

Supplementary Materials

Article information

Interleukin-17 receptor A1 gene knockout causes weight loss and reduction of intestinal metabolism-related genes in the Japanese medaka, *Oryzias latipes*

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Table S1

Table S1. crRNA and Primer sequences used in this study.

Sequence name	Nucleotide sequence (5'-3')	Purpose
crRNA1-1	GAGCGAGCGGGUCCUGGUUC	Genome Editing
crRNA1-2	UAUGACCGCGAAGCGACAUG	Genome Editing
crRNA7-1	UGCUGAUGUUCGGCUGCCAC	Genome Editing
crRNA7-2	UCUCUGACCGUCAGCUUCAG	Genome Editing
IL-17RAF1	CACATTCAACGCGCTCGAGA	HMA
IL-17RAF2	TCCCTGAAATGGAGAACACC	HMA
IL-17RAR1	GTGACATCCAGCAGTTCCAT	HMA
Chr.23IL-17RA-ORF-F	ATGAGGACTTTCCTAACCATCC	ORF amplification of WT's IL-17RA1
Chr.23IL-17RA-ORF-R	TCACGACGCAGTCAAGCTGTTG	ORF amplification of WT's IL-17RA1
IL-17RAmu-ORF-F2	ATGCTCTCCAAGTGCCGAG	ORF amplification of mutated IL-17RA1
IL-17RAmu-ORF-R2	TCACGACGCAGTCAAGCTGTT	ORF amplification of mutated IL-17RA1
Chr. 23IL-17RA-exF2	CTTTGTGGAGCGGTAGTTCC	qPCR
Chr. 23IL-17RA-exR2	CTCCAGACGCTCCTTTTCTG	qPCR
mvda-exF1	TGTCCTTGTGGCTAGTGCTG	qPCR
mvda-exR1	GACTCTGCCCGATGCTTTAG	qPCR
acat2-exF1	CAGATGGTGTGTGGTTCTGG	qPCR
acat2-exR1	ATCTTCACGCCTGCTCTCAT	qPCR
hmgcs1-exF1	TGATGCTCAACGACTTCCTG	qPCR
hmgcs1-exR1	TTTCCTCTGGCTTCACGTCT	qPCR
hmgcra-exF1	AAGGTGGTCCAGGAGTTCT	qPCR
hmgcra-exR1	GTAGATGGCAGCCACCAGAT	qPCR
il17c-exF1	CCTGGAAATACACGGAAGTCA	qPCR
il17c-exR1	AGGGGCTTGGAGTTGAAGTT	qPCR
rorc-exF1	TGCACAAGCTGTACCAGAGG	qPCR
rorc-exR1	TACCGCTGACTGAACCAGTG	qPCR
il17af1-exF1	TTCAGCAACCAGCTTCTGC	qPCR
il17af1-exR1	GGTCACCATCATCCTCATCA	qPCR
stat3-exF1	TCACCACACTGGCTGAGAAG	qPCR
stat3-exR1	AGCCCATGATGTATCCTTCG	qPCR
apoa1b-exF1	CAGGTGAAGCAGGGTTTGAT	qPCR
apoa1b-exR1	CAGAAATGGTGGTGACAACG	qPCR
pla2g12b-exF1	GCTATGACCAAGTGCTGCAA	qPCR
pla2g12b-exR1	TGTACAGAGCGTCTGCCATC	qPCR
mogat2-exF1	TACATCCTGGGCTTTCATCC	qPCR
mogat2-exR1	CTGCACACATGGCGTAGTCT	qPCR
ctsbb-exF1	CTGTCCCACACTCAAGCAGA	qPCR
ctsbb-exR1	AAGCAGCAGAAGGAAAACCA	qPCR
neu1-exF1	GTGGTGGTGGACGAAGAAGT	qPCR
neu1-exR1	CGAGCTCAATGGAGAGGTTT	qPCR
man2b1-exF1	CCCTGACAGTGCAGCAGATA	qPCR
man2b1-exR1	TGTCAGGAGATGGACAGCAG	qPCR
β -actin-exF1	CCACCATGTACCCTGGAATC	qPCR
β -actin-exR1	GCTGGAAGGTGGACAGAGAG	qPCR

Table S2

Table S2. List of top 50 genes with significantly higher expression in WT anterior intestine compared to posterior intestine.

Gene_ID	Gene name	Gene Symbol	FPKM*1		p_value	Fold increases*2
			Anterior/WT	Posterior/WT		
ENSORLG00000007755	GLIS family zinc finger 3	glis3	0.653783	0	0.016566	N/A
ENSORLG00000009829	Complement C8 beta chain	c8b	0.492892	0	0.031607	N/A
ENSORLG00000024779	Solute carrier family 35 member D3	slc35d3	0.321644	0	0.039025	N/A
ENSORLG00000012756	Calcium voltage-gated channel auxiliary subunit gamma 3	cacng3b	4.807693	0.045551	0.009076	105.545
ENSORLG00000000064	Rho-related GTP-binding protein RhoU	si:ch211-133l11.10	2.219903	0.034217	0.019288	64.87631
ENSORLG00000010752	C->U-editing enzyme APOBEC-2	apobec2	0.847848	0.013898	0.021198	61.0031
ENSORLG00000024637	Prostaglandin F receptor	ptgfr	2.224133	0.038282	0.022838	58.09819
ENSORLG00000006353	Fatty acid desaturase 2	fads2 (1 of many)	3.371598	0.081094	0.00766	41.57652
ENSORLG00000019113	Synaptotagmin 14	syt14a	3.188745	0.079672	0.010874	40.0232
ENSORLG00000004922	Ethanolamine-phosphate phospho-lyase	etnpl	3.178797	0.092583	0.004795	34.33442
ENSORLG000000006187	Vitellogenin II	vit-6	1.259741	0.058377	0.014287	21.57933
ENSORLG00000027981	Apolipoprotein Eb	apoea	8585.838	450.1285	0.005669	19.07419
ENSORLG00000016142	Ankyrin repeat and EF-hand domain containing 1	ankef1a	0.935558	0.049295	0.023324	18.97874
ENSORLG00000017640	Solute carrier family 15 member 1	slc15a1a	122.0398	6.475649	0.00594	18.84595
ENSORLG00000022823	Sodium-dependent neutral amino acid transporter B(0)AT1	slc6a19 (1 of many)	4.751944	0.271305	0.008755	17.51516
ENSORLG00000017374	GATA binding protein 4	gata4	52.02527	3.145251	0.00788	16.5409
ENSORLG000000006357	Fatty acid desaturase 2	fads2 (1 of many)	24.18572	1.490078	0.007918	16.23118
ENSORLG000000002980	Phosphoethanolamine N-methyltransferase	pmt	65.8878	4.262961	0.00757	15.45588
ENSORLG00000011725	Phosphatase and actin regulator 3	phactr3b	11.37623	0.749912	0.010681	15.17008
ENSORLG000000007815	Netrin receptor UNC5C	unc5c	1.127791	0.076471	0.017489	14.748
ENSORLG000000003870	Monocarboxylate transporter 12-B-like	slc16a12a	13.99971	0.989398	0.012428	14.14972
ENSORLG00000004027	Alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5	st6galnac5b	3.692379	0.274829	0.02827	13.43521
ENSORLG00000011814	Thiamine transporter 2-like	slc19a3a	27.78263	2.309222	0.011914	12.03117
ENSORLG000000002121	Malic enzyme 1	me1	125.0096	10.53937	0.010791	11.8612
ENSORLG000000009477	Alkaline phosphatase	alp3	15.46531	1.305906	0.011808	11.84259
ENSORLG000000015744	Apolipoprotein A-I	apoa1b	15041.67	1319.021	0.010975	11.40367
ENSORLG000000009193	Apolipoprotein A-IV	apoa4a	5928.088	542.2786	0.011591	10.93181
ENSORLG00000025647	Alkaline phosphatase	alpi.1	6.145193	0.565984	0.01551	10.85755
ENSORLG000000002620	Ankyrin repeat and SOCS box protein 16	asb16	2.634954	0.25279	0.026138	10.4235
ENSORLG00000010369	Vasorin	vasna	2.081763	0.204753	0.03799	10.16718
ENSORLG000000004492	PR/SET domain 16	si:ch211-263k4.2	5.068484	0.51757	0.015939	9.792839
ENSORLG000000003390	Cysteine dioxygenase type 1	cdo1	1348.553	138.0702	0.013512	9.767155
ENSORLG000000003115	Phosphoethanolamine/phosphocholine phosphatase 1	phospho1	16.5748	1.722852	0.02226	9.62056
ENSORLG00000019522	Fatty acid binding protein 2	gucy1b1	904.988	94.53033	0.01377	9.573521
ENSORLG000000000838	Fatty acid hydroxylase domain containing 2	faxdc2	174.7019	18.27045	0.013947	9.561994
ENSORLG000000004048	Amine oxidase copper containing 1	aoc1	112.0085	12.22091	0.014769	9.165321
ENSORLG000000001556	Glycine decarboxylase	gldc	52.87319	5.841827	0.015317	9.050797
ENSORLG0000000027036	Nicotinate-nucleotide pyrophosphorylase	qprt	4.908366	0.544889	0.02059	9.008012
ENSORLG00000011461	Lysoplasmalogenase	tmem86b	112.4113	12.74677	0.015882	8.818807
ENSORLG00000011713	Metallophosphoesterase domain-containing protein 1	mpped1	3.986476	0.46433	0.023314	8.585442
ENSORLG000000007987	Cholesterol 25-hydroxylase-like protein 1, member 1	ch25hl1.1	61.09696	7.274462	0.018683	8.398828
ENSORLG00000011403	Sodium- and chloride-dependent GABA transporter ine	si:ch211-283g2.1	7.485715	0.89201	0.020658	8.391961
ENSORLG00000017885	Calsequestrin-2	casq2	18.92542	2.256656	0.019194	8.38649
ENSORLG000000003516	CaM kinase-like vesicle-associated protein	camkva	1.621987	0.196389	0.037955	8.259056
ENSORLG000000004121	SCO-spondin	sco-spondin	0.564595	0.067877	0.033838	8.317951
ENSORLG000000006998	Intestinal-type alkaline phosphatase 1	alpi.2	55.19508	6.879683	0.018209	8.022911
ENSORLG00000018506	Mitochondrial uncoupling protein 2	ucp1	745.7533	94.70658	0.017872	7.874356
ENSORLG000000006858	WSC domain containing 2	wscd2	7.044699	0.919192	0.027045	7.664016
ENSORLG000000005805	G protein-coupled receptor 149	gpr149	0.832364	0.109615	0.040802	7.593535
ENSORLG00000028067	Group XIIB secretory phospholipase A2-like protein	pla2g12b (1 of many)	26.39515	3.570286	0.020539	7.393009

