

The gene expression gradient through the intestine tract of European sea bass (*Dicentrarchus labrax*)

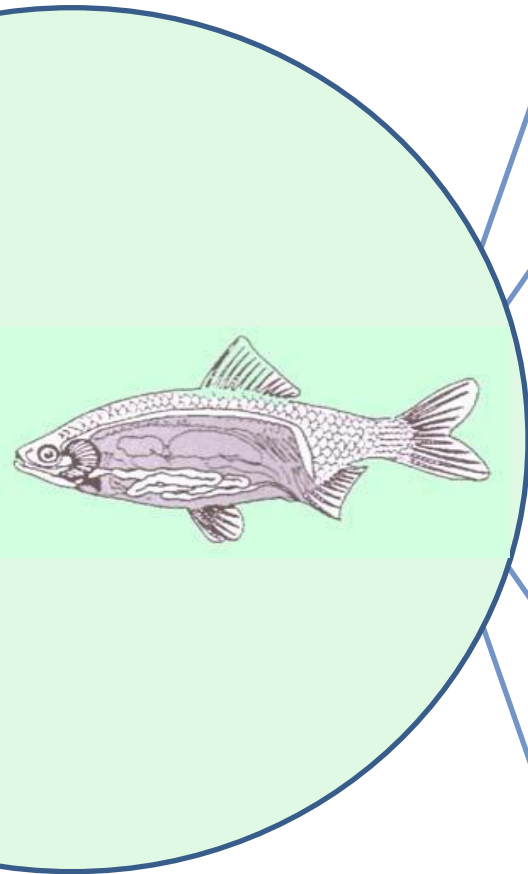


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www.nutrigroup-iats.org

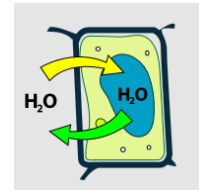
Fish intestine functions



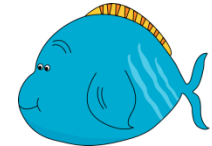
Digestion & feed absorption



Water & electrolyte balance



Endocrine regulation of digestion & metabolism



Physical & chemical barrier



Immunity



Genomic tools in gilthead sea bream: targeted and non-targeted approaches

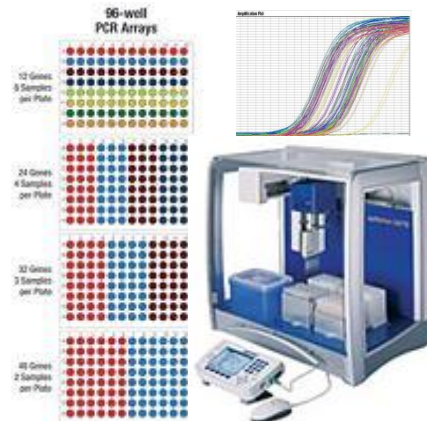
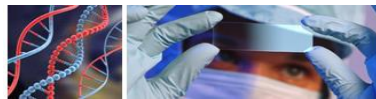


Gilthead sea bream

 Nutrigenomics and Fish Growth Endocrinology Group
Institute of aquaculture Torre de la Sal, CSIC



Array type	Target tissue	Challenge	Reference
cDNA microarray	Liver	Crowding stress	Calduch-Giner et al., BMC Genomics 2010
Oligo-microarray	SKM, RM, Heart	Nutritional	Calduch-Giner et al., Mar. Biotechnol. 2014
cDNA microarray	Intestine/HK	Parasite infection	Davey et al., Mol. Immunol. 2011
Oligo-microarray	Intestine	Parasite x nutritional	Calduch-Giner et al., BMC Genomics 2012
PCR-Array (Gut Chip)	Intestine	Nutritional	Estensoro et al. (NEXT COMMUNICATION)



