



Supplementary Material

10.1302/2046-3758.1112.BJR-2022-0215.R1

Table i. Characteristics of all patients.

Tissue	Name	Samples ID	Disease state	Mean OA score (SD)	Sex	Age, yrs
Cartilage	NC_AC_1	GSM5176138	Normal cartilage	Normal	N/A	N/A
	NC_AC_2	GSM5176139	Normal cartilage		N/A	N/A
	NC_AC_3	GSM5176140	Normal cartilage		N/A	N/A
	NC_AC_4	GSM5176141	Normal cartilage		N/A	N/A
	NC_AC_5	GSM5176142	Normal cartilage		N/A	N/A
	OA_AC_1	GSM5176143	Late-stage OA cartilage	Late-stage	N/A	N/A
	OA_AC_2	GSM5176144	Late-stage OA cartilage		N/A	N/A
	OA_AC_3	GSM5176145	Late-stage OA cartilage		N/A	N/A
	OA_AC_4	GSM5176146	Late-stage OA cartilage		N/A	N/A
	OA_AC_5	GSM5176147	Late-stage OA cartilage		N/A	N/A
	OA_AC_6	GSM5176148	Late-stage OA cartilage		N/A	N/A
	Meniscus	NC_M_1	GSM471665	Normal	Grade 0	Female
NC_M_2		GSM471666	Normal	Normal appearing surface	Male	43

	NC_M_3	GSM471667	Normal		Female	12		
	OA_M_1	GSM471668	OA	Grade 4 Severe fibrillation and degeneration, multiple incomplete tears, or complete tears	Female	65		
	OA_M_2	GSM471669	OA		Female	56		
	OA_M_3	GSM471670	OA		Female	50		
	OA_M_4	GSM471671	OA		Female	52		
	OA_M_5	GSM471672	OA		Male	61		
Synovium	NC_S_1	GSM2183532	Healthy control		N/A	N/A	N/A	
	NC_S_2	GSM2183533	Healthy control	N/A		N/A		
	NC_S_3	GSM2183534	Healthy control	N/A		N/A		
	NC_S_4	GSM2183535	Healthy control	N/A		N/A		
	NC_S_5	GSM2183536	Healthy control	N/A		N/A		
	NC_S_6	GSM2183537	Healthy control	N/A		N/A		
	NC_S_7	GSM2183538	Healthy control	N/A		N/A		
	OA_S_1	GSM2183539	OA	N/A	N/A	N/A		
	OA_S_2	GSM2183540	OA		N/A	N/A		
	OA_S_3	GSM2183541	OA		N/A	N/A		
	OA_S_4	GSM2183542	OA		N/A	N/A		
	OA_S_5	GSM2183543	OA		N/A	N/A		
	OA_S_6	GSM2183544	OA		N/A	N/A		
	OA_S_7	GSM2183545	OA		N/A	N/A		
	OA_S_8	GSM2183546	OA		N/A	N/A		
	OA_S_9	GSM2183547	OA		N/A	N/A		
	OA_S_10	GSM2183548	OA		N/A	N/A		
	Subchondral bone	NC_SB_1	GSM1248759		Normal	OARSI, histological scoring system to grade severity of osteoarthritis 3.00 (1.85)	Female	35
		NC_SB_2	GSM1248760		Normal		Female	35
		NC_SB_3	GSM1248761		Normal		Male	41
NC_SB_4		GSM1248762	Normal	Female	22			
NC_SB_10		GSM1248768	Normal	Male	59			
NC_SB_5		GSM1248763	Normal	OARSI, histological scoring system to grade severity of osteoarthritis 3.75 (1.67)	Male	59		
NC_SB_6		GSM1248764	Normal		Female	35		
NC_SB_7		GSM1248765	Normal		Female	35		
NC_SB_8		GSM1248766	Normal		Male	41		

