

Analysis

LCHNL

combined (1–3)

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Experiment Name	combined (1–3)
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Scanned	
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redo with

- vsn2
- detection filter

for Julia Brenndörfer

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1 Raw Data

The data for this experiment were obtained from ILLUMINA[®] gene expression arrays (array type Array type), yielding 46657 gene probes from 78 samples (using 13 arrays).

1.1 Coverage

The following 666 probes (out of 47323 probes listed in the annotation) were not sampled on at least one array and thus dropped:

The list of lost genes has been written to LCHNLallnew_lostgenes.txt.

1.2 Samples

The 78 samples were assigned the following array slots:

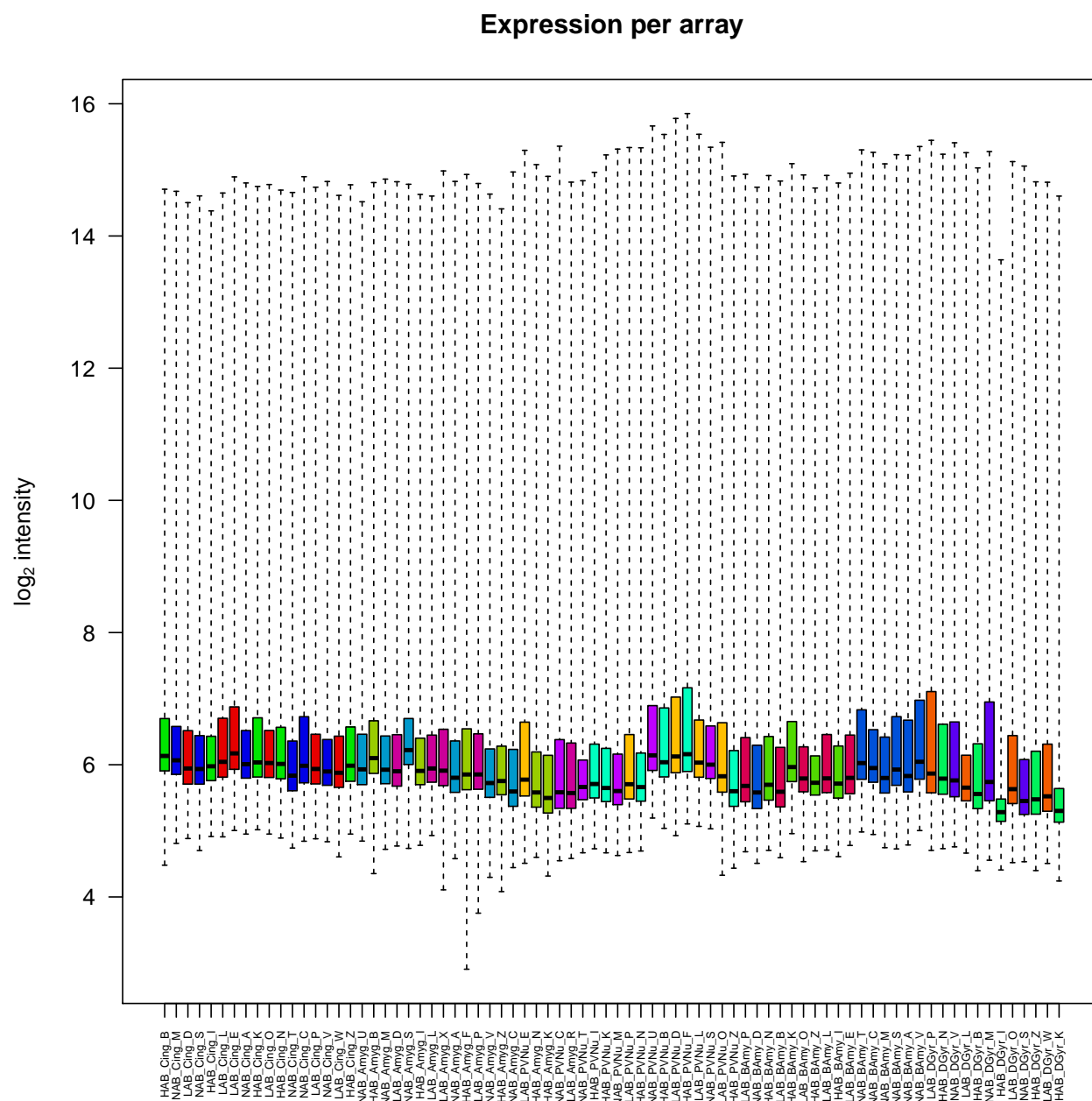
	Sample_Group	Sentrix_ID	Sentrix_Position
1	HAB_Cing_B	1736925168	A
2	NAB_Cing_M	1736925168	B
3	LAB_Cing_D	1736925168	C
4	NAB_Cing_S	1736925168	D
5	HAB_Cing_I	1736925168	E
6	LAB_Cing_L	1736925168	F
7	LAB_Cing_E	1736925185	A
8	NAB_Cing_A	1736925185	B
9	HAB_Cing_K	1736925185	C
10	LAB_Cing_O	1736925185	D
11	HAB_Cing_N	1736925185	E
12	NAB_Cing_T	1736925185	F
13	NAB_Cing_C	1736925219	A
14	LAB_Cing_P	1736925219	B
15	NAB_Cing_V	1736925219	C
16	LAB_Cing_W	1736925219	D
17	HAB_Cing_Z	1736925219	E
18	NAB_Amyg_U	1736925219	F
19	HAB_Amyg_B	1736925265	A
20	NAB_Amyg_M	1736925265	B
21	LAB_Amyg_D	1736925265	C
22	NAB_Amyg_S	1736925265	D
23	HAB_Amyg_I	1736925265	E
24	LAB_Amyg_L	1736925265	F
25	LAB_Amyg_X	1736925266	A
26	NAB_Amyg_A	1736925266	B
27	HAB_Amyg_F	1736925266	C
28	LAB_Amyg_P	1736925266	D
29	NAB_Amyg_V	1736925266	E
30	HAB_Amyg_Z	1736925266	F
31	NAB_Amyg_C	1736925270	A
32	LAB_PVNu_E	1736925270	B
33	HAB_Amyg_N	1736925270	C

continued on next page

	Sample_Group	Sentrix_ID	Sentrix_Position
34	HAB_Amyg_K	1736925270	D
35	NAB_PVN <u>u</u> _C	1736925270	E
36	LAB_Amyg_R	1736925270	F
37	NAB_PVN <u>u</u> _T	1736925183	A
38	HAB_PVN <u>u</u> _I	1736925183	B
39	HAB_PVN <u>u</u> _K	1736925183	C
40	NAB_PVN <u>u</u> _M	1736925183	D
41	LAB_PVN <u>u</u> _P	1736925183	E
42	HAB_PVN <u>u</u> _N	1736925183	F
43	NAB_PVN <u>u</u> _U	1736925333	A
44	HAB_PVN <u>u</u> _B	1736925333	B
45	LAB_PVN <u>u</u> _D	1736925333	C
46	HAB_PVN <u>u</u> _F	1736925333	D
47	LAB_PVN <u>u</u> _L	1736925333	E
48	NAB_PVN <u>u</u> _S	1736925333	F
49	LAB_PVN <u>u</u> _O	1736925330	A
50	HAB_PVN <u>u</u> _Z	1736925330	B
51	LAB_Bamy_P	1736925330	C
52	NAB_Bamy_D	1736925330	D
53	HAB_Bamy_N	1736925330	E
54	LAB_Bamy_B	1736925330	F
55	HAB_Bamy_K	1736925328	A
56	LAB_Bamy_O	1736925328	B
57	HAB_Bamy_Z	1736925328	C
58	LAB_Bamy_L	1736925328	D
59	HAB_Bamy_I	1736925328	E
60	LAB_Bamy_E	1736925328	F
61	NAB_Bamy_T	1736925184	A
62	NAB_Bamy_C	1736925184	B
63	NAB_Bamy_M	1736925184	C
64	NAB_Bamy_S	1736925184	D
65	NAB_Bamy_A	1736925184	E
66	NAB_Bamy_V	1736925184	F
67	LAB_Dgyr_P	1736925172	A
68	HAB_Dgyr_N	1736925172	B
69	NAB_Dgyr_V	1736925172	C
70	LAB_Dgyr_L	1736925172	D
71	HAB_Dgyr_B	1736925172	E
72	NAB_Dgyr_M	1736925172	F
73	HAB_Dgyr_I	1736925271	A
74	LAB_Dgyr_O	1736925271	B
75	NAB_Dgyr_S	1736925271	C
76	HAB_Dgyr_Z	1736925271	D
77	LAB_Dgyr_W	1736925271	E
78	HAB_Dgyr_K	1736925271	F