www.nutrigroup-iats.org/seabreamdb

Sparus aurata
transcriptomic database

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BLAST your query sequence in FASTA format:

```

CTCATGCTCTGGGTGATGCTCTGGGCTCTCTCAGCCGATCAGACAGCCAGCGTCTGTCTCCA
TCGCTGTACGACAGATTCAACACTCCACTCTGCTGAGACTCTTCTCTGACTTTGAGACTCTCT
GCAGACGGGAGCCGCGCCACTCCACAAATCTCTGGAGATTCTGTACTGTGATTAATCATC
AGCCCATCGACAGCAGCAGCAGCCAGCTCAGTGTGAGCTGCTGTATCTTATCGAATGG
TCGACTGTGGAGATTCCCGACTTCTCTGTCTGCGGTTCTCTCCAGAGACAGATTACCCCA
ACTCTCTGACTGAGACGGCATCTCTCTGTGACGGCCATGAGACGGCAGATCTCTCTCT
GATAGTCCGCTCCAGCTGCTCTTATGGAACTACTACCAAGTCTGGCAGCAGAGTCTGTA
GACGACC
    
```

Select database and search: Database: Matrx:

Calduch-Giner et al., BMC Genomics 2013

European sea bass



- **Genome sequencing**

European seabass Sequencing Consortium
Max Planck Institute for Molecular Genetics



- **Brain and liver transcriptome is characterized**

Magnanou et al., Gene 2014

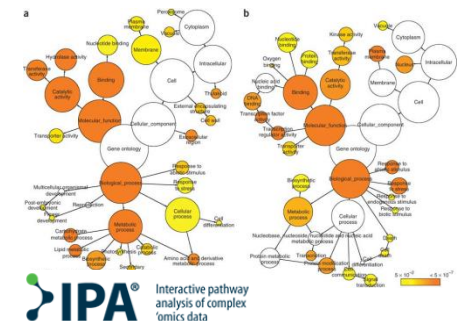
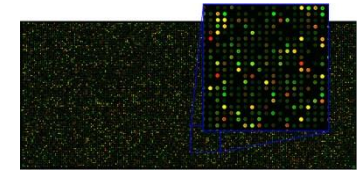
- **INTESTINE TRANSCRIPTOME MAPPING & REGULATION IS LACKING**

Objectives

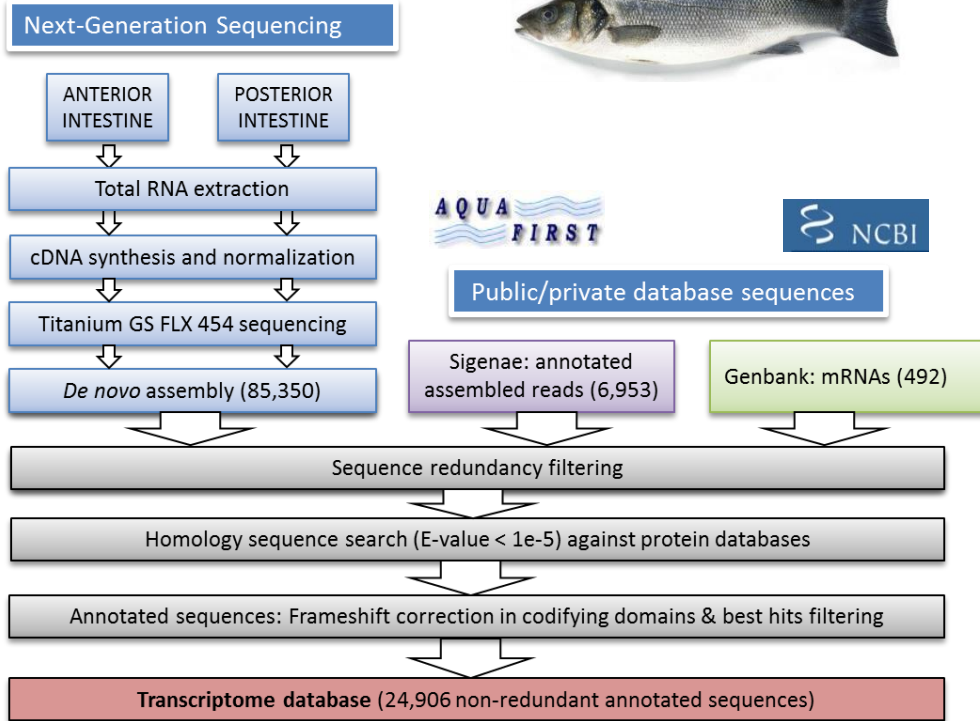
1. To construct a transcriptomic database enriched in intestinal-related genes
2. To generate new and powerful genomic resources for targeted and non-targeted gene expression profiling (microarray and RNA-seq approaches)
3. To build a functional map of the main genes and functions through the intestine tract of European sea bass



