

Default **miRComb** output

/media/Iomega_HDD/Projecte

January 19, 2015

1 Exploratory analysis of miRNA dataset

Number of miRNAs analysed	1733
Number of samples	12
Samples	

Table 1: Basic information of the miRNA dataset.

	group	DvH
H_1	H	0.00
H_2	H	0.00
H_3	H	0.00
D_1	D	1.00
D_2	D	1.00
D_3	D	1.00
D_4	D	1.00
D_5	D	1.00
D_6	D	1.00
D_7	D	1.00
D_8	D	1.00
D_9	D	1.00

Table 2: Phenotypical information of the miRNA dataset.

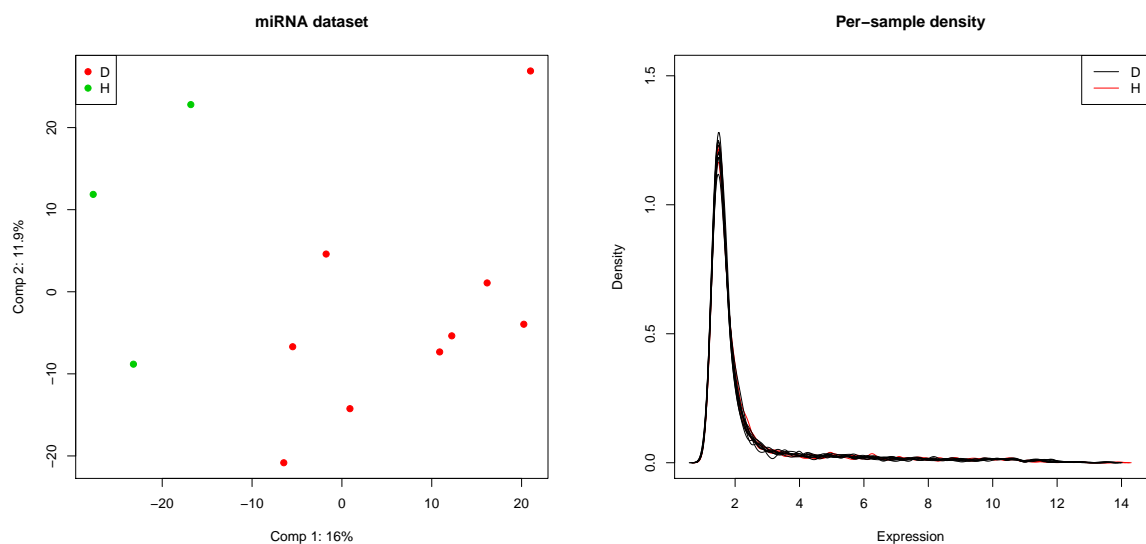


Figure 1: PCA and density plot for miRNAs.

2 Exploratory analysis of mRNA dataset

Number of mRNAs analysed	18900
Number of samples	12
Samples	

Table 3: Basic information of the miRNA dataset.

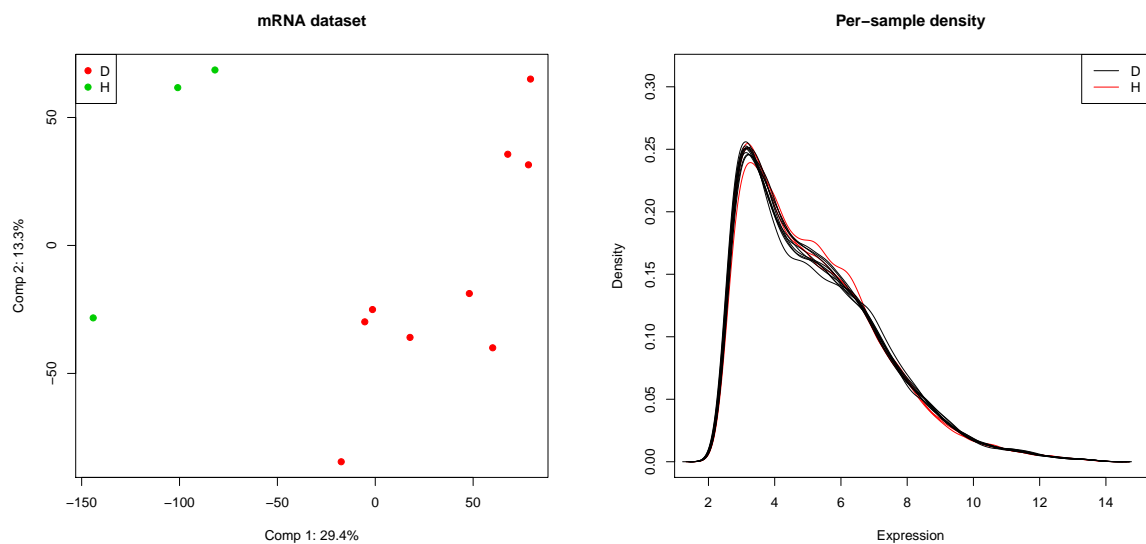


Figure 2: PCA and density plot for mRNAs.