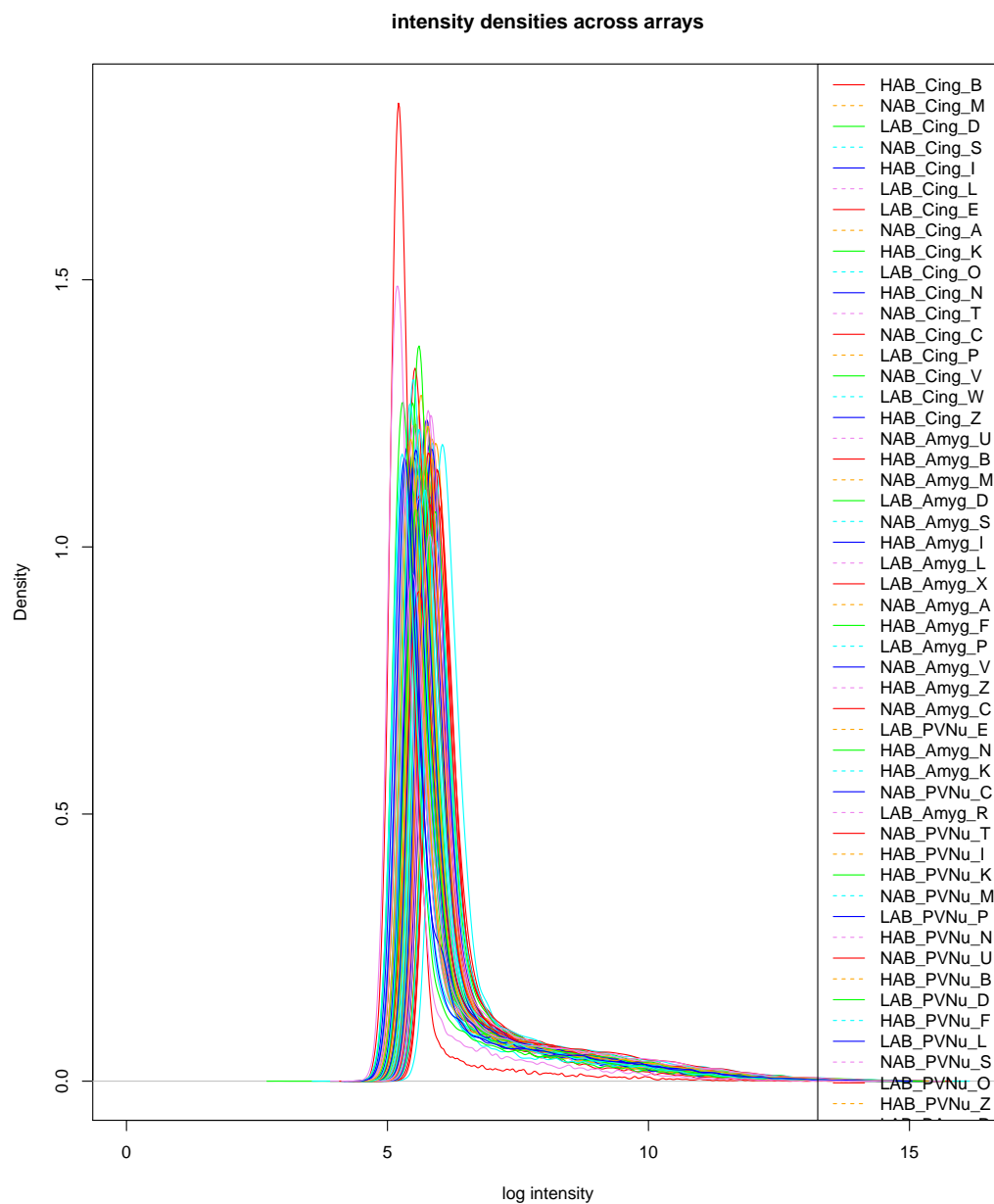
1.3 Simple boxplots

Simple boxplots of expression levels and number of each bead type. For each section the boxes extend from the first to the third quartile of the intensity distribution, the horizontal lines indicate the medians, the whiskers extend to the extreme data points.



1.4 Raw Intensity distribution across arrays

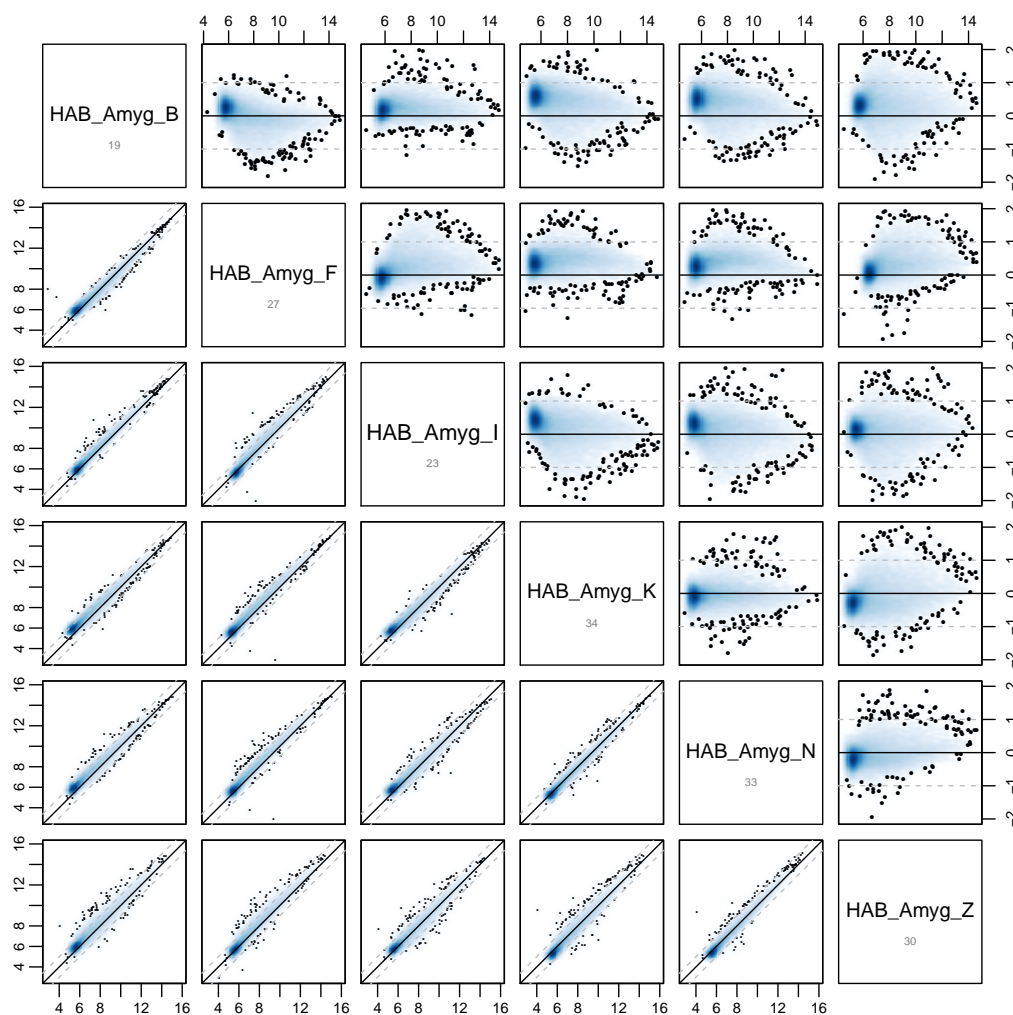
The raw data show the following intensity distribution across arrays



1.5 Groupwise pair plots

The following pages show similar plots for the data within each sample group, as these should be more similar and deviations are more apparent. The plots show the density distribution of the genes on the array, i. e., darker shading indicates more genes at a given point in the graphs, with “border genes” highlighted by individual dots. The plots in the lower left show \log_2 intensity in one section vs. \log_2 intensity in the other, the plots in the upper right show so-called MA-plots¹, which essentially rotate the lower left plots, showing the expression ratios more clearly.

Pairwise plots for group HAB_Amyg

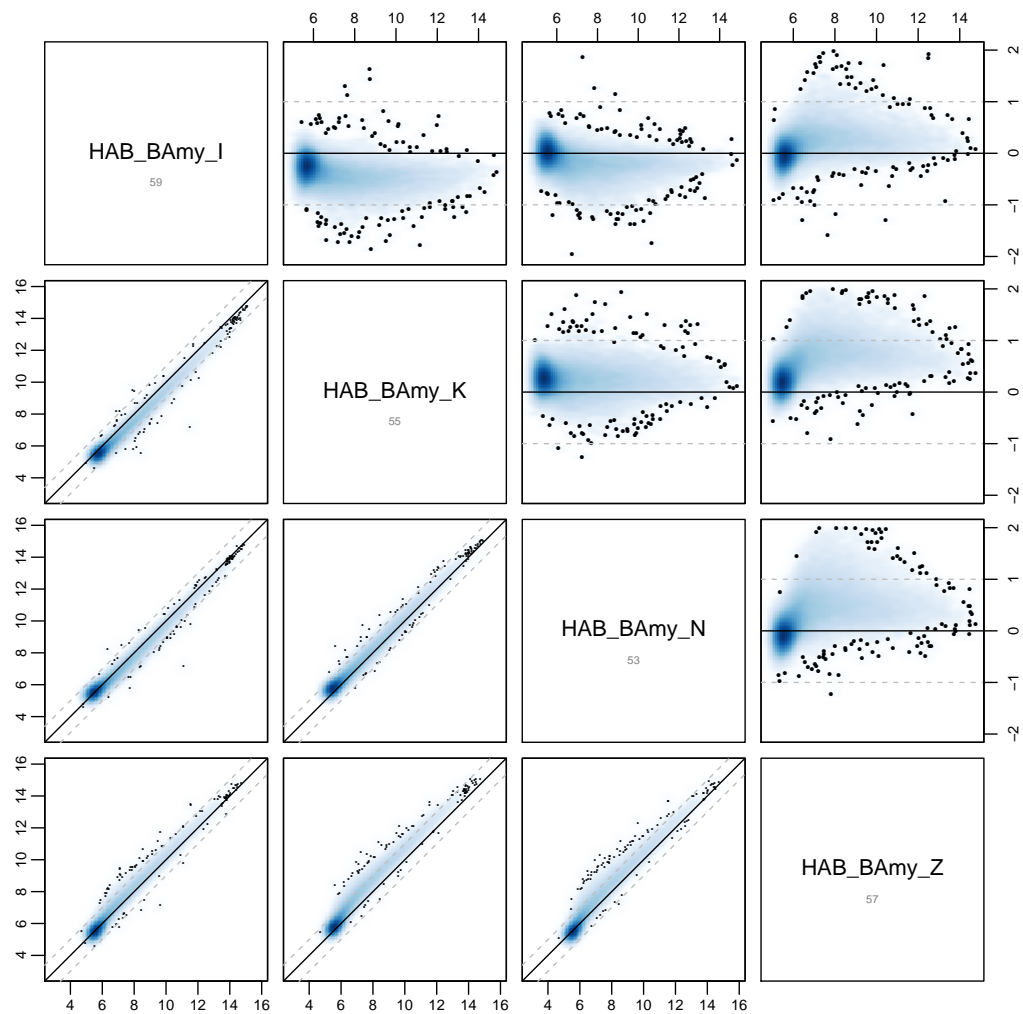


¹The MA-plot (proposed by Dudoit[2]) is a graphical way to see log-ratios and fluorescence intensity at the same time using the transformations:

