MASTER DEGREE IN BIOINFOMATICS AND SYSTEMS BIOLOGY

SUPPLEMENTARY INFORMATION

Understanding the biology of Morpholinos in zebrafish through integrated gene expression analysis

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TABLE OF CONTENTS

1) INTRODUCTION

The current study analyses a pool of microarray datasets which were collected from GEO public repository through supervised machine learning. The supplementary information is divided in three chapters. The first chapter gives a deeper insight into the criteria used for the microarray selection and annotation. The second part describes the normalization strategies for the integration of the two microarray platforms; the final part provides further results which give more detailed information about the main results shown in the paper.

2) MATERIAL AND METHODS

2.1 GEO repository details and experiment information from literature

Table S.2.1 – Microarray data curation: the attributes below are assigned to each microarray dataset. GPL, GSE, GSM, Title and Pubmed attributes are used as identification for retrieving the microarray in the GEO repository. MO target, MOseq, COseq, MOtarget, source, Hpf, Treatment, MO type, MO dose and phenotype are directly extracted from the annexed scientific article. Dev. Stage and MO dose are created additionally from the provided information.

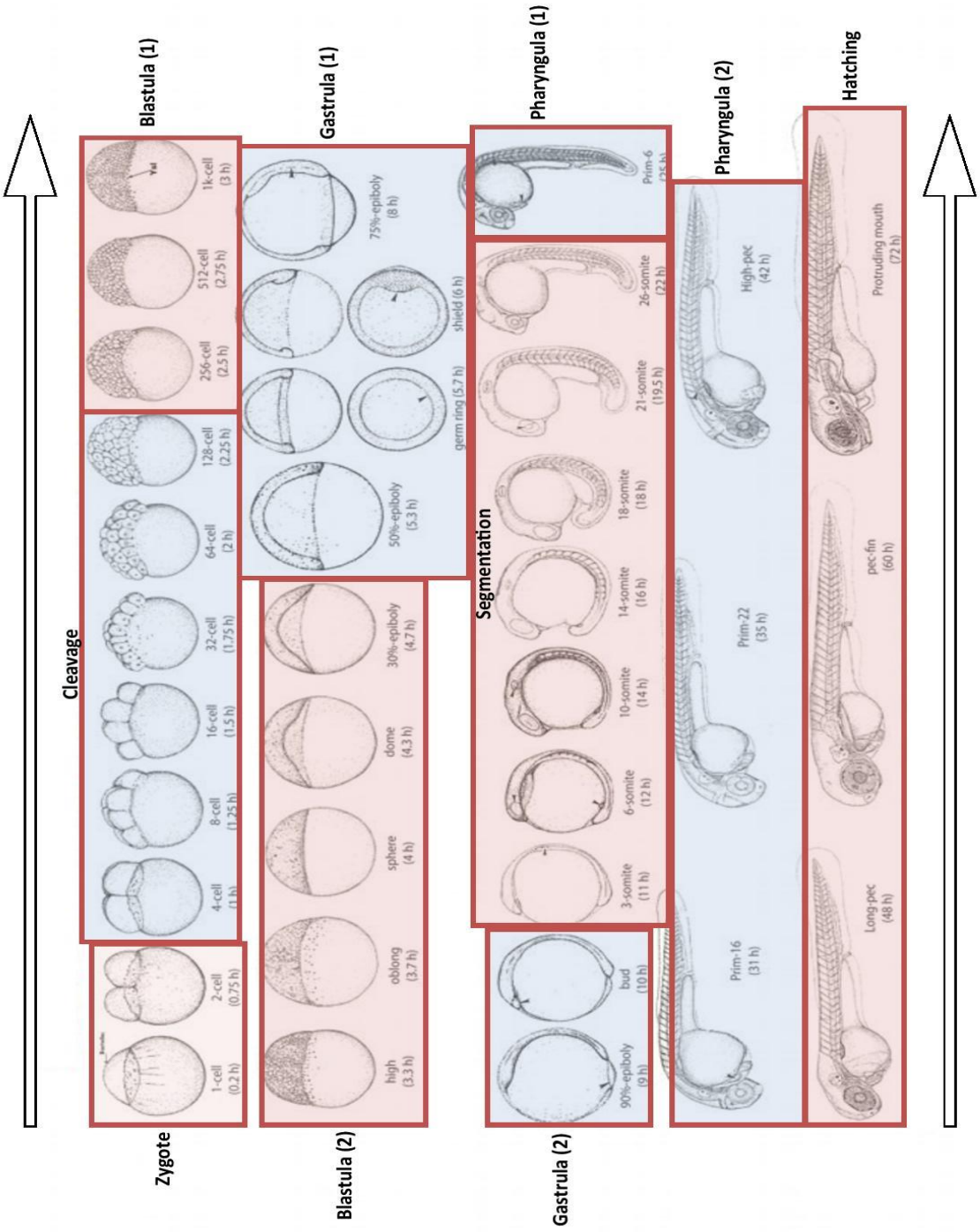
Attribute	Type	Levels	Description
GPL	Descriptive	-	Type of technology
GSE	Descriptive	-	Study ID (coupled to unique publication)
GSM	Descriptive	-	Data set ID
Title	Descriptive	-	Data set description
Pubmed	Descriptive	-	Associated publication ID
MO target	Descriptive	-	Gene targeted by morpholino
MOseq	Descriptive	-	Morpholino sequence
COseq	Descriptive	-	Sequence of the control morpholino (if available)
MO target	Descriptive	-	Gene targeted by morpholino
Source	Categorical	kidney, endothelial cells, hearts, whole embryo, embryo trunk	Tissue type
Hpf	Continuous	-	Age (hours post fertilization) of the sampled embryos
Treatment	Categorical	Morpholino, Control	Type of treatment
MO type	Categorical	Translation, splicing	Mechanism of gene product inhibition
MO dose	Continuous	-	Nanograms of morpholino injected
Phenotype	Categorical	Normal, various	Phenotype induced by the injection
Dev. Stage	Categorical	Blastula, Gastrula, Segmentation, Pharyngula, Hatching	Developmental stage of the sampled embryos*
MO dose PM	Continuous	-	PicoMolar dose of the injected morpholino**

* From: Zebrafish developmental staging series: http://zfin.org/zf_info/zfbook/stages/ - ZFin data base
Detailed description of the zebrafish developmental stages on page in section 2.2

** Calculated from the morpholino sequence molecular weight and the injected quantity (MO dose).
Molecular weights:
Morpholino ring: 87.12 g/mol, A subunit residue: 339.3 g/mole, C subunit residue: 315.3 g/mole, G subunit residue: 355.3 g/mole, T subunit residue: 330.3 g/mole, Additional weight of the ends of the chain: 101 g/mole

2.2 Zebrafish developmental stages

Figure S.2.2 – The "Hours post fertilization" attributes extracted from the literature information is assigned to one of the developmental stages below. The stage in this case is used as a categorical variable



2.3 Affymetrix microarray profiles used for integrated data analysis

Table S.2.3 – Relevant information used for the integrated microarray study- Affymetrix

GSE	GSM	Description	Treatment *	Replicates	Source	MO dose pM	Dev stage
GSE12012	GSM303576	zebrafish_48hpf_control_replicate1	WT	1	endothelial	0	Pharyngula
GSE12012	GSM303577	zebrafish_48hpf_miR-126 MO-1_replicate1	miR-126	1	endothelial	0.455	Pharyngula
GSE12012	GSM303578	zebrafish_48hpf_miR-126 MO-2_replicate1	miR-126	1	endothelial	0.563	Pharyngula
GSE12012	GSM303579	zebrafish_48hpf_control_replicate2	WT	2	endothelial	0	Pharyngula
GSE12012	GSM303580	zebrafish_48hpf_miR-126 MO-1_replicate2	miR-126	2	endothelial	0.455	Pharyngula
GSE12012	GSM303581	zebrafish_48hpf_miR-126 MO-2_replicate2	miR-126	2	endothelial	0.563	Pharyngula
GSE12012	GSM303582	zebrafish_48hpf_control_replicate3	WT	3	endothelial	0	Pharyngula
GSE12012	GSM303583	zebrafish_48hpf_miR-126 MO-1_replicate3	miR-126	3	endothelial	0.455	Pharyngula
GSE12012	GSM303584	zebrafish_48hpf_miR-126 MO-2_replicate3	miR-126	3	endothelial	0.563	Pharyngula
GSE12012	GSM303585	zebrafish_48hpf_control_replicate4	WT	4	endothelial	0	Pharyngula
GSE12012	GSM303586	zebrafish_48hpf_miR-126 MO-1_replicate4	miR-126	4	endothelial	0.455	Pharyngula
GSE12012	GSM303587	zebrafish_48hpf_miR-126 MO-2_replicate4	miR-126	4	endothelial	0.563	Pharyngula
GSE13157	GSM329381	Embryos injected with 15uM ERbeta2 MO biological repl. 1	esr2a	1	embryos	0.015	Hatching
GSE13157	GSM329382	Embryos injected with 15uM ERbeta2 MO biological repl. 2	esr2a	2	embryos	0.015	Hatching
GSE13157	GSM329383	Embryos injected with 15uM coMO biological repl. 1	CO	1	embryos	0.015	Hatching
GSE13157	GSM329384	Embryos injected with 15uM coMO biological repl. 2	CO	2	embryos	0.015	Hatching
GSE13157	GSM329385	Embryos uninjected biological repl. 1 (15uM)	WT	1	embryos	0	Hatching
GSE13157	GSM329386	Embryos uninjected biological repl. 2 (15uM)	WT	2	embryos	0	Hatching
GSE13158	GSM329399	Embryos injected with 50uM ERbeta2 MO biological repl. 1	esr2a	1	embryos	0.05	Hatching
GSE13158	GSM329400	Embryos injected with 50uM ERbeta2 MO biological repl. 2	esr2a	2	embryos	0.05	Hatching
GSE13158	GSM329401	Embryos injected with 50uM coMO biological repl. 1	CO	1	embryos	0.05	Hatching
GSE13158	GSM329402	Embryos injected with 50uM coMO biological repl. 2	CO	2	embryos	0.05	Hatching
GSE13158	GSM329403	Embryos uninjected biological repl. 1 (50uM)	WT	1	embryos	0	Hatching
GSE13158	GSM329404	Embryos uninjected biological repl. 2 (50uM)	WT	2	embryos	0	Hatching
GSE16740	GSM419445	RNA from embryos of 3 groups of Wildtype AB zebrafish at 36 hpf_1	CO	1	embryos	0.38	Pharyngula
GSE16740	GSM419446	RNA from embryos of 3 groups of Wildtype AB zebrafish at 36 hpf_2	CO	2	embryos	0.38	Pharyngula
GSE16740	GSM419447	RNA from embryos of 3 groups of Wildtype AB zebrafish at 36 hpf_3	CO	3	embryos	0.38	Pharyngula
GSE16740	GSM419448	RNA from embryos of 3 groups of tnnt2 morpholino fish at 36 hpf_1	tnnt2	1	embryos	0.377	Pharyngula
GSE16740	GSM419449	RNA from embryos of 3 groups of tnnt2 morpholino fish at 36 hpf_2	tnnt2	2	embryos	0.377	Pharyngula
GSE16740	GSM419450	RNA from embryos of 3 groups of tnnt2 morpholino fish at 36 hpf_3	tnnt2	3	embryos	0.377	Pharyngula
GSE16740	GSM419451	RNA from embryos of 3 groups of Wildtype AB zebrafish at 48 hpf_1	CO	1	embryos	0.38	Pharyngula
GSE16740	GSM419452	RNA from embryos of 3 groups of Wildtype AB zebrafish at 48 hpf_2	CO	2	embryos	0.38	Pharyngula
GSE16740	GSM419453	RNA from embryos of 3 groups of Wildtype AB zebrafish at 48 hpf_3	CO	3	embryos	0.38	Pharyngula
GSE16740	GSM419454	RNA from embryos of 3 groups of tnnt2 morpholino fish at 48 hpf_1	tnnt2	1	embryos	0.377	Pharyngula
GSE16740	GSM419455	RNA from embryos of 3 groups of tnnt2 morpholino fish at 48 hpf_2	tnnt2	2	embryos	0.377	Pharyngula
GSE16740	GSM419456	RNA from embryos of 3 groups of tnnt2 morpholino fish at 48 hpf_3	tnnt2	3	embryos	0.377	Pharyngula
GSE16740	GSM419457	RNA from embryos of 3 groups of Wildtype AB zebrafish at 60 hpf_1	CO	1	embryos	0.38	Hatching

