

SUPPLEMENTAL MATERIAL

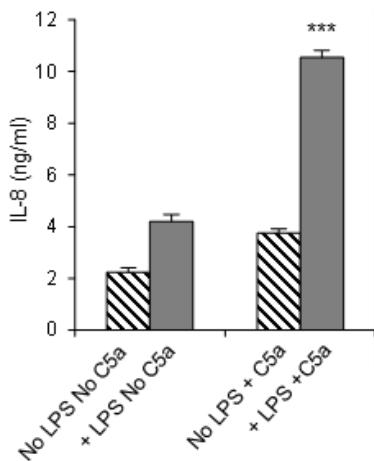
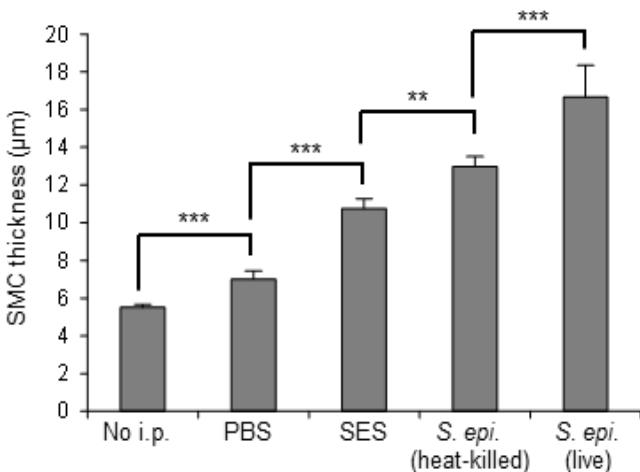


Figure 1. Co-stimulation via TLR4 and C5aR in peripheral blood mononuclear cells results in a synergistically enhanced pro-inflammatory response. Levels of IL-8 (ELISA) in the culture supernatant of PBMC (1.5×10^5 cells/ well in triplicates) cultured (14h) in the presence or absence of LPS (10 ng/ml) and C5a (2.5 nM). Synergism was assessed by comparing the additive response to each individual ligand (No LPS + C5a or + LPS No C5a) with that of the combination of ligands (+ LPS + C5a). Results are from one experiment (\pm SD) representative of three. ***, $P < 0.005$, C5a treatment + LPS treatment vs C5a + LPS treatment.



animal, 6 measurements were made per field and the average of the 10 highest measurements was taken as mean of SMC thickness. **, $P < 0.01$; ***, $P < 0.005$.

- ✖ Bacterial DNA standard curve
- Positive control
- ◆ Sterile PDE samples (x5)
- ◇ Non-sterile PDE sample

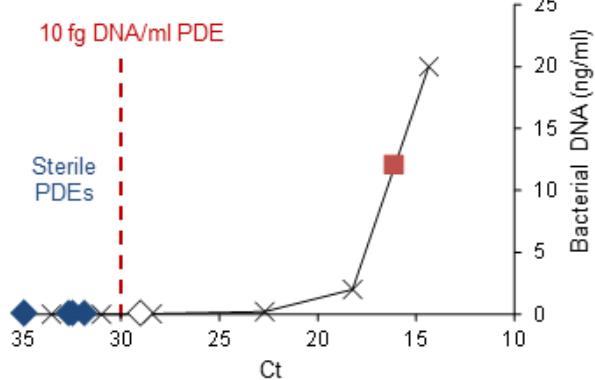


Figure 3. Testing for bacterial DNA in non-infected PD effluents. Total DNA was extracted from non-infected cell-free PDE by a chelex-based method as previously described⁵⁴. One PDE sample was spiked with heat-killed *S. epidermidis* prior to extraction to serve as a positive control. Pan-bacterial DNA was then amplified by qPCR using the Femto™ Bacterial DNA Quantification kit (Zymo research), and the amount of DNA in PDE was determined using the kit's internal standard curve as a reference. A Ct of 30 cycles, corresponding to 10 fg of bacterial DNA per 1ml of PDE, was set as PDE sterility cut off. Representative examples of the Ct values obtained for non-infected PDE (blue diamonds) and positive controls (red square) are shown together with a typical standard curve.