European sea bass



Transcriptomic European sea bass database



www.nutrigroup-iats.org/seabassdb

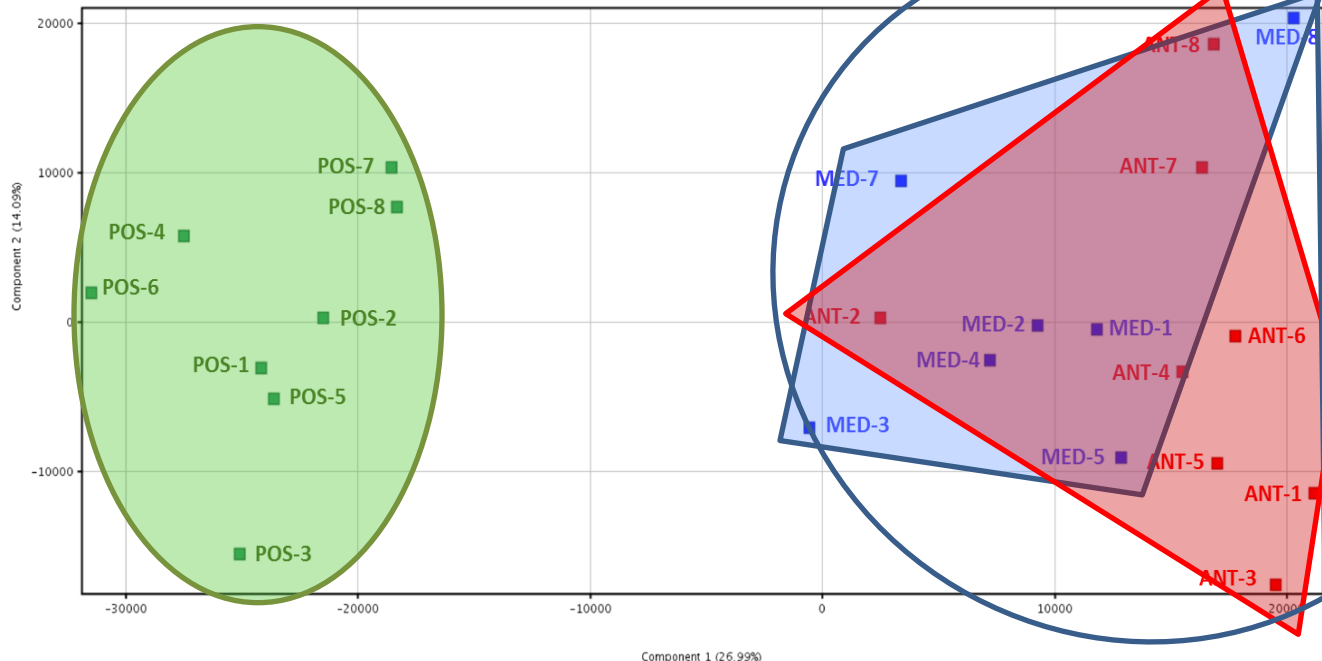
- 24,906 non-redundant annotated sequences
- 15,367 different gene descriptions

Gene expression profiling

Sea bass oligo-microarray (8 x 15K)