	NC_SB_9	GSM1248767	Normal		Female	22
	OA_SB_1	GSM1248769	OA	OARSI, histological scoring system to grade severity of osteoarthritis 4.7 (1.34)	Female	55
	OA_SB_2	GSM1248770	OA		Male	68
	OA_SB_3	GSM1248771	OA		Male	66
	OA_SB_4	GSM1248772	OA		Female	71
	OA_SB_5	GSM1248773	OA		Female	71
	OA_SB_6	GSM1248774	OA		Male	81
	OA_SB_7	GSM1248775	OA		Female	67
	OA_SB_8	GSM1248776	OA		Female	59
	OA_SB_9	GSM1248777	OA		Male	77
	OA_SB_10	GSM1248778	OA		Female	71
	OA_SB_11	GSM1248779	OA		Female	63
	OA_SB_12	GSM1248780	OA		Female	53
	OA_SB_13	GSM1248781	OA		Female	77
	OA_SB_14	GSM1248782	OA		Male	68
	OA_SB_15	GSM1248783	OA		Male	75
	OA_SB_16	GSM1248784	OA		Female	67
	OA_SB_17	GSM1248785	OA		Male	89
	OA_SB_18	GSM1248786	OA		Female	68
	OA_SB_19	GSM1248787	OA		Female	76
	OA_SB_20	GSM1248788	OA		Male	81
	OA_SB_21	GSM1248789	OA	OARSI, histological scoring system to grade severity of osteoarthritis 20.8 (1.62)	Female	55
	OA_SB_22	GSM1248790	OA		Male	68
	OA_SB_23	GSM1248791	OA		Male	66
	OA_SB_24	GSM1248792	OA		Male	68
	OA_SB_25	GSM1248793	OA		Female	63
	OA_SB_26	GSM1248794	OA		Male	65
	OA_SB_27	GSM1248795	OA		Female	71
	OA_SB_28	GSM1248796	OA		Female	60
	OA_SB_29	GSM1248797	OA		Female	63
	OA_SB_30	GSM1248798	OA		Female	83
	OA_SB_31	GSM1248799	OA		Female	77

	OA_SB_32	GSM1248800	OA		Male	52
	OA_SB_33	GSM1248801	OA		Male	74
	OA_SB_34	GSM1248802	OA		Male	68
	OA_SB_35	GSM1248803	OA		Female	68
	OA_SB_36	GSM1248804	OA		Male	69
	OA_SB_37	GSM1248805	OA		Male	89
	OA_SB_38	GSM1248806	OA		Female	68
	OA_SB_39	GSM1248807	OA		Female	76
	OA_SB_40	GSM1248808	OA		Male	81

N/A, not available; OA, osteoarthritis; OARSI, Osteoarthritis Research Society International; SD, standard deviation.

Table ii. Ligand and receptor pairing within and between tissues.

