

**S1 Table. Transcriptome analysis of gene expressed in inflamed areas of AD patients relative to their non-AD counterparts.**

Gene	p value	FC
<b>FLG</b>	<.0001	-33,4620368
<b>LOR</b>	<.0001	-37,8871287

<b>S100A7</b>	0.0018	6,69256792
<b>S100A8</b>	0.0002	28,2174085
<b>S100A9</b>	0.0002	21,1013902
<b>NLRP3</b>	0.0003	280,416897
<b>CASP1</b>	0.0612	-6,59843344
<b>IL1<math>\beta</math></b>	0.0412	10,8693377

<b>LL37</b>	0.0044	119,54566
<b>HBD2</b>	0.0037	6,6670778
<b>HBD3</b>	0.0029	11,8114083
<b>RNASE7</b>	0.0008	-6,07797538

<b>CCL3</b>	0.0306	12,5081269
<b>CCL17</b>	0.0181	10,2317651
<b>IL-8</b>	0.0009	32,1584301
<b>IL-13</b>	0.0009	643,855732
<b>IL-22</b>	0.0019	693,153442

Skin samples were taken by scratching the skin surface and reverse-transcribed RNA submitted to PCR with primers for genes as indicated. Results are expressed as Fold Change (FC) in AD (N=21) vs non-AD samples (N=14). Associated p values are shown according to methods described in statistical section.