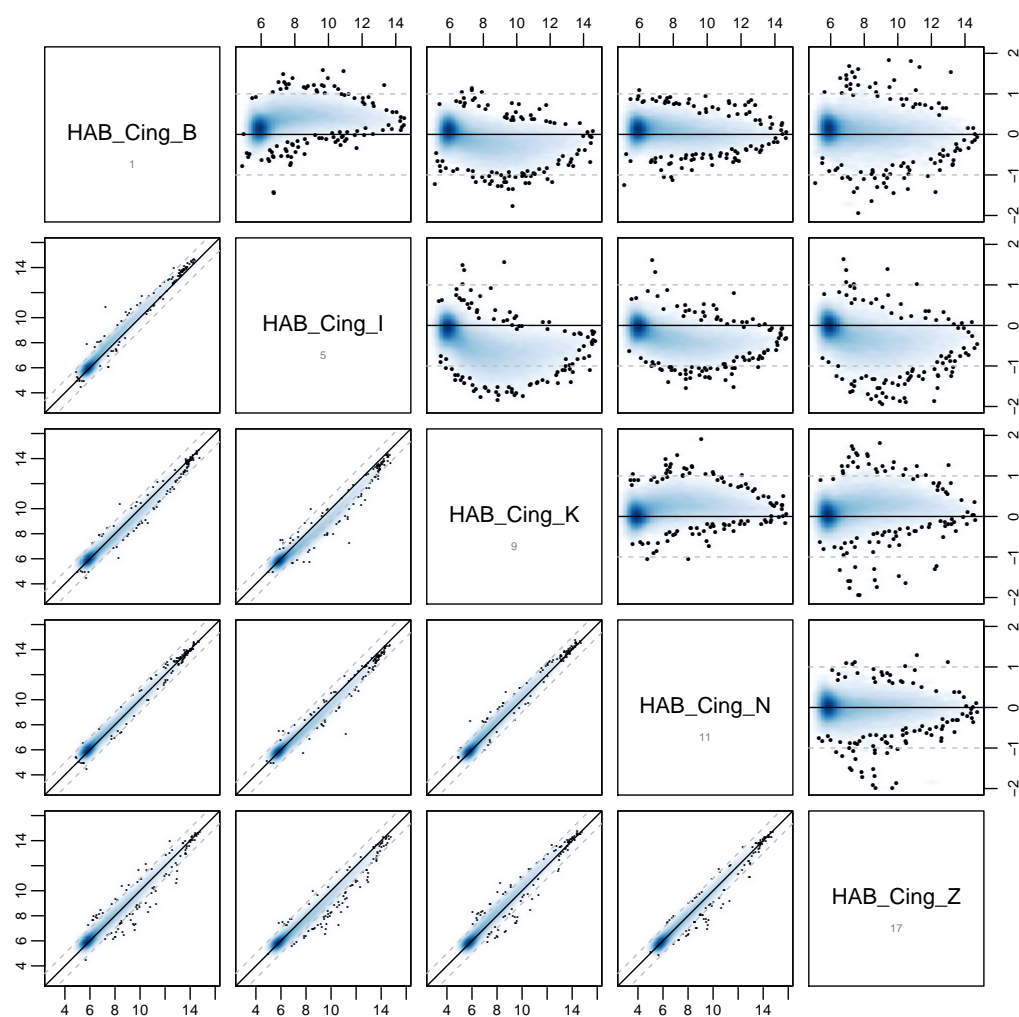
$$A = \frac{1}{2}(\log_2(I_1) + \log_2(I_2)) \quad (1)$$