	group	DvH
H.1	H	0.00
H.2	H	0.00
H.3	H	0.00
D.1	D	1.00
D.2	D	1.00
D.3	D	1.00
D.4	D	1.00
D.5	D	1.00
D.6	D	1.00
D.7	D	1.00
D.8	D	1.00
D.9	D	1.00

Table 4: Phenotypical information of the mRNA dataset.

3 Differentially expressed miRNAs

Number of miRNAs analysed	1733
Number of differentially expressed miRNAs	45 (15 upregulated, 30 downregulated)
Number of samples	12
Samples	
Criteria for selecting miRNAs	pval.cor: 0.05

Table 5: Basic statistics

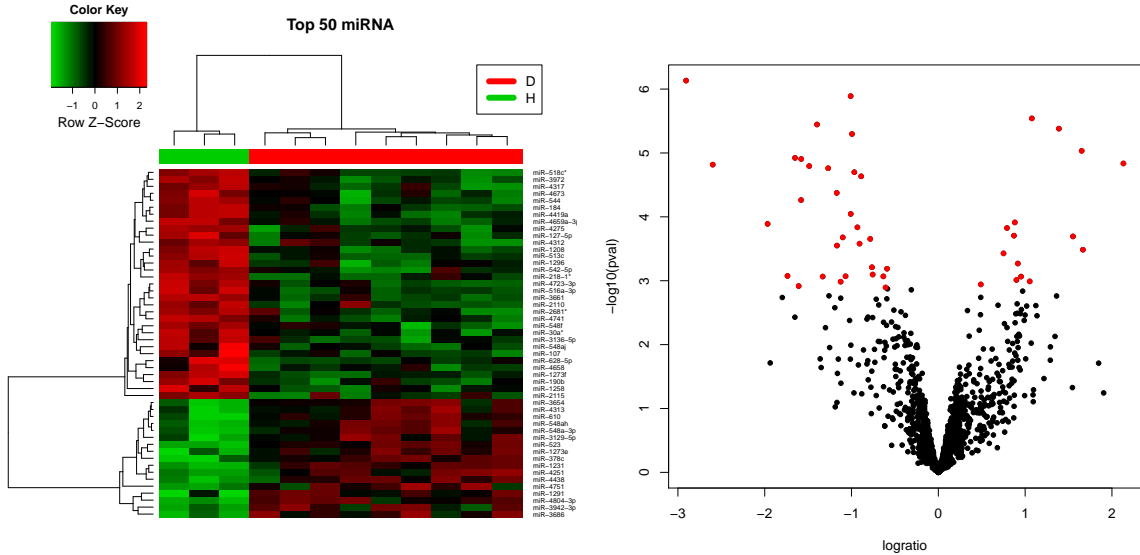


Figure 3: Significant miRNAs. Comparative used: DvH; method used: limma. Red dots highlight the selected miRNAs.

4 Differentially expressed mRNAs

Number of mRNAs analysed	18900
Number of differentially expressed mRNAs	2025 (1139 upregulated, 886 downregulated)
Number of samples	12
Samples	
Criteria for selecting mRNAs	logratio: 0.58
Criteria for selecting mRNAs	FC: 1.5
Criteria for selecting mRNAs	pval.cor: 0.05