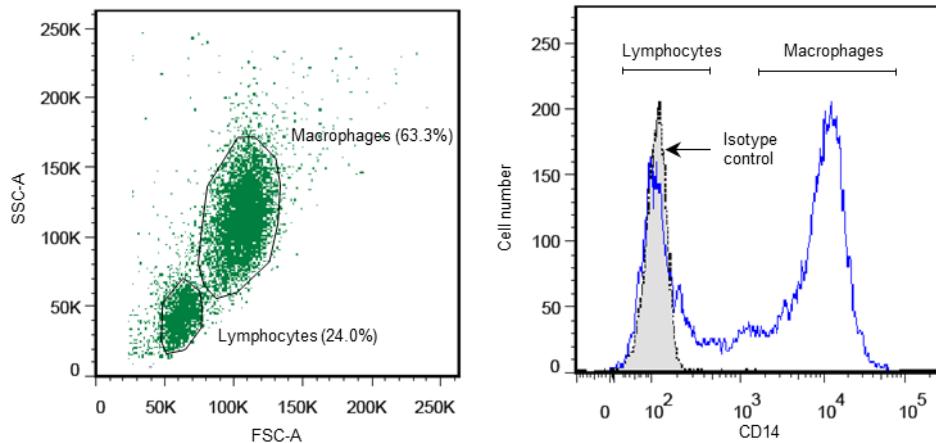


Figure 4. Flow cytometric analysis of leukocytes in non-infected PD effluents. Peritoneal leukocytes were prepared from non-infected PDE and analysed by flow cytometry as described in Concise Methods. The dot plot and fluorescence histogram show a representative forward and side scatter and the typical CD14 expression profile, respectively, of the total live peritoneal leukocyte population

following dead cells exclusion (eFluor viability dye, <15%). Lymphocytes and macrophages (representative percentages shown) were identified based on their forward and side scatter profiles and CD14 expression levels.

Table 1. Effect of blocking TLR2 in uremic peritoneal leukocytes on *S. epidermidis*-induced fibrosis-related gene expression (complete array).^{*}