$$M = \log_2(I_1) - \log_2(I_2) \quad (2)$$

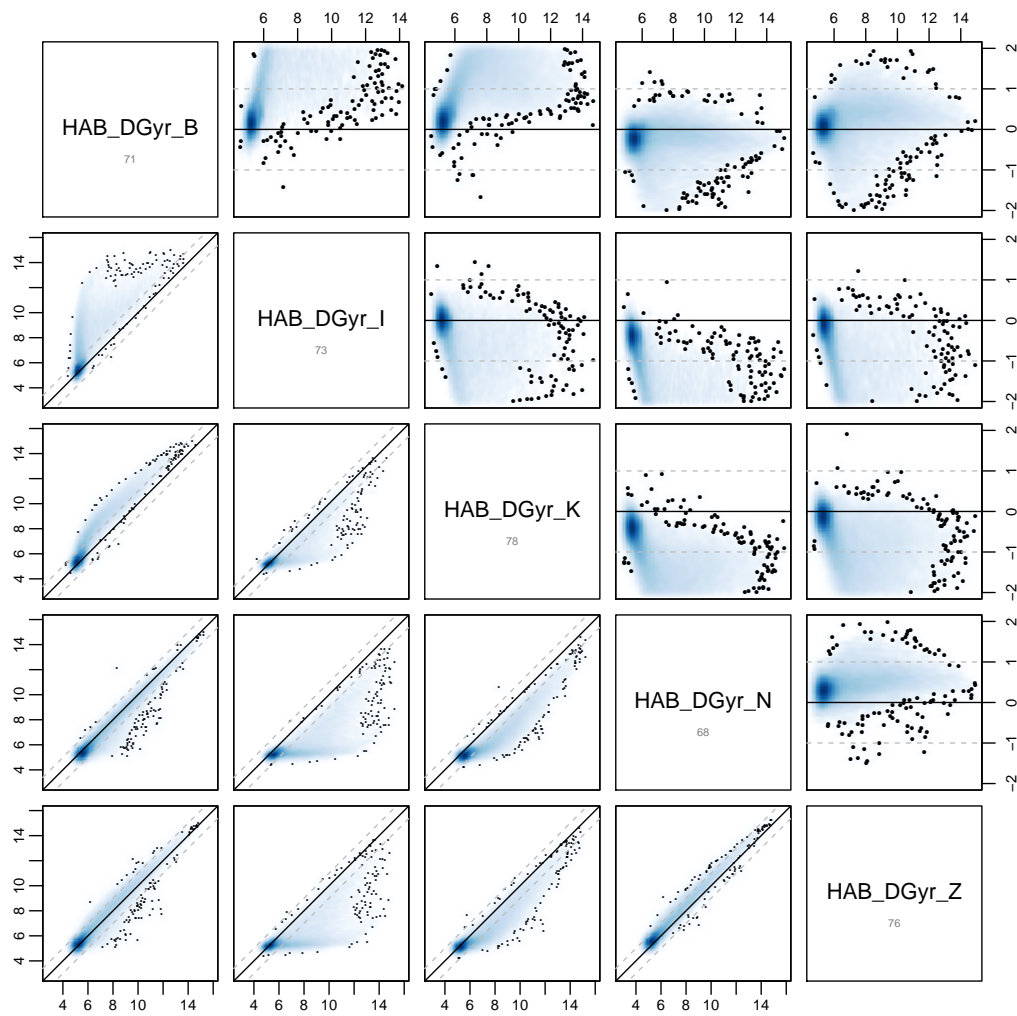
Pairwise plots for group HAB_BAmy



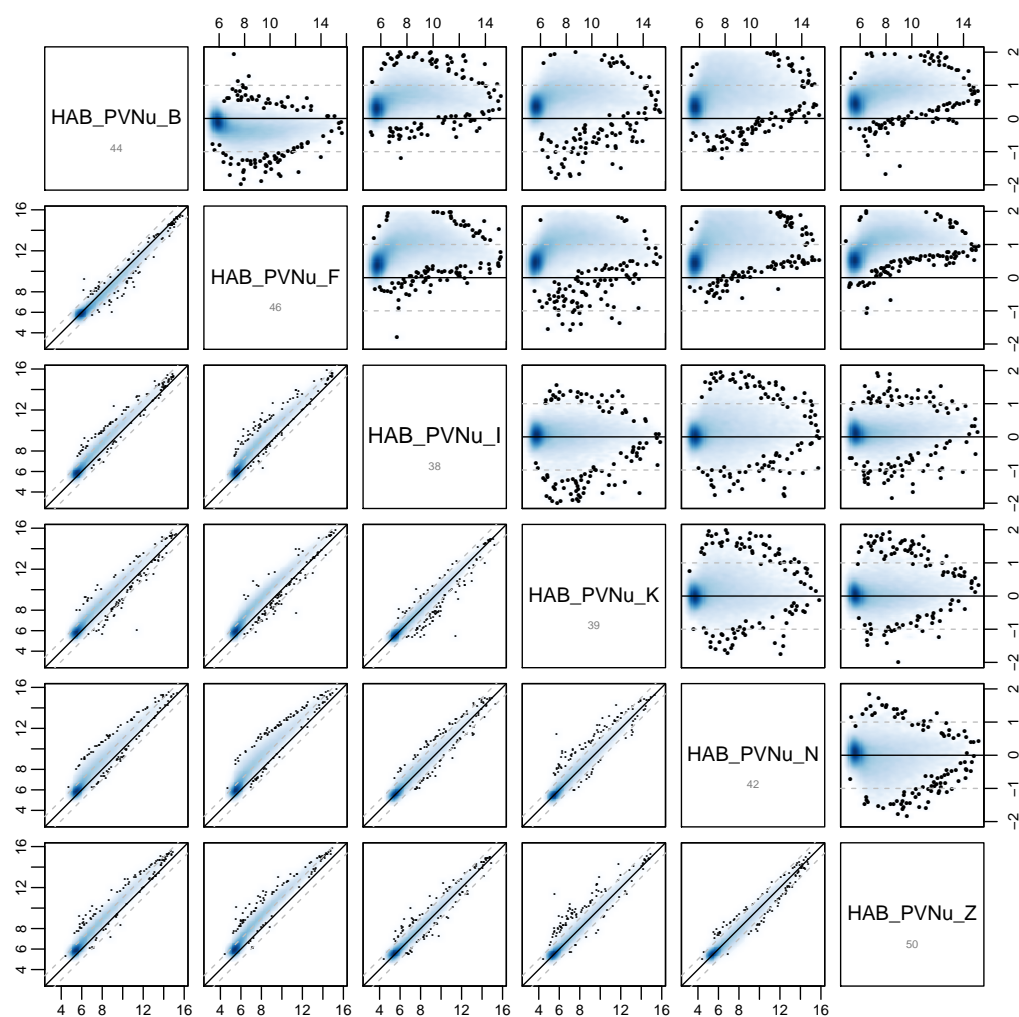
Pairwise plots for group HAB_Cing



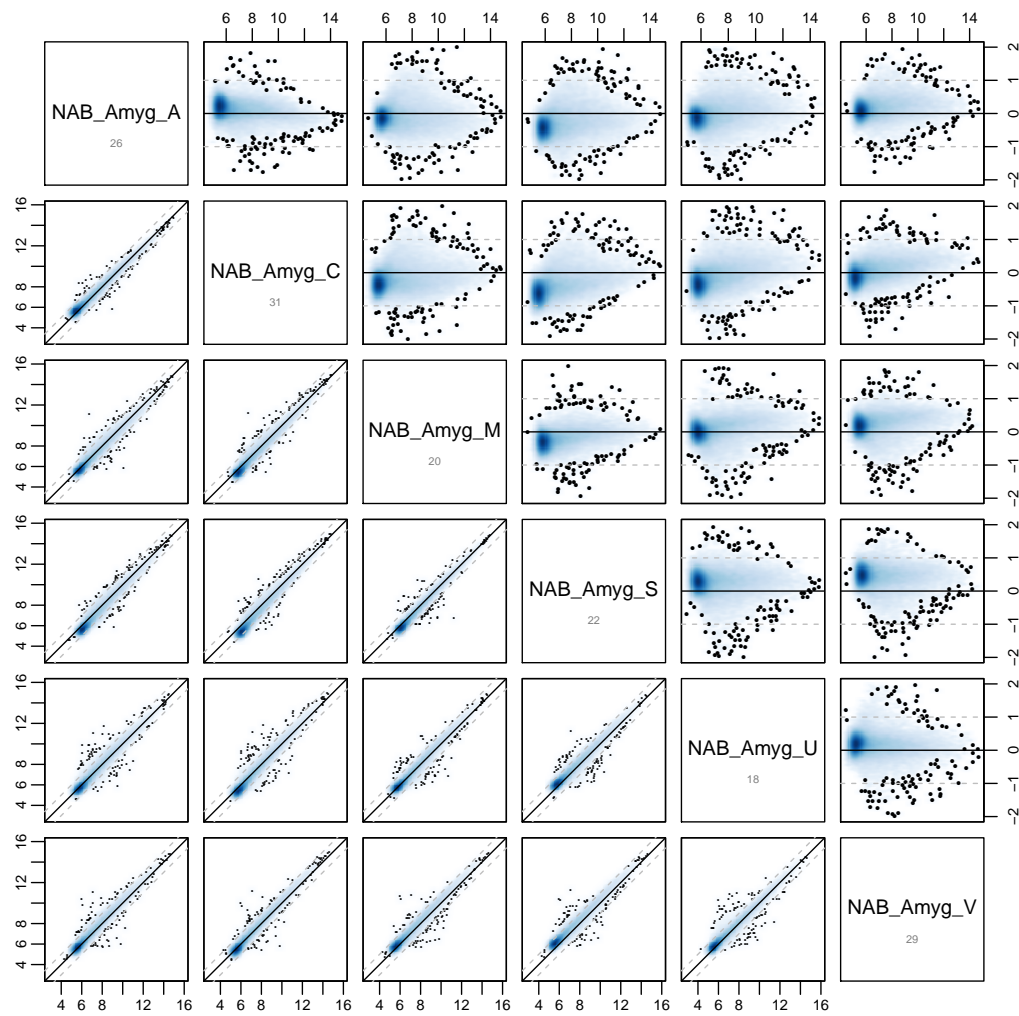
Pairwise plots for group HAB_DGyr



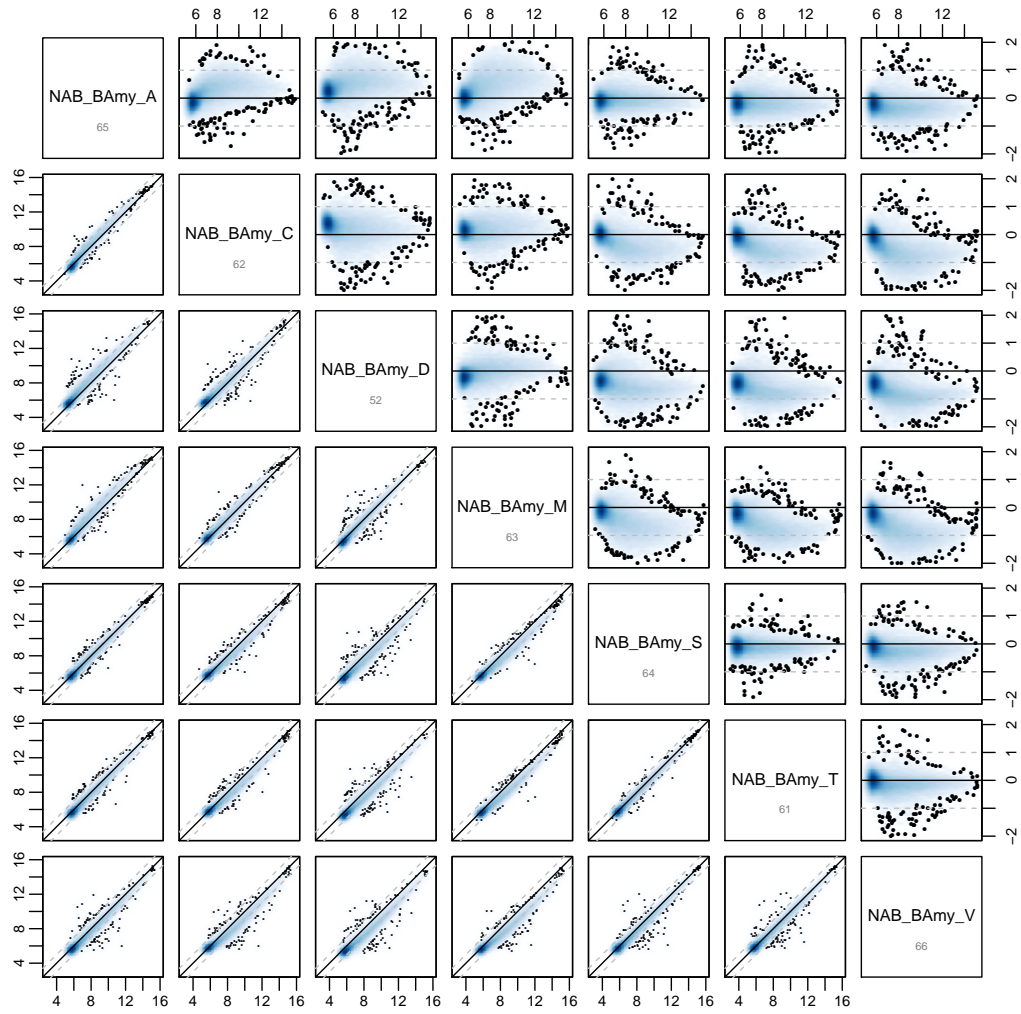