AC	M	S	SB
AC_L-AC_R	M_L-AC_R	S_L-AC_R	SB_L-AC_R
COL1A1_ITGA5	THBS1_SDC1	COL18A1_ITGA5	COL18A1_ITGA5
FBN1_ITGA5	THBS1_SDC4	FN1_ITGA5	CTGF_ITGA5
MYOC_FZD7	M_L-S_R	FN1_NT5E	FGG_ITGA5
TNC_ITGA5	THBS1_CD36	TNC_ITGA5	FN1_ITGA5
TNC_NT5E	THBS1_CD47	TNC_NT5E	FN1_NT5E
TNC_SDC1	THBS1_SDC1	TNC_SDC1	MYOC_FZD7
TNC_SDC4	THBS1_SDC4	TNC_SDC4	TGFB1_TGFBFR3
AC_L-S_R	M_L-SB_R	S_L-S_R	THBS1_SDC1
COL1A1_CD36	THBS1_ITGA2B	BGN_LY96	THBS1_SDC4
COL1A1_ITGA5	THBS1_ITGA3	C1QA_CSPG4	SB_L-M_R
COL1A2_CD36	THBS1_ITGA4	CALM3_MYLK2	CTGF_ITGB2
COL4A1_CD47	THBS1_LRP1	CALM3_SCN4A	FGG_ITGB2
COL4A1_ITGB8	THBS1_SCARB1	CALM3_SELL	HP_ITGB2
FBN1_ITGA5	THBS1_SDC4	COL18A1_ITGA5	SPON2_ITGB2
HLA-E_SLC16A4	THBS1_TNFRSF11B	FN1_C5AR1	SB_L-S_R
LTBP1_ITGB5		FN1_ITGA5	BGN_LY96
MYOC_FZD1		FN1_ITGB8	COL18A1_ITGA5
SERPING1_SELE		FN1_NT5E	COL1A2_CD36
SERPING1_SELP		FN1_PLAUR	CTGF_ITGA5
TNC_ITGA5		TNC_ITGA5	FAT4_DCHS1
TNC_NT5E		TNC_NT5E	FGG_ITGA5
TNC_SDC1		TNC_SDC1	FN1_C5AR1
TNC_SDC4		TNC_SDC4	FN1_ITGA5
VCAN_SELL		S_L-SB_R	FN1_ITGB8
VCAN_SELP		ADIPOQ_ADIPOR1	FN1_NT5E
AC_L-SB_R		ADIPOQ_ADIPOR2	FN1_PLAUR
CD14_ITGA4		BGN_TLR2	LTBP1_ITGB5
COL1A1_DDR2		C1QA_CR1	MYOC_FZD1
COL1A1_ITGA11		C1QA_CSPG4	TGFB1_CD109
COL1A1_ITGAV		C1QB_LRP1	TGFB1_CXCR4
COL1A2_ITGA11		CALM3_KCNQ3	TGFB1_ITGB8
COL1A2_ITGA2B		CALM3_MYLK	THBS1_CD36
COL1A2_ITGAV		CALM3_PDE1C	THBS1_CD47
COL3A1_DDR2		COL18A1_GPC4	THBS1_SDC1
COL4A1_ITGAV		FN1_C5AR1	THBS1_SDC4
F13A1_ITGA4		FN1_COL13A1	SB_L-SB_R
FBN1_ITGAV		FN1_ITGA2B	A2M_LRP1
LTBP1_ITGB5		FN1_ITGA3	AZGP1_ITGAV
MYOC_FZD1		FN1_ITGA4	BGN_TLR2
MYOC_FZD7		FN1_ITGAV	CAMP_FPR2
NID2_COL13A1		FN1_NT5E	COL18A1_GPC4
SERPING1_LRP1		FN1_PLAUR	COL1A2_ITGA11
SERPING1_SELE		FN1_ROBO4	COL1A2_ITGA2B
SERPING1_SELP		FN1_TNFRSF11B	COL1A2_ITGAV
TNC_ITGAV		HSP90B1_ERBB2	COL3A1_DDR2
TNC_NT5E		HSP90B1_LRP1	CTGF_ITGAM

TNC_PTPRZ1		HSP90B1_TLR2	CTGF_ITGB2
TNC_SDC4		HSP90B1_TLR7	CTGF_LRP1
VCAN_ITGA4		IGFBP4_FZD8	F13A1_ITGA4
VCAN_SELP		NID2_COL13A1	FAT4_DCHS1
VCAN_TLR2		TIMP2_ITGA3	FCN2_LRP1
		TNC_ITGAV	FGG_ITGA2B
		TNC_NT5E	FGG_ITGAV
		TNC_PTPRZ1	FGG_ITGB2
		TNC_SDC4	FN1_C5AR1
			FN1_COL13A1
			FN1_ITGA2B
			FN1_ITGA3
			FN1_ITGA4
			FN1_ITGAV
			FN1_NT5E
			FN1_PLAUR
			FN1_ROBO4
			FN1_TNFRSF11B
			HP_ITGAM
			HP_ITGB2
			LTBP1_ITGB5
			MYOC_FZD1
			MYOC_FZD7
			NCAM1_FGFR1
			NCAM1_FGFR2
			NID2_COL13A1
			ORM1_CCR5
			SAA1_FPR1
			SAA1_FPR2
			SAA1_SCARB1
			SPON2_ITGAM
			SPON2_ITGB2
			TFPI_LRP1
			TFPI_SDC4
			TGFB1_ACVRL1
			TGFB1_CD109
			TGFB1_CXCR4
			TGFB1_ITGAV
			THBS1_ITGA2B
			THBS1_ITGA3
			THBS1_ITGA4
			THBS1_LRP1
			THBS1_SCARB1
			THBS1_SDC4
			THBS1_TNFRSF11B

