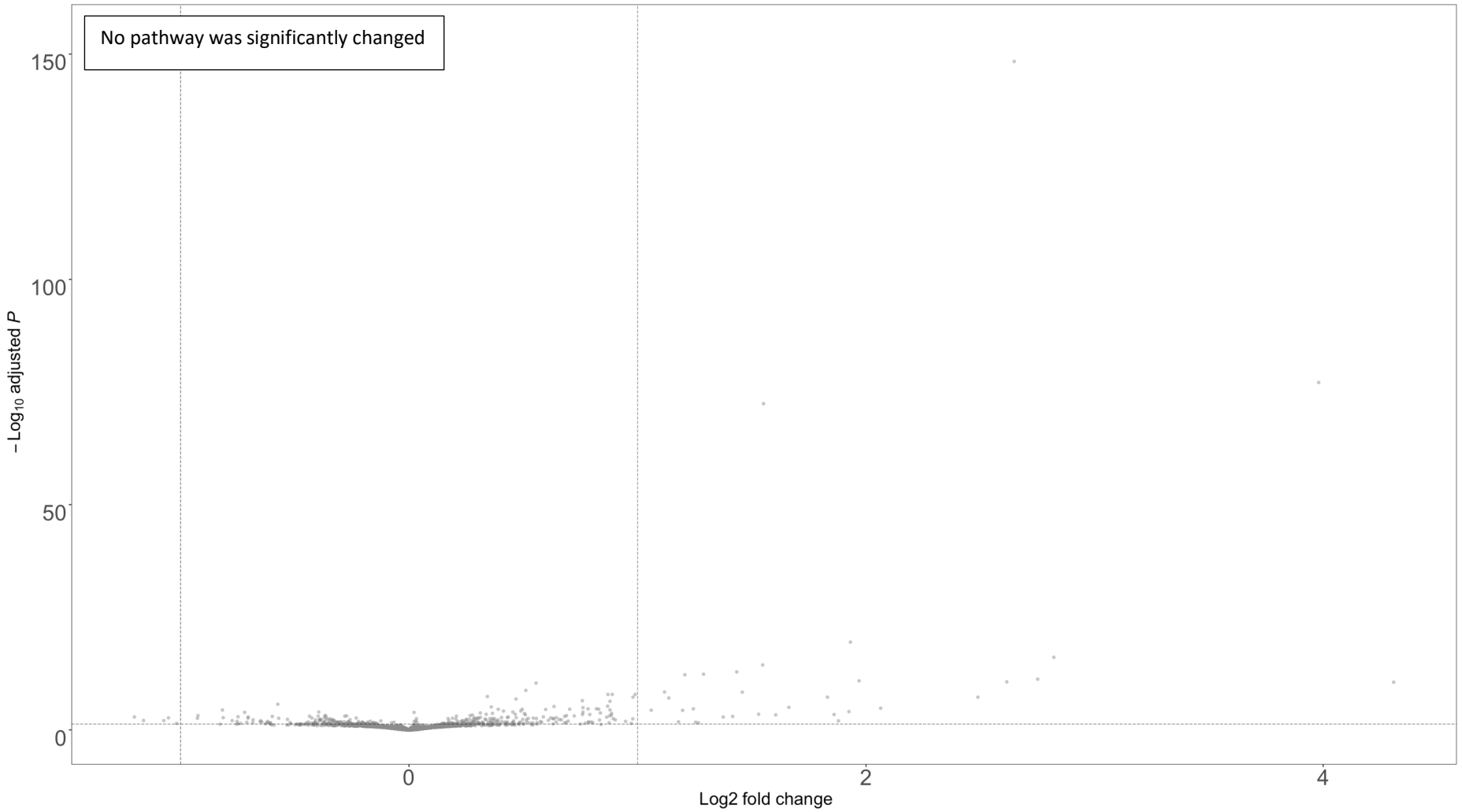

Figure C4-15. *Volcano plot representing genes changed by IL-17F treatment in chondrocytes, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots*.