Table 6: Basic statistics

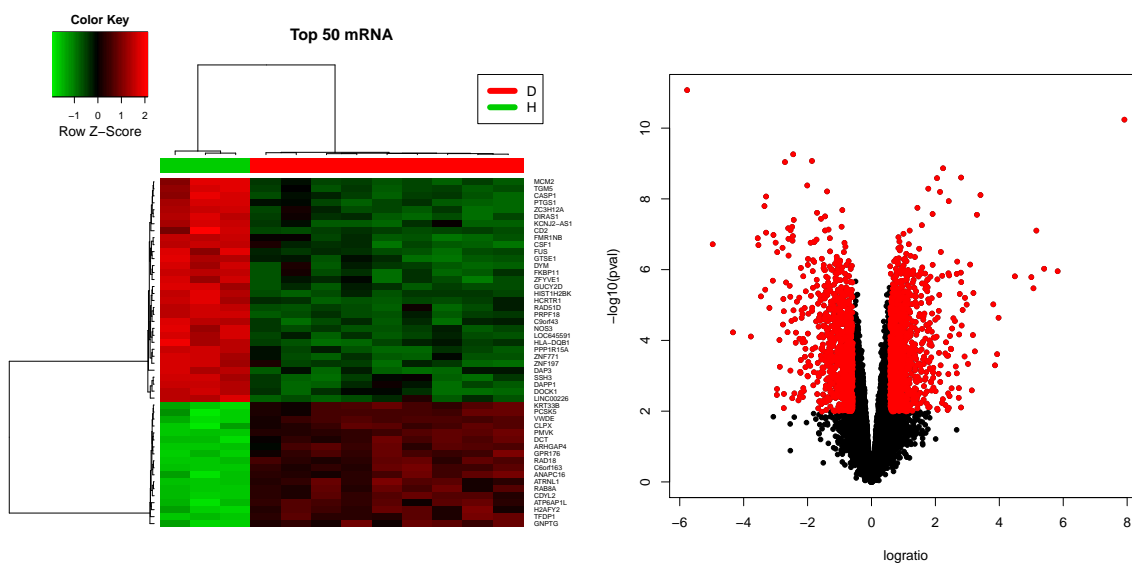


Figure 4: Significant mRNAs. Comparative used: DvH; method used: limma. Red dots highlight the selected mRNAs.

5 Correlation & intersection with databases

Number of miRNAs	45
Number of mRNAs	2025
Total miRNA-mRNA combinations	91125
Number of samples	12
Samples	

Table 7: Number of miRNAs, mRNAs and samples used for correlation.

	Number	%
Total correlations	91125	100
Total negative correlations	47460	52.08
Total correlations $p < 0.05$	44437	48.76
Total correlations $p < 0.01$	32267	35.41
Total correlations p-corrected < 0.05	38956	42.75
Total correlations p-corrected < 0.01	17465	19.17

Table 8: Basic statistics for correlation results. Correlation hypothesis: less.

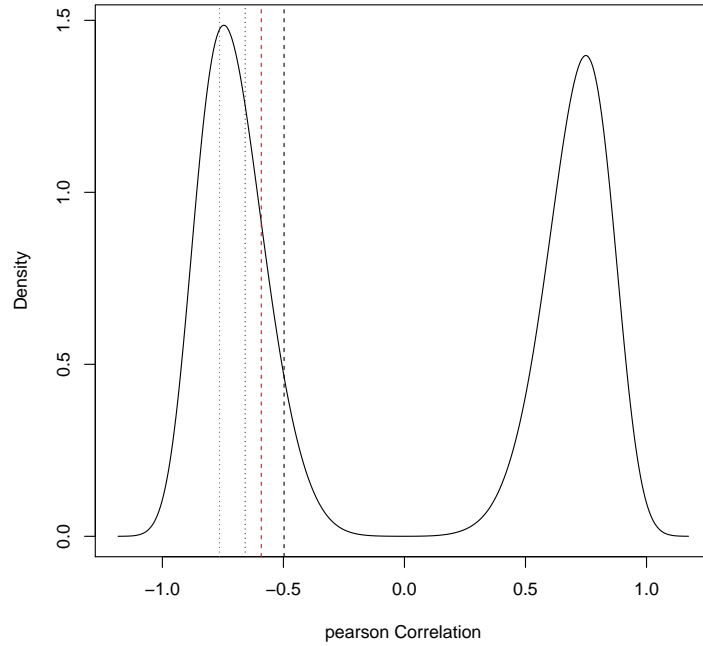


Figure 5: Density of a total of 91125 miRNA-mRNA pairs. Dashed lines distinguish correlations whose p-value is lower than 0.05, dotted lines for 0.01. Black is for raw p-value and red for adjusted p-value.