AC, articular cartilage; M, meniscus; S, synovium; SB, subchondral bone; COL1A1, collagen type I alpha 1 chain; FBN1, fibrillin 1; MYOC, myocilin; TNC, tenascin C; COL1A2, collagen type I alpha 2 chain; COL4A1, collagen type IV alpha 1 chain; HLA-E, major histocompatibility complex class I E; LTBP1, latent transforming growth factor beta binding protein 1; SERPING1, serpin family G member

1; VCAN, versican; CD14, CD14 molecule; COL3A1, collagen type III alpha 1 chain; F13A1, coagulation factor XIII A chain; NID2, nidogen 2; THBS1, thrombospondin 1; COL18A1, collagen type XVIII alpha 1 chain; FN1, fibronectin 1; BGN, biglycan; C1QA, complement C1q A chain; CALM3, calmodulin 3; ADIPOQ, adiponectin C1Q and collagen domain containing; C1QB, complement C1q B chain; HSP90B1, heat shock protein 90 beta family member 1; IGFBP4, insulin like growth factor binding protein 4; TIMP2, TIMP metalloproteinase inhibitor 2; CTGF, connective tissue growth factor; FGG, fibrinogen gamma chain; TGFB1, transforming growth factor beta 1; HP, haptoglobin; SPON2, spondin 2; FAT4, FAT atypical cadherin 4; A2M, alpha-2-macroglobulin; AZGP1, alpha-2-glycoprotein 1 zinc-binding; CAMP, cathelicidin antimicrobial peptide; FCN2, ficolin 2; NCAM1, neural cell adhesion molecule 1; ORM1, orosomucoid 1; SAA1, serum amyloid A1; TFPI, tissue factor pathway inhibitor; ITGA5, integrin subunit alpha 5; FZD7, frizzled class receptor 7; NT5E, 5'-nucleotidase ecto; SDC1, syndecan 1; SDC4, syndecan 4; CD36, CD36 molecule; CD47, CD47 molecule; ITGB8, integrin subunit beta 8; SLC16A4, solute carrier family 16 member 4; ITGB5, integrin subunit beta 5; FZD1, frizzled class receptor 1; SELE, selectin E; SELP, selectin P; SELL, selectin L; ITGA4, integrin subunit alpha 4; DDR2, discoidin domain receptor tyrosine kinase 2; ITGA11, integrin subunit alpha 11; ITGAV, integrin subunit alpha V; ITGA2B, integrin subunit alpha 2b; COL13A1, collagen type XIII alpha 1 chain; LRP1, LDL receptor related protein 1; PTPRZ1, protein tyrosine phosphatase receptor type Z1; TLR2, toll like receptor 2; ITGA3, integrin subunit alpha 3; SCARB1, scavenger receptor class B member 1; TNFRSF11B, TNF receptor superfamily member 11b; LY96, lymphocyte antigen 96; CSPG4, chondroitin sulphate proteoglycan 4; MYLK2, myosin light chain kinase 2; SCN4A, sodium voltage-gated channel alpha subunit 4; C5AR1, complement C5a receptor 1; PLAUR, plasminogen activator, urokinase receptor; ADIPOR1, adiponectin receptor 1; ADIPOR2, adiponectin receptor 2; CR1, complement C3b/C4b receptor 1; KCNQ3, potassium voltage-gated channel subfamily Q member 3; MYLK, myosin light chain kinase; PDE1C, phosphodiesterase 1C; GPC4, glypican 4; ROBO4, roundabout guidance receptor 4; ERBB2, erb-b2 receptor tyrosine kinase 2; TLR7, toll like receptor 7; FZD8, frizzled class receptor 8; TGFBR3, transforming growth factor beta receptor 3; ITGB2, integrin subunit beta 2; DCHS1, dachshous cadherin-related 1; CD109, CD109 molecule; CXCR4, C-X-C motif chemokine receptor 4; FPR2, formyl peptide receptor 2; ITGAM, integrin subunit alpha M; FGFR1, fibroblast growth factor receptor 1; FGFR2, fibroblast growth factor receptor 2; CCR5, C-C motif chemokine receptor 5; FPR1, formyl peptide receptor 1; ACVRL1, activin A receptor like type 1.