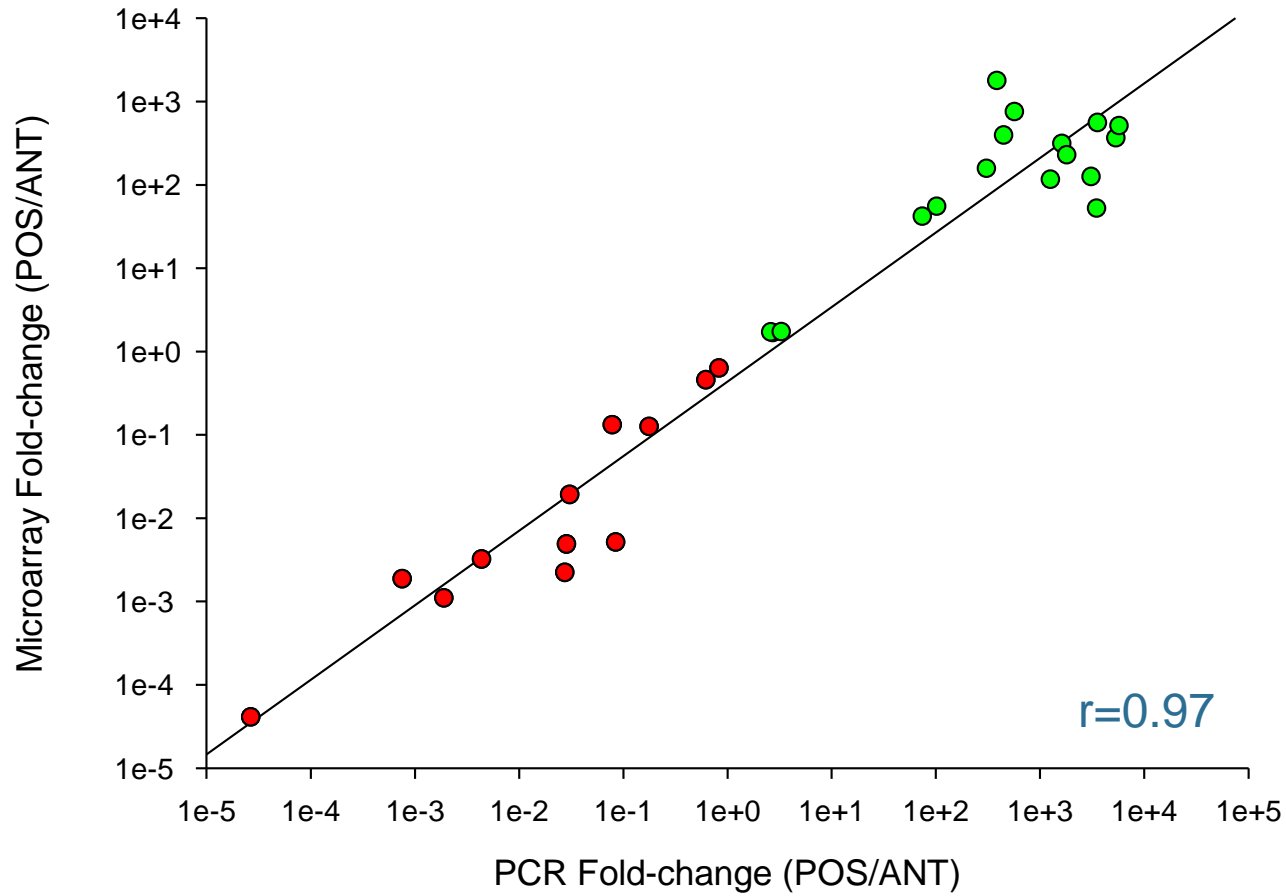


Principal Components Analysis



- Anterior and middle sections samples are grouped in a unique category (**MID-ANT**)