GSE16740	GSM419458	RNA from embryos of 3 groups of Wildtype AB zebrafish at 60 hpf_2	CO	2	embryos	0.38	Hatching
GSE16740	GSM419459	RNA from embryos of 3 groups of Wildtype AB zebrafish at 60 hpf_3	CO	3	embryos	0.38	Hatching
GSE16740	GSM419460	RNA from embryos of 3 groups of tnnt2 morpholino fish at 60 hpf_1	tnnt2	1	embryos	0.377	Hatching
GSE16740	GSM419461	RNA from embryos of 3 groups of tnnt2 morpholino fish at 60 hpf_2	tnnt2	2	embryos	0.377	Hatching
GSE16740	GSM419462	RNA from embryos of 3 groups of tnnt2 morpholino fish at 60 hpf_3	tnnt2	3	embryos	0.377	Hatching
GSE18830	GSM466790	Zebrafish wt embryo_ 30%E_biological rep1	WT	1	embryos	0	Blastula
GSE18830	GSM466791	Zebrafish wt embryo_ 30%E_biological rep2	WT	2	embryos	0	Blastula
GSE18830	GSM466792	Zebrafish wt embryo_ 75%E_biological rep1	WT	1	embryos	0	Gastrula
GSE18830	GSM466793	Zebrafish wt embryo_ 75%E_biological rep2	WT	2	embryos	0	Gastrula
GSE18830	GSM466794	Zebrafish wt embryo_ TB_biological rep1	WT	1	embryos	0	Gastrula
GSE18830	GSM466795	Zebrafish wt embryo_ TB_biological rep2	WT	2	embryos	0	Gastrula
GSE18830	GSM466796	Zebrafish QKD embryo_ 30%E_biological rep1	sox2/3/19a/19b	1	embryos	0.068	Blastula
GSE18830	GSM466797	Zebrafish QKD embryo_ 30%E_biological rep2	sox2/3/19a/19b	2	embryos	0.068	Blastula
GSE18830	GSM466798	Zebrafish QKD embryo_ 75%E_biological rep1	sox2/3/19a/19b	1	embryos	0.068	Gastrula
GSE18830	GSM466799	Zebrafish QKD embryo_ 75%E_biological rep2	sox2/3/19a/19b	2	embryos	0.068	Gastrula
GSE18830	GSM466800	Zebrafish QKD embryo_TB_biological rep1	sox2/3/19a/19b	1	embryos	0.068	Gastrula
GSE18830	GSM466801	Zebrafish QKD embryo_TB_biological rep2	sox2/3/19a/19b	2	embryos	0.068	Gastrula
GSE21539	GSM537962	zebrafish 12hpf control-1	WT	1	embryos	0	Segmentation
GSE21539	GSM537963	zebrafish 12hpf control-2	WT	2	embryos	0	Segmentation
GSE21539	GSM537964	zebrafish 12hpf control-3	WT	3	embryos	0	Segmentation
GSE21539	GSM537965	zebrafish 12hpf Ovo1 morphant-1	Ovo1	1	embryos	0.286	Segmentation
GSE21539	GSM537966	zebrafish 12hpf Ovo1 morphant-2	Ovo1	2	embryos	0.286	Segmentation
GSE21539	GSM537967	zebrafish 12hpf Ovo1 morphant-3	Ovo1	3	embryos	0.286	Segmentation
GSE27569	GSM683599	control embryos at 24hpf, biological rep 1	WT	1	embryos	0	Segmentation
GSE27569	GSM683600	control embryos at 24hpf, biological rep 2	WT	2	embryos	0	Segmentation
GSE27569	GSM683601	control embryos at 24hpf, biological rep 3	WT	3	embryos	0	Segmentation
GSE27569	GSM683602	control embryos at 24hpf, biological rep 4	WT	4	embryos	0	Segmentation
GSE27569	GSM683603	esco2 MO injected embryos at 24hpf, biological rep 1	esco2	1	embryos	0.189	Segmentation
GSE27569	GSM683604	esco2 MO injected embryos at 24hpf, biological rep 2	esco2	2	embryos	0.189	Segmentation
GSE27569	GSM683605	esco2 MO injected embryos at 24hpf, biological rep 3	esco2	3	embryos	0.189	Segmentation
GSE27569	GSM683606	esco2 MO injected embryos at 24hpf, biological rep 4	esco2	4	embryos	0.189	Segmentation
GSE27569	GSM683607	control embryos at 48hpf, biological rep 1	WT	1	embryos	0	Pharyngula
GSE27569	GSM683608	control embryos at 48hpf, biological rep 3	WT	2	embryos	0	Pharyngula
GSE27569	GSM683609	control embryos at 48hpf, biological rep 4	WT	3	embryos	0	Pharyngula
GSE27569	GSM683610	esco2 MO injected embryos at 48hpf, biological rep 1	esco2	1	embryos	0.189	Pharyngula
GSE27569	GSM683611	esco2 MO injected embryos at 48hpf, biological rep 2	esco2	2	embryos	0.189	Pharyngula
GSE27569	GSM683612	esco2 MO injected embryos at 48hpf, biological rep 3	esco2	3	embryos	0.189	Pharyngula
GSE27569	GSM683613	esco2 MO injected embryos at 48hpf, biological rep 4	esco2	4	embryos	0.189	Pharyngula
GSE32914	GSM814795	zebrafish_SB_4.3h_1	Sox31	1	embryos	1.2	Blastula
GSE32914	GSM814796	zebrafish_SB_4.3h_2	Sox31	2	embryos	1.2	Blastula
GSE32914	GSM814797	zebrafish_SB_4.3h_3	Sox31	3	embryos	1.2	Blastula
GSE32914	GSM814798	zebrafish_WT_4.3h_1	WT	1	embryos	0	Blastula
GSE32914	GSM814799	zebrafish_WT_4.3h_2	WT	2	embryos	0	Blastula
GSE32914	GSM814800	zebrafish_WT_4.3h_3	WT	3	embryos	0	Blastula
GSE32914	GSM814801	zebrafish_WT_2.5h_1	WT	1	embryos	0	Blastula
GSE32914	GSM814802	zebrafish_WT_2.5h_2	WT	2	embryos	0	Blastula
GSE32914	GSM814803	zebrafish_WT_4h_1	WT	1	embryos	0	Blastula
GSE32914	GSM814804	zebrafish_WT_4h_2	WT	2	embryos	0	Blastula
GSE46844	GSM1139092	Multiciliated cell_control_rep1	CO	1	kidney	1	Hatching

GSE46844	GSM1139093	Multiciliated cell_control_rep2	CO	2	kidney	1	Hatching
GSE46844	GSM1139094	Multiciliated cell_miR-34B morphants_rep1	mir-34B	1	kidney	1	Hatching
GSE46844	GSM1139095	Multiciliated cell_miR-34B morphants_rep2	mir-34B	2	kidney	1	Hatching
GSE51541	GSM1247632	Uninjected control biological replicate 1	WT	1	heart	0	Hatching
GSE51541	GSM1247633	Uninjected control biological replicate 2	WT	2	heart	0	Hatching
GSE51541	GSM1247634	Uninjected control biological replicate 3	WT	3	heart	0	Hatching
GSE51541	GSM1247635	Control Morpholino biological replicate 2	CO	1	heart	0.65	Hatching
GSE51541	GSM1247636	Control Mopholino biological replicate 3	CO	2	heart	0.65	Hatching
GSE51541	GSM1247637	atg5 Mopholino biological replicate 1	atg5	1	heart	0.65	Hatching
GSE51541	GSM1247638	atg5 Mopholino biological replicate 2	atg5	2	heart	0.65	Hatching
GSE51541	GSM1247639	atg5 Mopholino biological replicate 3	atg5	3	heart	0.65	Hatching
GSE51541	GSM1247640	becn1 Mopholino biological replicate 1	becn1	1	heart	0.65	Hatching
GSE51541	GSM1247641	becn1 Mopholino biological replicate 2	becn1	2	heart	0.65	Hatching
GSE51541	GSM1247642	becn1 Mopholino biological replicate 3	becn1	3	heart	0.65	Hatching
GSE51541	GSM1247643	atg7 Mopholino biological replicate 1	atg7	1	heart	0.65	Hatching
GSE51541	GSM1247644	atg7 Mopholino biological replicate 2	atg7	2	heart	0.65	Hatching
GSE8800	GSM218665	MO	C1q-like	1	embryos	0.473	Segmentation
GSE8800	GSM218666	Cont MO	CO	2	embryos	0.474	Segmentation

* Treatment
Control: **WT** – uninjected, **CO** – injected morpholino sequence
Morpholino treatment: **microRNA**- mir34B, mir126, **genes:** C1q-like, atg7, becn1, atg5, Sox31, esco2, Ovo1, sox2/3/19a/19b, tnnt2, esr2a

Table S.2.3.1 – Number of microarrays per attribute factor. The table is a summary of Table S.2.3

Developmental stage	Blastula: 14 Gastrula: 8 Segmentation: 16 Pharyngula: 31 Hatching: 35
Treatment	Morpholino: 52 Control: 52 (WT:34 -CO:18)
Source	Embryos: 75 Kidney: 4 Hearts: 13 Endothelial cells: 12
Dosage:	0-0.189: 56 0.289-0.65: 41 1-1.2: 7

2.4 Agilent microarray profiles used for integrated data analysis

Table S.2.4 – Relevant information used for the integrated microarray study- Agilent

gpl	gse	gsm	Description	Treatment*	Replicates	Source	MO.dose pM	Dev.stage
GPL14664	GSE32594	GSM807955	Injection of control MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	CO	1	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807956	Injection of control MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	CO	2	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807957	Injection of control MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	CO	3	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807961	Injection of Nrf2a MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a	1	embryos	0.025	Hatching
GPL14664	GSE32594	GSM807962	Injection of Nrf2a MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a	2	embryos	0.025	Hatching
GPL14664	GSE32594	GSM807963	Injection of Nrf2a MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a	3	embryos	0.025	Hatching
GPL14664	GSE32594	GSM807967	Injection of Nrf2a and Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a/Nrf2b	1	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807968	Injection of Nrf2a and Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a/Nrf2b	2	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807969	Injection of Nrf2a and Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2a/Nrf2b	3	embryos	0.05	Hatching
GPL14664	GSE32594	GSM807973	Injection of Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2b	1	embryos	0.025	Hatching
GPL14664	GSE32594	GSM807974	Injection of Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2b	2	embryos	0.025	Hatching
GPL14664	GSE32594	GSM807975	Injection of Nrf2b MO at 1-4 cell stage. DMSO exposure at 48 hpf. RNA sampled at 52 hpf.	Nrf2b	3	embryos	0.025	Hatching
GPL14664	GSE42070	GSM1031965	whole fish, 6h, control, replicate 1	CO_R	1	embryos	0.5	Gastrula
GPL14664	GSE42070	GSM1031966	whole fish, 6h, control, replicate 2	CO_R	2	embryos	0.5	Gastrula
GPL14664	GSE42070	GSM1031967	whole fish, 6h, control, replicate 3	CO_R	3	embryos	0.5	Gastrula
GPL14664	GSE42070	GSM1031968	whole fish, 24h, control, replicate 1	CO_R	1	embryos	0.5	Segmentation
GPL14664	GSE42070	GSM1031969	whole fish, 24h, control, replicate 2	CO_R	2	embryos	0.5	Segmentation
GPL14664	GSE42070	GSM1031970	whole fish, 24h, control, replicate 3	CO_R	3	embryos	0.5	Segmentation
GPL14664	GSE42070	GSM1031971	whole fish, 6h, PCSK7+P53 morpholinos, replicate 1	PCSK7/P53	1	embryos	1.25	Gastrula
GPL14664	GSE42070	GSM1031972	whole fish, 6h, PCSK7+P53 morpholinos, replicate 2	PCSK7/P53	2	embryos	1.25	Gastrula
GPL14664	GSE42070	GSM1031973	whole fish, 6h, PCSK7+P53 morpholinos, replicate 3	PCSK7/P53	3	embryos	1.25	Gastrula
GPL14664	GSE42070	GSM1031974	whole fish, 24h, PCSK7+P53 morpholinos, replicate 1	PCSK7/P53	1	embryos	1.25	Segmentation
GPL14664	GSE42070	GSM1031975	whole fish, 24h, PCSK7+P53 morpholinos, replicate 2	PCSK7/P53	2	embryos	1.25	Segmentation