Gene symbol	Description	S. epidermidis		S. epidermidis + anti-TLR2	
		Fold Change**	P-value**	Fold Change**	P-value**
<i>Acta2</i>	Actin, alpha 2, smooth muscle, aorta	1.0	0.789	1.0	0.946
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.0	0.757	1.0	0.903
<i>Akt1</i>	V-akt murine thymoma viral oncogene homolog 1	1.1	0.691	0.9	0.796
<i>Bcl2</i>	B-cell CLL/lymphoma 2	0.8	0.232	0.8	0.383
<i>Bmp7</i>	Bone morphogenetic protein 7	1.6	0.291	0.6	0.199
<i>Cav1</i>	Caveolin 1, caveolae protein, 22kDa	0.5	0.034	0.5	0.039
<i>Ccl11</i>	Chemokine (C-C motif) ligand 11	0.5	0.018	0.7	0.137
<i>Ccl2</i>	Chemokine (C-C motif) ligand 2	12.0	0.001	14.5	0.001
<i>Ccl3</i>	Chemokine (C-C motif) ligand 3	16.5	0.001	3.2	0.065
<i>Ccr2</i>	Chemokine (C-C motif) receptor 2	0.3	0.010	0.4	0.015
<i>Cebpb</i>	CCAAT/enhancer binding protein (C/EBP), beta	1.6	0.215	1.5	0.351
<i>Col1a2</i>	Collagen, type I, alpha 2	0.7	0.101	0.7	0.063
<i>Col3a1</i>	Collagen, type III, alpha 1	0.7	0.021	0.7	0.015
<i>Ctgf</i>	Connective tissue growth factor	0.4	0.048	0.4	0.040
<i>Cxcr4</i>	Chemokine (C-X-C motif) receptor 4	1.8	0.102	1.8	0.056
<i>Dcn</i>	Decorin	1.1	0.402	1.0	0.928
<i>Edn1</i>	Endothelin 1	14.9	0.001	11.0	0.006
<i>Egf</i>	Epidermal growth factor	1.0	0.757	1.0	0.903
<i>Eng</i>	Endoglin	0.5	0.011	0.5	0.016
<i>Faslg</i>	Fas ligand (TNF superfamily, member 6)	1.6	0.001	1.9	0.001
<i>Grem1</i>	Gremlin 1	0.2	0.001	0.4	0.001
<i>Hgf</i>	Hepatocyte growth factor (hepatopoietin A; scatter factor)	0.6	0.026	0.5	0.020
<i>Ifng</i>	Interferon, gamma	55.2	0.001	63.5	0.001
<i>Il10</i>	Interleukin 10	240.8	0.001	188.9	0.001
<i>Il13</i>	Interleukin 13	10.1	0.026	9.5	0.047
<i>Il13ra2</i>	Interleukin 13 receptor, alpha 2	1.9	0.002	1.7	0.002
<i>Il1a</i>	Interleukin 1, alpha	19.7	0.001	18.9	0.001
<i>Il1b</i>	Interleukin 1, beta	31.8	0.011	30.1	0.004
<i>Il4</i>	Interleukin 4	1.0	0.757	1.0	0.903
<i>Il5</i>	Interleukin 5	1.3	0.221	0.4	0.035
<i>Ilk</i>	Integrin-linked kinase	1.5	0.049	1.3	0.199
<i>Inhbe</i>	inhibin, beta E	1.0	0.757	1.0	0.903
<i>Itga1</i>	Integrin, alpha 1	9.5	0.001	9.4	0.001
<i>Itga2</i>	Integrin, alpha 2	1.4	0.118	1.2	0.362
<i>Itga3</i>	Integrin, alpha 3	0.7	0.066	0.6	0.076
<i>Itgav</i>	Integrin, alpha V	2.6	0.004	3.3	0.002
<i>Itgb1</i>	Integrin, beta 1	1.3	0.266	1.4	0.180
<i>Itgb3</i>	Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	5.7	0.001	6.6	0.002
<i>Itgb5</i>	Integrin, beta 5	0.3	0.001	0.3	0.004
<i>Itgb6</i>	Integrin, beta 6	1.9	0.013	1.2	0.339
<i>Itgb8</i>	Integrin, beta 8	12.6	0.004	13.7	0.011
<i>Jun</i>	Jun proto-oncogene	0.9	0.628	0.9	0.930
<i>Lox</i>	Lysyl oxidase	1.0	0.841	0.9	0.478
<i>Ltbp1</i>	Latent transforming growth factor beta binding protein 1	0.6	0.134	0.6	0.209
<i>Mmp1</i>	Matrix metallopeptidase 1 (interstitial collagenase)	67.1	0.001	61.1	0.001
<i>Mmp13</i>	Matrix metallopeptidase 13 (collagenase 3)	1.0	0.757	1.0	0.903
<i>Mmp14</i>	Matrix metallopeptidase 14 (membrane-inserted)	3.6	0.013	2.6	0.203
<i>Mmp2</i>	Matrix metallopeptidase 2 (gelatinase A)	2.0	0.008	1.7	0.022
<i>Mmp3</i>	Matrix metallopeptidase 3 (stromelysin 1, progelatinase)	5.5	0.001	3.6	0.001
<i>Mmp8</i>	Matrix metallopeptidase 8 (neutrophil collagenase)	3.5	0.001	4.7	0.002
<i>Mmp9</i>	Matrix metallopeptidase 9 (gelatinase B)	0.7	0.035	0.8	0.260
<i>Myc</i>	V-myc myelocytomatosis viral oncogene homolog (avian)	0.9	0.728	0.8	0.012
<i>Nfkb1</i>	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	1.5	0.228	1.7	0.140
<i>Pdgfa</i>	Platelet-derived growth factor alpha polypeptide	1.8	0.013	2.2	0.009
<i>Pdgfb</i>	Platelet-derived growth factor beta polypeptide	0.9	0.674	1.2	0.599
<i>Plat</i>	Plasminogen activator, tissue	0.2	0.092	0.2	0.086
<i>Plau</i>	Plasminogen activator, urokinase	1.1	0.828	1.1	0.712
<i>Plg</i>	Plasminogen	2.8	0.031	1.0	0.903
<i>Serpina1</i>	Serpin peptidase inhibitor, clade A, member 1	9.7	0.001	8.8	0.001