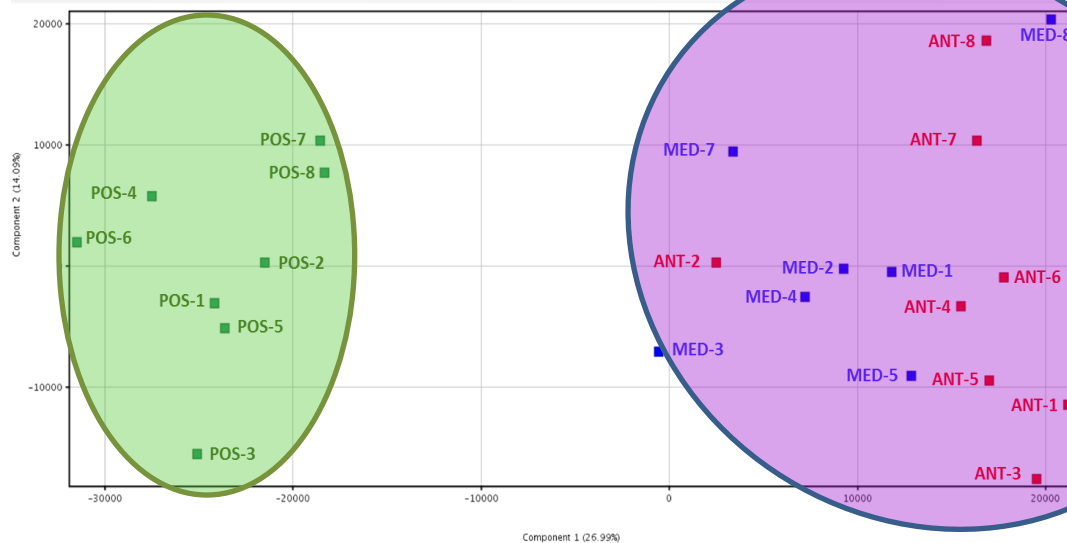
qPCR validation



Gene expression profiling Sea bass oligo-microarray (8 x 15K)



Principal Components Analysis



Differentially
expressed genes: 1906

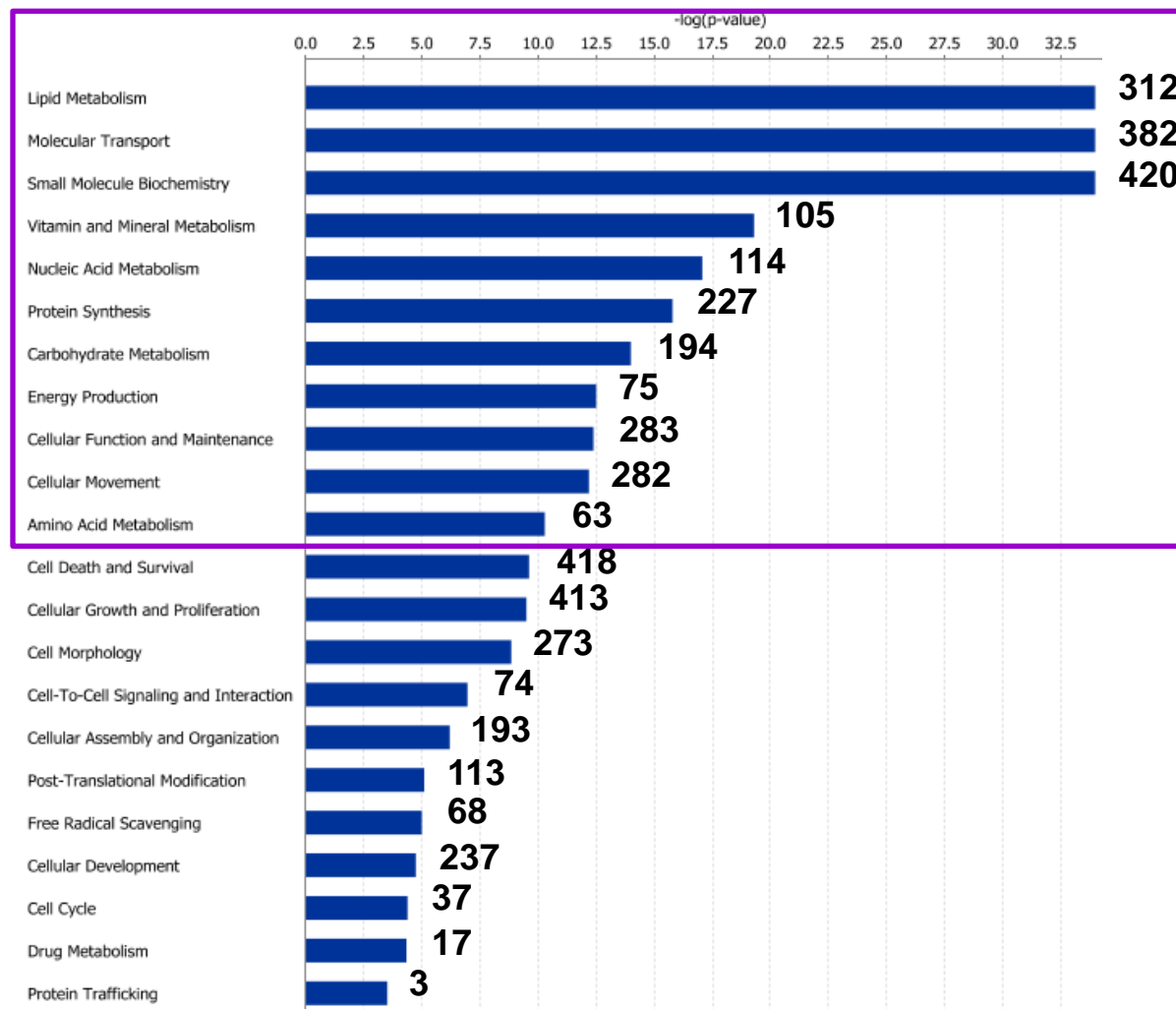
	MID-ANT	POS
MID-ANT	---	960
POS	946	---