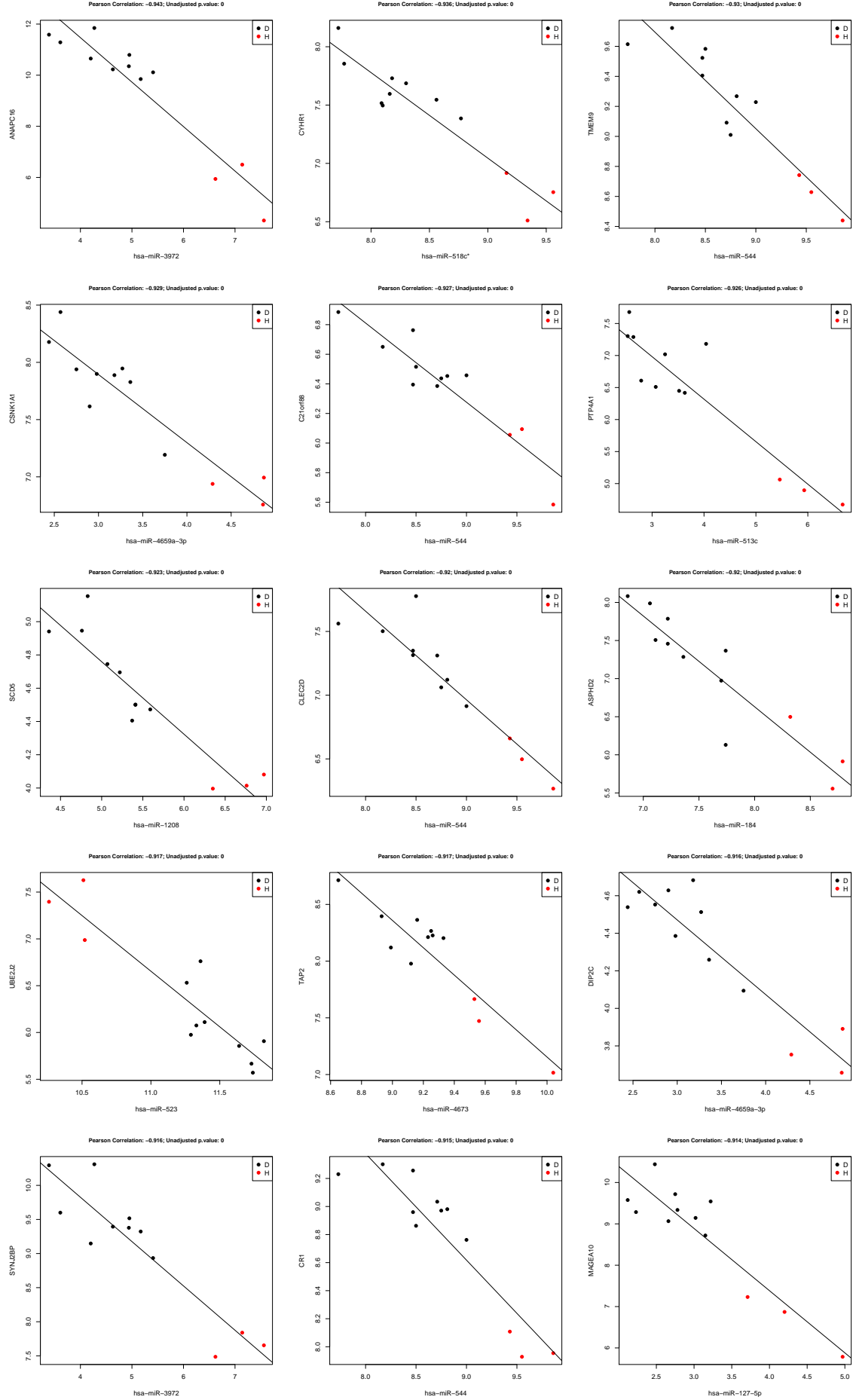


Figure 6: Plot of 15 top correlations

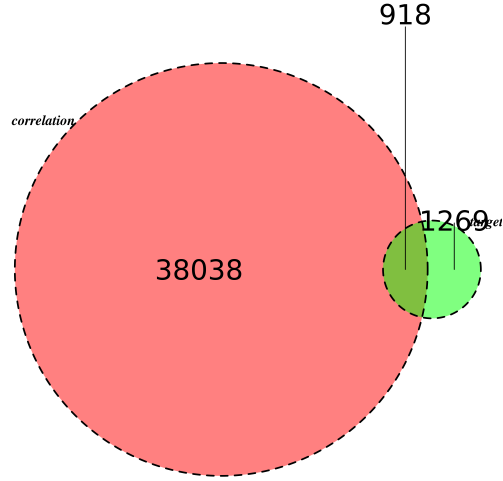


Figure 7: Venn Diagram. Database(s) selected: microCosm_v5_18, targetScan_v6.2_18 (minimum coincidences across databases: 1), Pval-adjusted cutoff: 0.05