<i>Serpine1</i>	Serpin peptidase inhibitor, clade E, member 1	1.7	0.035	1.5	0.095
<i>Serpinh1</i>	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1	1.2	0.002	1.2	0.094
<i>Smad2</i>	SMAD family member 2	1.3	0.099	1.3	0.111
<i>Smad3</i>	SMAD family member 3	0.6	0.281	0.5	0.193
<i>Smad4</i>	SMAD family member 4	1.4	0.320	1.4	0.304
<i>Smad6</i>	SMAD family member 6	0.6	0.007	0.3	0.001
<i>Smad7</i>	SMAD family member 7	1.0	0.979	1.0	0.961
<i>Snai1</i>	Snail homolog 1 (<i>Drosophila</i>)	7.2	0.049	5.3	0.063
<i>Sp1</i>	Sp1 transcription factor	1.0	0.894	1.4	0.135
<i>Stat1</i>	Signal transducer and activator of transcription 1, 91kDa	2.5	0.010	2.6	0.012
<i>Stat6</i>	Signal transducer and activator of transcription 6, interleukin-4 induced	1.0	0.915	1.1	0.619
<i>Tgfb1</i>	Transforming growth factor, beta 1	0.7	0.032	0.6	0.052
<i>Tgfb2</i>	Transforming growth factor, beta 2	1.4	0.077	1.4	0.066
<i>Tgfb3</i>	Transforming growth factor, beta 3	2.0	0.015	2.1	0.060
<i>Tgfbr1</i>	Transforming growth factor, beta receptor 1	0.9	0.589	0.8	0.515
<i>Tgfbr2</i>	Transforming growth factor, beta receptor II (70/80kDa)	0.4	0.064	0.4	0.066
<i>Tgif1</i>	TGFB-induced factor homeobox 1	2.3	0.032	2.3	0.041
<i>Thbs1</i>	Thrombospondin 1	0.7	0.126	0.5	0.035
<i>Thbs2</i>	Thrombospondin 2	0.8	0.143	0.5	0.018
<i>Timp1</i>	TIMP metallopeptidase inhibitor 1	1.9	0.093	1.6	0.193
<i>Timp2</i>	TIMP metallopeptidase inhibitor 2	0.6	0.093	0.6	0.118
<i>Timp3</i>	TIMP metallopeptidase inhibitor 3	0.3	0.001	0.3	0.001
<i>Timp4</i>	TIMP metallopeptidase inhibitor 4	0.4	0.021	0.4	0.022
<i>Tnf</i>	Tumor necrosis factor	4.9	0.002	4.7	0.001
<i>Vegfa</i>	Vascular endothelial growth factor A	6.8	0.001	6.8	0.000

*Statistically significant ($P<0.05$) and biologically relevant (≤ 0.5 , bold gold or ≥ 2 , bold red) *S. epidermidis*-induced fold changes are analysed in Results, Table 1

**Compared to Control group.

Table 2. Effect of blocking TLR2 in uremic peritoneal leukocytes on non-infected PDE-induced fibrosis-related gene expression (complete array). *