MID-ANT vs **POS** comparison ($P < 0.05$, T-test, Benjamini-Hochberg multiple testing correction)

Functional analysis (MID-ANT)



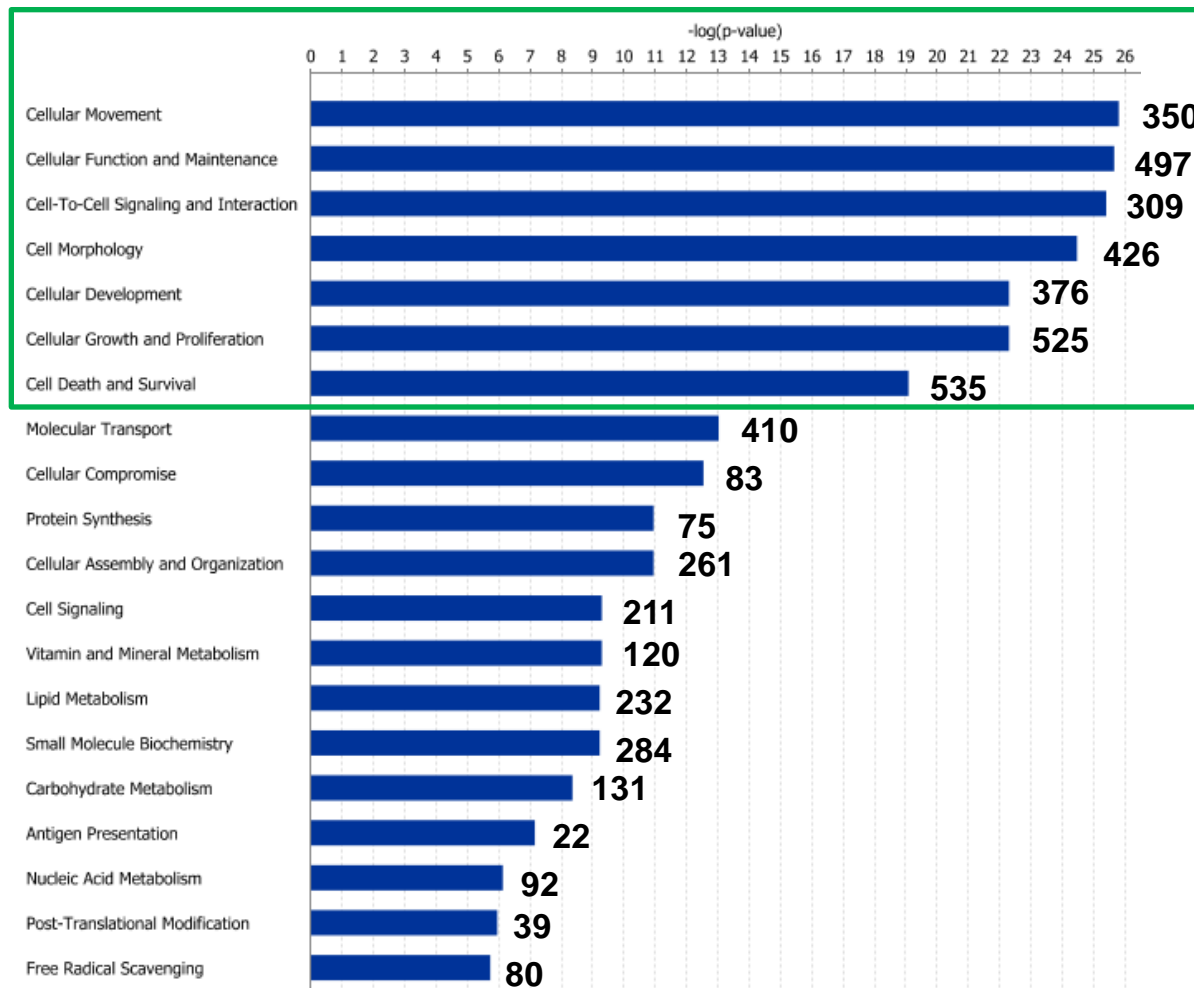
- MOLECULAR FUNCTIONS:
nutrient digestion
and absorption of
proteins, lipids,
carbohydrates,
vitamins, minerals
and nucleic acids