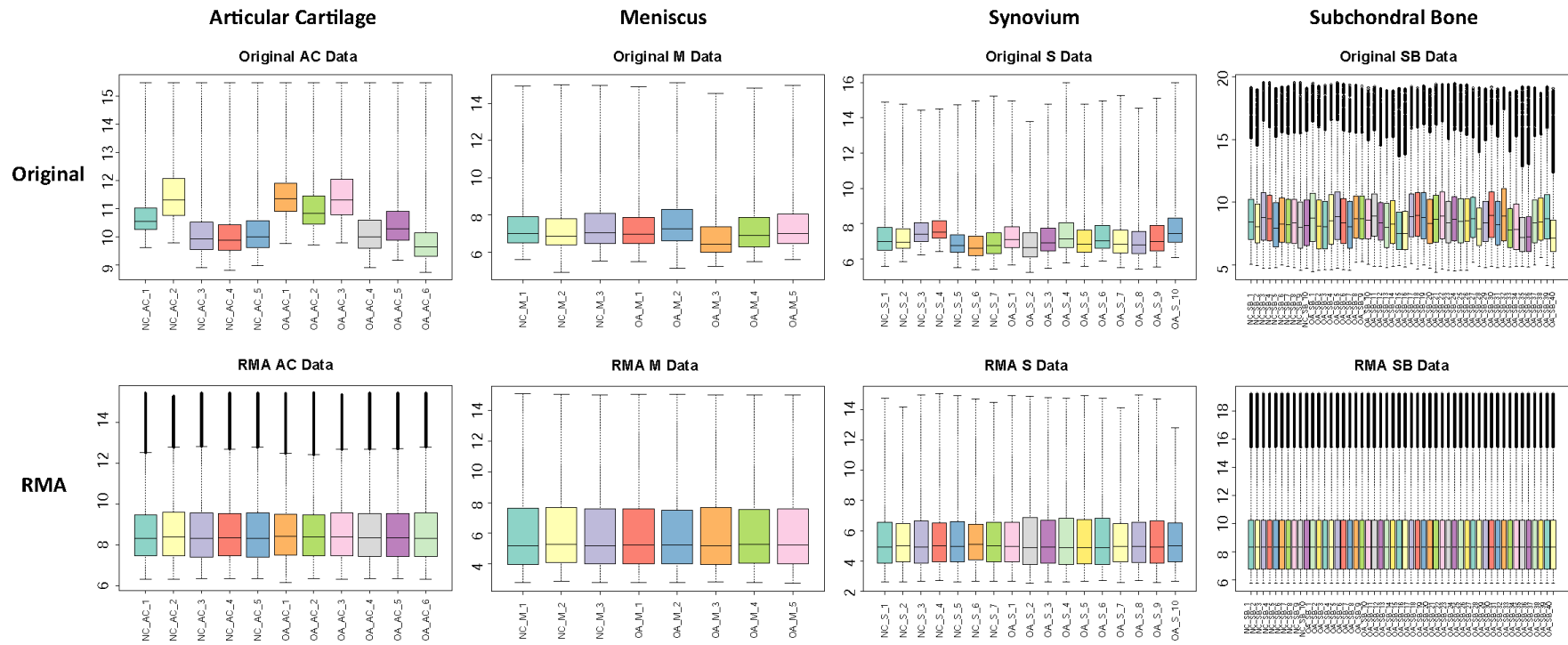


Fig a. Boxplot of all transcriptional profiles. The above figures represent the original microarray signals respectively. The below figures represent the signals after robust multiarray average (RMA) normalization. S, synovium; SB, subchondral bone.