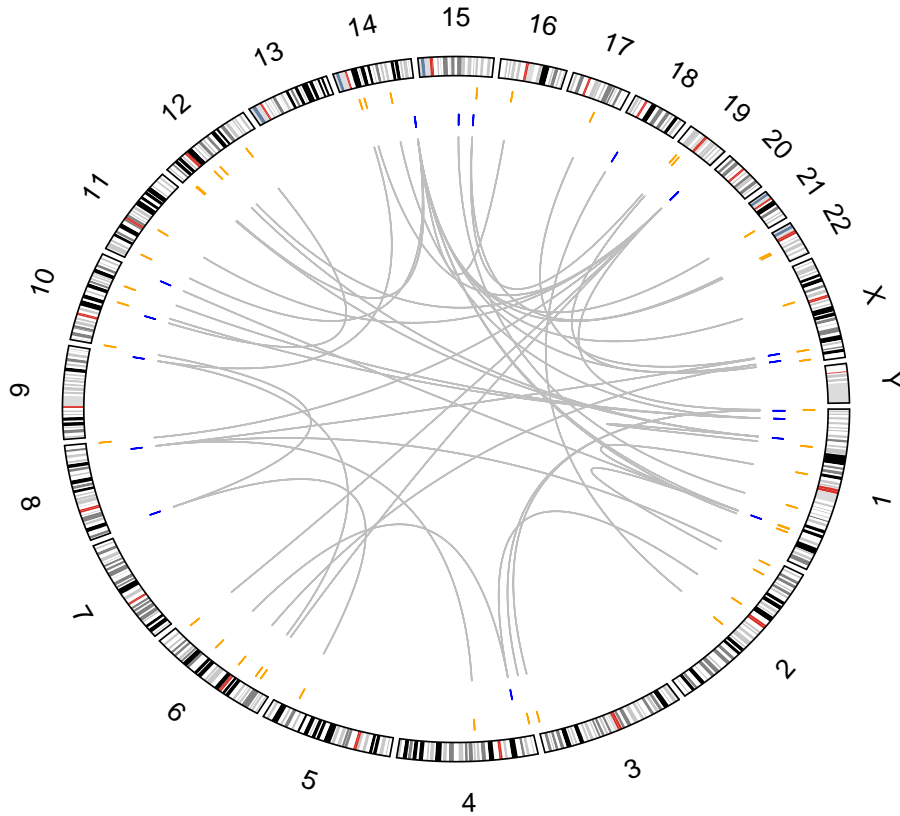


Figure 8: Circos for pval-corrected<0.05 and Targets=microCosm_v5_18, targetScan_v6.2_18 (minimum coincidences across databases: 1), restricted to first 45 miRNA-mRNA pairs, sorted by correlation.