Pairwise plots for group HAB_PVNu



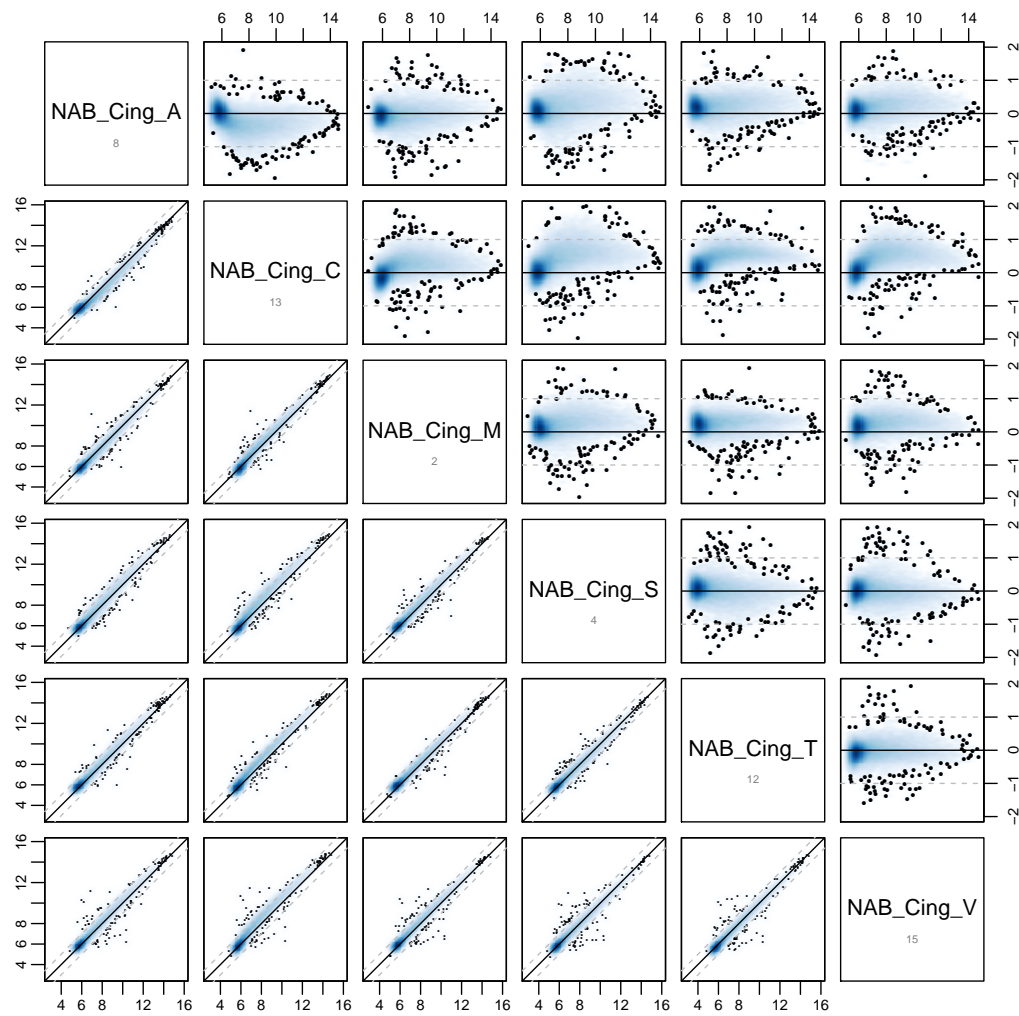
Pairwise plots for group NAB_Amyg



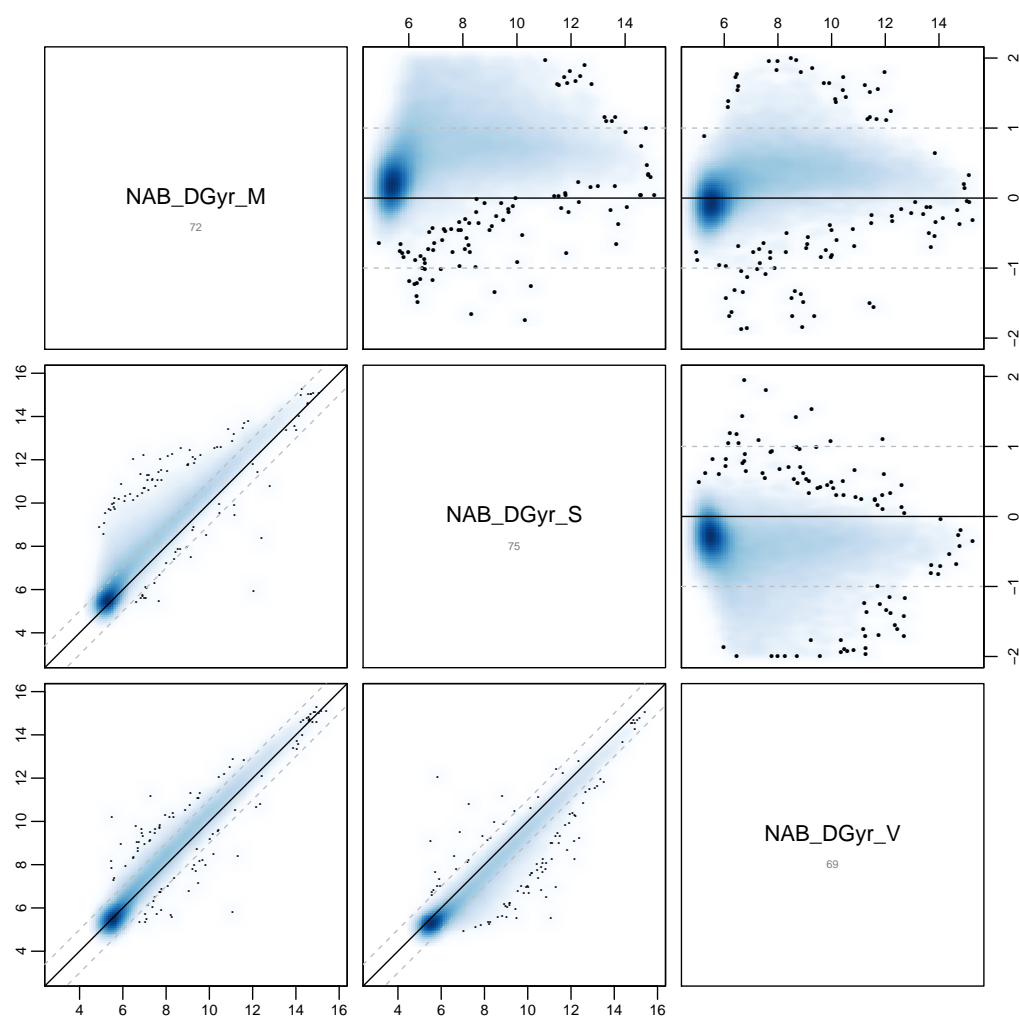
Pairwise plots for group NAB_BAmy



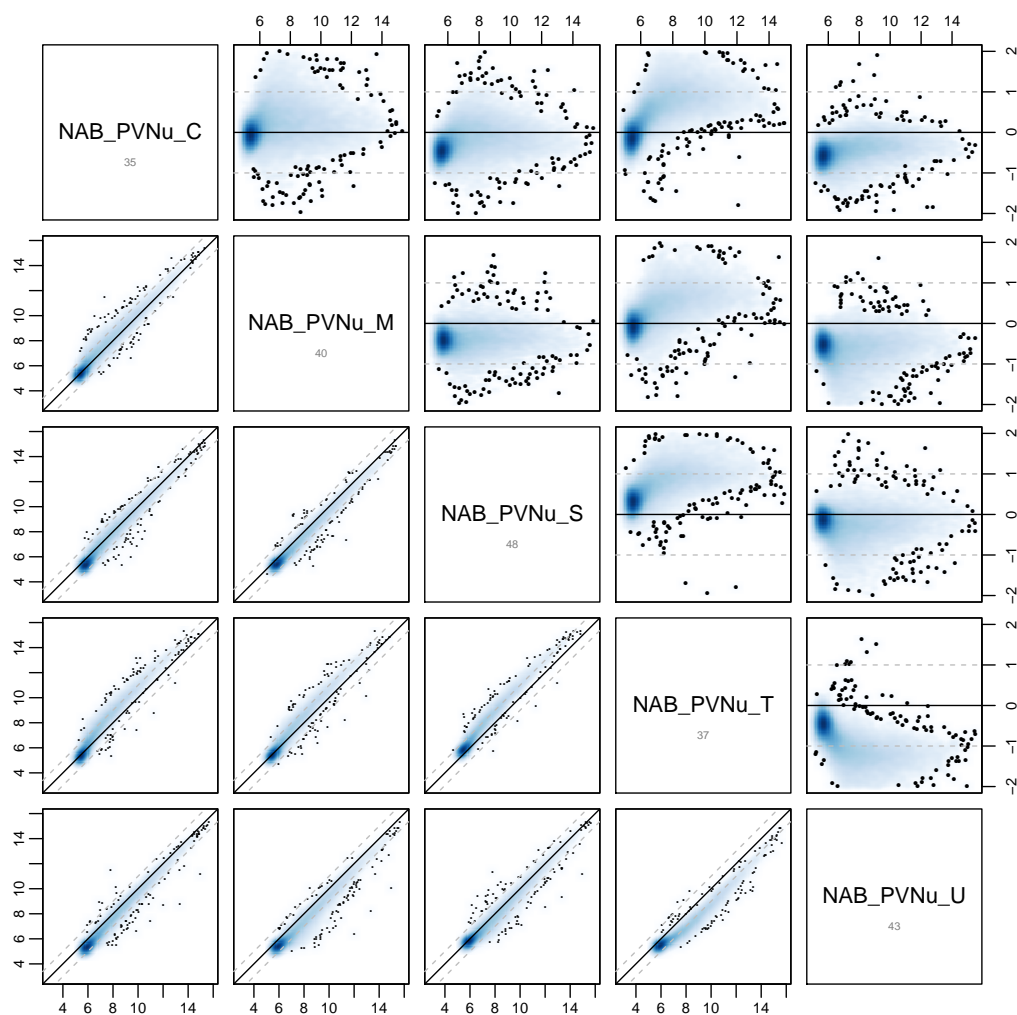
Pairwise plots for group NAB_Cing



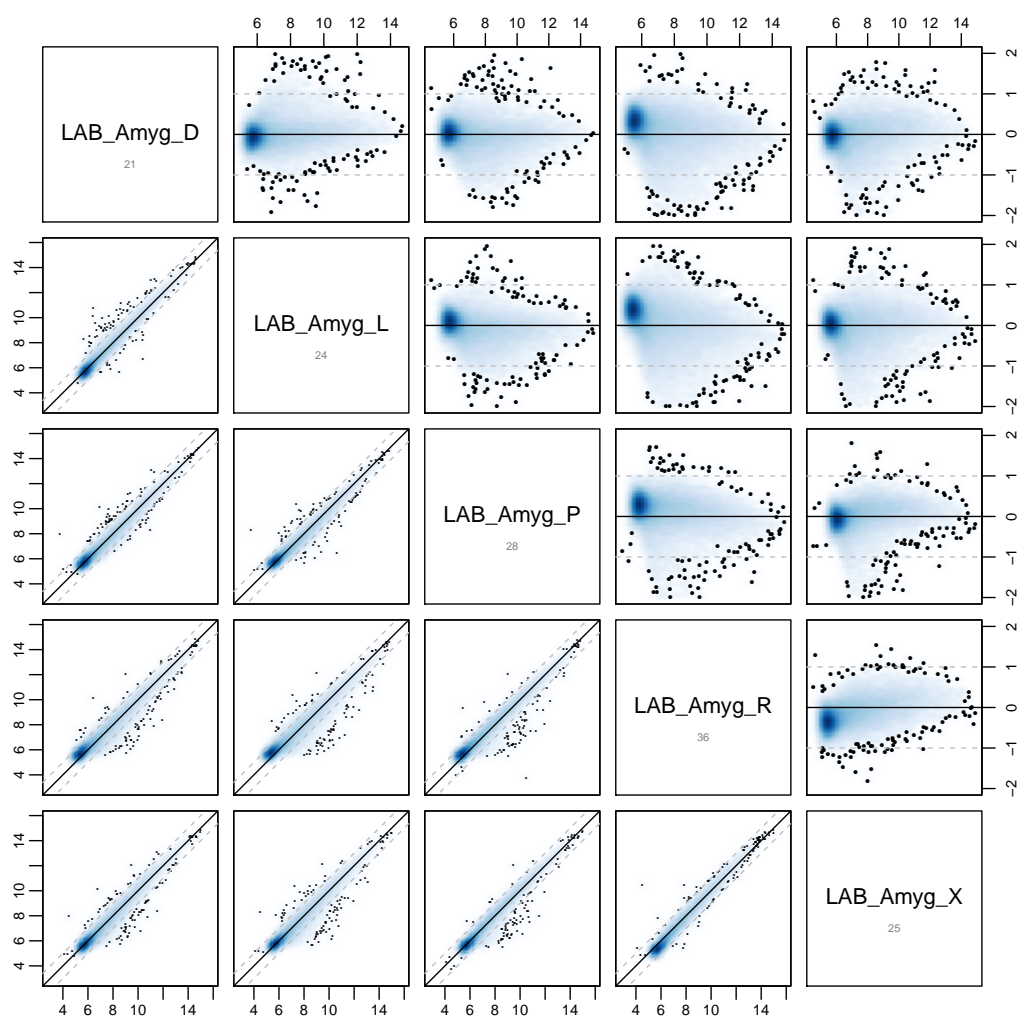
Pairwise plots for group NAB_DGyr