*1 Fragment per kilobase of exon length per million reads
*2 Fold increases of anterior intestine compared to posterior intestine in WT

Table S3

Table S3. List of top 50 genes with significantly higher expression in WT posterior intestine compared to anterior intestine.

Gene_ID	Gene name	Gene Symbol	FPKM ^{*1}		p_value	Fold increases ^{*2}
			Anterior/WT	Posterior/WT		
ENSORLG00000007896	Homeobox C13	hoxc13a	0	56.90971	0.042601	N/A
ENSORLG00000013898	Sodium-dependent neutral amino acid transporter B(0)AT3	slc6a18	0.014883	45.72621	0.031928	3072.385
ENSORLG00000012622	Gastrotropin	fabp6	2.02067	3802.423	0.032418	1881.763
ENSORLG000000029159	Transmembrane and immunoglobulin domain containing 1	tmigd1	0.106334	197.4546	0.033347	1856.933
ENSORLG000000007902	Homeobox protein Hox-C12a	hoxc12a	0.012779	19.66438	0.047384	1538.774
ENSORLG000000000412	Solute carrier family 12 member 3	slc12a3	0.190333	289.562	0.035663	1521.347
ENSORLG000000017347	Cathepsin B	ctsb	0.219461	292.9056	0.037311	1334.662
ENSORLG000000012785	Equisetin synthetase eqxS	si:dkey-61p9.11	0.034595	38.56171	0.041306	1114.665
ENSORLG000000005559	Novel gene	si:dkey-23i12.7	0	6.554478	0.019605	N/A
ENSORLG000000015795	PQ-loop repeat-containing protein 1	si:dkey-246g23.2	0	1.937674	0.020822	N/A
ENSORLG000000010475	Ring finger protein 32	rnf32	0	1.01096	0.034365	N/A
ENSORLG000000025010	Diacylglycerol kinase beta	dgkg	0	0.619658	0.039179	N/A
ENSORLG000000017540	Homeobox D10	hoxd9	0.005614	0.985636	0.006613	175.5649
ENSORLG000000002209	E3 ubiquitin-protein ligase TRIM39	btr01	0.013523	2.346265	0.006734	173.4994
ENSORLG000000003592	5-hydroxytryptamine receptor 7	htr7a	0	0.92148	0.045145	N/A
ENSORLG000000006424	Nerve growth factor-like	ngfb	0	2.09764	0.045145	N/A
ENSORLG000000019722	Calpain 9	capn9	0.042558	5.186289	0.004504	121.8627
ENSORLG000000013074	Phosphoribosyl transferase domain containing 1	unm_sa821	0.035953	4.195715	0.01238	116.699
ENSORLG000000030349	Serine palmitoyltransferase small subunit B sptssb		0.172073	18.65908	0.013849	108.4371
ENSORLG000000009791	DEP domain containing 7	depdc7a	0.04966	3.564347	0.010677	71.77504
ENSORLG000000012431	Transmembrane protein 182	tmem182a	0.013145	0.909533	0.027356	69.19321
ENSORLG000000004981	Homeobox protein Hox-A1a	hoxa1a	0.033067	1.997764	0.014159	60.41496
ENSORLG000000014516	Cytochrome P450, family 26, subfamily A, polypeptide 1	cyp26a1	0.027347	1.623931	0.014564	59.38223
ENSORLG000000017546	Homeobox D3	hoxd3a	0.104274	5.635614	0.0109	54.04644
ENSORLG000000029845	Ring finger protein 183	rnf183	0.262979	13.37569	0.00913	50.86217
ENSORLG000000013851	Inward rectifier potassium channel 16	kcnj16	0.06799	3.300122	0.020219	48.53852
ENSORLG000000013016	Calcium homeostasis modulator 1	si:dkeyp-80c12.5	0.152021	7.668066	0.005195	50.44092
ENSORLG000000017026	Homeobox protein XHOX-3	eve1	0.020928	0.961771	0.04911	45.95668
ENSORLG000000017782	Bone morphogenetic protein 3	bmp3	0.131324	6.181321	0.004294	47.06908
ENSORLG000000016368	Heme transporter hrg1-A	slc48a1b	0.151939	6.684492	0.009554	43.99449
ENSORLG000000003376	Zgc:110333	zgc:110333	0.108466	4.424661	0.026771	40.79301
ENSORLG000000005954	Arylacetamide deacetylase	aadac	0.337479	13.41827	0.006952	39.76028
ENSORLG000000012948	PR domain zinc finger protein 1-like	prdm1b	0.383341	15.11995	0.004756	39.44251
ENSORLG000000010789	RAB38, member RAS oncogene family	rab38 (1 of many)	0.077988	3.045075	0.006228	39.04531
ENSORLG000000022459	Erythrocyte band 7 integral membrane protein-like	stoml3a	0.020907	0.809671	0.02909	38.72754
ENSORLG000000020050	Microtubule associated protein 1 light chain 3 gamma	map1lc3c	0.864366	33.14002	0.008438	38.34027
ENSORLG000000018573	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase B	mgat4b	0.139553	4.611892	0.01071	33.0475
ENSORLG000000030486	DNA damage inducible transcript 4 like	ddit4l	0.063261	1.933554	0.018655	30.56465
ENSORLG000000023188	Homeobox A7	hoxa7	0.315432	10.33955	0.006283	32.77899
ENSORLG000000030640	Claudin b	cldnb	0.811916	24.9452	0.009414	30.72385
ENSORLG000000007148	Interferon-induced very large GTPase 1	si:dkey-202i22.6	0.012856	0.391662	0.042544	30.46567
ENSORLG000000016264	Sodium-dependent phosphate transport protein 2B	slc34a2b	0.82561	24.31788	0.00625	29.45445
ENSORLG000000014498	Transmembrane protein 120A	tmem120a	0.069441	1.989978	0.014869	28.65691
ENSORLG000000017272	Occludin	oclnb	0.055251	1.483541	0.021591	26.8511
ENSORLG000000023807	Sodium-dependent lysophosphatidylcholine symporter 1-B	mfsd2aa (1 of many)	0.04208	1.071956	0.037564	25.47412
ENSORLG000000024136	Mucin-12	si:ch211-168f7.5	0.017507	0.445988	0.037564	25.47412
ENSORLG000000019014	Calpain-1 catalytic subunit-like	zgc:136872 (1 of many)	0.053971	1.337694	0.029973	24.78563
ENSORLG000000011733	Rh family C glycoprotein	rhcg	0.82595	20.31174	0.008043	24.59199
ENSORLG000000001496	Ankyrin repeat domain 29	ankrd29	0.313211	7.493583	0.022472	23.92501
ENSORLG000000006603	Carbonic anhydrase 4	ca15b	7.246819	169.952	0.007115	23.45194

*1 Fragment per kilobase of exon length per million reads

*2 Fold increases of anterior intestine compared to posterior intestine in WT

Table S4

Table S4. List of the genes down-regulated by a third-fold in the anterior intestine of IL-17RA1-KO medaka.