miRNA	mRNA	cor	pval.corrected	FC.miRNA	FC.mRNA	dat.sum
hsa-miR-3972	ANAPC16	-0.94	1.25e-03	-6.06	35.75	1
hsa-miR-518c*	CYHR1	-0.94	1.37e-03	-2.25	1.91	1
hsa-miR-544	TMEM9	-0.93	1.42e-03	-2.15	1.72	1
hsa-miR-4659a-3p	CSNK1A1	-0.93	1.44e-03	-3.14	1.98	1
hsa-miR-544	C21orf88	-0.93	1.46e-03	-2.15	1.56	1
hsa-miR-513c	PTP4A1	-0.93	1.51e-03	-7.49	4.18	1
hsa-miR-1208	SCD5	-0.92	1.57e-03	-2.99	1.60	1
hsa-miR-544	CLEC2D	-0.92	1.62e-03	-2.15	1.80	1
hsa-miR-184	ASPHD2	-0.92	1.62e-03	-2.41	2.65	1
hsa-miR-523	UBE2J2	-0.92	1.70e-03	2.11	-2.44	1
hsa-miR-4673	TAP2	-0.92	1.70e-03	-1.52	1.85	1
hsa-miR-4659a-3p	DIP2C	-0.92	1.70e-03	-3.14	1.63	1
hsa-miR-3972	SYNJ2BP	-0.92	1.70e-03	-6.06	3.69	1
hsa-miR-544	CR1	-0.92	1.71e-03	-2.15	2.06	1
hsa-miR-127-5p	MAGEA10	-0.91	1.72e-03	-2.99	6.94	1
hsa-miR-628-5p	LMX1A	-0.91	1.74e-03	-3.91	2.06	1
hsa-miR-523	GANAB	-0.91	1.76e-03	2.11	-1.62	1
hsa-miR-1231	DPYSL5	-0.91	1.78e-03	2.62	-1.98	1
hsa-miR-518c*	GLS2	-0.91	1.84e-03	-2.25	6.35	1
hsa-miR-518c*	AP4S1	-0.91	1.91e-03	-2.25	4.50	1
hsa-miR-548a-3p	MEX3B	-0.91	1.91e-03	1.89	-4.46	1
hsa-miR-523	KIAA0319	-0.91	1.91e-03	2.11	-1.97	1
hsa-miR-518c*	SOD2	-0.91	1.91e-03	-2.25	1.58	1
hsa-miR-218-1*	SH2D6	-0.91	1.93e-03	-2.80	1.68	1
hsa-miR-184	TMED1	-0.91	1.94e-03	-2.41	7.60	1
hsa-miR-1208	SLC9A6	-0.91	1.94e-03	-2.99	3.09	1
hsa-miR-218-1*	SCML4	-0.91	1.94e-03	-2.80	2.18	1
hsa-miR-4251	RNF4	-0.90	1.95e-03	2.07	-1.58	1
hsa-miR-1231	NTNG1	-0.90	2.01e-03	2.62	-1.69	1
hsa-miR-544	CALCA	-0.90	2.20e-03	-2.15	1.55	1
hsa-miR-1273f	NECAP1	-0.90	2.24e-03	-2.01	2.01	1
hsa-miR-513c	RAB8A	-0.90	2.25e-03	-7.49	1.79	1
hsa-miR-1273f	ANO6	-0.90	2.26e-03	-2.01	1.59	1
hsa-miR-1208	ITGB1BP1	-0.89	2.35e-03	-2.99	1.94	1
hsa-miR-4741	POLR2D	-0.89	2.36e-03	-1.85	2.59	1
hsa-miR-1296	KIAA1033	-0.89	2.38e-03	-3.34	8.51	1
hsa-miR-3972	SCD	-0.89	2.43e-03	-6.06	5.91	1
hsa-miR-544	SCNN1B	-0.89	2.47e-03	-2.15	2.22	1
hsa-miR-544	WNK3	-0.89	2.47e-03	-2.15	6.11	1
hsa-miR-1273f	INADL	-0.89	2.47e-03	-2.01	1.52	1
hsa-miR-4251	FAM43A	-0.89	2.48e-03	2.07	-1.52	1
hsa-miR-127-5p	RASL10A	-0.89	2.49e-03	-2.99	1.64	1
hsa-miR-378c	IPO9	-0.89	2.53e-03	4.38	-2.41	1
hsa-miR-542-5p	SPATA20	-0.89	2.54e-03	-1.55	8.11	1
hsa-miR-4741	SBF1	-0.88	2.59e-03	-1.85	1.56	1

Table 9: Top 45 miRNA-mRNA pairs, sorted by correlation (minimum coincidences across databases: 1).