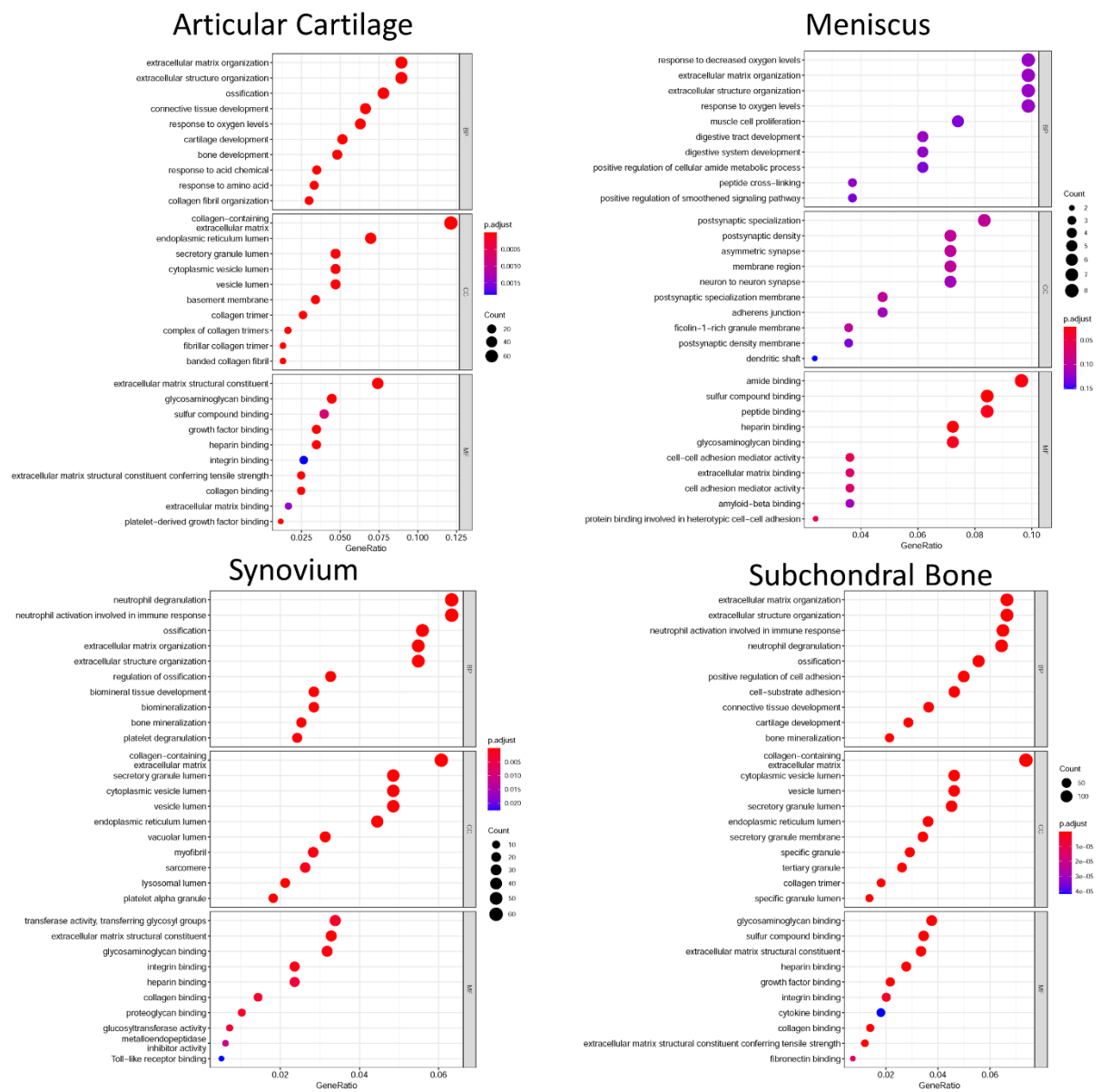


Fig b. Gene Ontology enrichment of articular cartilage, meniscus, synovium, and subchondral bone. The size of circle represents the number of genes, and the colour represents the p-adjust value. BP, biological process; CC, cellular component; MF, molecular function.