Gene_ID	Gene name	Gene Symbol	FPKM ^{*1}		p_value	Fold decreases ^{*2}
			WT	IL-17RA1-KO		
ENSORLGG00000008693	Striated muscle preferentially expressed protein kinase	spegb	0.10864732	0	0.017363	0
ENSORLGG00000008141	Melatonin receptor 1A	mtnr1aa	0.52907804	0.0121906	0.020256	0.02304128
ENSORLGG00000018249	Wnt family member 6	wnt6b	0.41128228	0.0126353	0.040303	0.0307217
ENSORLGG00000023466	Interleukin 17C	il17c	1.21599652	0.0611304	0.015992	0.05027187
ENSORLGG00000000705	Osteoprotegerin a	opga	1.22938927	0.12797	0.002707	0.10409235
ENSORLGG00000021993	Pleckstrin homology domain-containing family B member 1	si:ch211-176g13.7	1.32980513	0.1790465	0.009807	0.13464119
ENSORLGG00000025607	Lysosomal-associated transmembrane protein 4B	laptm4b	1.30325298	0.1767782	0.004008	0.13564377
ENSORLGG00000000922	Tescalcin	tesca	7.98641644	1.1715442	0.004757	0.1466921
ENSORLGG00000003196	Squalene epoxidase	sqlea	2.7959889	0.4495089	0.010949	0.1607692
ENSORLGG00000026984	Heat shock protein family A (Hsp70) member 2	hspa2	1.84464069	0.3331011	0.033266	0.18057776
ENSORLGG00000007442	Homogentisate 1,2-dioxygenase	hgd	1.10326382	0.21772	0.011977	0.19734174
ENSORLGG00000020877	Putative nucleotidyltransferase FAM46A	tent5bb	1.70985385	0.3565647	0.03044	0.20853518
ENSORLGG00000016350	Retinoic acid induced 2	rai2	2.83473821	0.6181476	0.029415	0.21806161
ENSORLGG00000014220	Potassium inwardly rectifying channel subfamily J member 1	kcnj15	12.504287	2.7600289	0.006425	0.22072661
ENSORLGG00000015759	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 2	sppock2	10.3870537	2.3000241	0.006511	0.22143181
ENSORLGG00000007210	Ubiquitin-protein ligase E3A	ube3a	1.76530105	0.4081267	0.029168	0.23119381
ENSORLGG00000007210	Transmembrane serine protease 13b	tmprss13b	13.1703941	3.1577095	0.005656	0.23975816
ENSORLGG00000017727	NADPH oxidase activator 1	nox1	31.6770444	7.6438289	0.004372	0.24130499
ENSORLGG00000010369	Vasorin	vasna	2.08176309	0.5262608	0.041744	0.2527957
ENSORLGG00000016652	Chemokine (C motif) receptor 1a, duplicate 1	xcr1a.1	4.05315773	1.0368187	0.04703	0.25580518
ENSORLGG00000011017	EF-hand calcium binding domain 1	efcab1	2.12098471	0.5659634	0.026834	0.26683991
ENSORLGG00000011713	Metallophosphoesterase domain-containing protein 1	mpped1	3.9864755	1.0681419	0.008908	0.26794142
ENSORLGG00000020852	ETS translocation variant 5	etv5a	6.82902261	1.8390215	0.004545	0.26929498
ENSORLGG00000002190	3 beta-hydroxysteroid dehydrogenase type 7-like	hsd3b7 (1 of many)	27.8564303	7.5955198	0.005036	0.27266666
ENSORLGG00000005554	Angiotensinogen	agt	3.37841726	0.9213204	0.031722	0.27270769
ENSORLGG00000014917	Protein FAM110C-like	si:ch211-107n13.1	4.48900818	1.2498693	0.034293	0.27842883
ENSORLGG00000012993	4-hydroxyphenylpyruvate dioxygenase-like	hpdh	6.43615544	1.8856336	0.036208	0.29297515
ENSORLGG00000009351	Mevalonate diphosphate decarboxylase	mvda	8.40529819	2.5234144	0.010287	0.30021712
ENSORLGG00000013807	Adhesion G protein-coupled receptor D1	adgrd1	3.32942799	1.0017981	0.018816	0.30089195
ENSORLGG00000017883	Clusterin-like protein 1	clul1	6.12055588	1.8542747	0.027416	0.30295855
ENSORLGG00000009486	Nuclear receptor ROR-alpha	rorc	2.03897188	0.6209598	0.044622	0.30454555
ENSORLGG00000023633	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1-like	b3gat1 (1 of many)	64.1275283	19.888825	0.005185	0.31014488
ENSORLGG00000010025	PR domain containing 1b, with ZNF domain	prdm1b	13.4870252	4.2060769	0.008451	0.31186098
ENSORLGG00000010075	Glutamate receptor-interacting protein 2	grip2a	5.2020519	1.6326101	0.011275	0.31383964
ENSORLGG00000014448	Ribonuclease ZC3H12A	z3h12a	9.96743482	3.131397	0.007713	0.31416278
ENSORLGG00000003479	Retinol dehydrogenase 7-like	dhrr9 (1 of many)	15.0659306	4.7656215	0.01387	0.31631776
ENSORLGG00000013226	Acetyl-CoA acetyltransferase 2	acat2	23.1530397	7.3427084	0.00851	0.31713798
ENSORLGG00000030080	Growth arrest and DNA damage-inducible protein GADD45 gamma	gadd45ga	7.46245909	2.4037782	0.012407	0.3221161
ENSORLGG00000009869	Retinol dehydrogenase 12	rdh12	9.46275831	3.129312	0.015325	0.33069766

*1 Fragment per kilobase of exon length per million reads
*2 Fold decrease in IL-17RA1-KO intestine compared to WT

Table S5. List of the genes down-regulated by a third-fold in the posterior intestine of IL-17RA1-KO medaka.

Gene_ID	Gene name	Gene Symbol	FPKM*1		p_value	Fold decreases*2
			WT	IL-17RA1-KO		
ENSORLGG0000007148	Interferon-induced very large GTPase 1	si:dkey-202l22.6	0.39166247	0.0161159	0.012546	0.04114739
ENSORLGG00000028123	Interleukin-17A/F-1	il-17a/f-1	7.41683241	0.6668821	0.014332	0.08991468
ENSORLGG00000003196	Squalene epoxidase	sqlea	0.97697843	0.0878447	0.038683	0.08991468
ENSORLGG00000009138	Delphinin	grid2ipa	0.28597647	0.0299991	0.035329	0.10490046
ENSORLGG00000012993	4-hydroxyphenylpyruvate dioxygenase-like	hpdh	8.36357271	1.0330214	0.008361	0.12351437
ENSORLGG00000026984	Heat shock protein family A (Hsp70) member 2	hspa2	3.27972465	0.6463311	0.026345	0.19706871
ENSORLGG00000017883	Clusterin-like protein 1	clul1	7.66644883	1.7472311	0.018615	0.22790618
ENSORLGG00000017149	Insulin-like growth factor-binding protein 3	igfbp3 (1 of many)	1.46759014	0.3457631	0.030308	0.23559921
ENSORLGG00000018249	Wnt family member 6	wnt6b	2.49537908	0.6158273	0.036883	0.24678709
ENSORLGG00000010353	Aldose reductase	akr1b1.1 (1 of many)	19.0860964	4.8474179	0.01489	0.25397639
ENSORLGG00000013056	Pappalysin 2	pappa2	0.99059785	0.2528197	0.042431	0.25521935
ENSORLGG00000000922	Tescalcin	tesca	5.18189358	1.3278956	0.046327	0.25625683
ENSORLGG00000002209	E3 ubiquitin-protein ligase TRIM39	btr01	2.34626488	0.6554942	0.038833	0.27937774
ENSORLGG00000014291	Macrophage stimulating 1 receptor	mst1rb	0.78372055	0.2203999	0.04643	0.2812225
ENSORLGG00000026741	Uncharacterized protein	gjd3 (1 of many)	21.794914	6.4284916	0.024864	0.29495375
ENSORLGG00000009169	Solute carrier family 26 member 6	si:ch211-117c9.2	3.18438331	0.9731168	0.044361	0.30559036
ENSORLGG00000022468	Adrenomedullin	adm	9.7391911	2.9799001	0.020302	0.30596998
ENSORLGG00000009979	Ribosomal protein S6 kinase alpha-2-like	rps6ka2	1.65320252	0.5117582	0.04837	0.30955565
ENSORLGG00000003493	Solute carrier family 6 member 20	slc6a20	7.74294972	2.4188471	0.021208	0.3123935
ENSORLGG00000011469	Cartilage acidic protein 1	aspi1	6.6680641	2.1122629	0.015024	0.31677304
ENSORLGG00000010295	Circadian-associated transcriptional repressor	ciart	8.17619954	2.6073687	0.01856	0.31889739
ENSORLGG00000004437	STEAP3 metalloredutase	steap3	36.8252461	12.029858	0.013637	0.32667422

*1 Fragment per kilobase of exon length per million reads

*2 Fold decrease in IL-17RA1-KO intestine compared to WT

Table S6

Table S6. List of the genes up-regulated over 3-fold in the anterior intestine of IL-17RA1-KO medaka.