6 Functional analysis

6.1 Network analysis

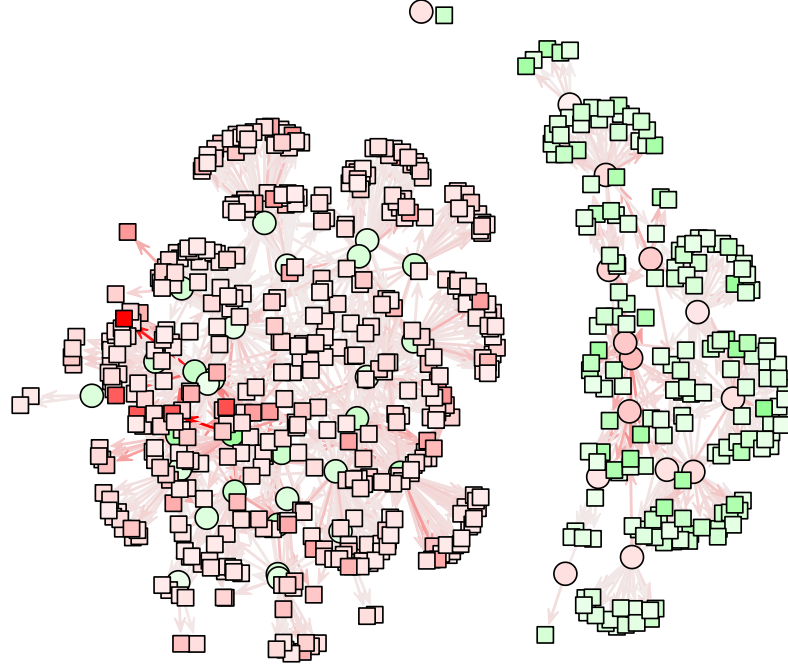


Figure 9: Network for $p\text{-val-corrected} < 0.05$ and Targets=microCosm_v5_18, targetScan_v6.2_18 (minimum coincidences between databases:1)

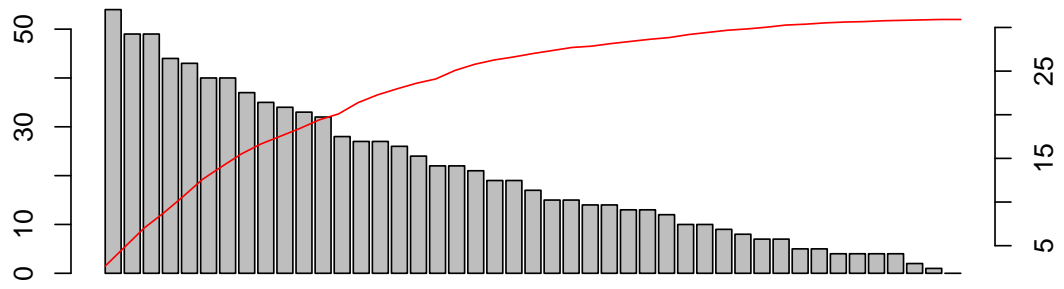


Figure 10: Barplot for miRNAs, $p\text{-val-corrected} < 0.05$ and Targets=microCosm_v5_18, targetScan_v6.2_18(minimum coincidences between databases:1). Red line (and right axis) represents the percentage of deregulated mRNAs that are targeted by the miRNAs.

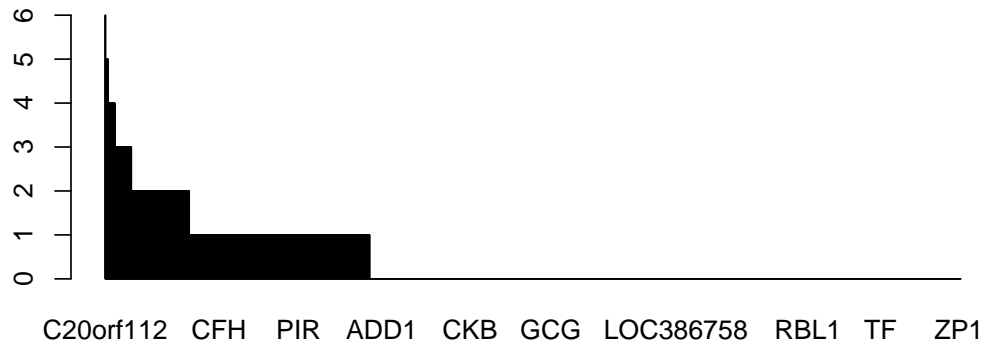


Figure 11: Barplot for mRNAs, $p\text{-val-corrected} < 0.05$ and Targets=microCosm_v5_18, targetScan_v6.2_18(minimum coincidences between databases:1).