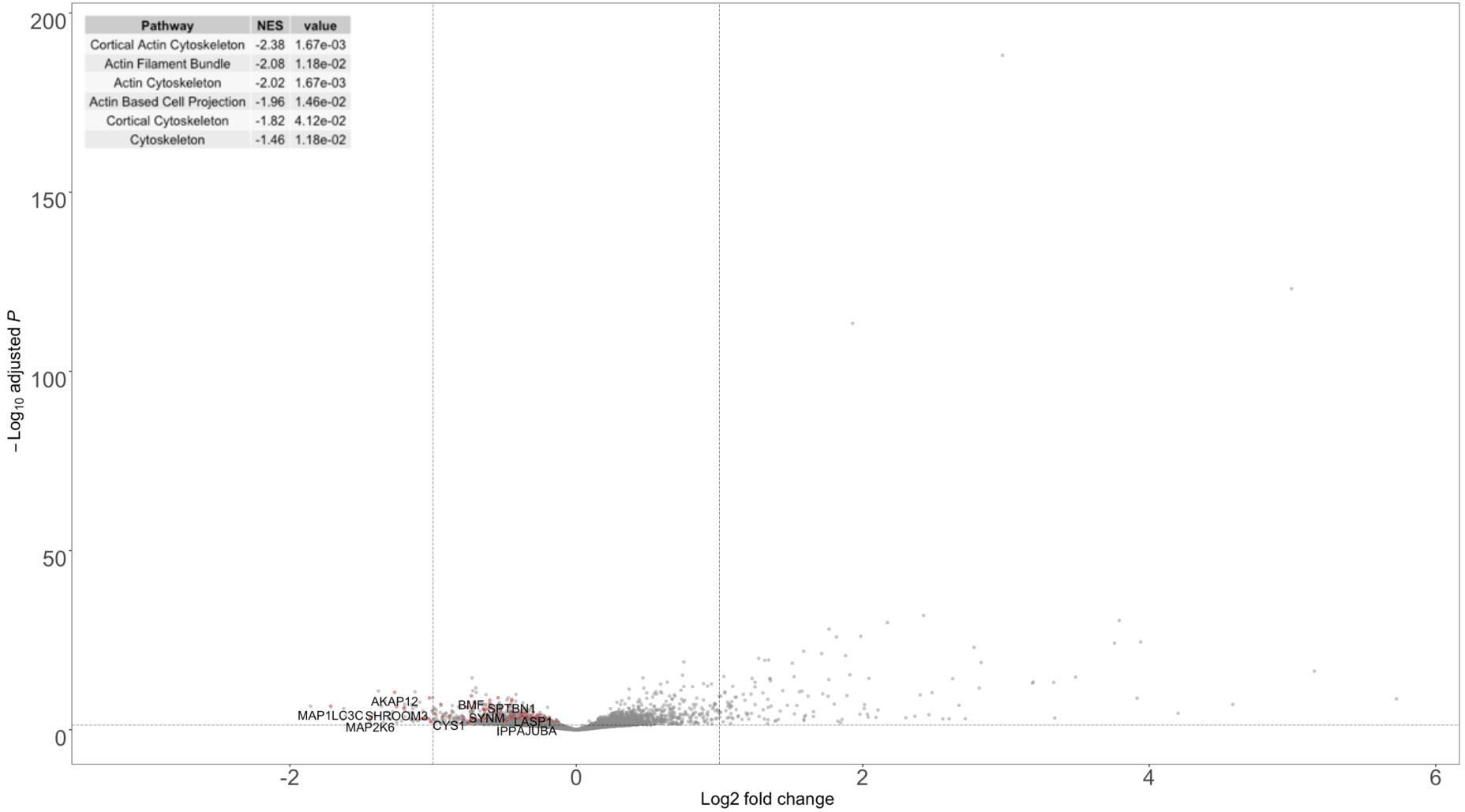

Figure C4-16. *Volcano plot representing genes changed by IL-17AF treatment in chondrocytes, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots.*