Gene_ID	Gene name	Gene Symbol	FPKM ^{*1}		p_value	Fold increases ^{*2}
			WT	IL-17RA1-KO		
ENSORLG00000012486	Kv channel-interacting protein 2	kchp2	0	0.9889816	0.019288	N/A
ENSORLG00000005999	Glutamate receptor ionotropic, NMDA 2D	grin2da	0	0.146159	0.022245	N/A
ENSORLG00000004952	Uncharacterized LOC101173774	si:ch73-244f7.3	0	0.4401883	0.032809	N/A
ENSORLG00000001465	Transmembrane protein 132C	si:dkey-215k6.1	0	0.1116154	0.042488	N/A
ENSORLG000000025271	Hemoglobin subunit beta-like	gb	0	1.3822466	0.042488	N/A
ENSORLG000000029206	Hyaluronan and proteoglycan link protein 1	hapln1a	0	0.1673572	0.042488	N/A
ENSORLG000000019408	Troponin C, slow skeletal and cardiac muscles	tnnc1b	0.02629792	0.9888903	0.023186	37.603361
ENSORLG000000015767	Myosin binding protein C, slow type	mybpc1	0.02355701	0.6339713	0.011789	26.9122093
ENSORLG000000013436	Col10a1	col10a1a	0.06381822	1.2045953	0.004315	18.8754126
ENSORLG000000004262	Olfactory receptor 52A5	or129-1	0.23517266	2.9824403	0.017554	12.6819178
ENSORLG000000004009	Coagulation factor III, tissue factor	f3	0.05114826	0.5326915	0.046677	10.4146564
ENSORLG000000013108	Papilin	paplnb	0.05338487	0.5609053	0.046677	10.5068215
ENSORLG000000021813	Anoctamin 9b	ano9 (1 of many)	0.10158819	1.0336626	0.03503	10.1750271
ENSORLG000000015485	Gap junction alpha-1 protein	cx43	0.24825775	2.0135017	0.03924	8.1105284
ENSORLG000000024663	Glutamate ionotropic receptor delta type subunit 2	grid2	0.05255807	0.4262737	0.03924	8.1105284
ENSORLG000000000201	C-X-C motif chemokine ligand 14	cxcl14	0.13137158	1.0239803	0.044232	7.79453421
ENSORLG000000024787	Cadherin-like protein 26	cdh26.1 (1 of many)	0.0581511	0.4682512	0.02571	8.0523193
ENSORLG000000009208	Glutamate decarboxylase 1	gad1	0.08834502	0.6513862	0.029295	7.37320804
ENSORLG000000002829	Supervillin	svlc	0.11902354	0.8704214	0.006497	7.31301858
ENSORLG000000012050	Solute carrier family 1 member 1	slc1a1	0.62578324	4.3623557	0.009071	6.97103305
ENSORLG000000026564	Hepatic leukemia factor	dbpb	0.43014092	2.9133716	0.003307	6.7730632
ENSORLG000000002168	Myosin light chain, phosphorylatable, fast skeletal muscle	mylpfa	0.21237206	1.2439915	0.02443	5.85760416
ENSORLG000000014422	Collagen type XVIII alpha 1 chain a	col18a1a	0.66609695	3.477497	0.005683	5.22070698
ENSORLG000000007685	Receptor tyrosine-protein kinase erbB-3	erb3b3	0.10448815	0.5347572	0.04247	5.11787381
ENSORLG000000006791	Pappalysin 1	pappaa	0.15320804	0.7669625	0.013681	5.00602019
ENSORLG000000012951	Protein tyrosine phosphatase domain containing 1	ptpdc1a	0.45529493	2.2199412	0.007541	4.87583112
ENSORLG000000001958	A disintegrin and metalloproteinase with thrombospondin motifs 12	adamts12	0.18261112	0.8830074	0.038243	4.83545271
ENSORLG000000004672	Thrombospondin type 1 domain containing 1	thsd1	0.26499676	1.2314562	0.018157	4.64706138
ENSORLG000000027772	SRY-box transcription factor 7	sox7	0.27567308	1.2631126	0.030107	4.58192214
ENSORLG000000001260	SRY-box containing gene 6a	sox6a	0.17204999	0.785689	0.026297	4.56663207
ENSORLG0000000029754	Endothelial cell adhesion molecule	esama	0.88530632	3.8328421	0.023182	4.32939651
ENSORLG000000000592	Kinase insert domain receptor	kdr	0.63411449	2.6517523	0.012806	4.18181948
ENSORLG000000011365	Adrenoreceptor beta 3a	adrb3a	0.99556425	4.159618	0.038145	4.17815122
ENSORLG000000010575	Leucine-rich repeat-containing protein 17	lrc17	1.09067787	4.5247207	0.01014	4.14853994
ENSORLG000000000985	Solute carrier organic anion transporter family member 2A1	slco2a1	0.27351561	1.1154803	0.038112	4.0783057
ENSORLG000000009315	Collagen, type IV, alpha 6	col4a6	0.75505908	3.0280178	0.011845	4.01030583
ENSORLG0000000006659	BCL6B transcription repressor	bcl6b	1.032437	4.0678617	0.01341	3.94005804
ENSORLG000000004792	Adhesion G protein-coupled receptor L3	adgrl3.1	0.34588935	1.3612302	0.013194	3.93544979
ENSORLG000000012201	Abnormal spindle microtubule assembly	aspm	0.9823633	3.7395604	0.004891	3.80669794
ENSORLG000000005094	MKL/myocardin-like protein 2	mrtfb	0.2219592	0.8387116	0.038645	3.77867459
ENSORLG0000000006686	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	cyp24a1	0.92827649	3.4526073	0.034153	3.71937383
ENSORLG000000004345	Patched 1	ptch1	0.36143953	1.3404396	0.020884	3.70861359
ENSORLG0000000028295	USH1 protein network component harmonin binding protein 1	ushbp1	0.82409441	3.0430644	0.013577	3.69261622
ENSORLG0000000005980	Neurogenic locus notch homolog protein 2	notch3	0.53482638	1.9756763	0.013426	3.6940517
ENSORLG0000000020628	Ectonucleotide pyrophosphatase/phosphodiesterase 6	enpp6	1.42252494	5.2755386	0.030875	3.70857371
ENSORLG000000017972	Fibroblast growth factor receptor 3	fgfr3	1.02999031	3.7793434	0.007583	3.66929996
ENSORLG000000019688	Stabilin 1	stab1	0.65858317	2.4045898	0.013358	3.6511559
ENSORLG0000000029633	Transcription factor SOX-4	sox4a	1.77602044	6.3766802	0.037961	3.59043174
ENSORLG000000017898	Voltage-dependent L-type calcium channel subunit beta-3	cacnb2b	0.48174987	1.7275841	0.04033	3.58606027
ENSORLG000000014800	Growth hormone receptor	ghr	1.80826977	6.4716266	0.008613	3.57890547
ENSORLG000000003448	Protocadherin-16	dchs1a	0.2699378	0.9632106	0.019485	3.56826858
ENSORLG000000014817	Receptor-type tyrosine-protein phosphatase S	ptpsra	0.57884969	2.0293033	0.015528	3.50575175
ENSORLG000000009171	DNA damage inducible transcript 4	ddit4	2.85733648	10.014593	0.011561	3.50487002
ENSORLG000000000356	Laminin subunit beta 1	lamb1a	0.51111855	1.7294184	0.027308	3.38359547
ENSORLG000000013150	Pleckstrin homology and RhoGEF domain containing G1	plekhg1	0.30899694	1.0445785	0.04009	3.38054633
ENSORLG000000016809	Lysyl oxidase homolog 2A	lox12a	0.64482463	2.1729736	0.028498	3.36986762
ENSORLG0000000025181	Tumor necrosis factor alpha-induced protein 2	exoc3l2a	0.78779878	2.6459866	0.012983	3.35870872
ENSORLG000000000843	Scavenger receptor class F member 2	scarf2	0.8934551	2.9863924	0.036108	3.34252098
ENSORLG000000020389	Teneurin-3	si:dkey-237h12.3	0.27793448	0.9270501	0.034366	3.33549887
ENSORLG000000007888	FYVE, RhoGEF and PH domain-containing protein 5	fgd5a	0.61589992	2.0528524	0.029021	3.33309404
ENSORLG000000006672	Rho GTPase activating protein 31	arhgap31	0.78826167	2.6121055	0.023931	3.31375429
ENSORLG000000001968	Collagen alpha-1(VIII) chain	col8a1 (1 of many)	1.01366542	3.336592	0.041584	3.29161073
ENSORLG000000003427	Dysferlin, limb girdle muscular dystrophy 2B (autosomal recessive)	dysf	1.03599713	3.409818	0.022446	3.29133926
ENSORLG000000011369	Secreted protein acidic and cysteine rich	sparc	18.659363	60.735316	0.00588	3.25495122
ENSORLG000000011277	ANTXR cell adhesion molecule 1	antr1a	0.94840143	3.0626523	0.030142	3.22927846
ENSORLG000000013548	Fli-1 proto-oncogene, ETS transcription factor	fli1a	0.56746722	1.8214278	0.026009	3.2097498
ENSORLG000000000636	Notch receptor 1	notch1b	0.53196943	1.6919165	0.020964	3.18047703
ENSORLG0000000024518	Ephrin A5	efna5	0.97601445	3.0898647	0.020038	3.16579805
ENSORLG0000000023423	NACHT and WD repeat domain containing 2	nwd2	0.37263421	1.1722707	0.02908	3.1459021
ENSORLG0000000004966	ADAM metalloproteinase with thrombospondin type 1 motif 5	adamts5	0.47992767	1.5039078	0.030278	3.13361342
ENSORLG000000002317	Potassium voltage-gated channel subfamily H member 6	kcnh6a	0.67998005	2.1251823	0.041359	3.12535982
ENSORLG0000000020663	FRAS1 related extracellular matrix 1	frem1a	0.48878925	1.525826	0.035581	3.12164392
ENSORLG0000000020551	FAT atypical cadherin 4	fat4	0.63047042	1.9655025	0.013035	3.11751744
ENSORLG000000012356	Platelet endothelial cell adhesion molecule	pecam1	1.58873635	4.931799	0.019974	3.10422744
ENSORLG0000000030619	Neuron derived neurotrophic factor	ndnf	0.4375226	1.349934	0.044989	3.08540398
ENSORLG0000000001940	Vascular endothelial growth factor receptor kdr-like	kdr1	1.44740164	4.4302285	0.01281	3.06081487
ENSORLG0000000023445	Dishevelled binding antagonist of beta catenin 2	dact2	1.62320259	4.9692009	0.023288	3.06135598
ENSORLG0000000024534	SH3 and multiple ankyrin repeat domains protein 3-like	shank3b	0.59891065	1.8350141	0.020886	3.06391966
ENSORLG000000017886	Collectin-12	colec12	2.48525047	7.509172	0.016693	3.02149505
ENSORLG000000008238	Guanidinoacetate N-methyltransferase	gamt	155.891072	468.9717	0.006186	3.00832944

^{*1} Fragment per kilobase of exon length per million reads

^{*2} Fold increase in IL-17RA1-KO intestine compared to WT

Table S7

Table S7. List of the genes up-regulated over 3-fold in the posterior intestine of IL-17RA1-KO medaka.