6.2 GO analysis

	freq	names
hsa-miR-544	54	AFF3, ANKRD32, ATG12, BAHCC1, BMP1, C16orf48, C1orf68, C21orf88, C6orf89, C7orf60, CALCA, CBFA2T2, CDKN2AIP, CLEC2D, CLYBL, CR1, CSDE1, DAZAP2, FAM123B, FRAS1, FRY, HIST1H4A, INVS, IRF2BP2, MAGEB6, MKI67, MPZL1, MTMR12, MYC, NOVA1, OGT, PEPD, PIR, PITRM1, PJA2, RRAGA, SCNN1B, SDK1, SELT, SGMS1, SLC35F2, SLC39A10, SNTG2, SOD2, STOM, SUB1, TMEM9, TMOD2, TTC12, UNC13B, USP48, WNK3, ZNF518B, ZNF629
hsa-miR-107	49	AFG3L2, AKAP12, BAIAP2, BAZ2A, BCAS4, BCOR, CACNA2D1, CARD14, CGGBP1, CREB3L3, CSNK1A1, EIF2C4, EN2, FAM176A, FAM49A, FBXW7, GLS2, HADH, HEMGN, IDUA, IRF2BP2, ISLR, KIAA1033, KPNA1, MCM7, MRPS16, MTMR3, NFIL3, NKTR, NMUR2, NOVA1, NRBP1, OGT, PEPD, PGD, PLCE1, PPP6C, PTH, RLN1, SATB2, SCML4, SIK2, SMAD9, SOD2, TFDP1, TRAF3, TSEN2, UBE2F, WASF3
hsa-miR-516a-3p	49	A2ML1, ADCK1, ALPK3, ANKRD27, ANTXR1, ARRB1, BAIAP2, BTBD16, C14orf102, CEP250, CHST2, CREB3L3, DCLRE1A, DOM3Z, EFNB1, EN2, EPG5, ESF1, GIN1, GOLT1A, GPR176, GPR35, GRPEL2, GSTP1, H2AFY2, HIVEP3, HPDL, KCNA6, LILRB5, LRP1, MOCS2, NCAPD3, NPC2, PHF7, PIK3CD, PLD4, RAC3, REL, RINT1, SCN3B, SDK1, SLC22A14, SLC26A11, TM6SF2, TMEM8B, TRAF3, TRPV4, WDR69, ZG16
hsa-miR-4659a-3p	44	AK4, ANKRD7, ANKS4B, ARL5A, BAZ2A, BHLHE40, CD84, CDADC1, CSGALNACT2, CSNK1A1, CSNK1D, DDX6, DIP2C, DSE, DUSP19, ELAVL4, EN2, EPG5, FAM123B, GIGYF1, INADL, ITGB1BP1, ITPK1, KCNQ3, KIAA1033, KIF3A, LPIN3, LRP6, MTMR12, NKTR, PAN3, PUM2, RBMS3, SLC9A6, SNTB2, SNX10, SRF, SSPN, SYT15, TFF2, TRAF3, UVRAG, VWDE, YEATS2
hsa-miR-184	43	AFG3L2, AMPD2, AP4S1, ARHGDI1, ASPHD2, BAD, BAI2, C19orf25, C20orf112, C9orf86, CALCA, DNAH17, GPBAR1, HIVEP3, HUWE1, IGSF9B, NENF, NMNAT3, PAN3, PGD, POLR3GL, PROK1, PXN, RPA1, RPN1, SCD5, SEMA7A, SIRT6, SIX2, SLC25A28, SLC4A7, SPIRE2, STC2, TBXA2R, TLX3, TMED1, TOP2B, TP53BP2, TSSK2, UROC1, WNT10B, ZNF784, ZSCAN2

Table 10: Top 5 miRNA with more targets (FDR <0.05 and minimum coincidences across databases: 1).

GOBPID	Pvalue	fdr	OddsRatio	ExpCount	Count	Size	Term
GO:0006470	4.10e-04	5.19e-01	3.11	4.92	14	140	protein dephosphorylation
GO:0046324	1.03e-03	5.19e-01	4.99	1.62	7	46	regulation of glucose import
GO:0034048	1.23e-03	5.19e-01	Inf	0.07	2	2	negative regulation of protein phosphatase type 2A activity
GO:0043408	1.25e-03	5.19e-01	1.92	16.54	30	471	regulation of MAPK cascade
GO:0010675	1.67e-03	5.19e-01	3.10	3.86	11	110	regulation of cellular carbohydrate metabolic process
GO:0005979	1.87e-03	5.19e-01	6.60	0.91	5	26	regulation of glycogen biosynthetic process
GO:0010962	1.87e-03	5.19e-01	6.60	0.91	5	26	regulation of glucan biosynthetic process
GO:0046323	1.92e-03	5.19e-01	4.42	1.79	7	51	glucose import
GO:0050655	1.95e-03	5.19e-01	9.22	0.56	4	16	dermatan sulfate proteoglycan metabolic process
GO:0070925	2.06e-03	5.19e-01	2.12	10.50	21	299	organelle assembly

Table 11: Biological Process Options used: adjusted-pval cutoff:; mininum coincidences across databases:1; organism: human.