Gene symbol	Description	Non-infected PDE		Non-infected PDE + anti-TLR2	
		Fold Change**	P-value**	Fold Change**	P-value**
<i>Acta2</i>	Actin, alpha 2, smooth muscle, aorta	1.0	0.886	1.0	0.836
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	0.8	0.291	1.1	0.835
<i>Akt1</i>	V-akt murine thymoma viral oncogene homolog 1	0.7	0.007	0.7	0.025
<i>Bcl2</i>	B-cell CLL/lymphoma 2	0.7	0.001	0.5	0.001
<i>Bmp7</i>	Bone morphogenetic protein 7	1.8	0.175	1.2	0.844
<i>Cav1</i>	Caveolin 1, caveolae protein, 22kDa	1.0	0.843	1.5	0.011
<i>Ccl11</i>	Chemokine (C-C motif) ligand 11	1.3	0.490	1.1	0.835
<i>Ccl2</i>	Chemokine (C-C motif) ligand 2	2.2	0.017	1.1	0.883
<i>Ccl3</i>	Chemokine (C-C motif) ligand 3	0.6	0.001	0.3	0.001
<i>Ccr2</i>	Chemokine (C-C motif) receptor 2	1.3	0.014	0.9	0.193
<i>Cebpb</i>	CCAAT/enhancer binding protein (C/EBP), beta	0.8	0.028	0.4	0.001
<i>Col1a2</i>	Collagen, type I, alpha 2	1.4	0.217	1.2	0.514
<i>Col3a1</i>	Collagen, type III, alpha 1	2.1	0.245	1.7	0.472
<i>Ctgf</i>	Connective tissue growth factor	1.0	0.640	0.9	0.006
<i>Cxcr4</i>	Chemokine (C-X-C motif) receptor 4	1.3	0.027	0.9	0.364
<i>Dcn</i>	Decorin	1.0	0.540	1.3	0.001
<i>Edn1</i>	Endothelin 1	1.7	0.120	0.5	0.163
<i>Egf</i>	Epidermal growth factor	6.5	0.001	1.1	0.835
<i>Eng</i>	Endoglin	0.9	0.552	0.7	0.034
<i>Faslg</i>	Fas ligand (TNF superfamily, member 6)	0.9	0.196	1.1	0.692
<i>Grem1</i>	Gremlin 1	0.8	0.068	1.2	0.405
<i>Hgf</i>	Hepatocyte growth factor (hepatopoietin A; scatter factor)	1.0	0.852	2.2	0.018
<i>Ifng</i>	Interferon, gamma	0.7	0.208	1.4	0.265
<i>Il10</i>	Interleukin 10	0.9	0.220	1.0	0.879
<i>Il13</i>	Interleukin 13	3.5	0.001	3.9	0.011
<i>Il13ra2</i>	Interleukin 13 receptor, alpha 2	7.3	0.002	6.7	0.004
<i>Il1a</i>	Interleukin 1, alpha	0.6	0.036	0.1	0.001
<i>Il1b</i>	Interleukin 1, beta	0.6	0.004	0.1	0.001
<i>Il4</i>	Interleukin 4	4.2	0.001	3.8	0.014
<i>Il5</i>	Interleukin 5	1.5	0.054	1.9	0.002
<i>Ilk</i>	Integrin-linked kinase	0.8	0.051	0.6	0.007
<i>Inhbe</i>	inhibin, beta E	1.0	0.708	0.4	0.435
<i>Itga1</i>	Integrin, alpha 1	1.3	0.001	0.9	0.501
<i>Itga2</i>	Integrin, alpha 2	1.6	0.001	1.8	0.077
<i>Itga3</i>	Integrin, alpha 3	0.7	0.031	0.8	0.479
<i>Itgav</i>	Integrin, alpha V	0.9	0.007	0.9	0.166
<i>Itgb1</i>	Integrin, beta 1	1.1	0.708	0.9	0.632
<i>Itgb3</i>	Integrin, beta 3 (platelet glycoprotein IIIa, antigen CD61)	0.8	0.009	0.6	0.001
<i>Itgb5</i>	Integrin, beta 5	1.0	0.973	1.2	0.328
<i>Itgb6</i>	Integrin, beta 6	0.8	0.291	1.1	0.835
<i>Itgb8</i>	Integrin, beta 8	1.6	0.032	0.5	0.030
<i>Jun</i>	Jun proto-oncogene	0.8	0.537	0.5	0.035
<i>Lox</i>	Lysyl oxidase	1.1	0.311	1.3	0.043
<i>Ltbp1</i>	Latent transforming growth factor beta binding protein 1	0.7	0.126	1.3	0.136
<i>Mmp1</i>	Matrix metallopeptidase 1 (interstitial collagenase)	1.4	0.001	0.9	0.404
<i>Mmp13</i>	Matrix metallopeptidase 13 (collagenase 3)	4.1	0.001	1.1	0.835
<i>Mmp14</i>	Matrix metallopeptidase 14 (membrane-inserted)	0.5	0.001	0.2	0.001
<i>Mmp2</i>	Matrix metallopeptidase 2 (gelatinase A)	0.9	0.214	1.1	0.289
<i>Mmp3</i>	Matrix metallopeptidase 3 (stromelysin 1, progelatinase)	0.9	0.344	0.6	0.014
<i>Mmp8</i>	Matrix metallopeptidase 8 (neutrophil collagenase)	1.1	0.794	1.1	0.759
<i>Mmp9</i>	Matrix metallopeptidase 9 (gelatinase B)	0.8	0.005	1.3	0.004
<i>Myc</i>	V-myc myelocytomatosis viral oncogene homolog (avian)	1.1	0.001	1.0	0.476
<i>Nfkbia</i>	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	0.6	0.001	0.3	0.001
<i>Pdgfa</i>	Platelet-derived growth factor alpha polypeptide	0.8	0.204	1.2	0.373
<i>Pdgfb</i>	Platelet-derived growth factor beta polypeptide	0.6	0.001	0.8	0.004
<i>Plat</i>	Plasminogen activator, tissue	0.5	0.001	0.5	0.001
<i>Plau</i>	Plasminogen activator, urokinase	1.0	0.724	0.4	0.001
<i>Plg</i>	Plasminogen	0.8	0.291	1.1	0.835