Functional analysis (POS)



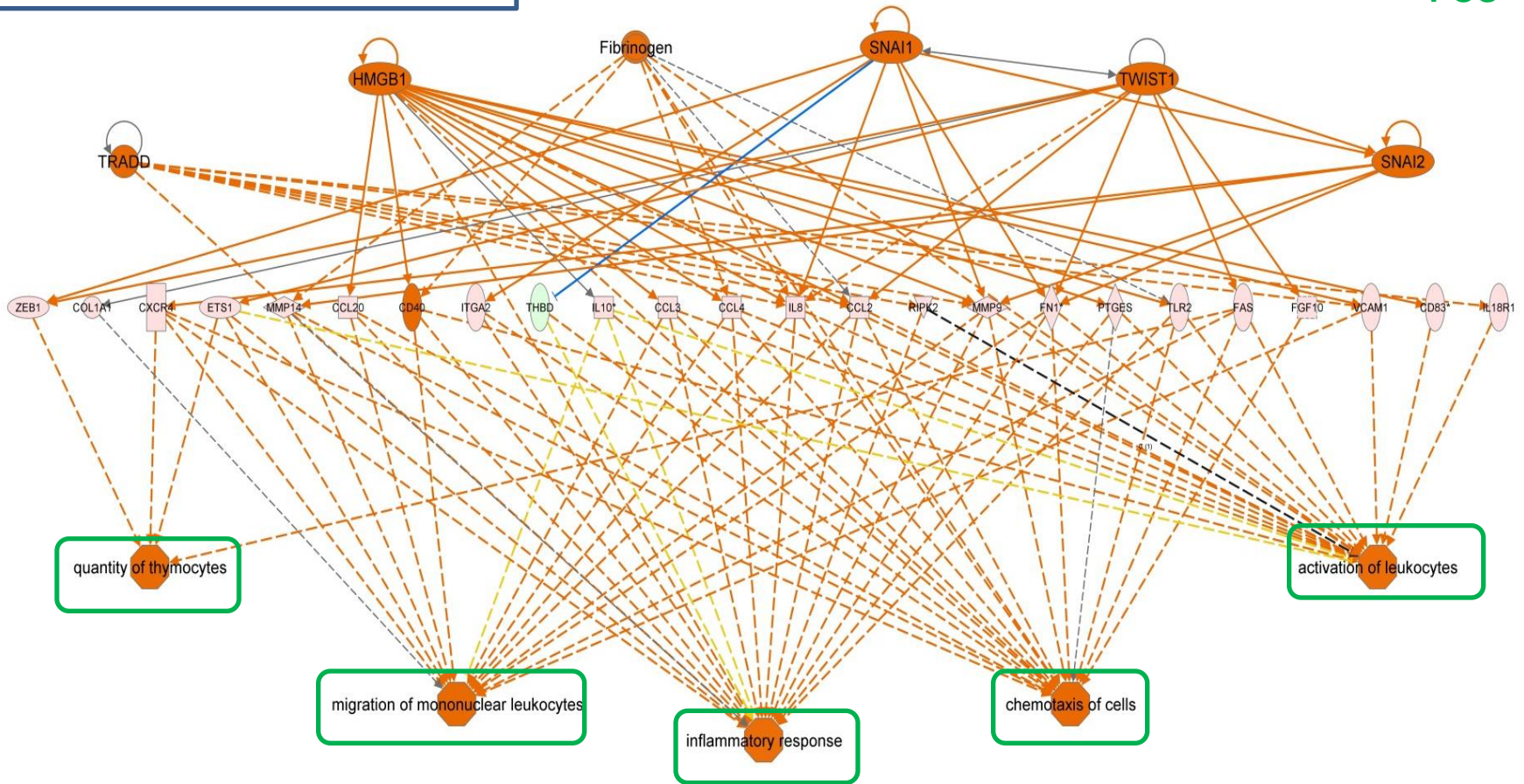
- MOLECULAR FUNCTIONS: movement, development, activation, chemotaxis and signaling of phagocytes, neutrophils and myeloid cells