GPL14664	GSE42070	GSM1031976	whole fish, 24h, PCSK7+P53 morpholinos, replicate 3	PCSK7/P53	3	embryos	1.25	Segmentation
GPL14664	GSE45012	GSM1095807	FoxD5 Morpholino injection	FoxD5	1	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095808	FoxD5 Morpholino injection	FoxD5	2	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095813	FoxD5 Morpholino injection	FoxD5	3	embryos	0.38	Blastula
GPL6457	GSE20179	GSM506241	Whole embryo TNNT2sp morphants	tnnt2	1	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506241	Whole embryo TNNT2sp morphants	CO	1	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506242	Whole embryo TNNT2sp morphants	tnnt2	2	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506242	Whole embryo TNNT2sp morphants	CO	2	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506243	Whole embryo TNNT2sp morphants	tnnt2	3	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506243	Whole embryo TNNT2sp morphants	CO	3	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506244	Whole embryo TNNT2sp morphants	tnnt2	4	embryos	0.471	Hatching
GPL6457	GSE20179	GSM506244	Whole embryo TNNT2sp morphants	CO	4	embryos	0.471	Hatching
GPL6457	GSE24934	GSM612962	MO2-ers2a embryos at 8 hours post fertilization	CO	1	embryos	0.974	Gastrula
GPL6457	GSE24934	GSM612962	MO2-ers2a embryos at 8 hours post fertilization	Ers2a	1	embryos	0.974	Gastrula
GPL6457	GSE24934	GSM612963	MO2-ers2a embryos at 48 hours post fertilization	CO	2	embryos	0.974	Pharyngula
GPL6457	GSE24934	GSM612963	MO2-ers2a embryos at 48 hours post fertilization	Ers2a	2	embryos	0.974	Pharyngula
GPL6457	GSE25517	GSM627464	MO2-nr3c1-5m, 5hpf	CO	1	embryos	0.783	Blastula
GPL6457	GSE25517	GSM627464	MO2-nr3c1-5m, 5hpf	MO	1	embryos	0.783	Blastula
GPL6457	GSE25517	GSM627465	WT, 5hpf	WT	1	embryos	0.783	Blastula
GPL6457	GSE25517	GSM627465	WT, 5hpf	MO	1	embryos	0.783	Blastula
GPL6457	GSE25517	GSM627466	MO2-nr3c1-5m, 10hpf	CO	2	embryos	0.783	Gastrula
GPL6457	GSE25517	GSM627466	MO2-nr3c1-5m, 10hpf	MO	2	embryos	0.783	Gastrula
GPL6457	GSE25517	GSM627467	WT, 10hpf	WT	2	embryos	0.783	Gastrula
GPL6457	GSE25517	GSM627467	WT, 10hpf	MO	2	embryos	0.783	Gastrula
GPL6457	GSE38441	GSM942059	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	WT	1	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942059	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	MO	1	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942060	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	WT	2	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942060	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	MO	2	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942061	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	WT	3	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942061	16 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	MO	3	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942062	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	WT	1	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942062	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	MO	1	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942063	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	WT	2	trunk	0.023	Segmentation

GPL6457	GSE38441	GSM942063	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	MO	2	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942064	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	WT	3	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942064	24 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	MO	3	trunk	0.023	Segmentation
GPL6457	GSE38441	GSM942065	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	WT	1	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942065	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	MO	1	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942066	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	WT	2	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942066	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	MO	2	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942067	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	WT	3	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942067	48 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	MO	3	trunk	0.023	Pharyngula
GPL6457	GSE38441	GSM942068	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	WT	1	trunk	0.023	Hatching
GPL6457	GSE38441	GSM942068	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 1	MO	1	trunk	0.023	Hatching
GPL6457	GSE38441	GSM942069	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	WT	2	trunk	0.023	Hatching
GPL6457	GSE38441	GSM942069	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 2	MO	2	trunk	0.023	Hatching
GPL6457	GSE38441	GSM942070	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	WT	3	trunk	0.023	Hatching
GPL6457	GSE38441	GSM942070	72 hpf trunk region of zebrafish embryos: WT vs MO-grnA injected Replicate 3	MO	3	trunk	0.023	Hatching
GPL14664	GSE45011	GSM1095795	Klf2a Morpholino injection	Klf2a	1	embryos	0.38	Blastula
GPL14664	GSE45011	GSM1095799	Klf2a+Klf2b Morpholino injection	Klf2a/Klf2b	1	embryos	0.19	Blastula
GPL14664	GSE45011	GSM1095800	Klf2a+Klf2b Morpholino injection	Klf2a/Klf2b	2	embryos	0.19	Blastula
GPL14664	GSE45011	GSM1095796	Klf2a Morpholino injection	Klf2a	2	embryos	0.38	Blastula
GPL14664	GSE45011	GSM1095797	Klf2b Morpholino injection	Klf2b	1	embryos	0.375	Blastula
GPL14664	GSE45011	GSM1095793	Control Morpholino injection	CO	1	embryos	0.38	Blastula
GPL14664	GSE45011	GSM1095794	Control Morpholino injection	CO	2	embryos	0.38	Blastula
GPL14664	GSE45011	GSM1095798	Klf2b Morpholino injection	Klf2b	2	embryos	0.375	Blastula
GPL14664	GSE45012	GSM1095801	FoxD3 Morpholino injection	FoxD3	1	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095802	FoxD3+FoxD5 Morpholino injection	FoxD3/FoxD5	1	embryos	0.19	Blastula
GPL14664	GSE45012	GSM1095803	FoxD3+FoxD5 Morpholino injection	FoxD3/FoxD5	2	embryos	0.19	Blastula
GPL14664	GSE45012	GSM1095804	FoxD3 Morpholino injection	FoxD3	2	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095805	FoxD3 Morpholino injection	FoxD3	3	embryos	0.38	Blastula

GPL14664	GSE45012	GSM1095806	FoxD3+FoxD5 Morpholino injection	FoxD3/FoxD5	3	embryos	0.19	Blastula
GPL14664	GSE45012	GSM1095809	Klf4 Morpholino injection	Klf4	1	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095810	Control Morpholino injection	CO	1	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095811	Klf4 Morpholino injection	Klf4	2	embryos	0.38	Blastula
GPL14664	GSE45012	GSM1095812	Control Morpholino injection	CO	2	embryos	0.38	Blastula

* Treatment
Control: **WT** – uninjected, **CO** – injected morpholino sequence
Morpholino treatment: **genes:** Klf4, FoxD3/FoxD5, FoxD3, Klf2b, Klf2a/Klf2b, tnnt2, FoxD5, PCSK7/P53, Nrf2b, Nrf2a/Nrf2b, Nrf2a

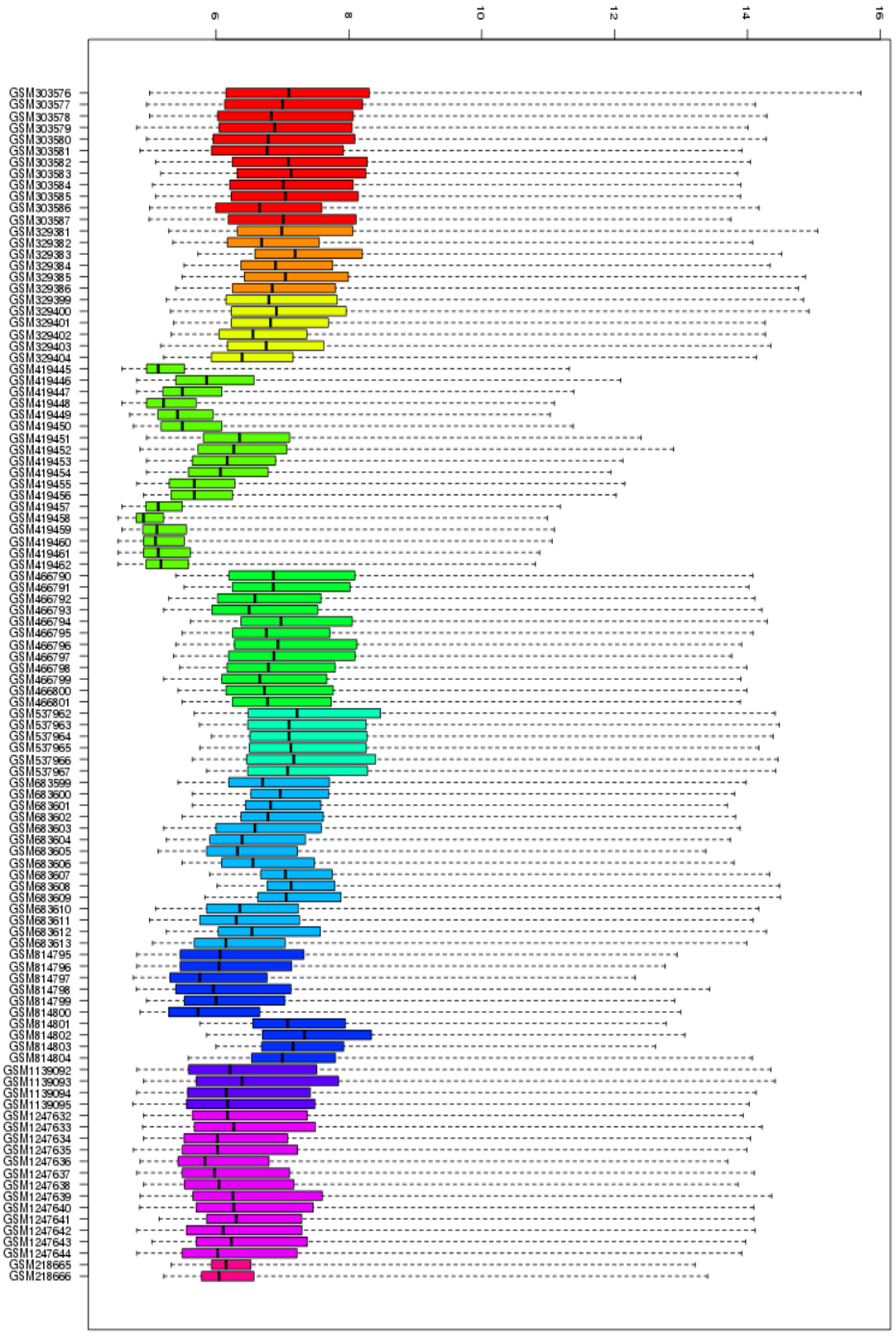
Table S.2.4.1 – Number of microarrays per attribute factor. The table is a summary of Table S.2.4

Developmental stage	Blastula: 25 Gastrula: 12 Segmentation: 18 Pharyngula: 8 Hatching: 26
Treatment	Morpholino: 54 Control: 32 (WT:14, CO:18)
Source	Embryos: 65 Trunk: 24
Dosage:	0-0.19: 43 0.38-0.783: 36 0.974-1.25: 10