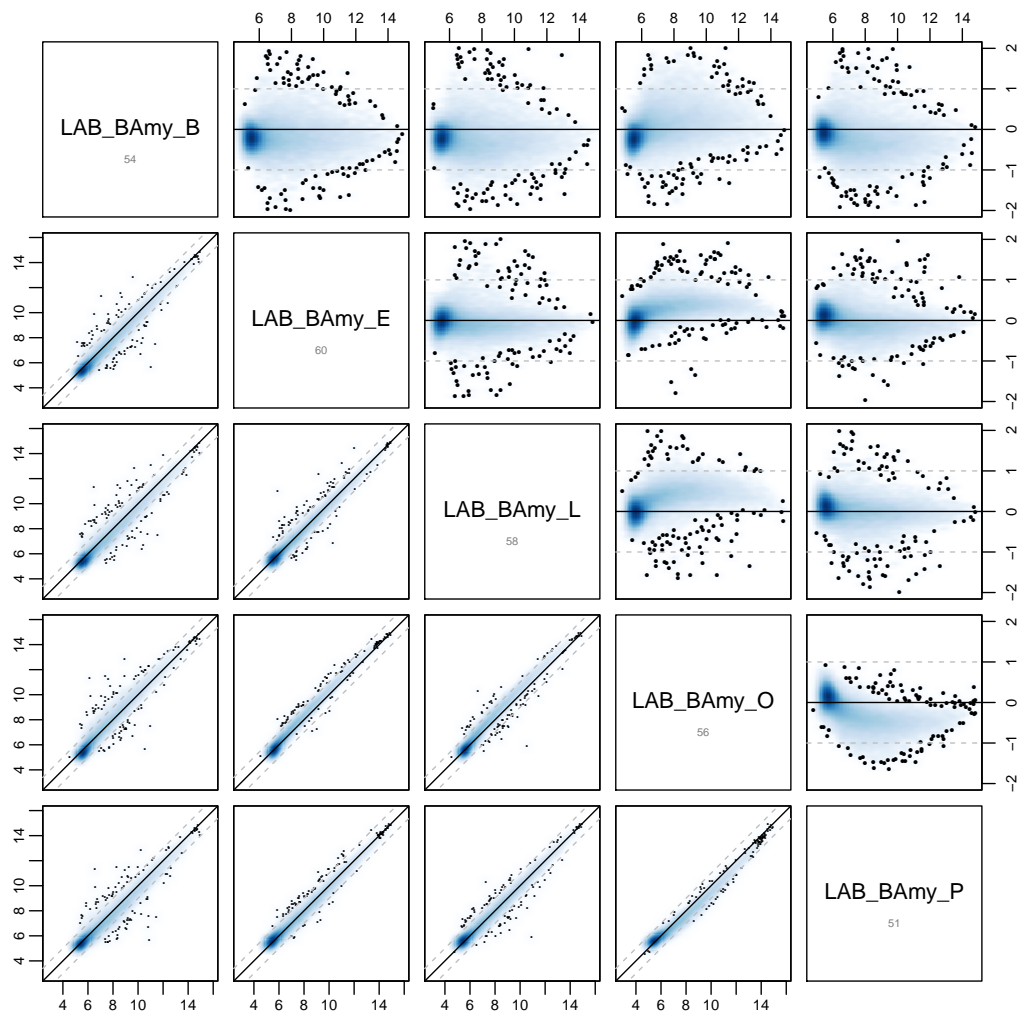
Pairwise plots for group NAB_PVNu



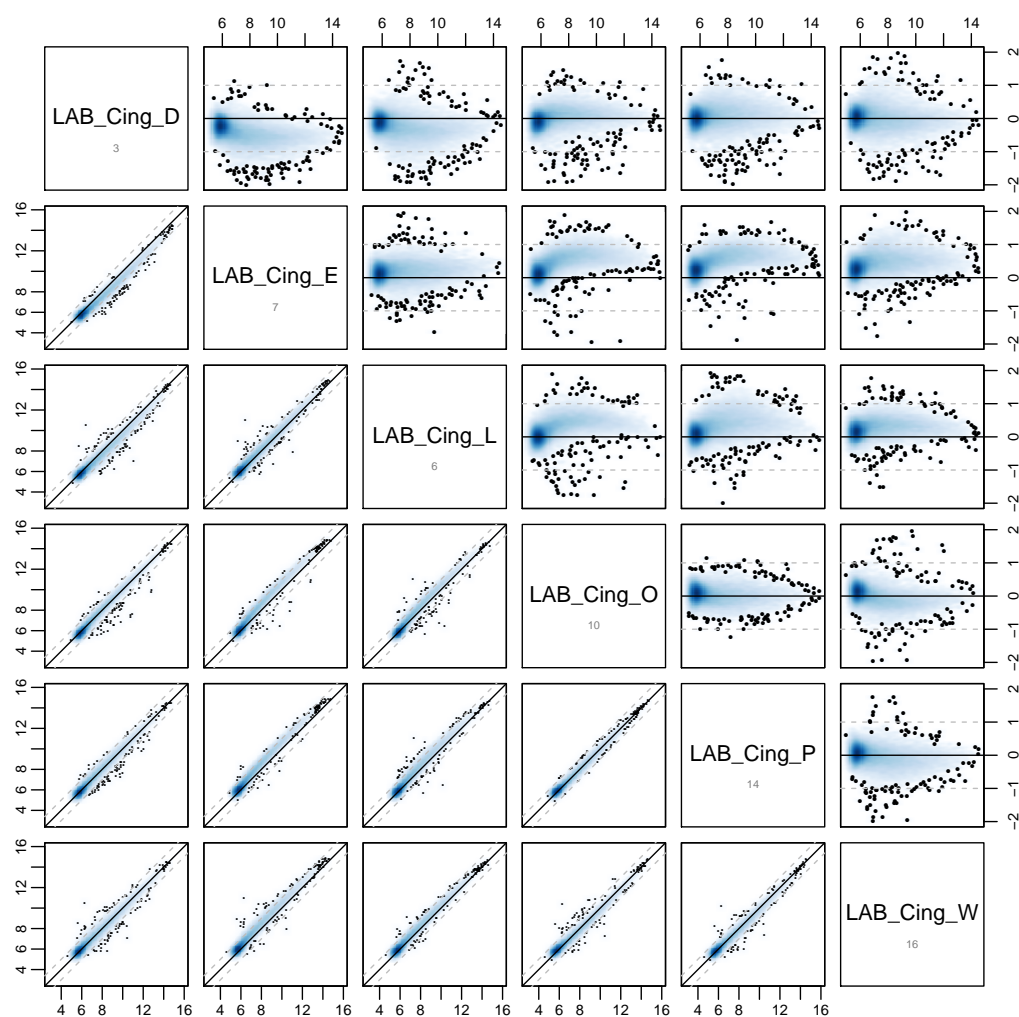
Pairwise plots for group LAB_Amyg



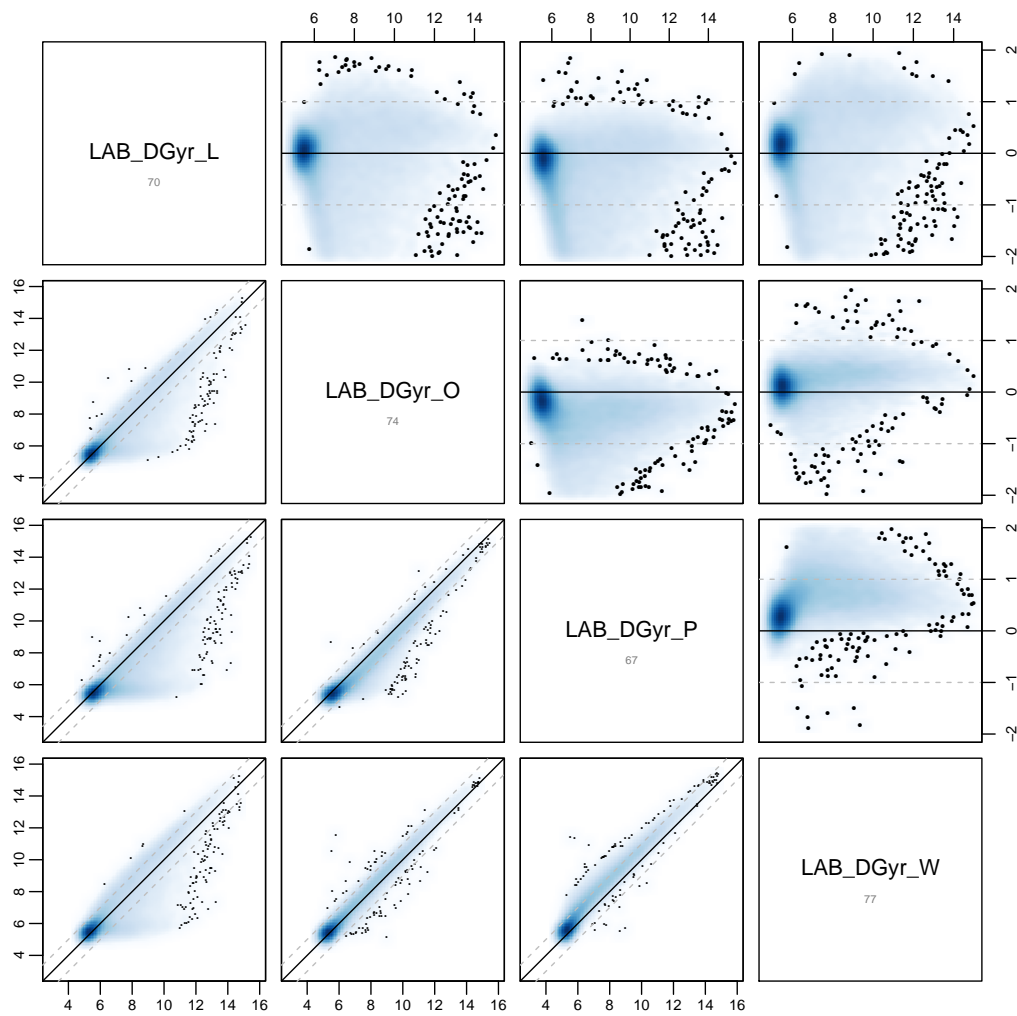
Pairwise plots for group LAB_BAmy



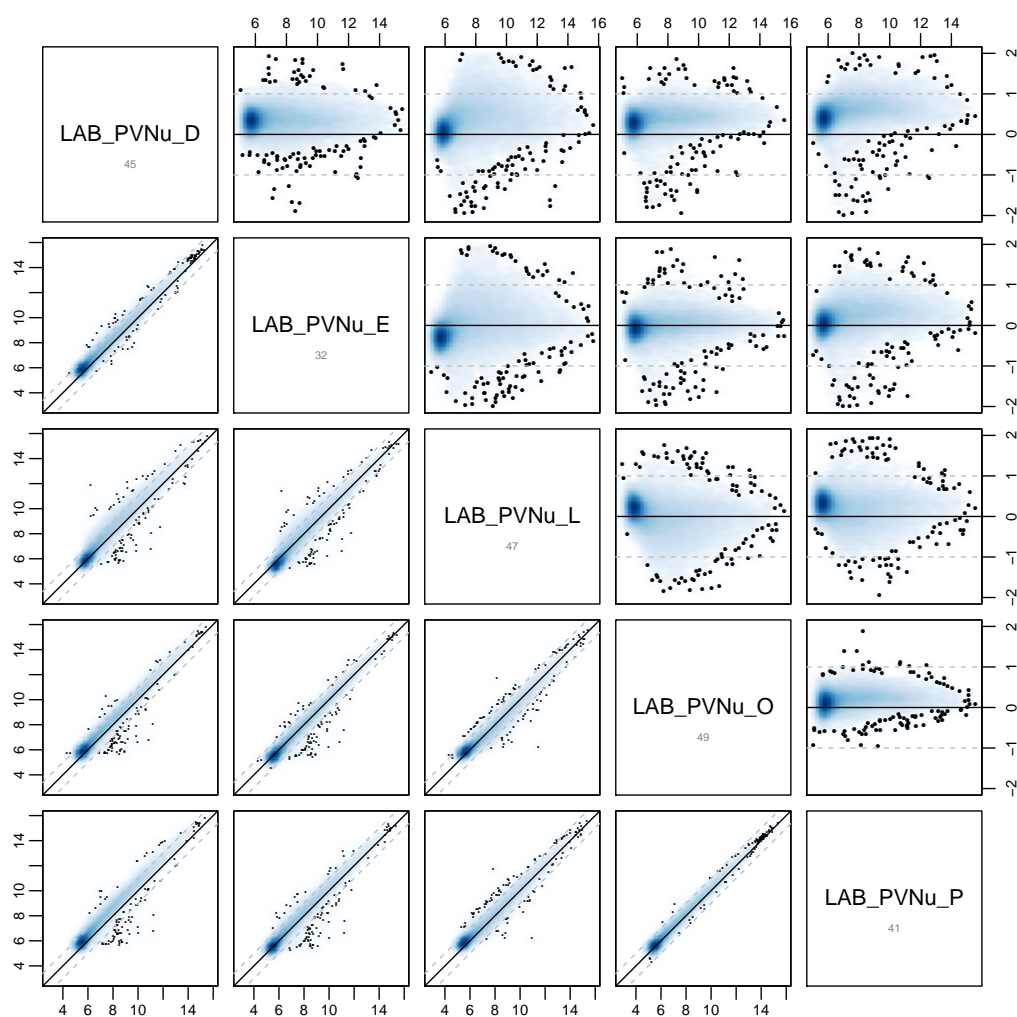
Pairwise plots for group LAB_Cing