Gene_ID	Gene name	Gene Symbol	FPKM ^{*1}		p_value	Fold increases ^{*2}
			WT	IL-17RA1-KO		
ENSORLG00000015892	Alpha-1-antitrypsin homolog	serpina11	0	67.848505	0.032797	N/A
ENSORLG00000013444	ADAM metallopeptidase with thrombospondin type 1 motif 13	adams13	0	0.113279	0.033191	N/A
ENSORLG00000030151	Aconitate decarboxylase 1	acod1	0	0.1630289	0.040635	N/A
ENSORLG000000021992	MORN repeat containing 2	morn2	0	0.2780739	0.046975	N/A
ENSORLG00000011267	Complement component C3-1	c3-1	0.03841095	150.68094	0.026869	3922.86403
ENSORLG00000003245	Uncharacterized LOC101168896	si:ch211-165i18.2	0.00946154	17.464654	0.043325	1845.85839
ENSORLG000000010251	Hemopexin	hpx	0.05807995	103.35336	0.035007	1779.50136
ENSORLG00000012653	Apolipoprotein B-100-like	apobb.2	0.01363348	11.837609	0.046451	868.274771
ENSORLG000000005801	Complement factor B	bf/c2	0.02706798	22.659973	0.047184	837.150593
ENSORLG00000018755	GTP cyclohydrolase 1	gch2	0.02762792	1.2520146	0.025248	45.3169968
ENSORLG00000002868	Thyroid hormone responsive	thrsp	0.21013356	7.056943	0.013574	33.5831316
ENSORLG000000030238	GRAM domain containing 2B	gramd2b	0.11841622	3.0983805	0.012117	26.1651708
ENSORLG00000009323	Proteoglycan 4	prg4b	0.08159948	1.9149547	0.006639	23.4677305
ENSORLG00000006084	Vitellogenin 1	ol-vit1	0.04479507	1.0431601	0.005936	23.2873874
ENSORLG000000004075	Histidine ammonia-lyase	hal	0.06530427	1.374004	0.01298	21.0400342
ENSORLG00000011150	Citrate lyase beta like	clybl	0.02697217	0.5129285	0.049137	19.016954
ENSORLG00000016001	Si:key-85n7.8	si:key-85n7.8	0.95960992	12.269445	0.03231	12.785867
ENSORLG00000016020	Serpin family A member 10	si:ch1073-416d2.3 (1 of many)	0.18613123	2.3669386	0.028633	12.7165042
ENSORLG00000010477	Angiopietin like 3	angptl3	0.05011502	0.5812838	0.031793	11.5989932
ENSORLG00000002247	Serpin family D member 1	serpind1	0.34136321	3.7753082	0.013787	11.0595052
ENSORLG00000011239	Nucleotide diphosphate kinase, mitochondrial	nme4	0.36166203	3.9217582	0.01865	10.84371
ENSORLG00000008088	Vitronectin	vtna	0.15331046	1.6541833	0.037954	10.7897612
ENSORLG00000022248	Uncharacterized LOC101165397	si:ch211-256m1.8	0.21020027	2.0929794	0.008012	9.95707306
ENSORLG00000013040	PDZ domain containing ring finger 4	pdzrn4	0.05822352	0.5732488	0.047262	9.84565705
ENSORLG000000018731	Glucose-6-phosphatase	g6pca.1	0.29806693	2.5628066	0.045345	8.59809092
ENSORLG00000016737	Uridine phosphorylase 2	upp2	0.72120996	5.982169	0.009182	8.29462888
ENSORLG00000017079	ATP binding cassette subfamily B member 11	abcb11a	0.12791009	0.9660835	0.028841	7.55283281
ENSORLG000000024787	Cadherin-like protein 26	cdh26.1 (1 of many)	0.16436007	1.2098379	0.016037	7.36089955
ENSORLG00000017559	Iodothyronine deiodinase 3	dio3	0.97490251	6.6362295	0.032689	6.8070699
ENSORLG00000015968	Von Willebrand factor A domain containing 5B1	vwa5b1	0.11432569	0.7401281	0.029253	6.47385669
ENSORLG000000006450	Sex hormone binding globulin	shbg	2.62057063	16.227581	0.009985	6.19238466
ENSORLG000000026149	Pentraxin 3	ptx3b	0.26501589	1.4721103	0.025609	5.55480025
ENSORLG000000000795	SEC14-like protein 2	sec14l7	1.01148073	5.5722504	0.035706	5.50900305
ENSORLG000000028914	Retinol-binding protein 2	rbp2b	0.44970407	2.4652429	0.032809	5.48192258
ENSORLG000000025673	Protein FAM131A	fam131a	0.83801551	4.4997184	0.012609	5.3694929
ENSORLG00000011365	Adrenoceptor beta 3a	adrb3a	0.85679457	4.4096784	0.044702	5.14671607
ENSORLG00000008872	Aquaporin-7	aqp7	0.81803716	4.1724921	0.034336	5.10061436
ENSORLG00000016809	Lysyl oxidase homolog 2A	loxl2a	0.47834595	2.3718927	0.024202	4.95852994
ENSORLG000000025647	Alkaline phosphatase	alpi.1	0.56598352	2.7607947	0.024064	4.87787119
ENSORLG00000013399	Venom prothrombin activator oscutarin-C non-catalytic subunit	f5	0.76013797	3.6961171	0.013448	4.86242932
ENSORLG00000024658	Rho guanine nucleotide exchange factor 19	arhgef19	1.65740422	8.0577452	0.012502	4.86166563
ENSORLG000000025559	Retinoic acid induced 1	rai1	0.3364866	1.6337745	0.024487	4.85539252
ENSORLG00000009228	Dopamine receptor D3	drd3	0.32365542	1.5025498	0.038692	4.64243671
ENSORLG00000010575	Leucine-rich repeat-containing protein 17	lrrc17	1.51993526	7.0504233	0.015635	4.63863392
ENSORLG000000025575	Suppressor of cytokine signaling 8	socs8	0.39042471	1.7247573	0.032654	4.41764337
ENSORLG00000002277	Uncharacterized LOC101171752	kcnk4a	1.29954825	5.7394379	0.017366	4.41648698
ENSORLG000000020391	Radical S-adenosyl methionine domain containing 2	rsad2	4.60374842	19.534332	0.011856	4.24313663
ENSORLG00000007987	Cholesterol 25-hydroxylase-like protein 1, member 1	ch25hl.1	7.27446231	30.602637	0.017842	4.206859
ENSORLG00000017352	Quiescin sulfhydryl oxidase 1	qsx1	1.29885397	5.4569474	0.028566	4.20135563
ENSORLG00000013447	Serpin family F member 1	serpinf1	0.54135429	2.2719098	0.045561	4.19671524
ENSORLG00000003719	Monocarboxylate transporter 7	slc16a6a	0.41235736	1.7305464	0.045561	4.19671524
ENSORLG000000027036	Nicotinate-nucleotide pyrophosphorylase	npbt	0.54488891	2.2555858	0.039821	4.13953336
ENSORLG000000005461	Inhibin beta B chain	inhb	0.94216247	3.8597923	0.044071	4.09673744
ENSORLG00000017972	Fibroblast growth factor receptor 3	fgfr3	1.04929309	4.2712685	0.016968	4.07061525
ENSORLG000000009477	Alkaline phosphatase	alp3	1.30590646	5.2809521	0.021442	4.04389766
ENSORLG000000005696	F-box protein 32	fbxo32	2.34743287	9.4615589	0.017456	4.03059828
ENSORLG000000006686	1,25-dihydroxyvitamin D(3) 24-hydroxylase, mitochondrial	cyp24a1	2.23688055	8.9301005	0.025158	3.99221163
ENSORLG00000004646	Ribosomal modification protein rimK like family member B	rimkla	0.41902104	1.635446	0.030058	3.90301627
ENSORLG000000028594	Peptide Y	pyyb	2.87062797	11.15042	0.037076	3.88431401
ENSORLG000000023476	Stanniocalcin 2	stc2a	0.90937252	3.4731418	0.028258	3.81927293
ENSORLG00000012173	Pyruvate dehydrogenase (acetyl-transferring) kinase isozyme 2, mitochondrial	pdk2a	7.38838564	27.827484	0.014819	3.76638216
ENSORLG00000001050	Nitric oxide synthase 1	nos1	0.64744033	2.4204067	0.025035	3.73842429
ENSORLG00000018068	Egl-9 family hypoxia inducible factor 3	egln3	13.4838469	50.230016	0.019329	3.72519918
ENSORLG00000009416	Collagen type IV alpha 5 chain	col4a5	0.9845519	3.625126	0.033003	3.68200599
ENSORLG000000009315	Collagen, type IV, alpha 6	col4a6	0.65615257	2.4009517	0.044613	3.65913639
ENSORLG00000015839	Semaphorin-6D	sema6e	0.35869883	1.2999093	0.045782	3.62395754
ENSORLG00000011397	Myomesin 1	myom1b	0.71801979	2.5104109	0.046256	3.4962976
ENSORLG00000015744	Apolipoprotein A-I	apoa1b	1319.02083	4603.7425	0.013515	3.49027275
ENSORLG00000015770	Beta-ureidopropionase 1	ubp1	5.20877759	18.129505	0.022013	3.48056811
ENSORLG00000002940	UTP--glucose-1-phosphate uridylyltransferase	ugp2a	3.29746437	11.363963	0.024609	3.44627317
ENSORLG000000029803	Solute carrier family 13 member 5	slc13a5b	5.52097197	19.010076	0.017319	3.44324814
ENSORLG00000003339	Transcription regulator protein BACH1	bach1a	0.97311041	3.3239157	0.044855	3.41576417
ENSORLG000000005019	Large neutral amino acids transporter small subunit 4	slc43a2b	18.4459519	62.878629	0.015417	3.40880371
ENSORLG000000004048	Amine oxidase copper containing 1	aoc1	12.2209084	41.399017	0.016561	3.38755644
ENSORLG000000025379	TSC22 domain family protein 3	si:ch211-220e11.3	16.210214	53.934329	0.017383	3.32718181
ENSORLG000000006281	Phosphoenolpyruvate carboxykinase 2, mitochondrial	pcck2	28.6519228	93.288896	0.017698	3.2559384
ENSORLG00000014358	Mepirin A subunit beta	mep1b	27.3325107	88.876214	0.017158	3.25166667
ENSORLG00000007656	Beta,beta-carotene 9,,10,-oxygenase	bco2a	4.17076991	13.51913	0.033402	3.24139924
ENSORLG000000024341	Eukaryotic translation initiation factor 4E binding protein 3	eif4ebp3l	9.6189782	30.802684	0.021794	3.20228232
ENSORLG000000026564	Hepatic leukemia factor	dbpb	1.67357807	5.3587326	0.036852	3.20196153
ENSORLG000000027016	Arachidonate 5-lipoxygenase activating protein	alox5ap	2.85089591	9.0818784	0.036294	3.18562256
ENSORLG00000001512	Beta,beta-carotene 15,15,-dioxygenase	bco1l	5.93552544	18.873249	0.025429	3.17970991
ENSORLG000000007741	Glutamic-oxaloacetic transaminase 1	got1	5.5833535	17.472311	0.030007	3.14344305
ENSORLG000000024518	Ephrin A5	efna5	1.11995971	3.5087041	0.042918	3.13288422
ENSORLG00000001185	Solute carrier family 22 member 5	slc22a5	7.76808197	23.647786	0.025397	3.04422453