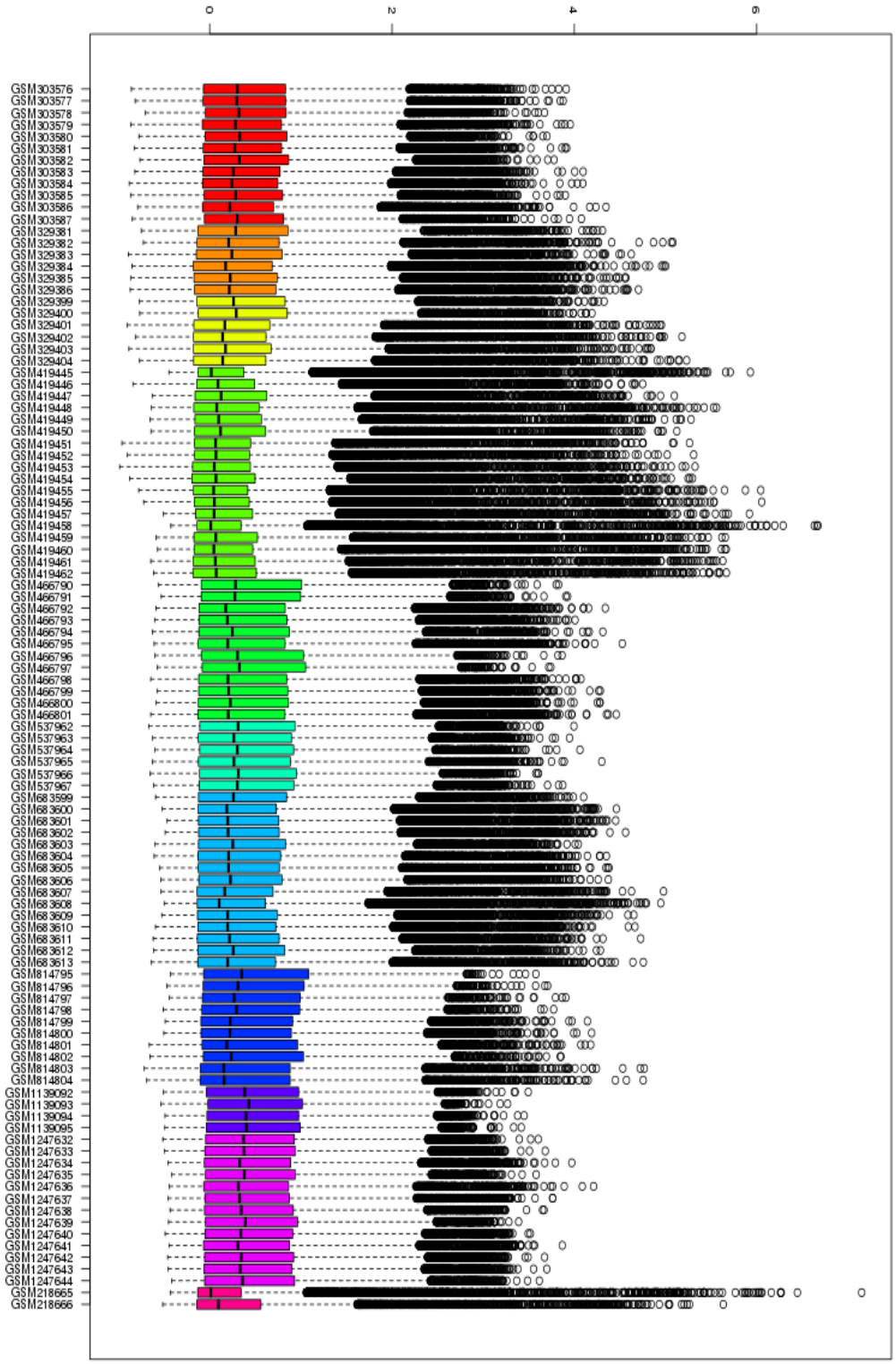
2.5 Data normalization and integration – Affymetrix GPL1319

Figure S.2.5 – Affymetrix: Boxplots of the microarray intensities. Each study is presented with different color. From the top: GSE12012, GSE13157, GSE13158, GSE16740, GSE18830, GSE21539, GSE27569, GSE32914, GSE46844, GSE51541, GSE8800

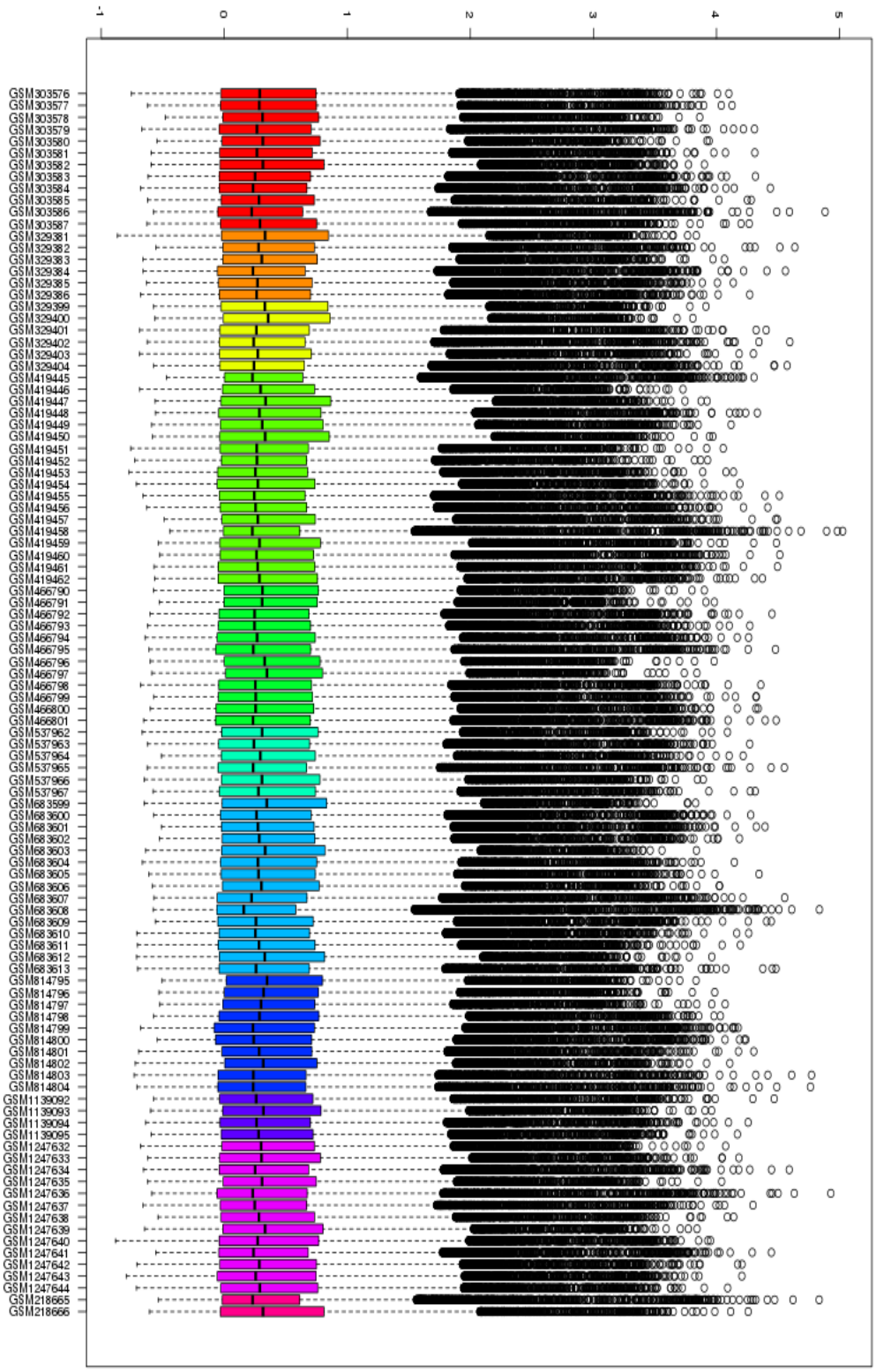
A) Raw intensities



B) Intensities normalized through Single Channel Array Normalization (SCAN)



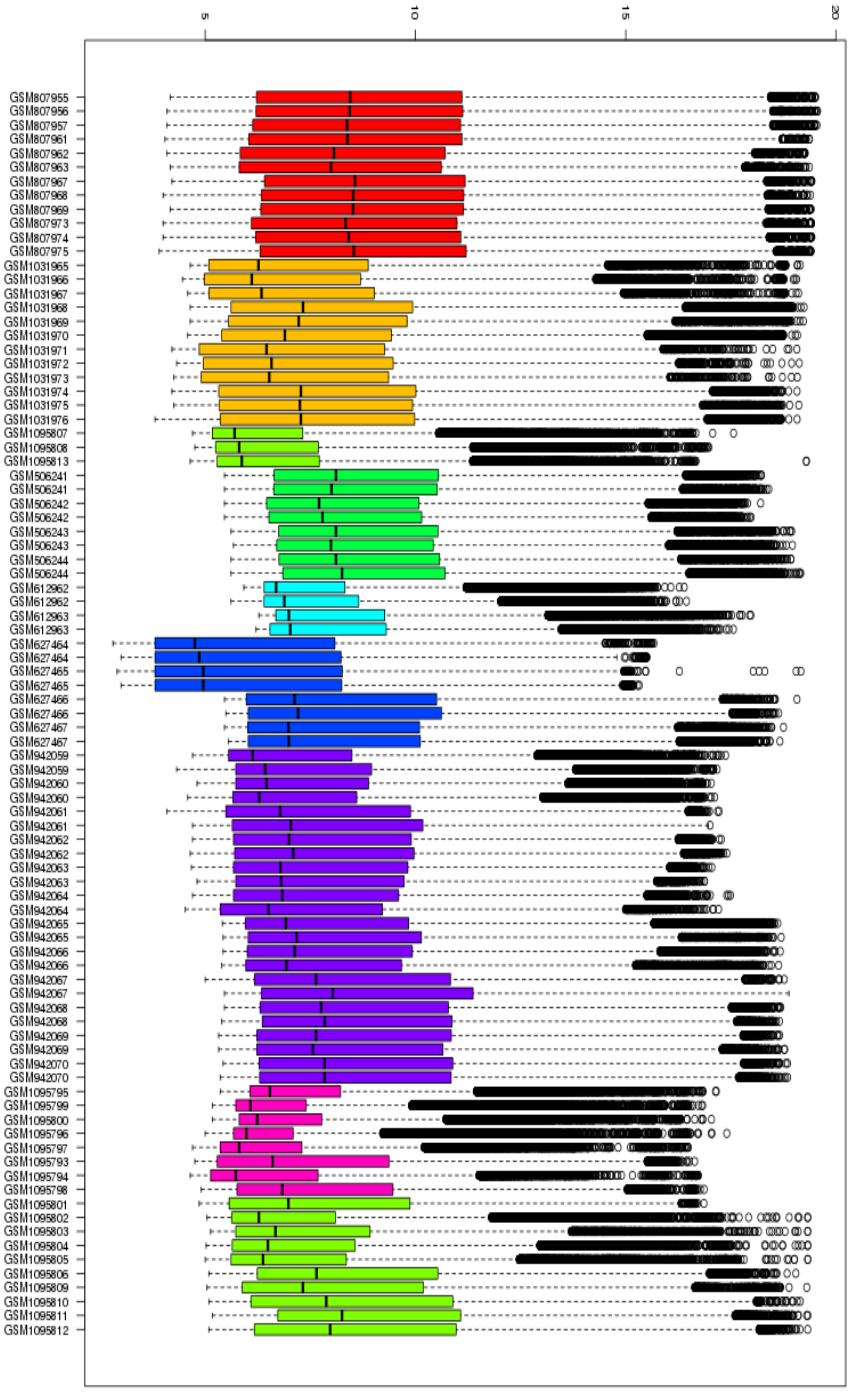
C) **Intensities after Empirical Bayes "batch" standardization. The levels of the *Batch* covariate are the different studies and no *model matrix* is included in the correction**