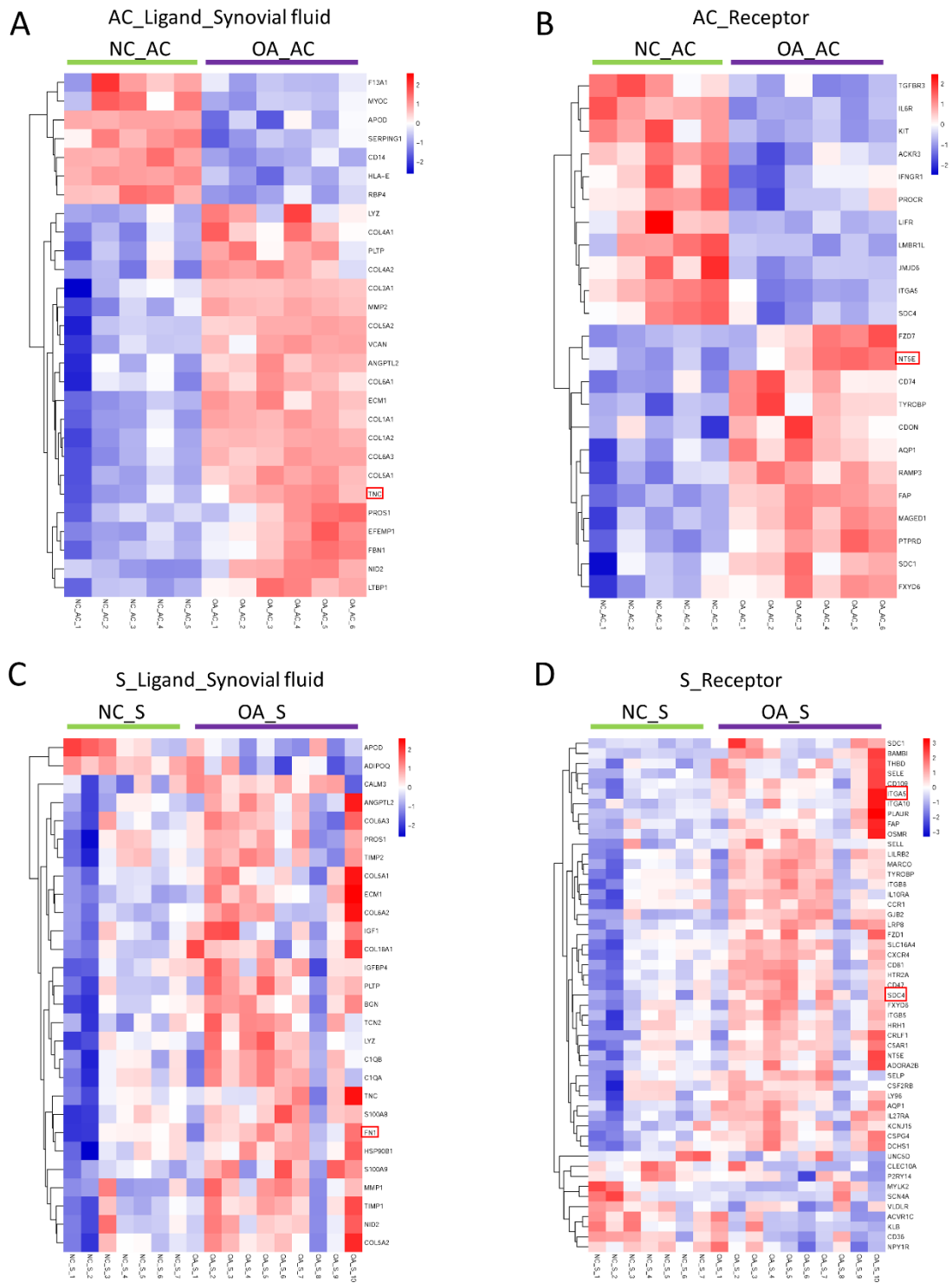
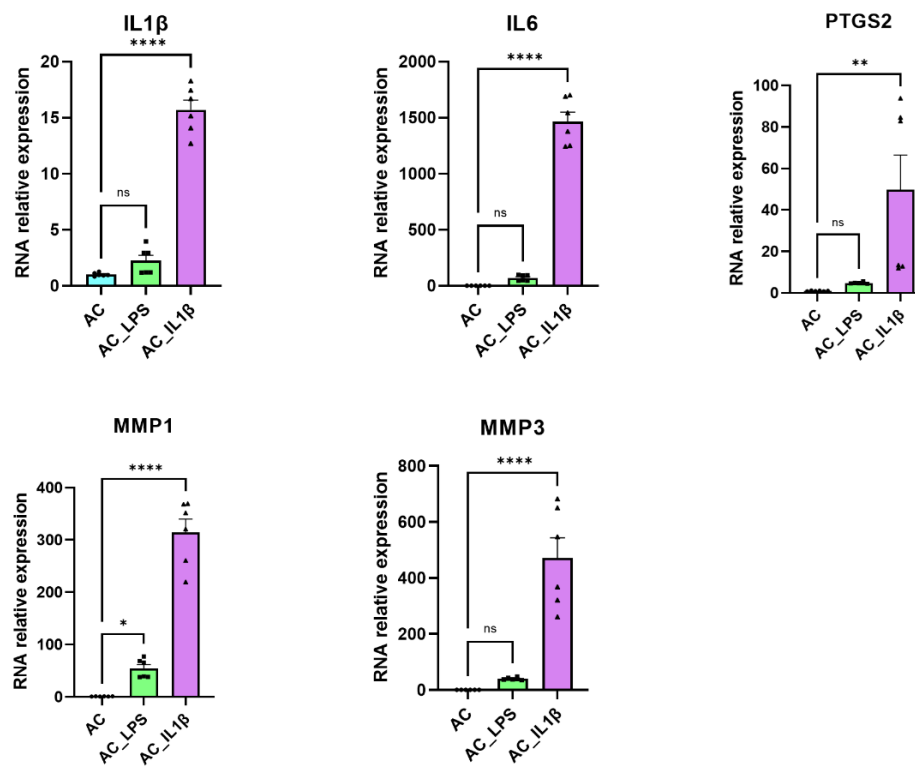