*1 Fragment per kilobase of exon length per million reads

*2 Fold increase in IL-17RA1-KO intestine compared to WT

Fig. S1.

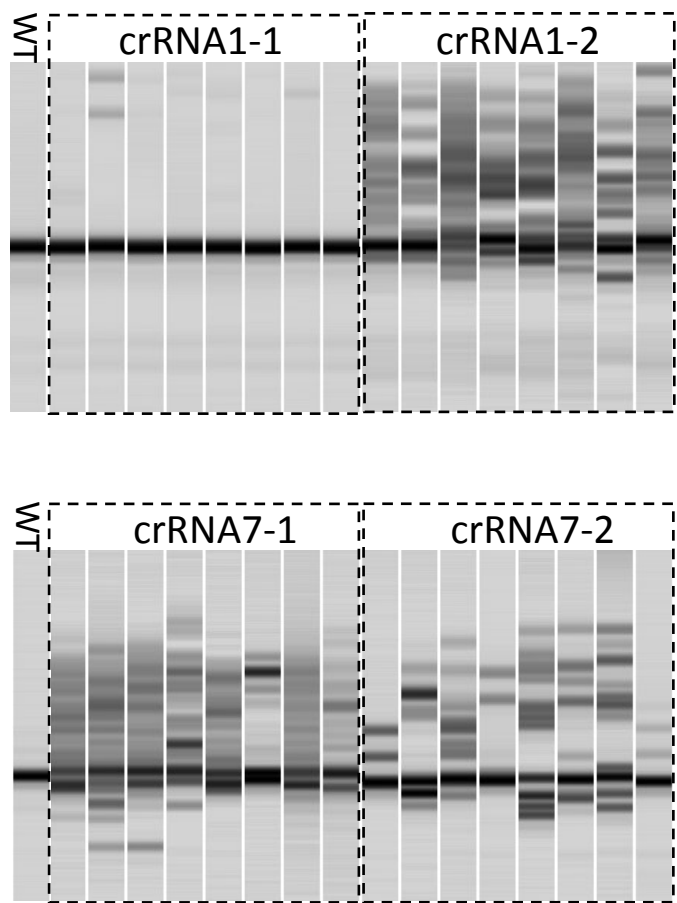


Fig. S1. Efficiency of mutation by each crRNA. The mutation efficiency was evaluated by HMA method. The results of HMA examined for the fertilized medaka eggs treated by crRNA1-1, crRNA1-2, crRNA7-1 and crRNA7-2 are shown. Of these, crRNA1-2, crRNA7-1 and crRNA7-2 showed high mutant efficiency.

Fig. S2. The mutation start and end point of mutated IL-17RA1. (A) Overall, we obtained six variants of the mutant. Mutant line B and K were inserted the nucleotide (KO line B: 1 bp inserted, KO line K: 12 bp inserted.). All mutations in KO line started the up-stream of start codon of WT's IL-17RA1 (B) and predicted coding sequence of mutated IL-17RA1 in each KO line are described (C). (D) Two forward primers and a reverse primer used for confirmation of genotype (F1-R1; 286 bp (amplification of the partial region of WT IL-17RA1), F2-R1; 181 bp (amplification of the partial region of mutated IL-17RA1 (line C))).

Fig. S3.

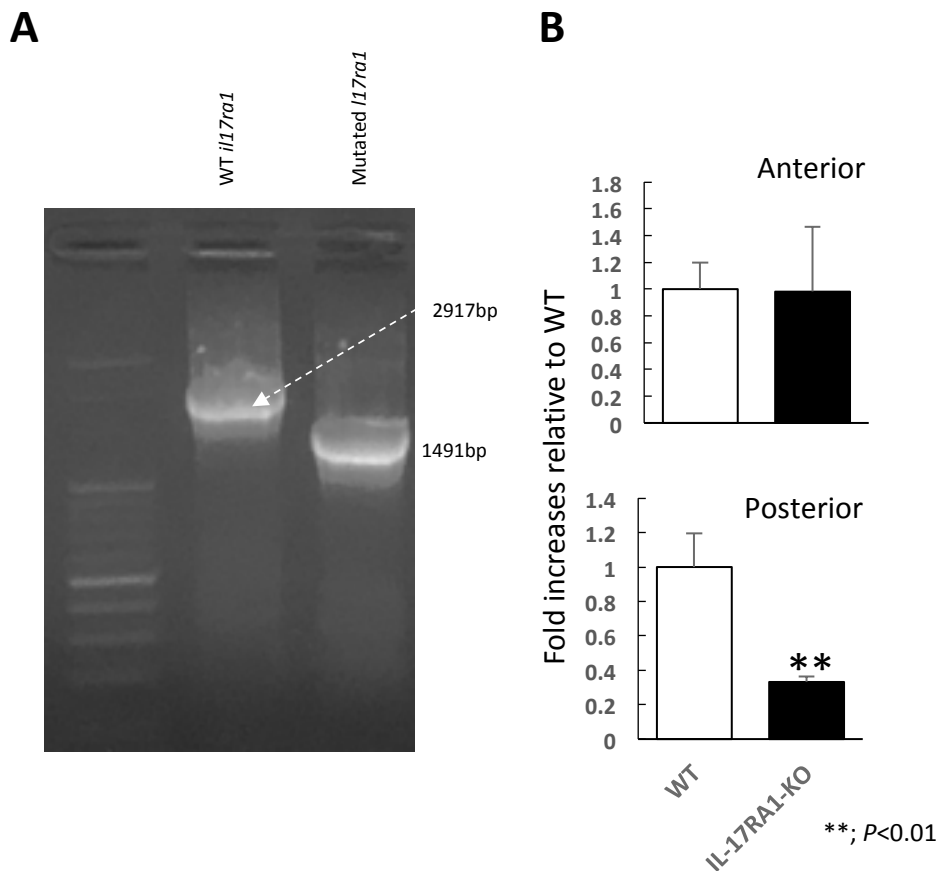


Fig. S3. The ORF comparison of WT and mutated *il17ra1* and its gene expression level in each section of the intestine. (A) The PCR product size of each ORF in WT's and mutated *il17ra1*. The mutated ORF sequence were confirmed by read sequencing and WT's *il17ra1* was not amplified in the cDNA sample of IL-17RA1-KO. (B) The comparison of the gene expression level of *il17ra1* in anterior and posterior intestine of WT and IL-17RA1-KO medaka. ** $P < 0.01$, * $P < 0.05$ (Student's *t*-test). Data are from one experiment with three individual fish ($n = 3$).

Fig. S4.

