Table S3. Least square means of ΔCt values of each gene for all diagnoses and stimuli; fold increase of stimuli and diagnoses

	least square means of ΔCt			least square means of ΔCt			fold increase				
GENE	NS	PS	AD	KGM	Th1	Th2	PS/NS	AD/NS	PS/AD	Th1/KGM	Th2/KGM
DEFB103	8.9	4.5	7.8	7.6	5.8	7.9	21.3	2.1	9.9	3.4	0.8
S100A9	3.1	2.6	5.6	4.8	0.4	6.2	1.4	0.2	8.1	20.4	0.4
S100A8	2.5	2.4	4.9	4.5	0.0	5.4	1.1	0.2	5.9	23.7	0.6
DEFB4	10.0	6.7	11.2	12.0	2.8	13.1	10.1	0.5	22.1	591.3	0.5
CST6	6.7	4.7	5.8	6.0	4.6	6.6	4.0	1.8	2.2	2.7	0.7
LCN2	6.3	6.6	7.4	7.4	4.4	8.4	0.8	0.5	1.8	8.1	0.5
IL1F9	9.9	10.8	12.3	12.5	7.8	12.7	0.5	0.2	2.7	27.1	0.9
CXCL10	12.6	12.5	14.9	16.0	8.5	15.6	1.0	0.2	5.3	187.7	1.3
SPRR2C	4.7	2.3	4.0	4.0	2.0	5.0	5.2	1.5	3.4	4.0	0.5
CTSL2	3.6	4.6	5.5	4.4	3.7	5.6	0.5	0.3	1.9	1.6	0.4
CCL20	10.2	10.2	12.4	12.3	8.5	12.0	1.0	0.2	4.4	13.4	1.2
IVL	8.0	7.6	9.1	7.8	7.2	9.8	1.3	0.5	2.8	1.5	0.2
IL1B	8.7	10.0	13.5	10.8	8.3	13.2	0.4	0.0	11.4	5.7	0.2
CXCL2	11.7	10.8	13.7	12.9	9.9	13.5	1.8	0.2	7.5	7.9	0.6
CCL5	11.0	9.6	11.9	12.2	8.8	11.6	2.6	0.5	4.9	10.6	1.5
CA2	2.5	1.9	1.8	2.8	2.8	0.6	1.5	1.5	1.0	1.0	4.6
CALML5	7.3	8.6	9.1	8.6	7.5	8.9	0.4	0.3	1.5	2.2	0.8
LGMN	7.6	8.0	8.9	8.6	7.2	8.7	0.8	0.4	1.8	2.5	0.9
TGM1	8.0	8.5	9.5	9.0	7.3	9.8	0.7	0.4	2.0	3.2	0.6
TLR2	11.0	11.7	12.9	13.1	10.6	11.9	0.7	0.3	2.3	5.4	2.2
SLPI	1.1	-0.2	0.9	0.8	-0.3	1.5	2.5	1.2	2.1	2.2	0.6
CTSL	8.8	8.3	9.6	9.1	8.3	9.1	1.4	0.6	2.4	1.8	1.0
PI3	1.6	0.3	3.4	2.8	-0.6	3.0	2.5	0.3	8.9	10.2	0.9
IL1A	6.9	7.8	8.4	8.1	6.3	8.7	0.6	0.4	1.6	3.4	0.6
IL1RN	7.1	7.1	8.5	7.8	6.5	8.5	1.0	0.4	2.7	2.5	0.6
IL8	13.5	9.2	16.0	14.1	10.3	14.4	19.2	0.2	110.2	14.2	0.8
KLK6	9.9	9.9	12.1	10.9	9.4	11.7	1.0	0.2	4.6	2.9	0.6
NELL2	13.6	14.2	14.7	14.9	14.8	12.8	0.6	0.4	1.4	1.1	4.2
CCL27	12.7	10.4	11.1	12.7	9.3	12.1	4.9	3.1	1.6	10.7	1.5
MT2A	4.7	3.0	5.9	4.8	2.7	6.1	3.2	0.4	7.5	4.2	0.4
IL1F8	15.7	14.5	15.3	15.5	13.5	16.4	2.2	1.3	1.7	4.1	0.5
TNF	13.0	12.0	12.7	13.9	10.2	13.5	2.1	1.2	1.7	13.0	1.3
KLK7	6.0	4.8	5.1	5.0	5.2	5.7	2.4	1.9	1.3	0.9	0.6
FABP5	2.6	2.7	2.9	2.6	2.1	3.4	0.9	0.8	1.1	1.4	0.6
IL18	4.7	4.6	5.1	4.6	4.8	5.0	1.1	0.8	1.4	0.8	0.8
Arg1	12.9	13.7	13.5	13.5	12.3	14.3	0.6	0.7	0.9	2.3	0.6
TGFA	8.4	9.5	9.9	9.4	8.3	10.1	0.5	0.3	1.3	2.2	0.6
TNC	8.8	8.4	10.8	10.4	9.3	8.3	1.4	0.3	5.3	2.2	4.3
KLK13	13.0	11.9	13.0	12.4	12.2	13.3	2.1	1.0	2.1	1.2	0.6
TLR3	12.5	14.3	13.5	14.5	12.3	13.5	0.3	0.5	0.6	4.5	1.9
IER3	11.3	11.4	14.1	12.8	11.0	13.0	0.9	0.1	6.3	3.5	0.8
AREG	5.6	5.1	5.9	5.5	5.0	6.2	1.4	0.8	1.7	1.4	0.6
KRT10	3.2	3.7	2.6	3.0	3.3	3.1	0.7	1.5	0.5	0.8	1.0
DKK1	10.8	9.2	10.0	10.1	9.6	10.4	3.2	1.8	1.8	1.4	0.8
CXCL1	10.5	7.1	11.6	10.5	7.7	11.0	10.3	0.5	21.8	7.1	0.7
GJA1	6.8	7.4	8.0	7.5	7.1	7.5	0.6	0.4	1.5	1.3	1.0
TNFRSF6	11.9	11.9	12.1	12.4	11.5	11.9	1.0	0.9	1.1	1.9	1.4
CAMP	14.7	13.6	14.0	14.2	13.6	14.5	2.2	1.7	1.3	1.4	0.8
KRT6A	-0.2	0.2	0.7	0.3	0.1	0.3	0.8	0.5	1.5	1.2	1.0
DEFB1	8.3	7.9	8.2	8.4	7.4	8.5	1.3	1.1	1.3	1.9	0.9
KRT17	1.8	2.4	2.5	2.2	2.0	2.5	0.6	0.6	1.0	1.1	0.8
IL1R1	13.8	12.7	13.9	13.4	13.6	13.4	2.2	0.9	2.4	0.9	1.0
KRT14	0.8	0.7	1.4	1.0	0.9	1.0	1.1	0.6	1.6	1.1	1.0
JUNB	7.3	7.2	7.6	7.6	7.0	7.5	1.0	0.8	1.3	1.5	1.1
TP73L	5.8	5.9	6.2	6.2	5.8	6.0	0.9	0.8	1.2	1.3	1.1

Least square means of the ΔCt values for each diagnosis (over all stimuli) and for each stimulus (over all diagnoses) are given. Fold increase in gene expression is given as calculated by the method of Livak et al. 2001, based on the least square means. Fold increases or decreases of >4 are marked in red.