<i>Serpina1</i>	Serpin peptidase inhibitor, clade A, member 1	1.0	0.505	0.6	0.001
<i>Serpine1</i>	Serpin peptidase inhibitor, clade E, member 1	0.9	0.531	0.7	0.089
<i>Serpinh1</i>	Serpin peptidase inhibitor, clade H (heat shock protein 47), member 1	1.0	0.357	1.3	0.004
<i>Smad2</i>	SMAD family member 2	0.9	0.399	0.8	0.214
<i>Smad3</i>	SMAD family member 3	0.4	0.019	0.2	0.005
<i>Smad4</i>	SMAD family member 4	1.1	0.647	0.9	0.435
<i>Smad6</i>	SMAD family member 6	0.6	0.022	0.6	0.005
<i>Smad7</i>	SMAD family member 7	1.0	0.972	0.6	0.432
<i>Snai1</i>	Snail homolog 1 (<i>Drosophila</i>)	1.3	0.307	0.7	0.336
<i>Sp1</i>	Sp1 transcription factor	1.1	0.319	0.9	0.707
<i>Stat1</i>	Signal transducer and activator of transcription 1, 91kDa	1.3	0.005	2.9	0.001
<i>Stat6</i>	Signal transducer and activator of transcription 6, interleukin-4 induced	1.2	0.270	1.0	0.899
<i>Tgfb1</i>	Transforming growth factor, beta 1	0.8	0.036	0.6	0.034
<i>Tgfb2</i>	Transforming growth factor, beta 2	1.0	0.914	0.6	0.002
<i>Tgfb3</i>	Transforming growth factor, beta 3	0.9	0.314	0.8	0.091
<i>Tgfbr1</i>	Transforming growth factor, beta receptor 1	0.9	0.753	0.7	0.008
<i>Tgfbr2</i>	Transforming growth factor, beta receptor II (70/80kDa)	1.2	0.587	0.9	0.523
<i>Tgif1</i>	TGFB-induced factor homeobox 1	1.4	0.258	1.3	0.356
<i>Thbs1</i>	Thrombospondin 1	1.0	0.940	0.2	0.004
<i>Thbs2</i>	Thrombospondin 2	0.9	0.170	0.7	0.004
<i>Timp1</i>	TIMP metallopeptidase inhibitor 1	1.0	0.835	0.7	0.037
<i>Timp2</i>	TIMP metallopeptidase inhibitor 2	1.5	0.040	1.5	0.103
<i>Timp3</i>	TIMP metallopeptidase inhibitor 3	0.8	0.023	2.3	0.001
<i>Timp4</i>	TIMP metallopeptidase inhibitor 4	0.5	0.007	1.3	0.042
<i>Tnf</i>	Tumor necrosis factor	0.8	0.030	0.3	0.001
<i>Vegfa</i>	Vascular endothelial growth factor A	1.2	0.088	0.5	0.003

*Statistically significant ($P<0.05$) and biologically relevant (≤ 0.5 , bold gold or ≥ 2 , bold red) PDE #1-induced fold changes are analysed in Results, Table 2

**Compared to Control group.

Table 3. Changes in fibrosis-related peritoneal gene expression (complete fibrosis array) at day 28 in mice infected with *S. epidermidis* or *S. epidermidis* + sTLR2.*