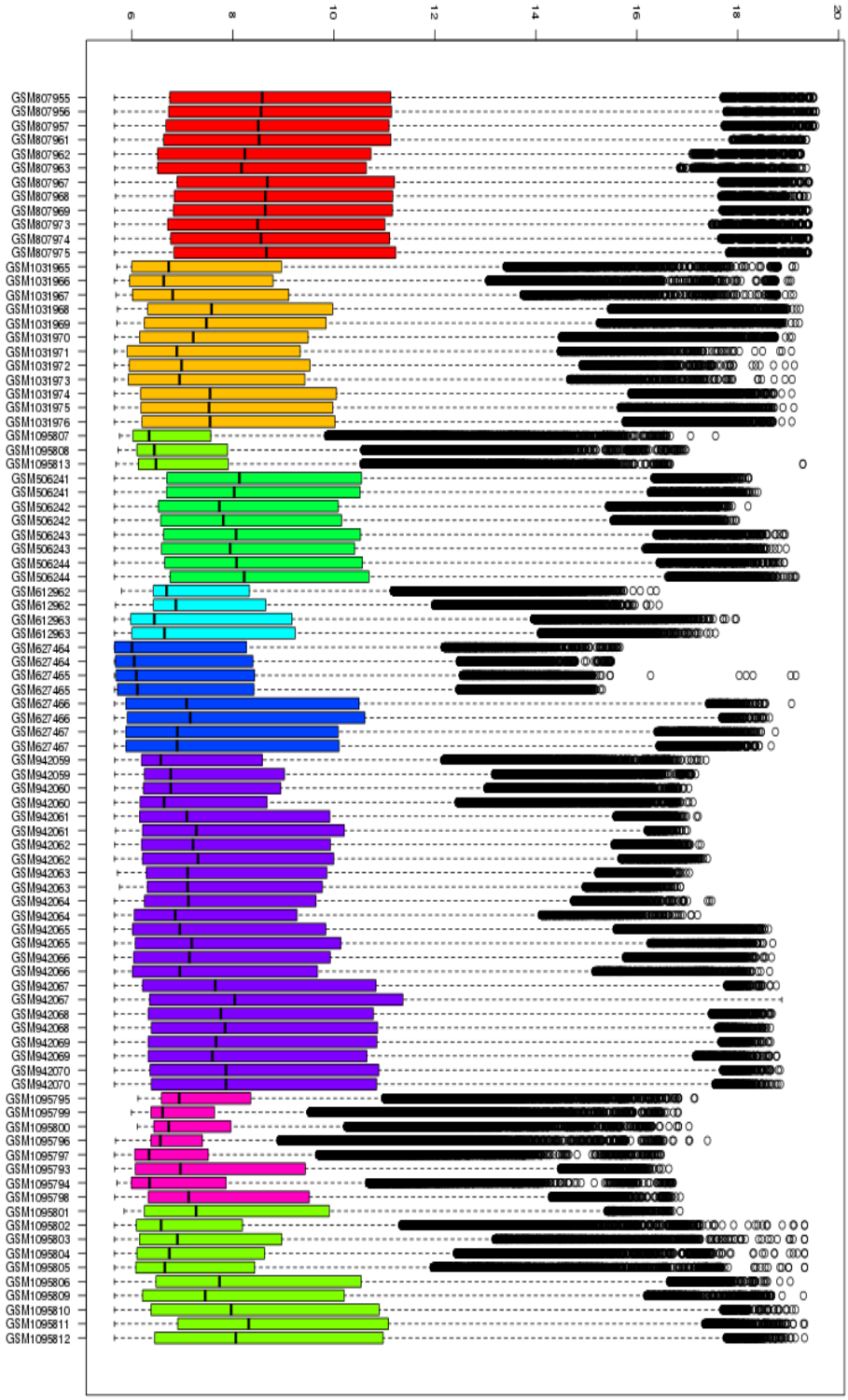
2.6 Data normalization and integration – Agilent GPL14664 – GPL6457

Figure S.2.6 – Agilent: Boxplots of the microarray intensities. Each study is presented with different color. From the top: Single channel: GSE32594, GSE42070, GSE45012, GSE45011, Double channel: GSE20179, GSE24934, GSE25517, GSE38441, GSE45011

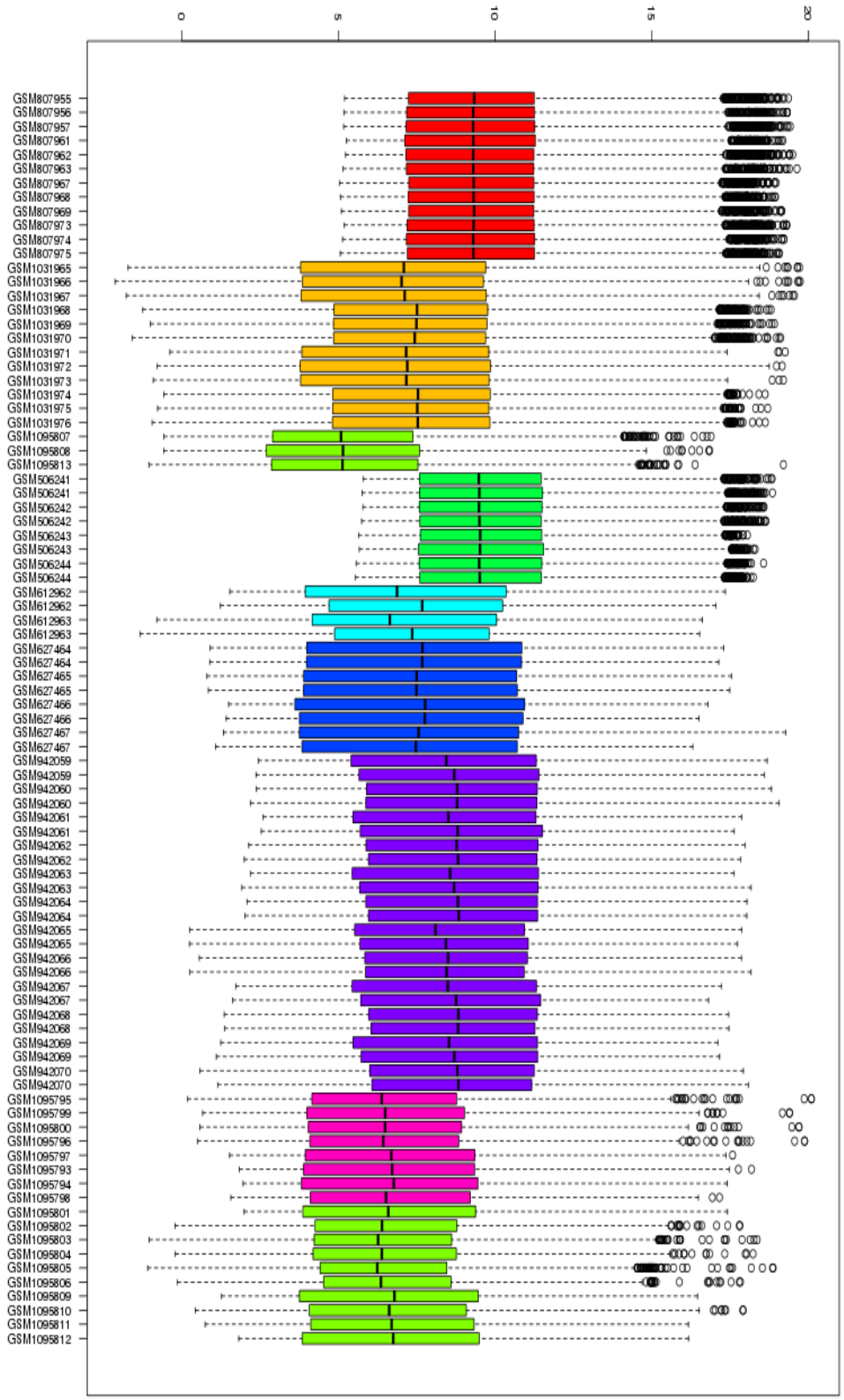
A) Row intensities



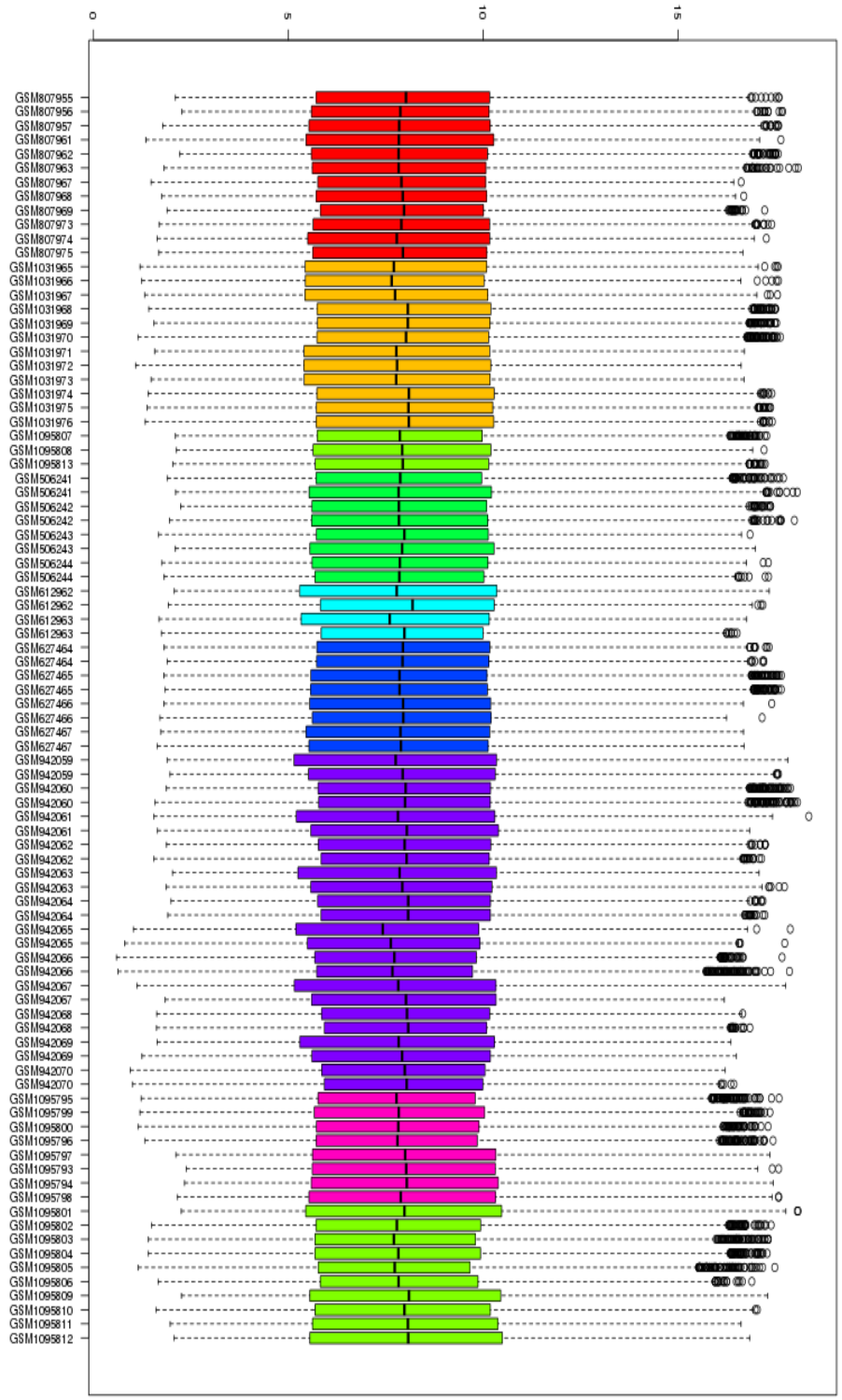
B) Background corrected intensities with "minimum" method and offset score of 50. The correction aimed to the removal of the negative intensity values. The offset score is selected to shrunk the log2 transformed intensities toward zero



C) Intensities values after Variance Stabilization Normalization (VSN)



D) Intensities after Empirical Bayes "batch" correction. The levels of the Batch covariate are the different studies. Studies with both single and double channel intensities are treated as two different levels of batch covariate. No model matrix is included in the "batch" correction