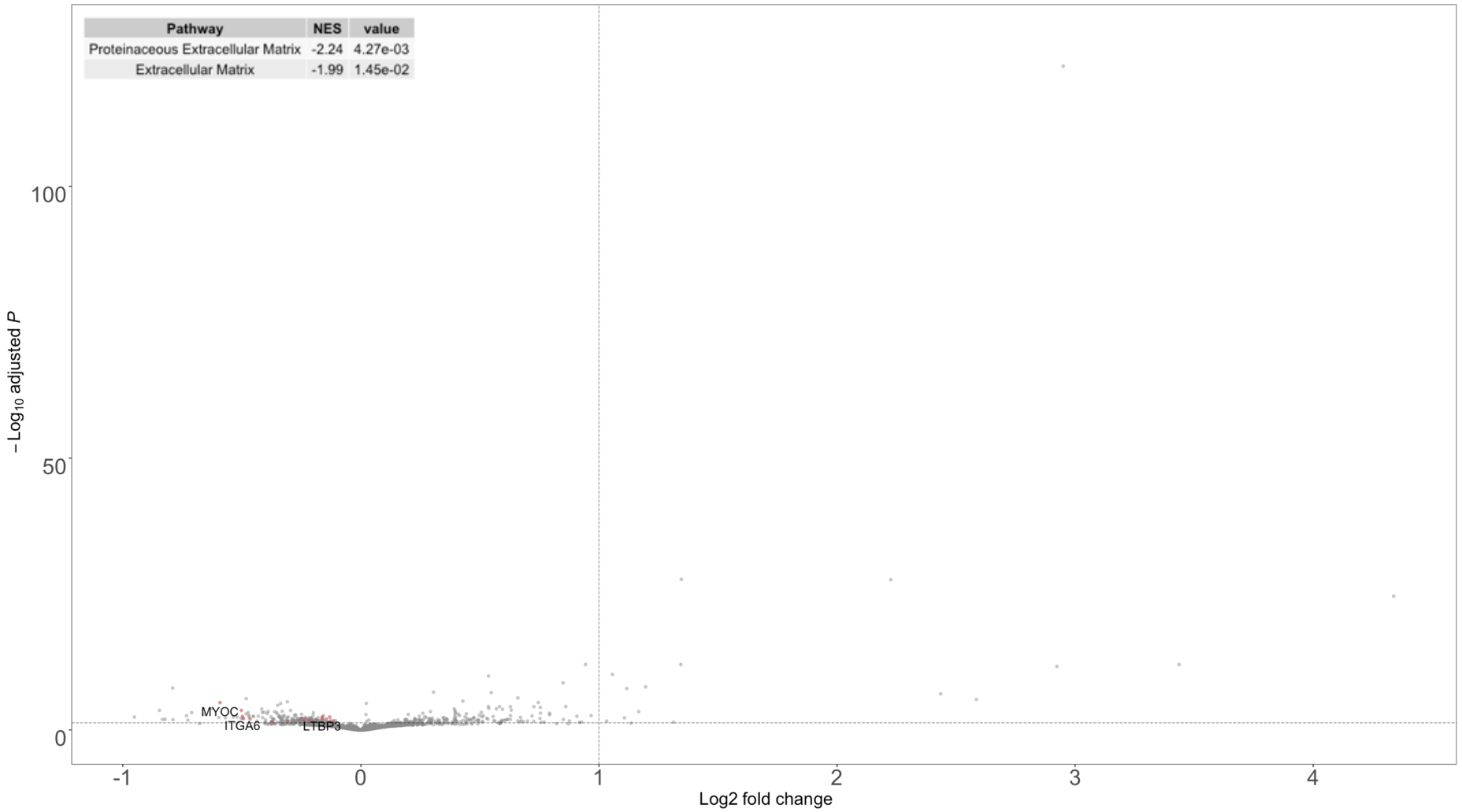

Figure C4-17. *Volcano plot representing genes changed by IL-17F treatment in synovial fibroblasts, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots*.