Gene symbol	Description	S. epidermidis		S. epidermidis + sTLR2	
		Fold Change**	P-value**	Fold Change**	P-value**
<i>Acta2</i>	Actin, alpha 2, smooth muscle, aorta	1.1	0.133	1.1	0.339
<i>Agt</i>	Angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	1.1	0.304	0.8	0.390
<i>Akt1</i>	Thymoma viral proto-oncogene 1	1.7	0.048	1.3	0.315
<i>Bcl2</i>	B-cell leukemia/lymphoma 2	1.5	0.167	1.3	0.333
<i>Bmp7</i>	Bone morphogenetic protein 7	1.9	0.029	1.7	0.068
<i>Cav1</i>	Caveolin 1, caveolae protein	1.5	0.062	1.2	0.283
<i>Ccl11</i>	Chemokine (C-C motif) ligand 11	1.0	0.772	1.0	0.992
<i>Ccl12</i>	Chemokine (C-C motif) ligand 12	12.4	0.008	9.4	0.023
<i>Ccl3</i>	Chemokine (C-C motif) ligand 3, MIP1a	4.3	0.033	5.2	0.005
<i>Ccr2</i>	Chemokine (C-C motif) receptor 2	4.2	0.043	2.5	0.082
<i>Cebpb</i>	CCAAT/enhancer binding protein (C/EBP), beta	1.8	0.001	1.4	0.099
<i>Col1a2</i>	Collagen, type I, alpha 2	1.1	0.625	0.7	0.105
<i>Col3a1</i>	Collagen, type III, alpha 1	1.1	0.507	0.9	0.760
<i>Ctgf</i>	Connective tissue growth factor	1.6	0.138	3.2	0.034
<i>Cxcr4</i>	Chemokine (C-X-C motif) receptor 4	2.1	0.036	1.7	0.113
<i>Dcn</i>	Decorin	1.1	0.593	1.1	0.669
<i>Edn1</i>	Endothelin 1	0.8	0.078	1.0	0.972
<i>Egf</i>	Epidermal growth factor	1.8	0.004	1.3	0.103
<i>Eng</i>	Endoglin	1.7	0.001	1.	0.080
<i>Fasl</i>	Fas ligand (TNF superfamily, member 6)	8.0	0.048	3.2	0.209
<i>Grem1</i>	Gremlin 1	1.2	0.527	0.8	0.283
<i>Hgf</i>	Hepatocyte growth factor	9.8	0.048	3.7	0.050
<i>Ifng</i>	Interferon gamma	14.1	0.018	15.3	0.004
<i>Il10</i>	Interleukin 10	8.7	0.010	2.5	0.001
<i>Il13</i>	Interleukin 13	0.7	0.152	1.0	0.688
<i>Il13ra2</i>	Interleukin 13 receptor, alpha 2	0.9	0.765	1.0	0.841
<i>Il1a</i>	Interleukin 1 alpha	1.0	0.714	0.4	0.091
<i>Il1b</i>	Interleukin 1 beta	7.8	0.046	5.5	0.049
<i>Il4</i>	Interleukin 4	0.9	0.677	1.1	0.515
<i>Il5</i>	Interleukin 5	2.3	0.234	2.7	0.251
<i>Il6</i>	Interleukin 6	3.1	0.001	1.4	0.218
<i>Ilk</i>	Integrin linked kinase	1.2	0.324	1.1	0.549
<i>Inhbe</i>	Inhibin beta E	1.2	0.530	1.1	0.841
<i>Itga1</i>	Integrin alpha 1	1.8	0.002	1.5	0.057
<i>Itga2</i>	Integrin alpha 2	5.4	0.019	3.6	0.076
<i>Itga3</i>	Integrin alpha 3	1.0	0.909	0.8	0.137
<i>Itgav</i>	Integrin alpha V	1.5	0.100	1.1	0.562
<i>Itgb1</i>	Integrin beta 1 (fibronectin receptor beta)	1.9	0.019	1.4	0.120
<i>Itgb3</i>	Integrin beta 3	2.2	0.000	1.6	0.000
<i>Itgb5</i>	Integrin beta 5	1.6	0.000	1.3	0.024
<i>Itgb6</i>	Integrin beta 6	1.2	0.138	0.9	0.245
<i>Itgb8</i>	Integrin beta 8	3.1	0.080	2.7	0.125
<i>Jun</i>	Jun oncogene	1.6	0.016	1.6	0.023
<i>Lox</i>	Lysyl oxidase	1.0	0.817	1.1	0.564
<i>Ltbp1</i>	Latent transforming growth factor beta binding protein 1	1.9	0.103	1.7	0.077
<i>Mmp13</i>	Matrix metallopeptidase 13	4.4	0.037	1.5	0.344
<i>Mmp14</i>	Matrix metallopeptidase 14 (membrane-inserted)	1.8	0.242	1.0	0.998
<i>Mmp1a</i>	Matrix metallopeptidase 1a (interstitial collagenase)	1.2	0.253	1.1	0.283
<i>Mmp2</i>	Matrix metallopeptidase 2	1.3	0.362	1.3	0.152
<i>Mmp3</i>	Matrix metallopeptidase 3	0.8	0.263	0.5	0.014
<i>Mmp8</i>	Matrix metallopeptidase 8	1.7	0.215	1.9	0.070
<i>Mmp9</i>	Matrix metallopeptidase 9	1.3	0.017	0.4	0.009
<i>Myc</i>	Myelocytomatosis oncogene	2.1	0.005	1.7	0.078
<i>Nfkb1</i>	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1	1.5	0.049	1.1	0.230
<i>Pdgfa</i>	Platelet derived growth factor, alpha	1.1	0.679	1.0	0.748
<i>Pdgfb</i>	Platelet derived growth factor, B polypeptide	1.6	0.060	1.3	0.001