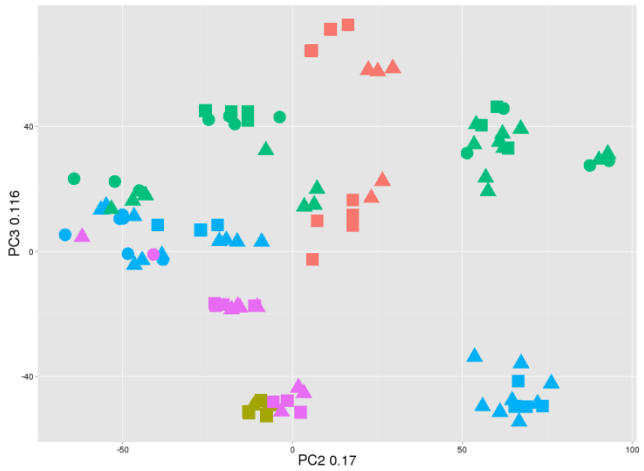


3) RESULTS

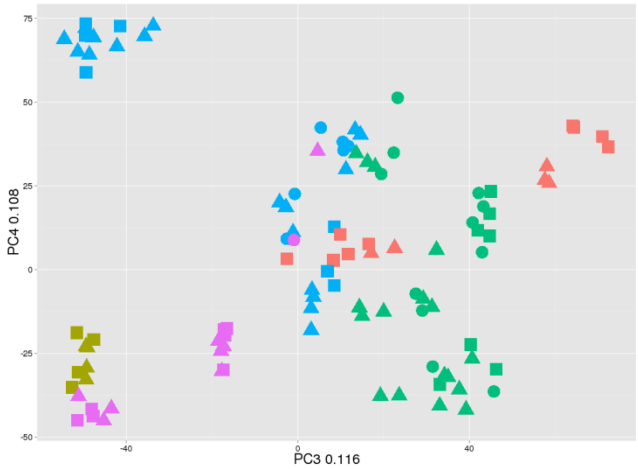
3.1 Principal component analysis -Affymetrix

Figure S.3.1 – PCA labeled by developmental stage and treatment (The number of samples is shown in brackets): Developmental stages (see more details in Table S.2.3.1): Blastula (14), Gastrula (8), Segmentation (13), Pharyngula (31), Hatching (35), Treatment: WT (32): uninjected, CO (18): injected with control, MO (52): injected with target morpholino

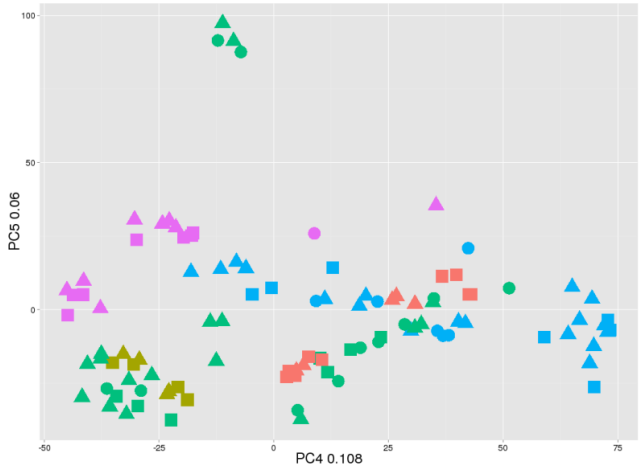
A) PC1-PC2



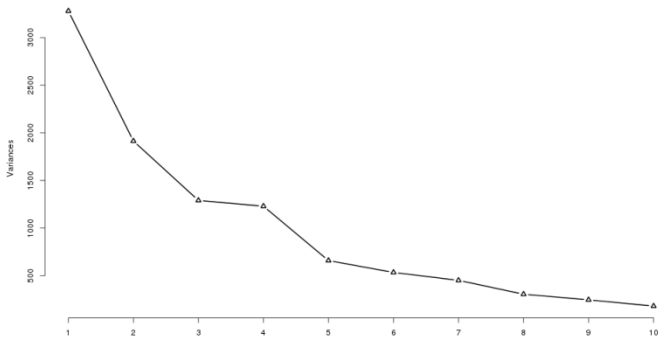
B) PC2-PC3



C) PC3-PC4



D) PC4-PC5



E) Eigenvalues of the principal components

3.2 Hierarchical clustering - Affymetrix

Figure S.3.2A – Hierarchical clustering with Euclidian distance, Pearson correlation score, Ward´s minimum variance method (Murtagh and Legendre, 2014). The samples are labeled by treatment: Wild type, Control and Morpholino

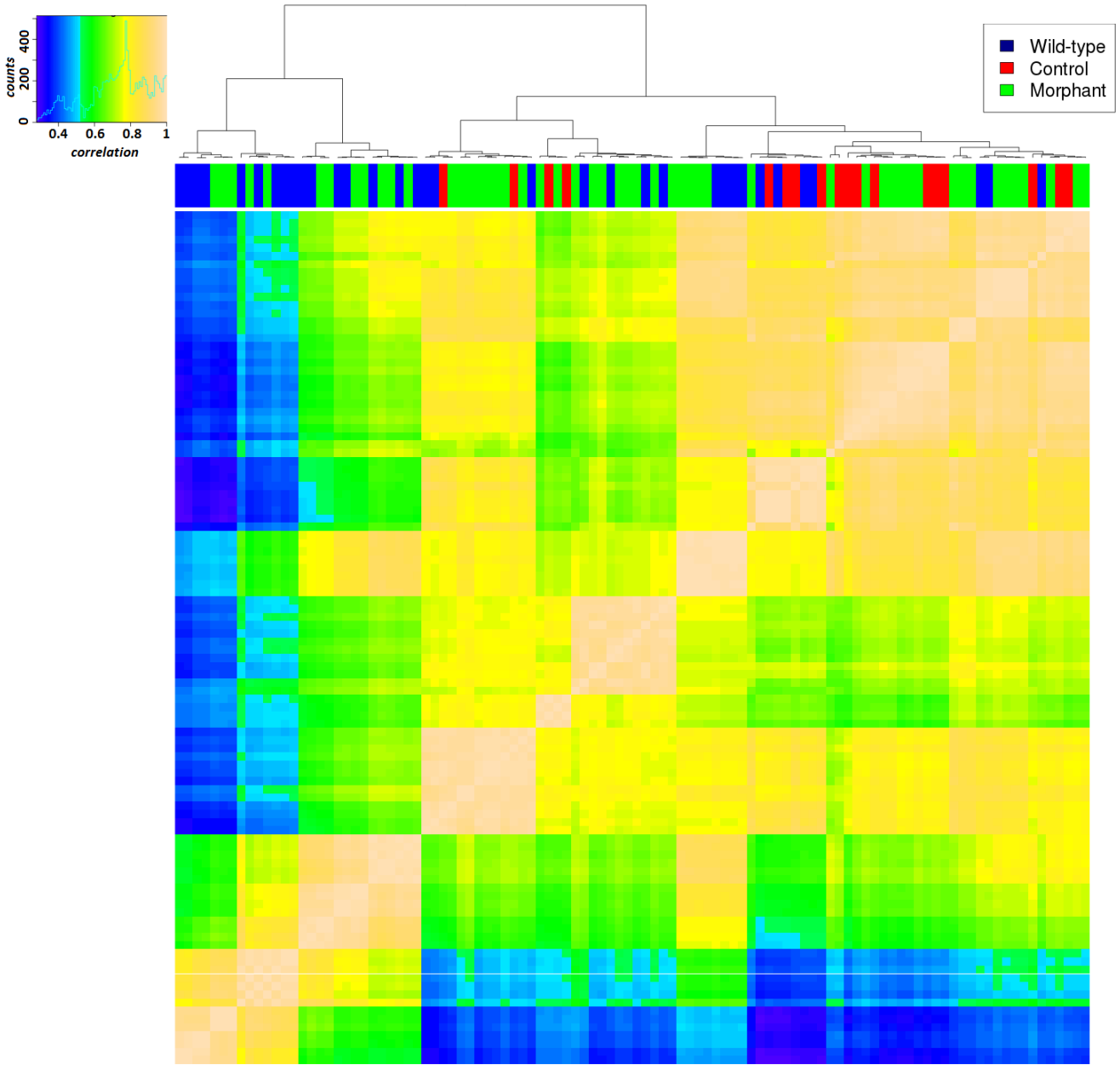
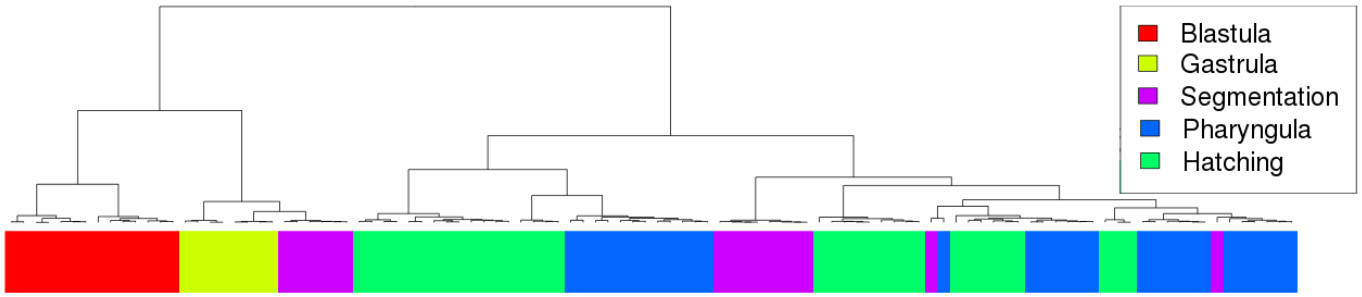
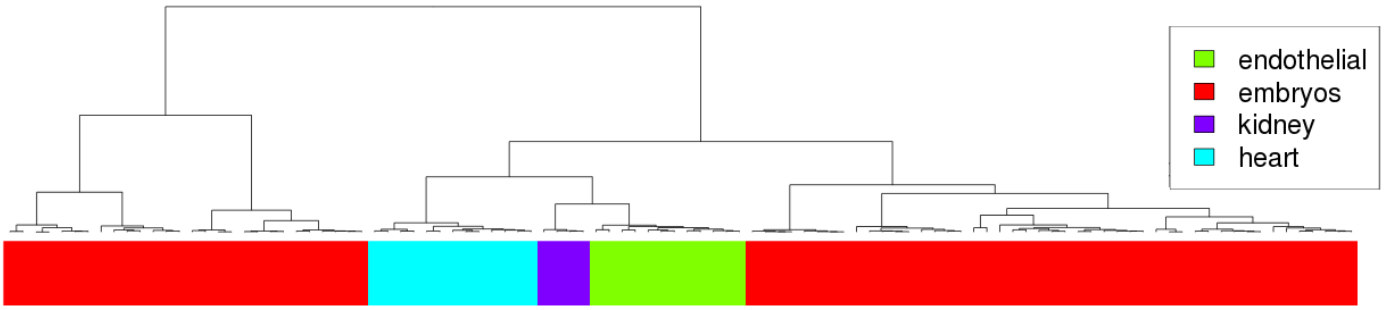


Figure S.3.2B, C – Hierarchical clustering with Euclidian distance, Pearson correlation score, Ward´s minimum variance method (Murtagh and Legendre, 2014) as the previous Figure S.3.2. The samples are labeled by developmental stage (B) or tissue type (C)

B)



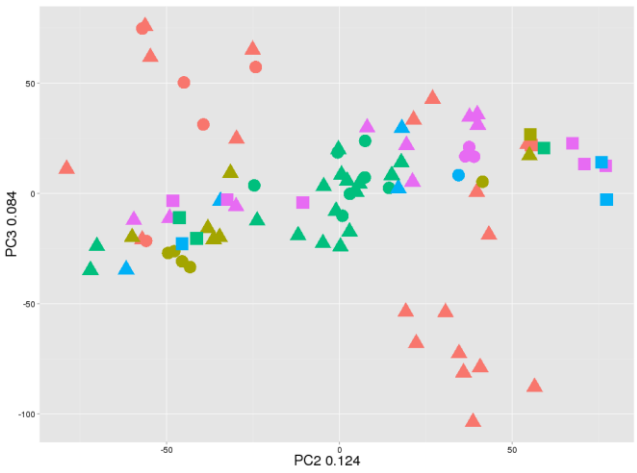
C)



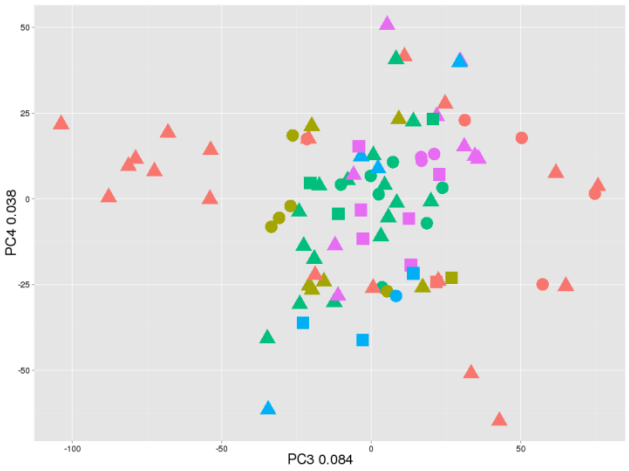
3.3 Principal Component Analysis - Agilent