Pairwise plots for group LAB_DGyr



Pairwise plots for group LAB_PVNu



2 Normalisation

Normalisation can be performed using various functions from R, here we employ `vsn`[4].

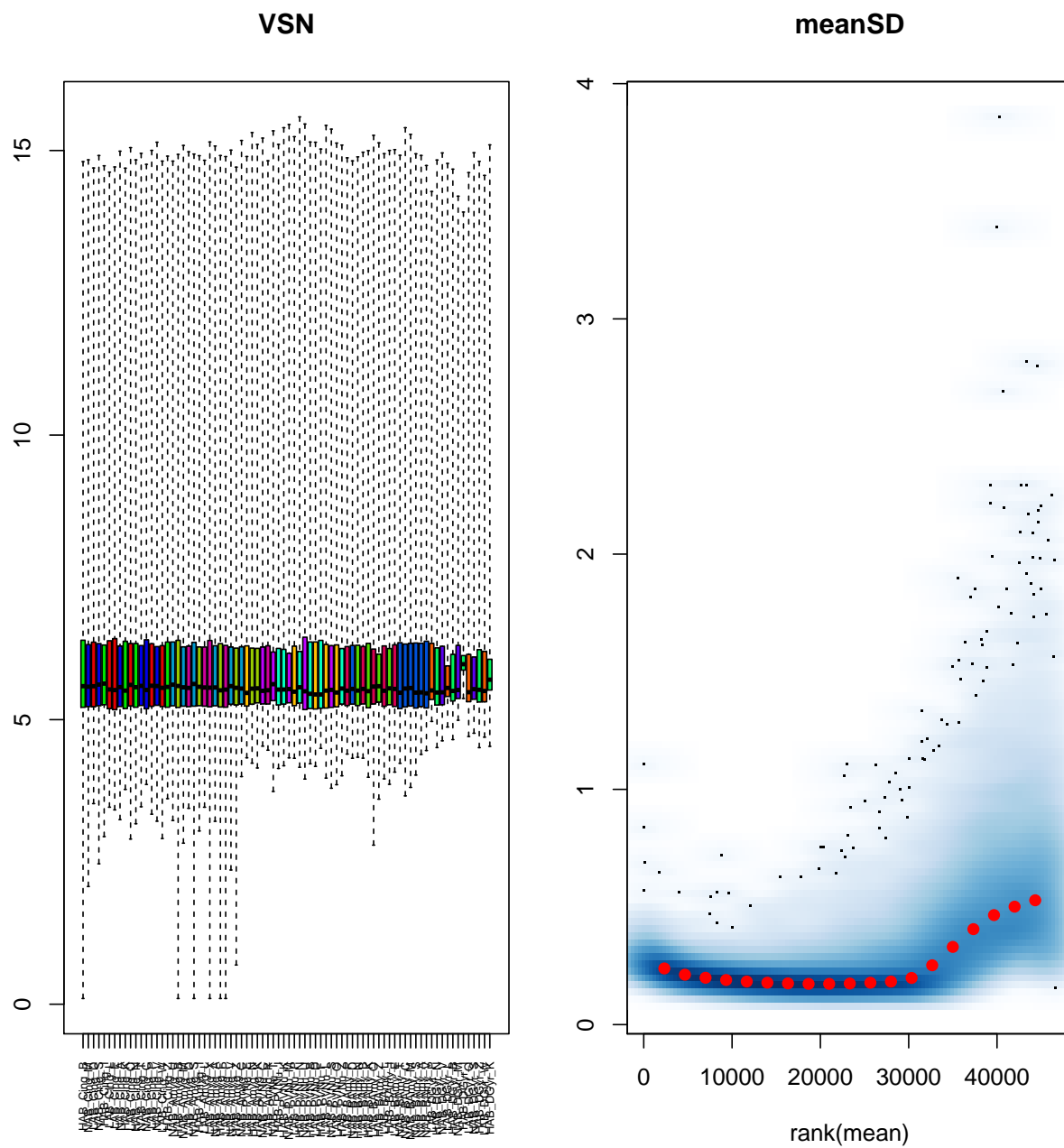
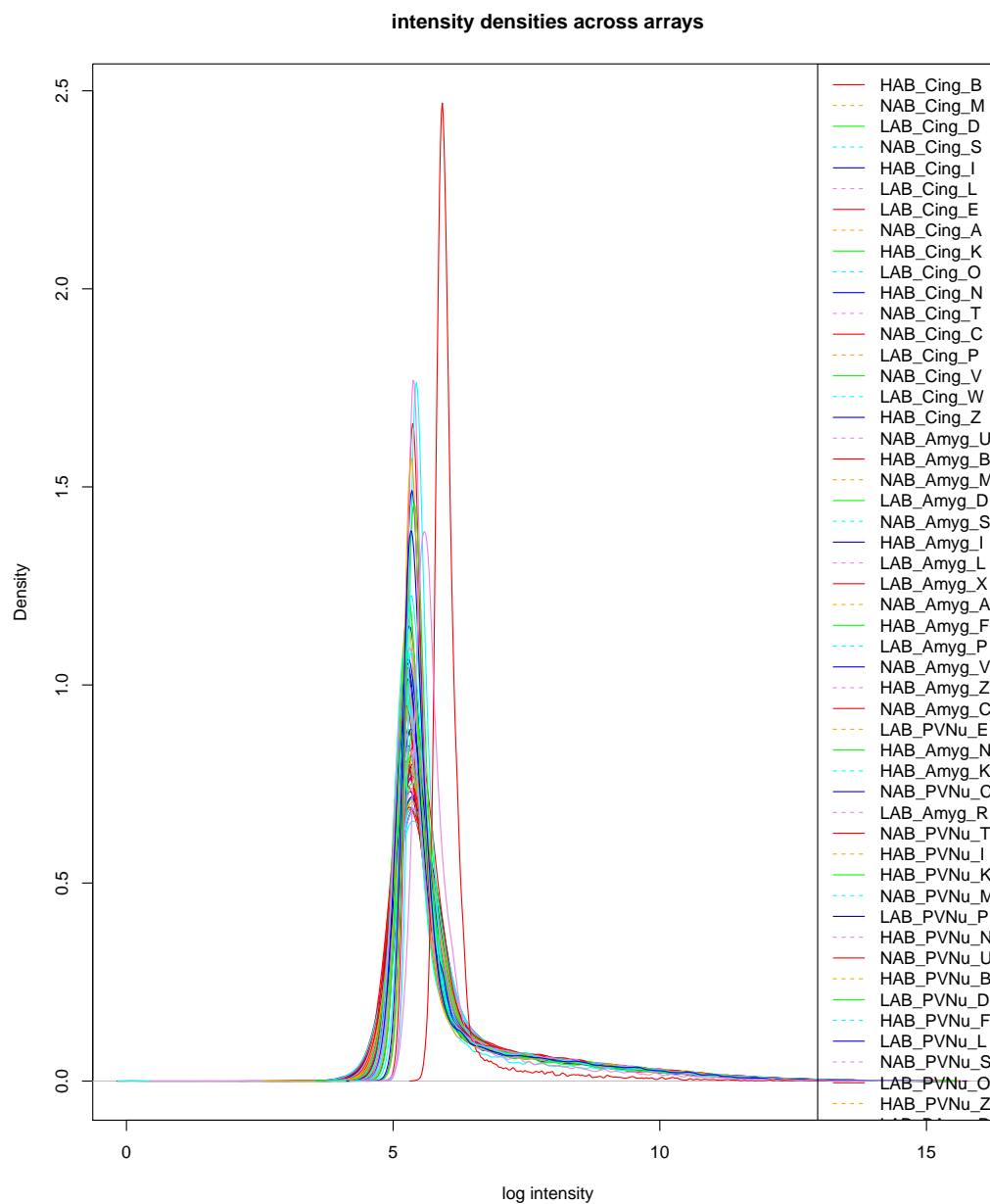


Figure 2: Data after normalization (left) and variance vs. intensity (right)