Genes highly expressed in POS: regulator effect networks

Connect

- Upstream regulators
- Dataset molecules
- Downstream functions

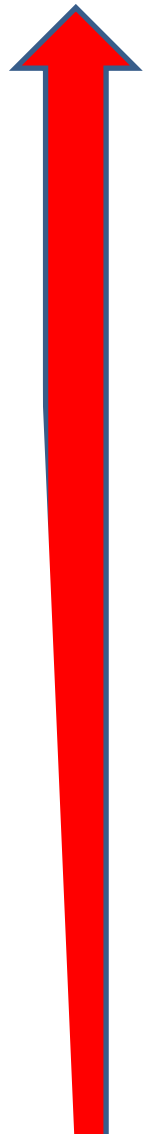


Top highly expressed genes (POS)



3825.29	TM236
1781.91	AMN
757.80	IGFN1
556.28	TMIGD1
513.32	CUBN
395.29	HAL
367.05	CTSL
314.06	SLC7A9
229.39	MYO5B
157.27	DEFB
125.59	SLC10A2
124.94	GIF
118.63	HOXC13A
116.11	EAAT3
113.58	HOXA13A
105.85	PTCHD3
95.66	FOXD2
55.27	SNX6
52.48	FABP6
52.26	SLC15A2
51.39	SLC30A10
50.83	HOXD4B
50.50	TPTE2
48.21	GRN
45.71	SNX10
42.50	MFSD4A
42.33	HYKK
42.14	TCN2
41.07	HOXA11A
38.13	R7VQC7

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- 1781.91 **AMN**
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- 42.14 **TCN2**
- 41.07 HOXA11A
- 38.13 **R7VQC7**

Vitamin B12 metabolism

Immune response

Bile acid metabolism



CONCLUDING REMARKS

1. Deep sequencing for *de novo* assembly of intestinal-related genes leads to construct an European sea bass transcriptome database with more than 15,000 unique sequences (www.nutrigroup.iats-org/seabassdb)
2. Gene expression and functional analysis allows to define different chemosensors and physiological functions along the intestine tract
3. Anterior and middle sections show almost identical gene expression profiles with an over-representation of nutrient digestion, absorption and transport processes
4. The posterior intestine emerges as a highly immuno-regulated tissue with also relevance on vitamin B12 and bile acid metabolism
5. These findings contribute to identify new nutritionally regulated biomarkers of intestine function and health in farmed fish



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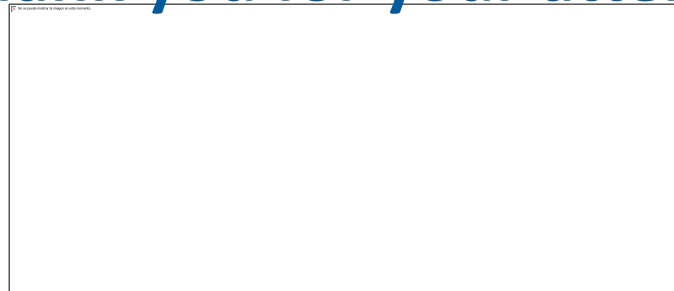


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Thank you for your attention



Website: www.arrassain.eu