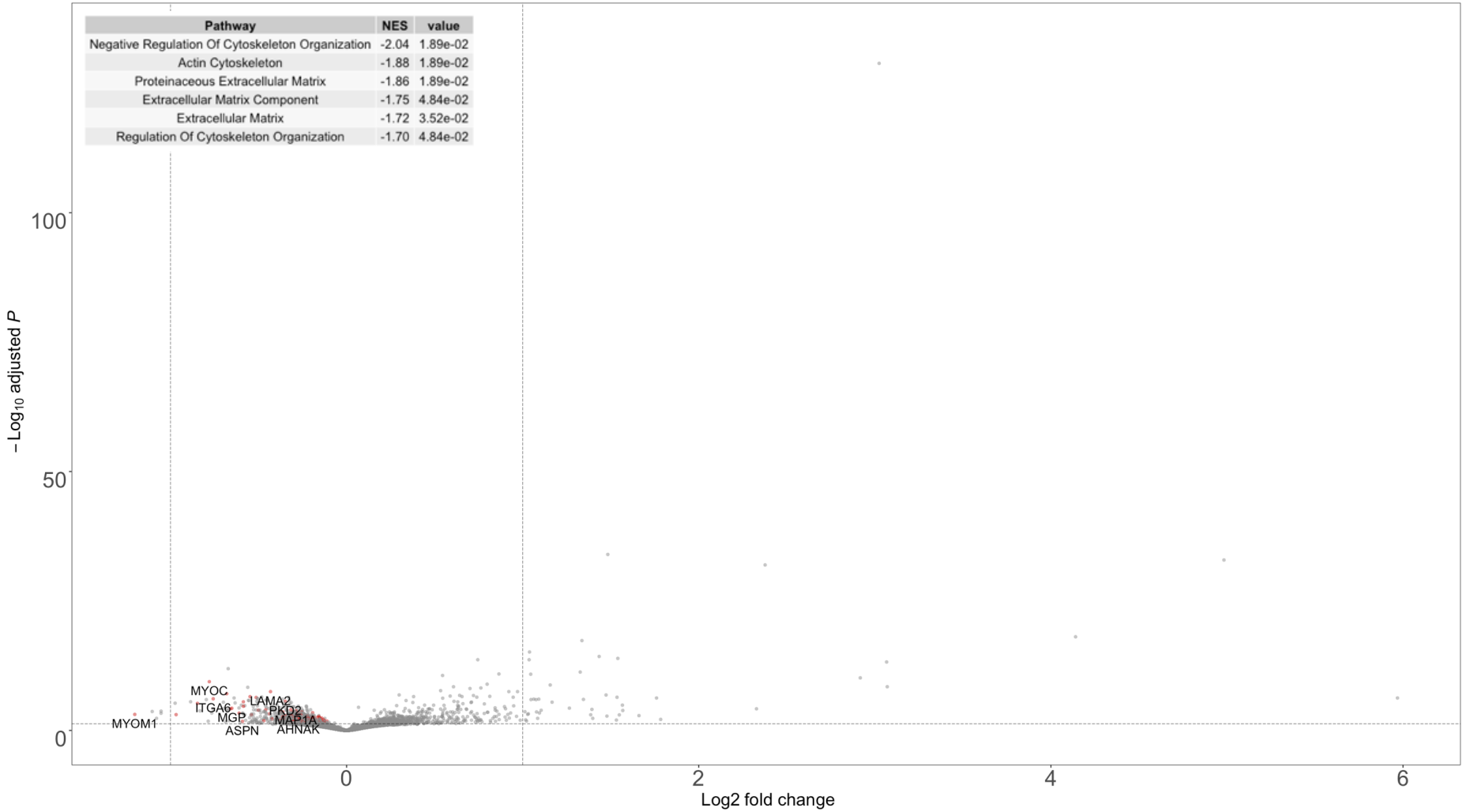

Figure C4-18. *Volcano plot representing genes changed by IL-17AF treatment in synovial fibroblasts, with the most important genes that correspond to the changes in matrix pathways highlighted by name and red dots*.

C5 Western blots

Representative western blots for each antibody using protein lysate from either end-stage OA chondrocytes or synovial fibroblasts.

