

Supplementary Table S5. FAE- and M-cell-related genes significantly induced > 2.0 fold in the intestinal epithelium in response to RANKL-stimulation. The putative functions of the genes listed in this table are presented in Figure 8.

Gene symbol ^a	Gene title	Fold change in intestinal epithelium after RANKL-treatment ^b	<i>P</i> value ^c	Day of peak expression level	Reported expression by FAE and/or M cells	Fold change in <i>in vitro</i> small intestinal organoids after RANKL-treatment ^d	Ref.
<i>Gp2</i>	glycoprotein 2 (zymogen granule membrane)	46.9	0.02	3	M cells	56.5	¹ , current study
<i>SpiB</i>	Spi-B transcription factor (Spi-1/PU.1 related)	31.9	0.0005	2	M cells	18.5	²
<i>Anxa5</i>	Annexin A5	12.7	9x10 ⁻⁵	2	M cells	35.6	³
<i>Ccl20</i>	chemokine (C-C motif) ligand 20	11.3	0.0002	2	FAE	158.5	⁴ , current study
<i>Tnfaip2</i>	tumor necrosis factor, alpha-induced protein 2 (M-Sec)	7.7	0.004	2	M cells	13.9	⁵
<i>Fabp5</i>	fatty acid binding protein 5, epidermal	7.4	0.008	2			
<i>Ctsh</i>	Cathepsin H	6.9	0.002	2	FAE	8.2	³
<i>Serpina1a/ Serpina1b</i>	serine (or cysteine) peptidase inhibitor, clade A, members 1A or 1B	5.6	1x10 ⁻⁵	2			
<i>Clu</i>	Clusterin	5.3	0.001	2	FAE and M cells	10.9	³
<i>9930023K05Rik</i>	RIKEN cDNA 9930023K05 gene	5.1	0.002	2		51.7	
<i>Clca2</i>	chloride channel calcium activated 2	5.0	3x10 ⁻⁵	2	Cluster 65:M cell- and FAE-related	3.1	current study
<i>Ccl9</i>	chemokine (C-C motif) ligand 9	4.9	4x10 ⁻⁶	2	M cells	32.0	⁶
<i>Mfge8</i>	milk fat globule-EGF factor 8 protein	4.9	0.004	3		5.0	
<i>Ncf4</i>	Neutrophil cytosolic factor 4	4.9	0.006	1		52.8	
<i>Akt3</i>	Thymoma viral	4.8	0.0005	2			

	proto-oncogene 3						
<i>Rac2</i>	RAS-related C3 botulinum substrate 2	4.6	0.001	2		23.5	
<i>Cd44</i>	CD44 antigen	4.1	0.006	1		2.2	
<i>Prnp</i>	Prion protein	3.7	0.0002	2	M cells	52.4	⁷
<i>Slc2a6</i>	solute carrier family 2 (facilitated glucose transporter), member 6	3.7	0.0002	1		35.6	
<i>Icam1</i>	Intercellular adhesion molecule 1	3.6	0.0001	1	M cells	87.7	⁸
<i>Marcks11</i>	MARCKS-like 1	3.6	0.0002	1	M cells	5.8	⁹
<i>Rnase1</i>	Ribonuclease, RNase A family, 1 (pancreatic)	3.6	0.002	2		2.2	
<i>Tmem176a</i>	Transmembrane protein 176A	3.4	0.006	1		n/a	
<i>Tmem176b</i>	Transmembrane protein 176B	3.4	0.005	1		n/a	
<i>Ubd</i>	Ubiquitin D	3.1	0.02	2	FAE and M cells	31.2	⁶ , current study
<i>Eno3</i>	Enolase 3,beta muscle	3.0	0.008	2		24.0	
<i>Slco3a1</i>	solute carrier organic anion transporter family, member 3a1	3.0	0.0001	3		3.3	
<i>Tr</i>	Transthyretin	2.9	0.008	3			
<i>Cxcl11</i>	chemokine (C-X-C motif) ligand 11	2.8	0.003	1	FAE and M cells		current study
<i>Mreg</i>	Melanoregulin	2.8	0.004	2			
<i>Fyb</i>	FYN binding protein	2.7	0.002	2			
<i>Kctd12</i>	potassium channel tetramerisation domain containing 12	2.6	0.0001	1		9.2	
<i>Scg5</i>	Secretogranin V (Sgpe-1)	2.6	0.0001	2	M cells		⁶
<i>Cyba</i>	cytochrome b-245, alpha polypeptide	2.5	0.0008	1		2.7	
<i>Blnk</i>	B-cell linker	2.4	0.0002	3		2.3	
<i>Far2</i>	fatty acyl CoA reductase 2	2.4	0.003	1		n/a	
<i>Rab32</i>	RAB32, member RAS oncogene family	2.4	0.01	2		16.2	
<i>Tmem184c</i>	Transmembrane protein 184C	2.4	4.3x10 ⁻⁵	3		n/a	
<i>Clca4</i>	Chloride channel	2.3	0.0002	1			

	calcium activated 4						
<i>Epb4.1l2</i>	Erythrocyte protein band 4.1- like 2	2.3	0.01	1		2.1	
<i>S100a11</i>	S100 calcium binding protein A11 (calgizzarin)	2.3	0.0003	1		2.9	
<i>Stk39</i>	Serine/threonine kinase 39, STE20/SPS1 homolog (yeast)	2.3	0.0009	3			
<i>Tmprss2</i>	Transmembrane protease, serine 2	2.3	0.0002	3			
<i>Gca</i>	Grancalcin	2.2	0.001	2			
<i>Gjb2</i>	Gap junction protein, beta 2	2.2	0.001	2	Cluster 65:M cell- and FAE- related	16.2	current study
<i>Pdia5</i>	Protein disulfide isomerise associated 5	2.2	0.007	3			
<i>Myo1b</i>	Myosin 1B	2.2	0.005	3		2.8	
<i>Reep1</i>	Receptor accessory protein 1	2.2	0.002	1			

^a, Data are presented in order of peak expression fold-change, with the highest score first. These data were performed on Affymetrix mouse gene 1.0 ST expression arrays (GSE37861).

^b, Fold-change in gene expression level at peak day when compared to controls (d 0).

^c, *P* values for those genes which were significantly upregulated > 2.0 fold on peak day after RANKL-treatments when compared to controls (*n* = 3/group).

^d, Fold-change in gene expression in RANKL-stimulated small intestinal organoid cultures when compared to controls. These data were performed on Agilent 4x44K whole mouse genome expression arrays (GSE38785) and equivalent gene probe sets were compared. n/a; an equivalent annotated probe set was not present on the array.

References

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