<i>Plat</i>	Plasminogen activator, tissue	0.9	0.482	0.7	0.024
<i>Plau</i>	Plasminogen activator, urokinase	1.4	0.227	1.0	0.698
<i>Plg</i>	Plasminogen	0.9	0.765	1.6	0.411
<i>Serpina1a</i>	Serine (or cysteine) peptidase inhibitor, clade A, member 1a	0.9	0.765	1.1	0.841
<i>Serpine1</i>	Serine (or cysteine) peptidase inhibitor, clade E, member 1	3.5	0.022	2.1	0.002
<i>Serph1</i>	Serine (or cysteine) peptidase inhibitor, clade H, member 1	1.3	0.051	1.0	0.874
<i>Smad2</i>	MAD homolog 2 (Drosophila)	2.0	0.018	1.4	0.037
<i>Smad3</i>	MAD homolog 3 (Drosophila)	1.6	0.014	1.4	0.192
<i>Smad4</i>	MAD homolog 4 (Drosophila)	1.4	0.126	1.2	0.355
<i>Smad6</i>	MAD homolog 6 (Drosophila)	1.4	0.048	1.1	0.598
<i>Smad7</i>	MAD homolog 7 (Drosophila)	1.7	0.099	1.5	0.178
<i>Snai1</i>	Snail homolog 1 (Drosophila)	1.7	0.120	1.0	0.864
<i>Sp1</i>	Trans-acting transcription factor 1	2.2	0.002	1.5	0.046
<i>Stat1</i>	Signal transducer and activator of transcription 1	8.1	0.046	6.4	0.041
<i>Stat6</i>	Signal transducer and activator of transcription 6	1.6	0.010	1.2	0.107
<i>Tgfb1</i>	Transforming growth factor, beta 1	1.9	0.170	1.2	0.042
<i>Tgfb2</i>	Transforming growth factor, beta 2	1.5	0.050	1.0	0.963
<i>Tgfb3</i>	Transforming growth factor, beta 3	1.2	0.299	1.2	0.002
<i>Tgfbr1</i>	Transforming growth factor, beta receptor I	2.4	0.001	1.6	0.101
<i>Tgfbr2</i>	Transforming growth factor, beta receptor II	1.6	0.021	0.9	0.708
<i>Tgif1</i>	TGFB-induced factor homeobox 1	1.5	0.575	1.1	0.793
<i>Thbs1</i>	Thrombospondin 1	2.6	0.139	2.2	0.019
<i>Thbs2</i>	Thrombospondin 2	1.1	0.477	0.9	0.856
<i>Timp1</i>	Tissue inhibitor of metalloproteinase 1	3.2	0.028	1.5	0.233
<i>Timp2</i>	Tissue inhibitor of metalloproteinase 2	1.1	0.528	0.8	0.383
<i>Timp3</i>	Tissue inhibitor of metalloproteinase 3	1.6	0.006	1.6	0.033
<i>Timp4</i>	Tissue inhibitor of metalloproteinase 4	0.8	0.834	1.5	0.086
<i>Tnf</i>	Tumor necrosis factor	8.1	0.042	14.3	0.043
<i>Vegfa</i>	Vascular endothelial growth factor A	1.2	0.313	0.9	0.420

*Statistically significant ($P<0.05$) and biologically relevant (≤ 0.5 or ≥ 2) *S. epidermidis*-induced fold changes in bold red are analysed in Results, Table 3

**Compared to Control group.