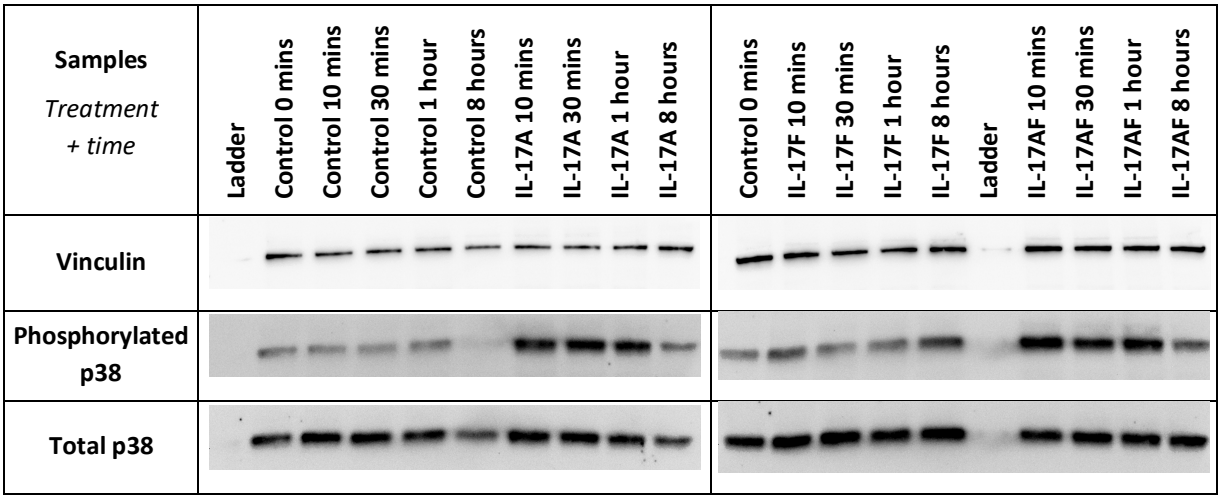

***Figure C5.1**. Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, of medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p38, and total p38, and visualised with an enhanced chemiluminescent reagent.*