Figure S.3.3 – PCA labeled by developmental stage and treatment (The number of samples is shown in brackets): Developmental stages (see more details in Table S.2.4.1): Blastula (25), Gastrula (12), Segmentation (18), Pharyngula (8), Hatching (26), Treatment: WT (14): uninjected, CO (18): injected with control, MO (54): injected with target morpholino

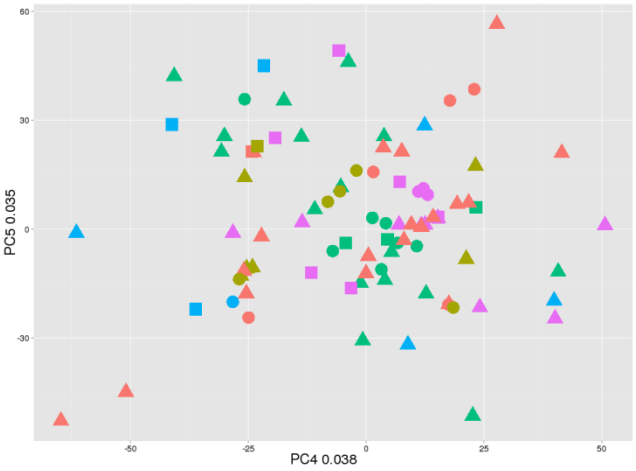
A) PC1-PC2



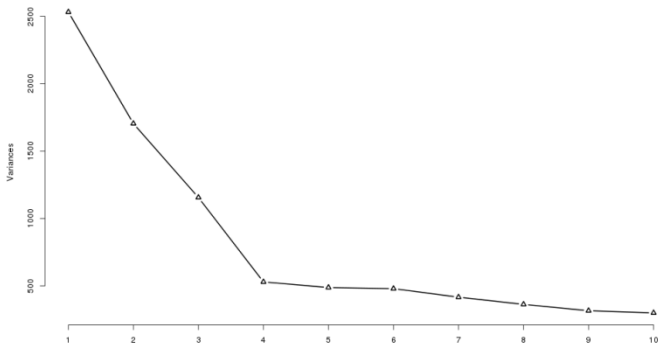
B) PC2-PC3



C) PC3-PC4



D) PC4-PC5



E) Eigenvalues of the principal components

3.4 Machine learning performance - Agilent

Table S.3.4A – LOOCV accuracy performance of Embedded feature selector methods

Feature selector	LOOCV	LOOCV scrambled
Glmnet	0.764	0.584 ± 0.042
Gaussian Linear process	0.652	0.494 ± 0.045
SVM Linear kernel	0.652	0.494 ± 0.045
Random Forest	0.706	0.539 ± 0.086
J48	0.741	0.526 ± 0.037
Naive Bayes	0.685	0.557 ± 0.032
SVM Radial kernel	0.674	0.517 ± 0.054
SVM Polynomial kernel	0.741	0.55 ± 0.053
PAM	0.674	0.52 ± 0.045
KNN	0.607	0.559 ± 0.072

Table S.3.4A – LOOCV accuracy performance of filter feature selector methods tested with K-nearest neighbour

Feature selector	Max LOOCV	Max LOOCV scrambled	Max distance to scramble
t-test	0.805 (54 feat.)	0.635 (1 feat.)	0.803 (83 feat.)
Relief	0.783 (189 feat.)	0.643 (121 feat.)	0.78 (232 feat.)
mRMR	0.673 (25 feat.)	0.69 (63 feat.)	0.657 (278 feat.)

3.5 Optimized parameters of embedded feature selectors

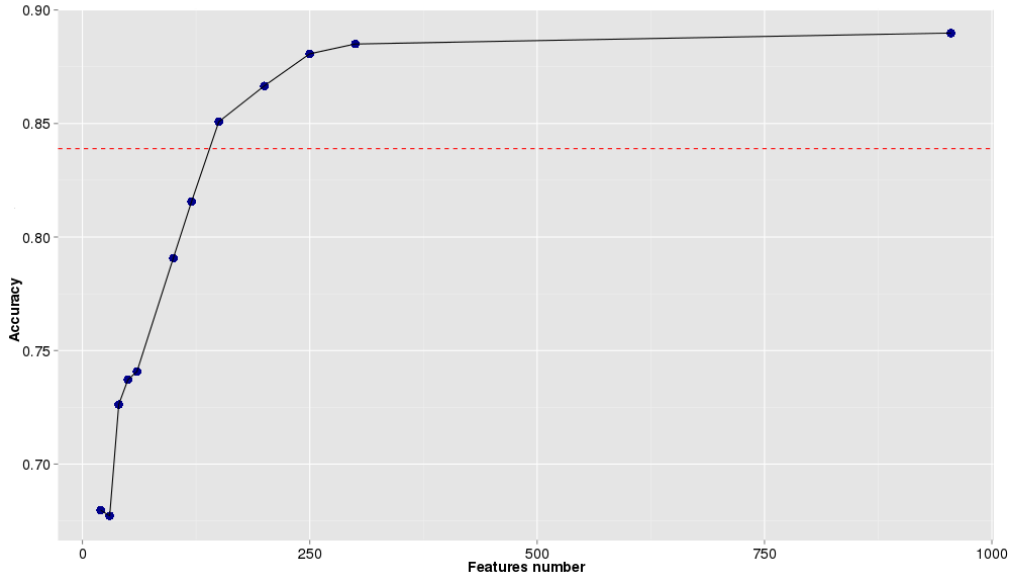
Table S.3.5 – Algorithms optimal parameters for the Affymetrix and Agilent datasets

Method	Parameters
Affymetrix	
GlmNet	Alpha: 0.1, Lambda: 0.1
Gaussian Linear	No parameters
SVM Linear	C: 1
Random Forest	Mtry: 3763 (max)
J48	C: 0.25
Naïve Bayes	fL: 0, usekerel: FALSE
SVM Radial kernel	Sigma: 0.00019, C: 0.5
SVM Polynomial kernel	Degree: 1 , Scale: 0.01 , C: 1
PAM	Threshold: 1.435
KNN	K: 5
Agilent	
GlmNet	Alpha: 1 , Lambda: 0.0986
Gaussian Linear	No parameters
SVM Linear	C: 1
Random Forest	Mtry: 103
J48	C: 0.25
Naïve Bayes	fL: 0, usekerel: TRUE
SVM Radial kernel	Sigma: 0.00011, C: 1
SVM Polynomial kernel	Degree: 2, Scale: 0.01, C: 0.25
PAM	Threshold: 0.849
KNN	K: 9

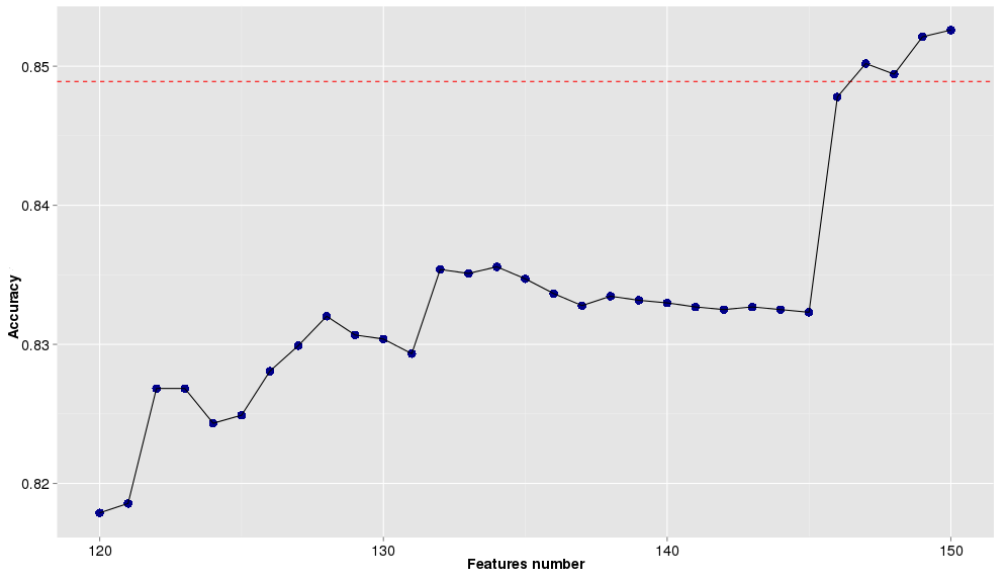
3.6 Recursive feature elimination – Affymetrix

Figure S.3.6– A) Model´s accuracy for features number equal to 20, 30, 40, 50, 60, 100, 120, 150, 200, 250, 300 and 955. The red line shows the 5% tolerance interval **B)** Model´s accuracy for features number from 120 to 150. The red line shows the 5% tolerance interval

A)



B)



3.7 Complete list of selected genes

Table S.3.7 – Feature selection: list of the genes selected with Gaussian Linear model. The regulation is the observed gene expression in Morphants (+ Upregulated, -Downregulated). The score is the importance value assigned by the model for separating the two classes.

Entrez gene ID	Gene name	Regulation in MO	Score
100534720	isg20	+	100.000
368779	phlda3	+	97.530
406311	pik3r3a	+	89.021
30590	tp53	+	88.747
393939	atf3	+	85.087
445220	riok3	+	83.806
792924	wu:fb55g09	+	82.708
555812	ucp2	-	78.957
559540	bmb	+	76.578
406397	mmp9	+	76.304
336967		+	75.206
100004299	arhgap35a	+	74.748
394198	fos	+	73.193
58081	baxa	+	72.736
677743	rps27.2	+	72.187
80963	rnd3a	+	71.272
100334953	nck1b	+	71.089
567253	atf5b	+	71.089
553721	rpp14	+	70.906
447811	rassf1	+	70.723
30637	mdm2	+	70.357
568593	sdc4	+	69.625
503589	gna12a	+	69.076
386815		+	68.893
30682	vegfaa	+	68.618
323503		+	68.253
336462		+	68.253
553212	st8sia6	+	68.253
368359	txnipa	+	67.887
100322182		+	67.521
393548	gadd45aa	+	67.521
100536496		+	67.429
30248	calr	-	67.246
556363	GPR108	+	67.063
561938	thumpd3	+	66.972
100003476	FAM117B (1 of 2)	+	66.880

114424	cdh1	+	66.514
323607	tmx1	+	66.514
559260	ENDOD1 (8 of 13)	-	66.514
406172	fat1a	+	66.423
678623	slc11a2	+	66.331
140744	ckbb	-	66.240
321708		+	66.240
445149		+	66.240
555328	serpinh1a	+	66.148
564994	rbms1a	+	66.148
335963		+	65.874
57965		+	65.874
323226	wsb1	+	65.691
246093	id3	+	65.599
566151	gas2l3	+	65.508
65231	mdkb	-	65.142
100004977	mthfd2	+	64.684
324215	igf2b	+	64.593
337513		+	64.593
325181	gpd1b	-	64.501
335839	cnbpb	+	64.501
793663	timm8b	+	64.227
334086	hspa4b	+	63.952
402843	sfrp1a	-	63.952
321197		+	63.769
335542		+	63.769
116991	ugdh	-	63.586
336335	si:ch211-51e12.7	-	63.586
321314	lmbr1l	-	63.403
386590	hsp90b1	-	63.312
58094	dap1b	-	63.312
100537724		+	63.038
406528	tdh	+	63.038
554119	mlx	+	62.946
555997	C2H1orf123	+	62.946
140614	xbp1	-	62.855
334393	iars	+	62.855
30719	gbp	-	62.397
406562	anp32e	-	62.397
322292		+	62.306
393109	rasl11b	+	62.031