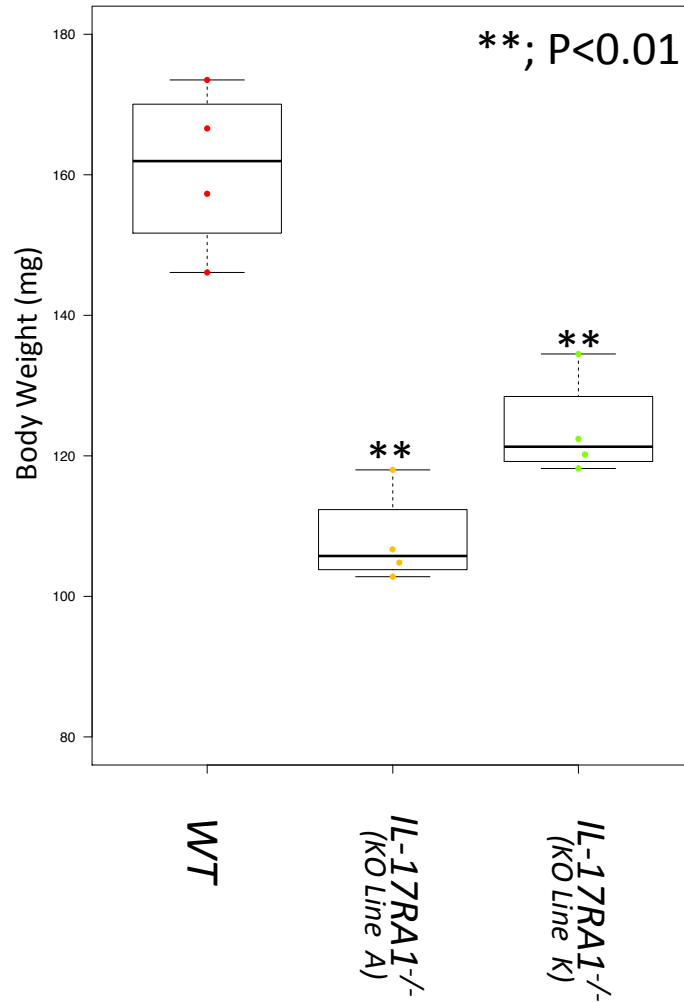


Fig. S4. The Weight losses seen in other lines (KO lines A and K) homologous mutant of IL-17RA1-KO medaka. In 4 months after hatching, body weight were measured (n=4).

Fig. S5.

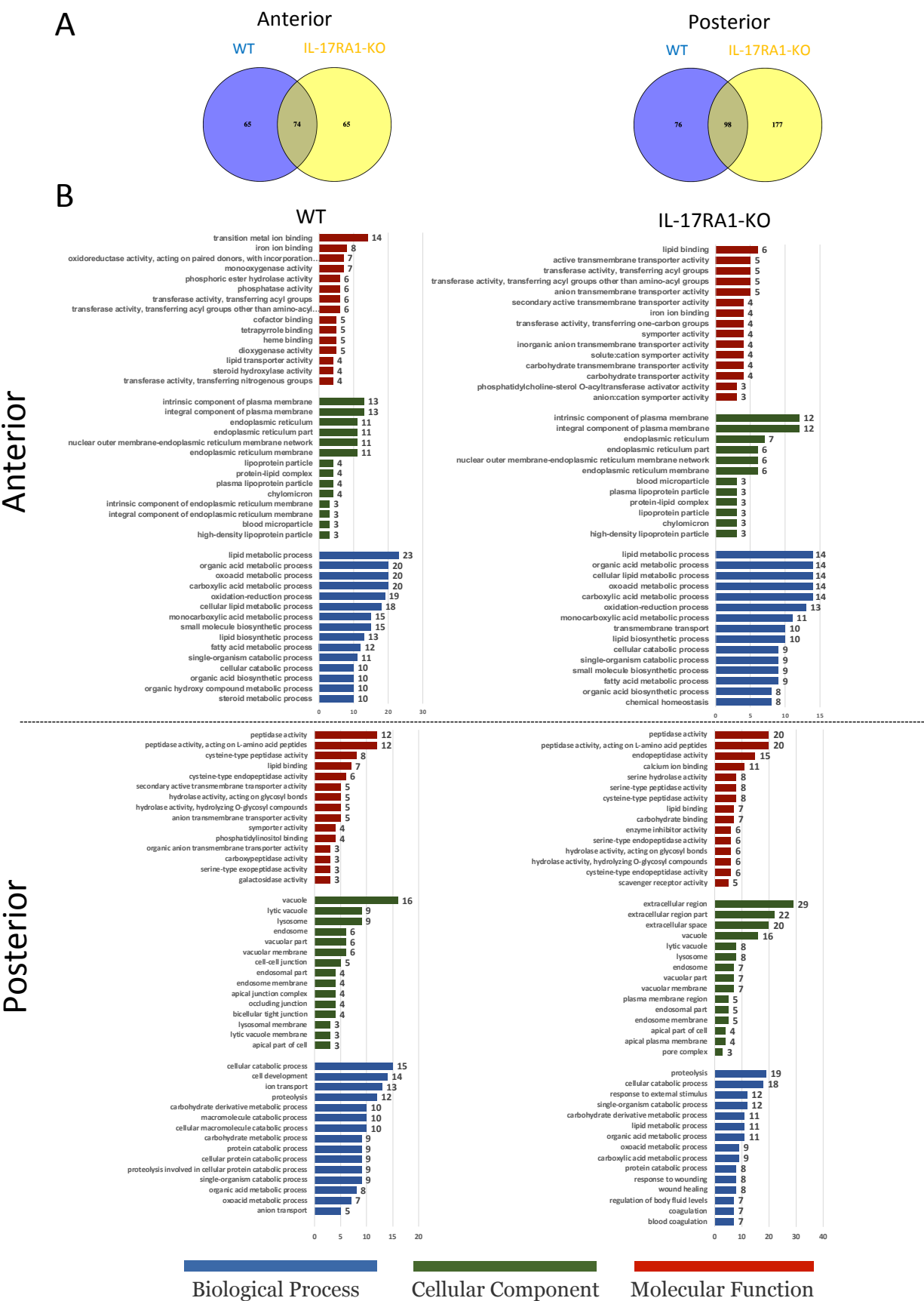


Fig. S5. Enrichment of Gene Ontology (GO) classification of the differentially expressed gene (DEG) when comparing between anterior and posterior intestine. Significant different genes ($P<0.05$) were extracted as DGEs. (A) In WT's comparison of anterior and posterior intestine, and IL-17RA1-KO's comparison of anterior and posterior intestine, Anterior 74 genes and posterior 98 genes were consensus DEGs in both of WT and KO. (B) Anterior intestine develops the expression of lipid metabolism-related genes.

Fig. S6.

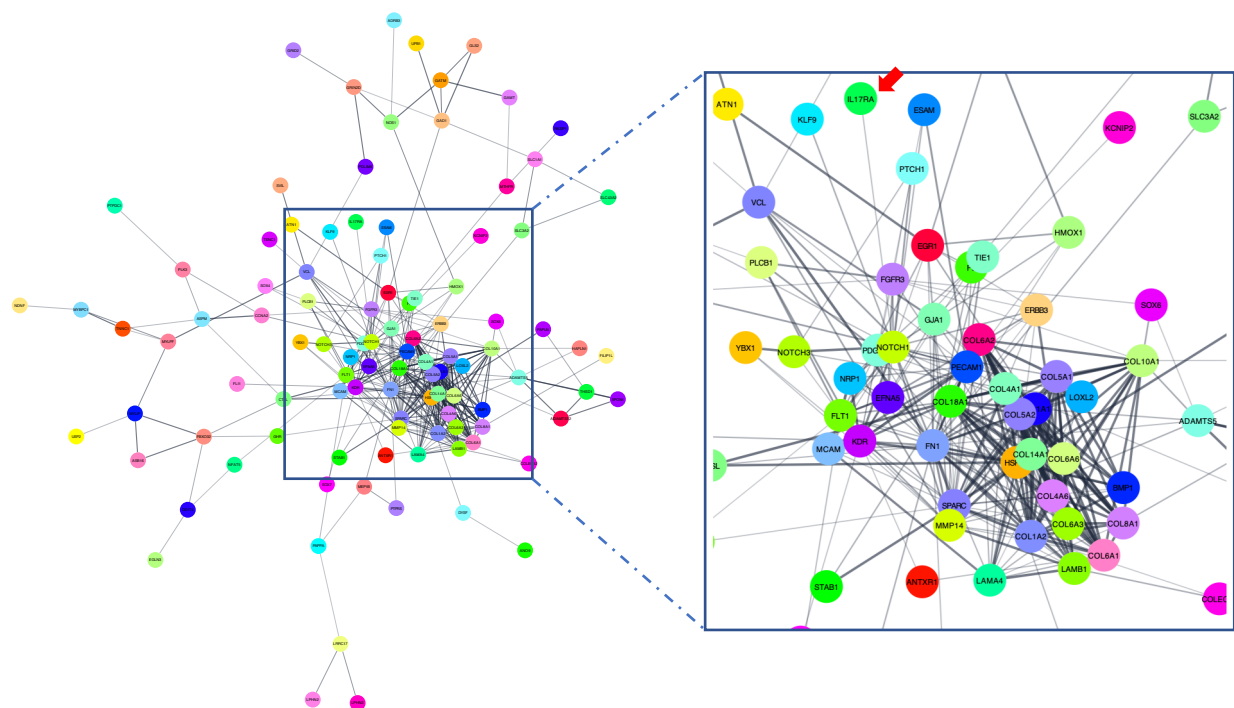
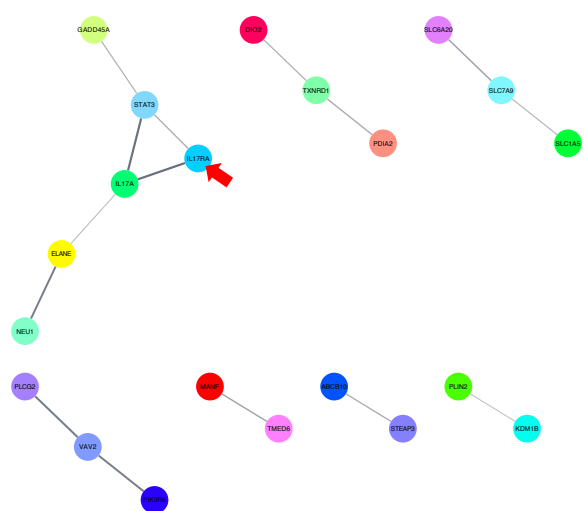


Fig. S6. The prediction of the interaction among DEGs up-regulated in IL-17RA1-KO and IL-17RA. Interaction network of these genes as defined by Cytoscape's software STRING. Of 167 DEGs, 102 genes formed the most complex cluster and contained IL-17RA. Red arrow shows IL-17RA.