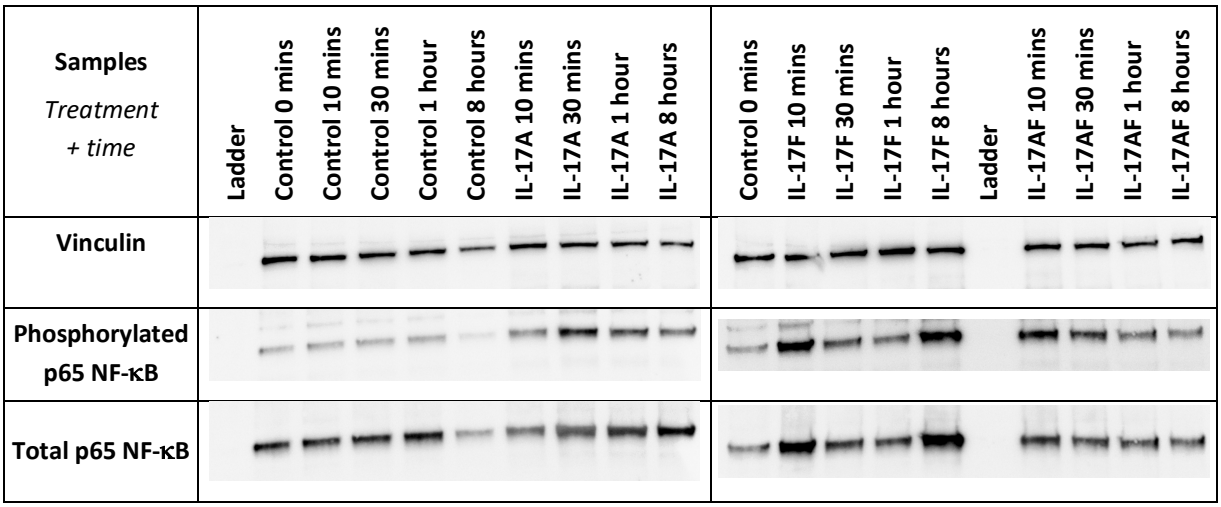

***Figure C5.2**. Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent.*

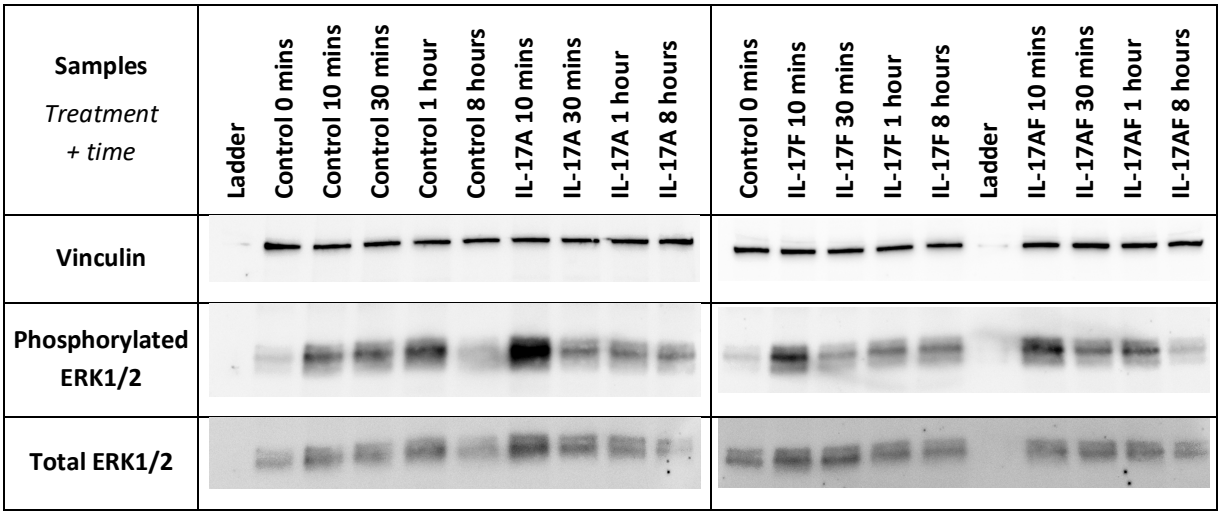

Figure C5.3. *Representative western blots using protein lysate from end-stage chondrocytes treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated ERK1/2, and total ERK1/2, and visualised with an enhanced chemiluminescent reagent.*

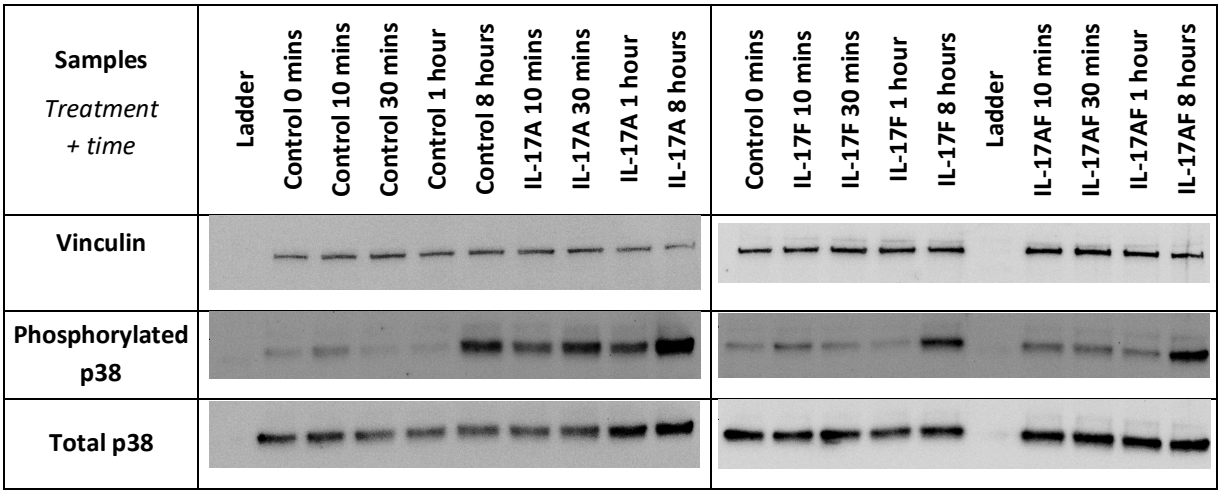

Figure C5.4. *Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained with antibodies against vinculin, phosphorylated p38, and total p38, and visualised with an enhanced chemiluminescent reagent.*