567241	lepr	+	62.031
30081	ptpn1	+	61.940
325029		+	61.940
337130		+	61.665
393421	etnppl	-	61.665
572231	pfdn4	+	61.299
335072		+	61.208
563060	s100u	+	61.208
64603	eomesa	-	61.208
100148022	APOD (3 of 3)	-	61.116
564413	hipk3a	+	61.116
280647	kars	+	60.750
322841		+	60.750
352925		-	60.750
406787	kctd10	+	60.659
553622	phlda2	+	60.659
393834	arl4aa	+	60.567
407084	riok2	+	60.567
553715		+	60.476
30295	rho	-	60.293
799566	eif4ebp1	+	60.201
321177	sb:cb252	+	60.110
321986		+	60.110
336470	pak1ip1	+	60.110
337658		+	60.110
335838	lrrfip2	+	60.018
436766	jdp2	+	60.018
449555	zgc:101858	+	60.018
30596	hbbe3	+	59.927
325586	cyth1b	+	59.927
100007768	MRPL52	+	59.835
325557	anxa2a	+	59.744
117508	klf2a	-	59.652
436988	zgc:92360	+	59.652
335732	elovl4b	-	59.561
100331225	atad2b	+	59.561
751707	acsf2	-	59.469
553799	C9H2orf15	+	59.378
797137		+	59.286
326758		+	59.195
323343		+	59.103

570360	ppp6r2b	+	59.103
100536814	dnali1	+	59.012
100003675	p4ha1b	+	59.012
336227	cdr2l	-	59.012
337391		+	59.012
100334857	uqcrfs1	-	58.920
337093		+	58.920
322404	gltscr2	+	58.829
436826	polr3k	+	58.737
140620	prps1a	+	58.646
325655		+	58.646
445229	naa50	+	58.646
566223	atf5a	+	58.554
321298	col14a1a	+	58.463
322065		+	58.463
561159		+	58.463
317638	igfbp1a	+	58.371
564805	arhgap29a	+	58.371
79380	eif4ea	+	58.371
325269		+	58.280
386850	eif6	+	58.280
325637	nr2f6a	+	58.280
171473	ccng1	+	58.188
30698	nkx2.3	+	58.188
140820	ptprsa	+	58.097
325009		+	58.097
677757	mycbp	+	58.097
323672	naa15a	+	58.005

Table S.3.7.1 Genes filtered during the data processing with a strong correlation to the selected features (>0.95 Pearson correlation score)

387293	mmp13a	+	**327494**	zgc:66472	+
793785	rab6a	+	**558677**	zp3a.2	+
567949	piezo1	+	**559966**	kbtbd8	+
1E+08	zgc:173837	+	**664700**	zp2.5	+
1E+08	wu:fi42e03	+	**327506**	ckmt2a	+
1E+08	si:zfos-1505d6.3	+	**559073**	galnt1	+
114438	zp2.2	+	**336236**		+
114439	zp2.3	+	**336000**		+
114440	si:zfos-1505d6.3	+	**567632**	dnali1	+
30593	zp2.1	+	**406359**	uqcrfs1	+
327453	pfkfb1	+			

3.8 Detailed results from GSEA

Table S.3.8 A) Significant biological process GO terms and annexed genes

Description	P-value	Genes
intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	5.25E-6	phlda3 - pleckstrin homology-like domain, family a, member 3 tp53 - tumor protein p53
stress fiber assembly	1.01E-4	sdc4 - syndecan 4 gna12a - guanine nucleotide binding protein (g protein) alpha 12a
response to external stimulus	1.26E-4	wipi2 - wd repeat domain, phosphoinositide interacting 2 ap1b1 - adaptor-related protein complex 1, beta 1 subunit ctsd - cathepsin d pcna - proliferating cell nuclear antigen defbl1 - defensin, beta-like 1 atf3 - activating transcription factor 3 junba - jun b proto-oncogene a cebpb - ccaat/enhancer binding protein (c/ebp), beta mcm4 - mcm4 minichromosome maintenance deficient 4, mitotin (s. cerevisiae) jun - jun proto-oncogene atg4c - autophagy-related 4c (yeast) angptl4 - angiopoietin-like 4 mmp9 - matrix metalloproteinase 9 nuak2 - nuak family, snf1-like kinase, 2 ins - preproinsulin hadhaa - hydroxyacyl-coenzyme a dehydrogenase/3-ketoacyl-coenzyme a thiolase/enoyl-coenzyme a hydratase, alpha subunit a hspa5 - heat shock protein 5 pik3r4 - phosphoinositide-3-kinase, regulatory subunit 4 cyp26a1 - cytochrome p450, subfamily xxvia, polypeptide 1 lamc1 - laminin, gamma 1 rho - rhodopsin nbr1 - neighbor of brca1 gene 1 lamb1a - laminin, beta 1a
positive regulation of cell death	2.9E-4	phlda3 - pleckstrin homology-like domain, family a, member 3 tp53 - tumor protein p53 baxa - bcl2-associated x protein, a
actin filament bundle assembly	8.13E-4	sdc4 - syndecan 4 gna12a - guanine nucleotide binding protein (g protein) alpha 12a
positive regulation of peptidase activity	8.29E-4	tp53 - tumor protein p53 baxa - bcl2-associated x protein, a
response to stimulus	8.44E-4	sdc4 - syndecan 4 mmp9 - matrix metalloproteinase 9 phlda3 - pleckstrin homology-like domain, family a, member 3 atf3 - activating transcription factor 3 tmx1 - thioredoxin-related transmembrane protein 1 tp53 - tumor protein p53 gadd45aa - growth arrest and dna-damage-inducible, alpha, a mdm2 - transformed 3t3 cell double minute 2 homolog (mouse) baxa - bcl2-associated x protein, a
cell migration involved in heart development	8.95E-4	vegfaa - vascular endothelial growth factor aa gna12a - guanine nucleotide binding protein (g protein) alpha 12a

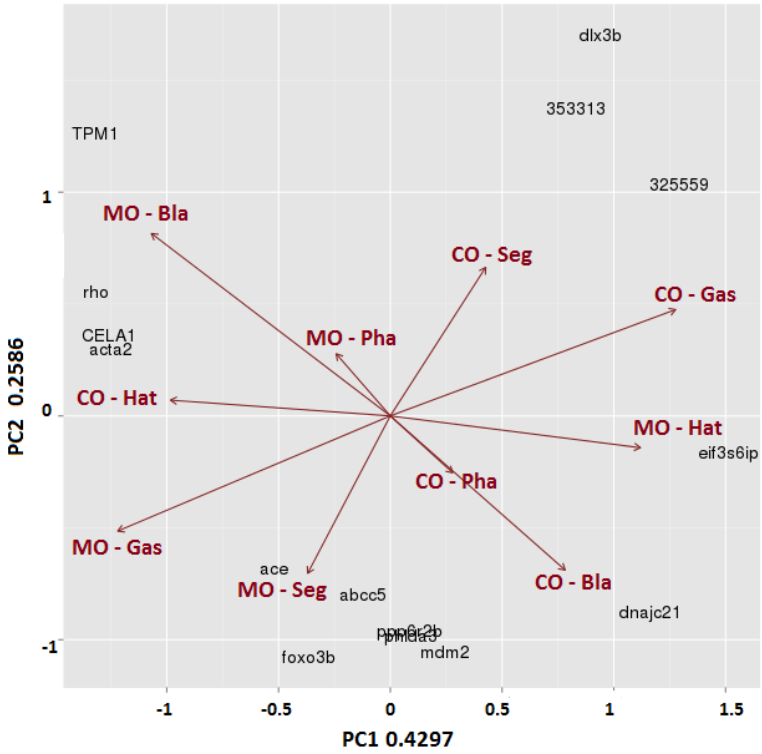
Table S.3.8 B) Significant molecular function GO terms and annexed genes

Description	P-value	Genes
phosphatidylinositol-4,5-bisphosphate binding	9.01E-5	sdc4 - syndecan 4 phlda3 - pleckstrin homology-like domain, family a, member 3
phosphatidylinositol-5-phosphate binding **phosphatidylinositol-3,4-bisphosphate binding** **phosphatidylinositol-3,4,5-trisphosphate binding**	3.84E-4	phlda3 - pleckstrin homology-like domain, family a, member 3
phosphatidylinositol 3-kinase regulator activity	7.67E-4	pik3r3a - phosphoinositide-3-kinase, regulatory subunit 3a (gamma)

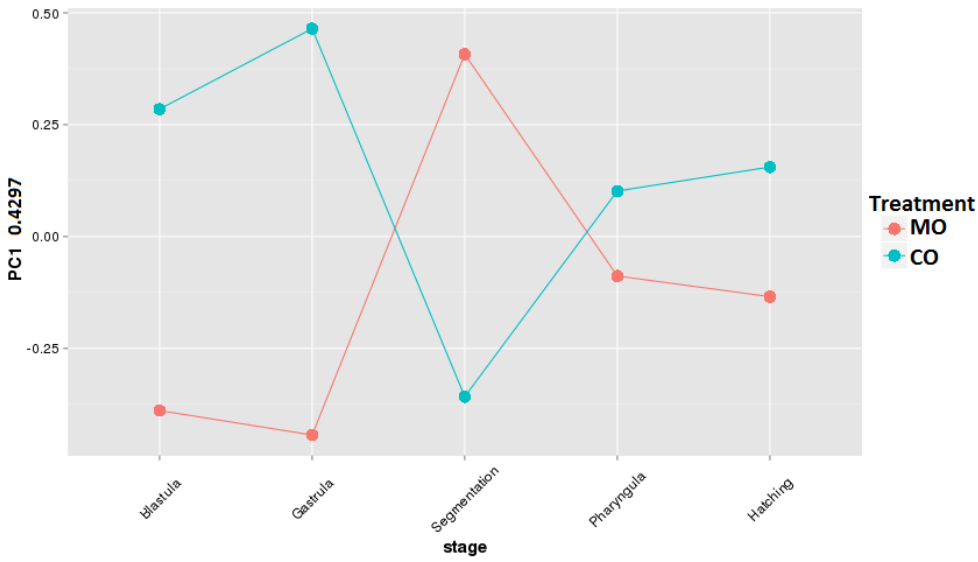
3.9 Interaction effect between developmental stage and treatment

Figure S.3.9– A) Biplot of th interaction coefficients: Developmental stage - Treatment **B)** Loadings of Bioplot´s principal component 1 (PC1)

A)



B)



3.10 Significant genes for developmental stage and treatment interaction in 2-way ANOVA and linear model

Table S.3.10 List of significant genes after ANOVA and linear model

Entrez gene ID	Gene name	Significant	Entrez gene ID	Gene name	Significant
30295	rho	0.001	**335166**		0.05
30296	foxo3b	0.001	**335716**	nme2a	0.05
30585	dlx3b	0.001	**368359**	txnipa	0.05
30637	mdm2	0.001	**369193**	aldocb	0.05
322509	acta2	0.001	**373080**	tuba1b	0.05
325559		0.001	**393117**	ccdc94	0.05
336147	abcc5	0.001	**394087**	arl6ip1	0.05
336984	dnajc21	0.001	**402863**	gtpbp1l	0.05
353313		0.001	**403023**	matn1	0.05
368779	phlda3	0.001	**406460**	ptp4a3	0.05
393908	TPM1 (2 of 2)	0.001	**406840**	sesn3	0.05
406402	eif3s6ip	0.001	**407696**	ddx52	0.05
445282	CELA1 (1 of 7)	0.001	**415236**	ppil3	0.05
565980	ace	0.001	**445030**	pomp	0.05
570360	ppp6r2b	0.001	**445133**	kctd15a	0.05
100003142	rpz5	0.05	**556995**	lig1	0.05
100148022	apoda.2	0.05	**558540**	mybl1	0.05
100534720	isg20	0.05	**558911**	nol7	0.05
100535672	prss59.2	0.05	**559540**	bmb	0.05
171481	fabp10a	0.05	**561947**		0.05
259189	hgd	0.05	**563328**	lamp1	0.05
30289	her3	0.05	**564608**	tmem198b	0.05
30590	tp53	0.05	**565144**	cenpk	0.05
30710	igf2a	0.05	**566445**	KRT78 (2 of 2)	0.05
321114	nhp2l1b	0.05	**568021**	tp53inp1	0.05
323401		0.05	**568155**	bnip4	0.05
325853		0.05	**58216**	atoh7	0.05
326088	ccnl1b	0.05	**64812**	sox19b	0.05
326098	med7	0.05	**677743**	rps27.2	0.05