Fig. S7.

A



B

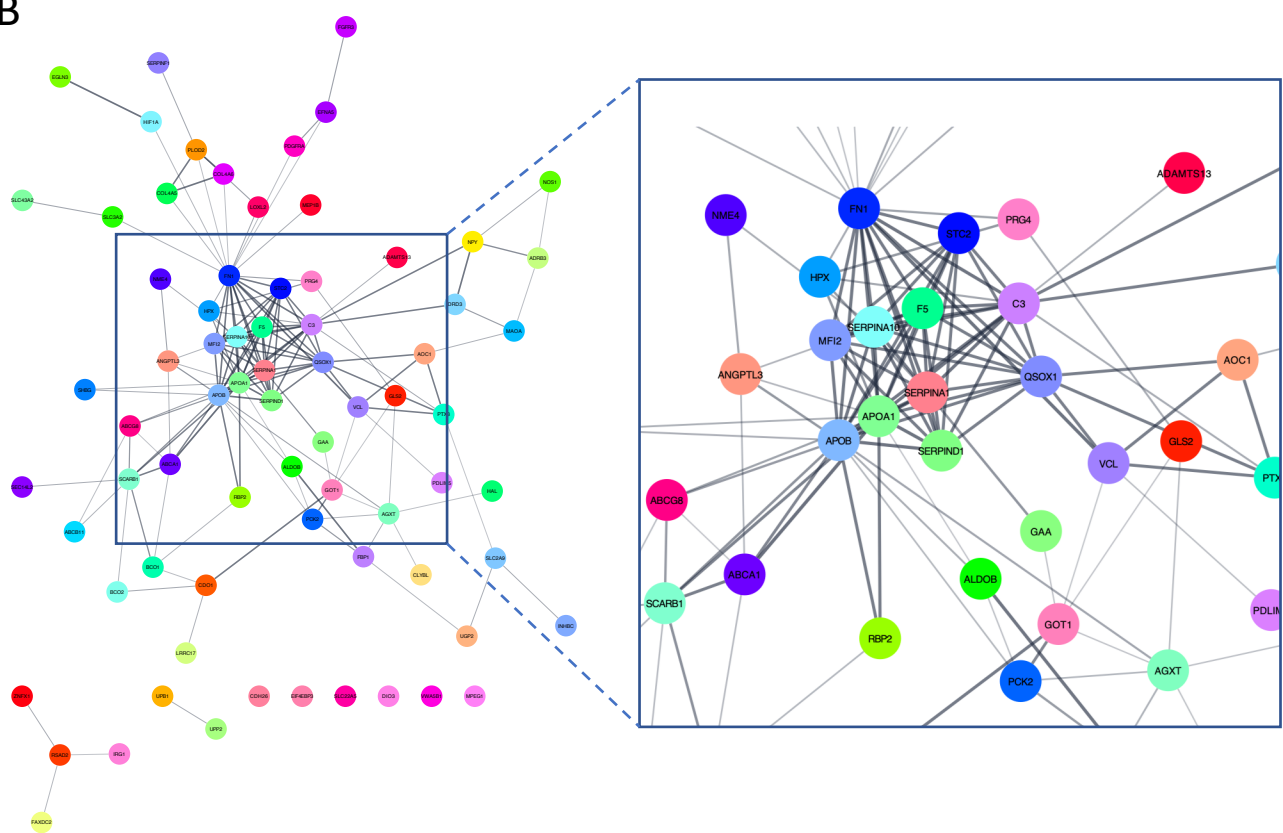


Fig. S7. The prediction of the interaction between posterior DEGs in IL-17RA1-KO and IL-17RA. Interaction network of these genes as defined by software STRING in Cytoscape. (A) down-regulated DEGs in posterior intestine of IL-17RA1-KO. IL-17RA containing cluster contains IL-17 signaling related genes such as IL-17A/F1 ligands and transcriptional factor STAT3. Red arrow shows IL-17RA. (B) Up-regulated DEGs in the posterior intestine of IL-17RA1-KO. Up-regulated DEGs in the posterior intestine of IL-17RA1-KO did not form same cluster with IL-17RA.

Fig. S8.

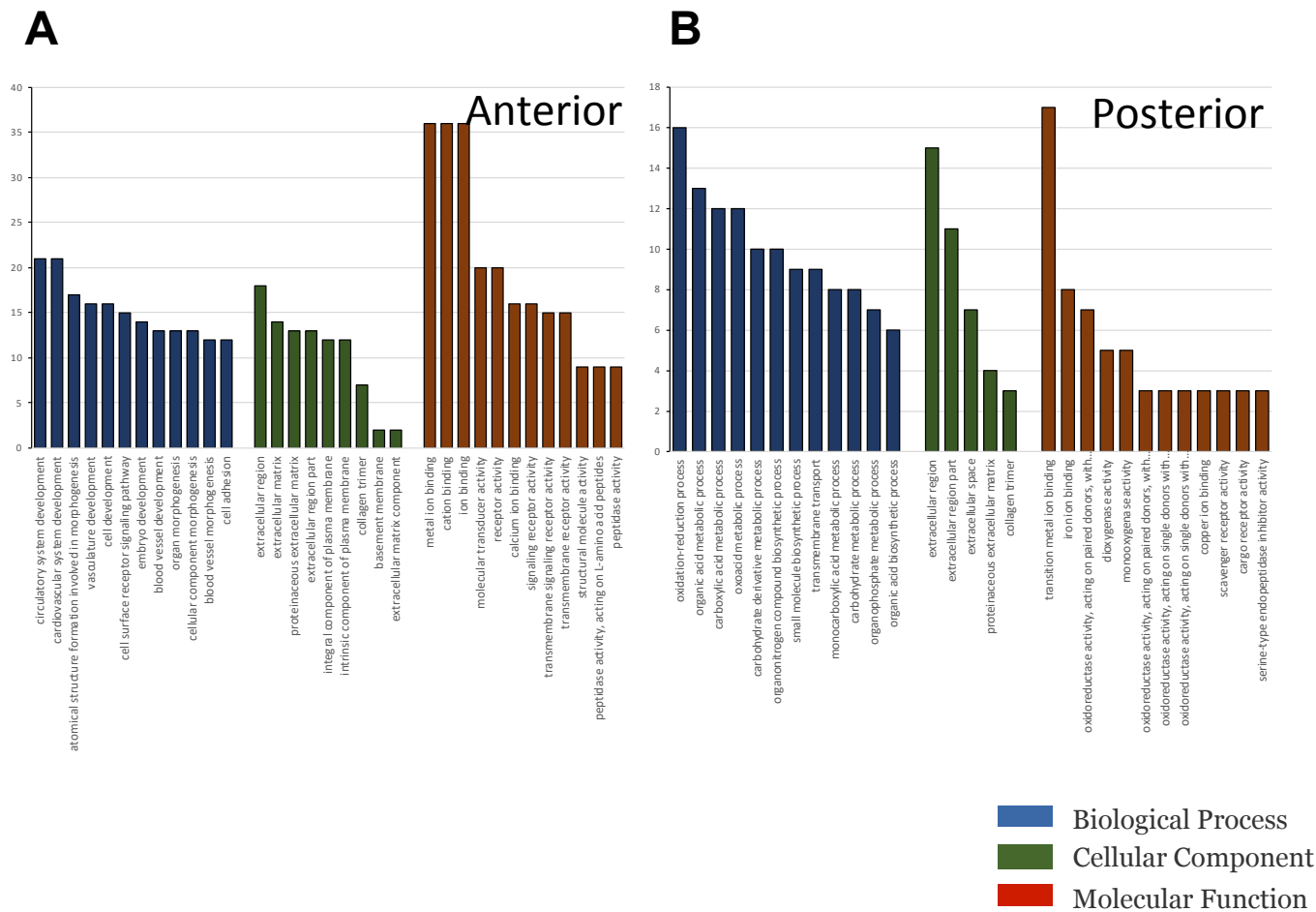


Fig. S8. Top 12 classification of Gene Ontology (GO) enrichment of up-regulated DEGs in anterior and posterior intestine of IL-17RA1-KO. (A) GO term in anterior intestine and (B) posterior intestine.