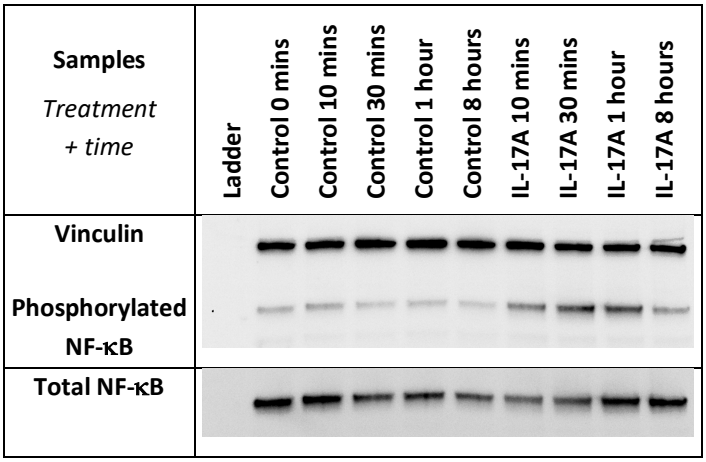

***Figure C5.5**. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent.*

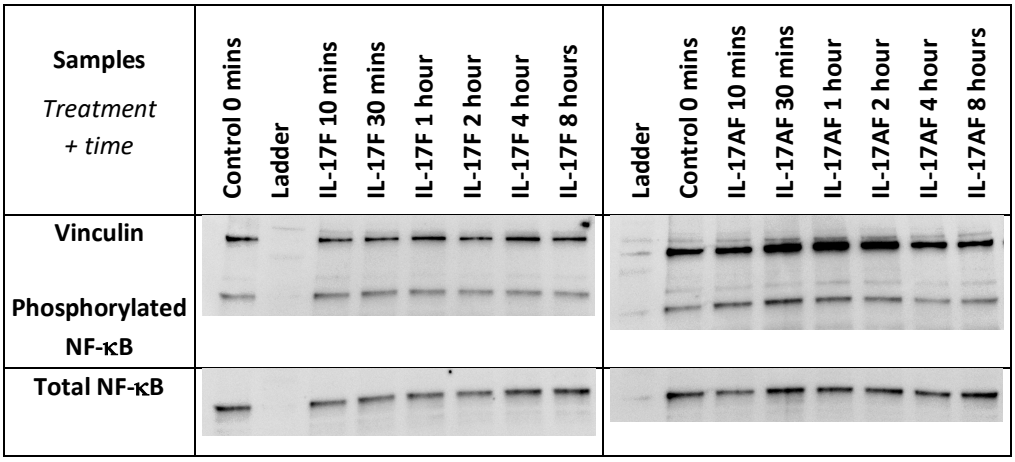

***Figure C5.6**. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17F or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated p65 NF-κB, and total p65 NF-κB, and visualised with an enhanced chemiluminescent reagent.*

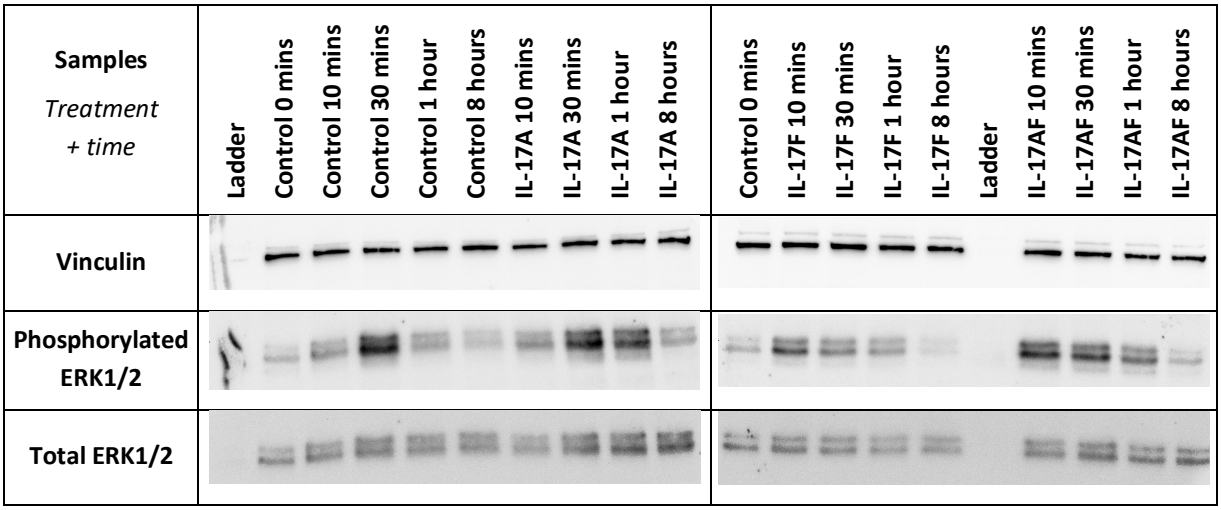

***Figure C5.7**. Representative western blots using protein lysate from end-stage synovial fibroblasts treated with vehicle control medium, or medium containing 10 ng/ml IL-17A, IL-17F, or IL-17AF for different durations. Blots were stained using antibodies against vinculin, phosphorylated ERK1/2, and total ERK1/2, and visualised with an enhanced chemiluminescent reagent.*