Fig c. Heatmap of ligands and receptors in articular cartilage and synovium. a) and b) Ligands and receptors in articular cartilage. c) and d) Ligands and receptors in synovium. AC, articular cartilage; M, meniscus; NC, negative control; OA, osteoarthritis; S, synovium; SB, subchondral bone.

A



B

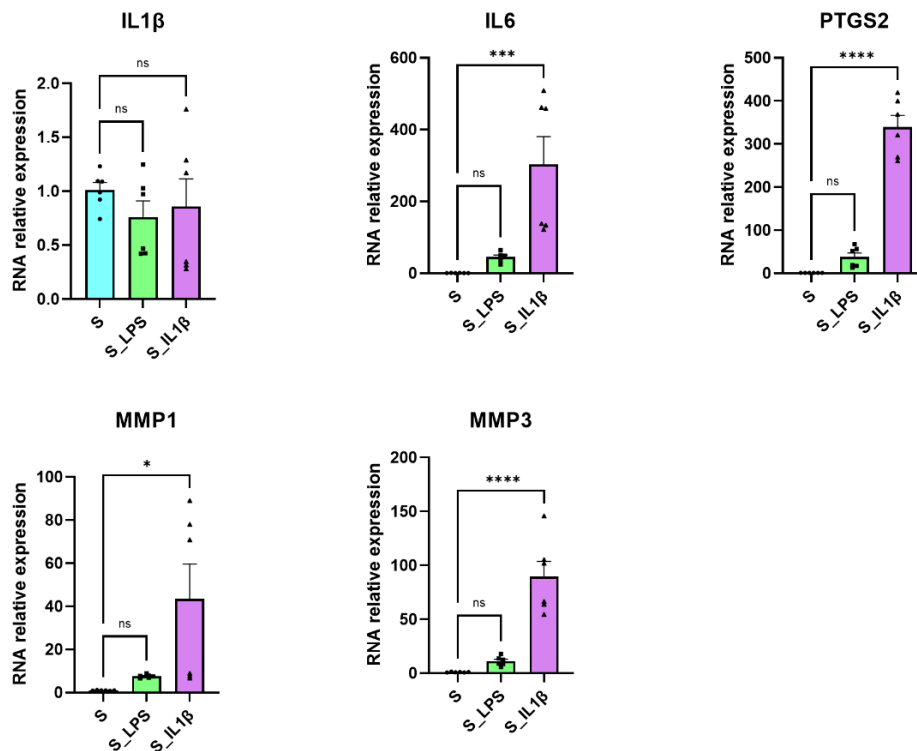


Fig d. Relative expression of interleukin (IL)-1 β , IL-6, PTGS2, matrix metalloproteinase 1 (MMP1), and MMP3 in a) chondrocytes and b) synovial cells after LPS and IL-1 β stimulation. Data are presented as the mean (standard error of the mean (SEM)). *Statistical significance; ns, no statistical significance. AC, articular cartilage; M, meniscus; S, synovium; SB, subchondral bone.