2.1 Intensity distribution across arrays

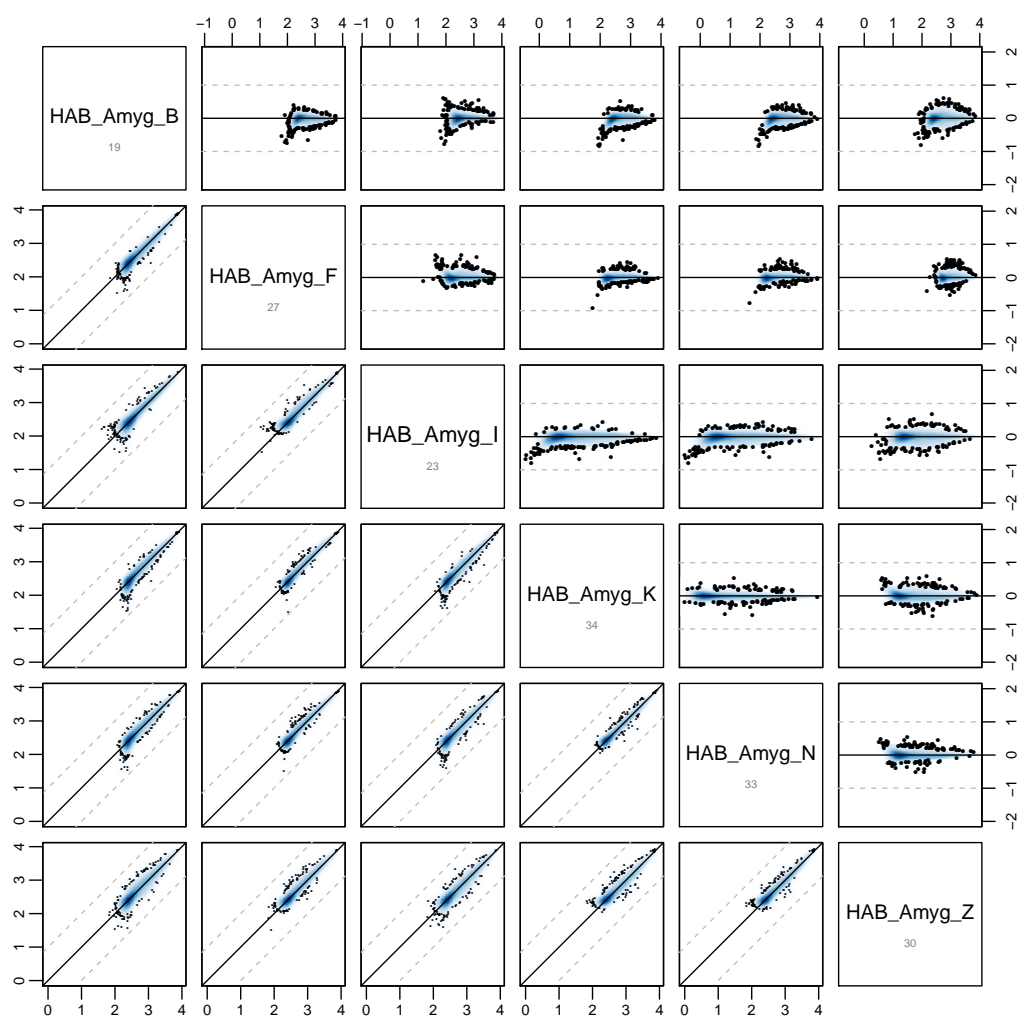
To get a more detailed impression of the effect of the normalization, we look at the intensity distribution across arrays



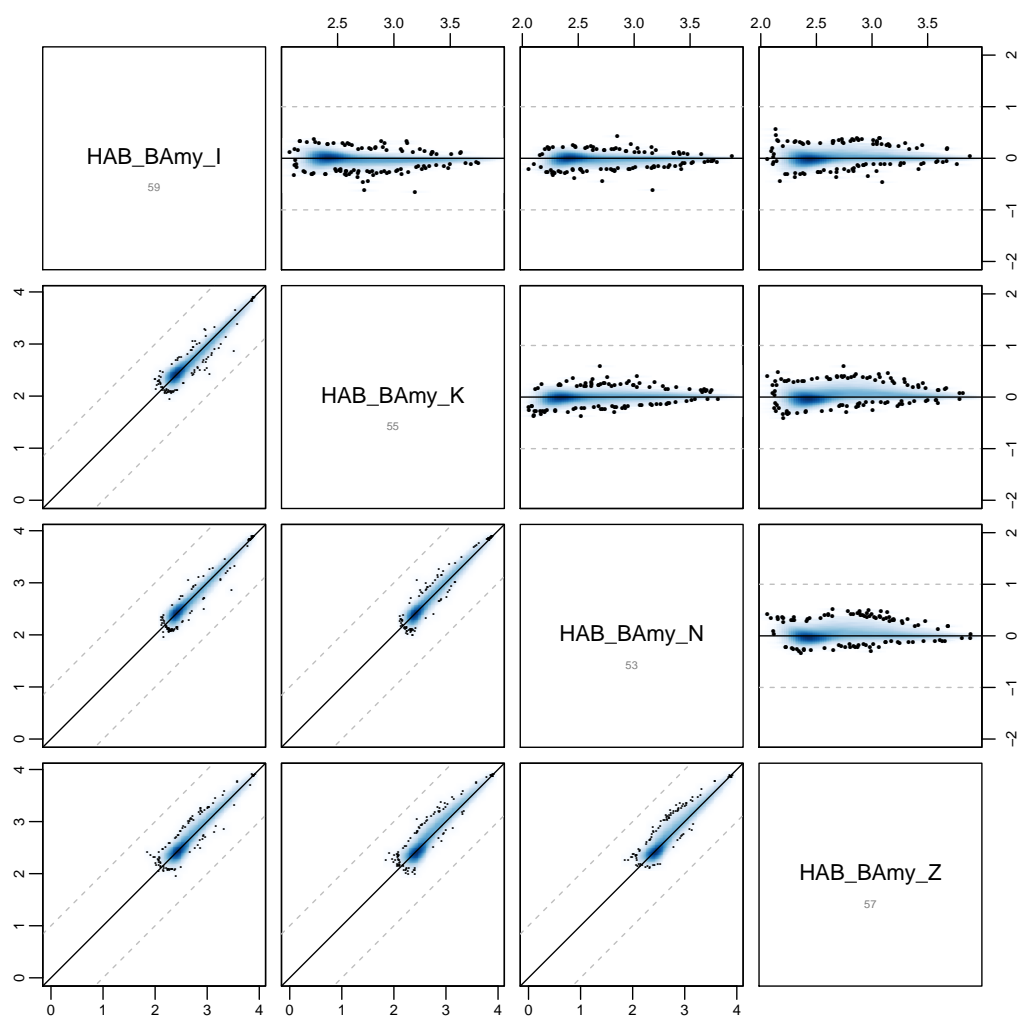
2.2 Groupwise pair plots after normalisation

The following pages show similar plots for the data within each sample group, as these should be more similar and deviations are more apparent.

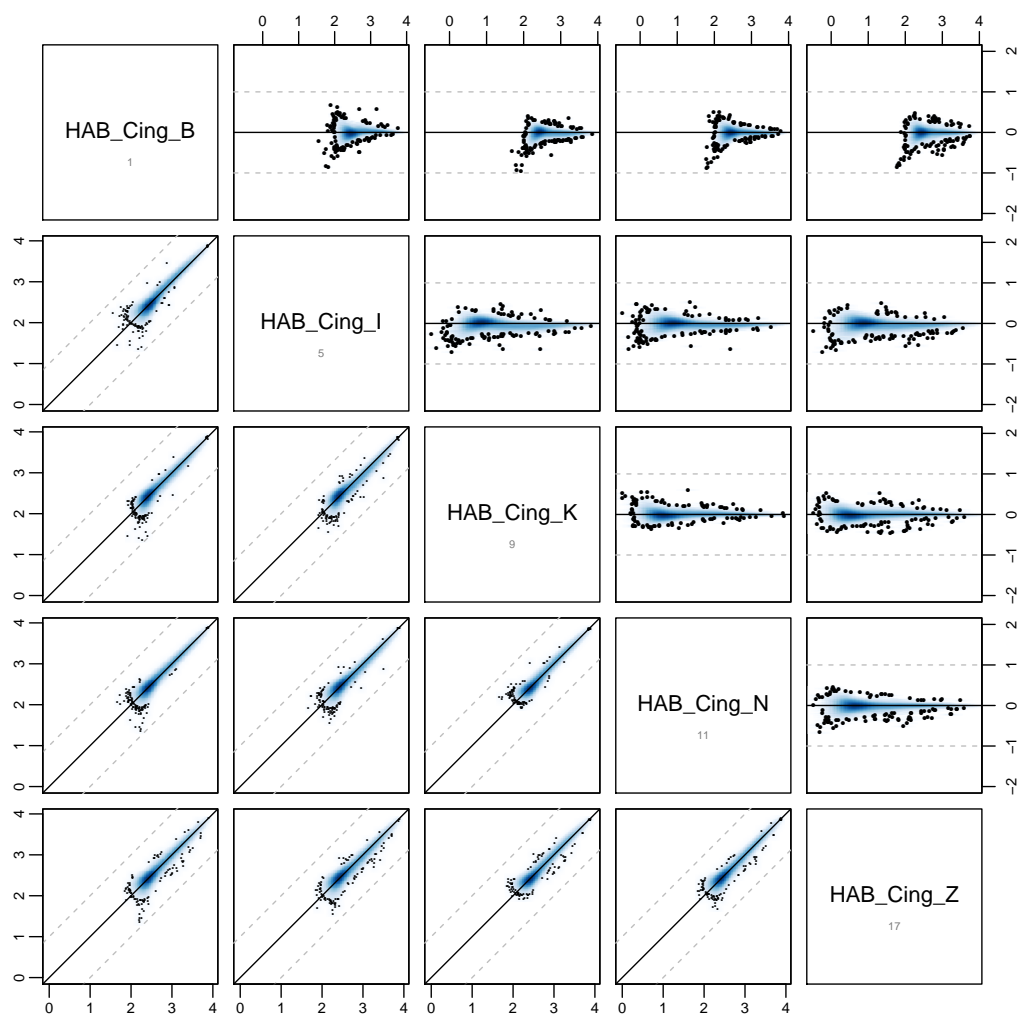
Pairwise plots for group HAB_Amyg



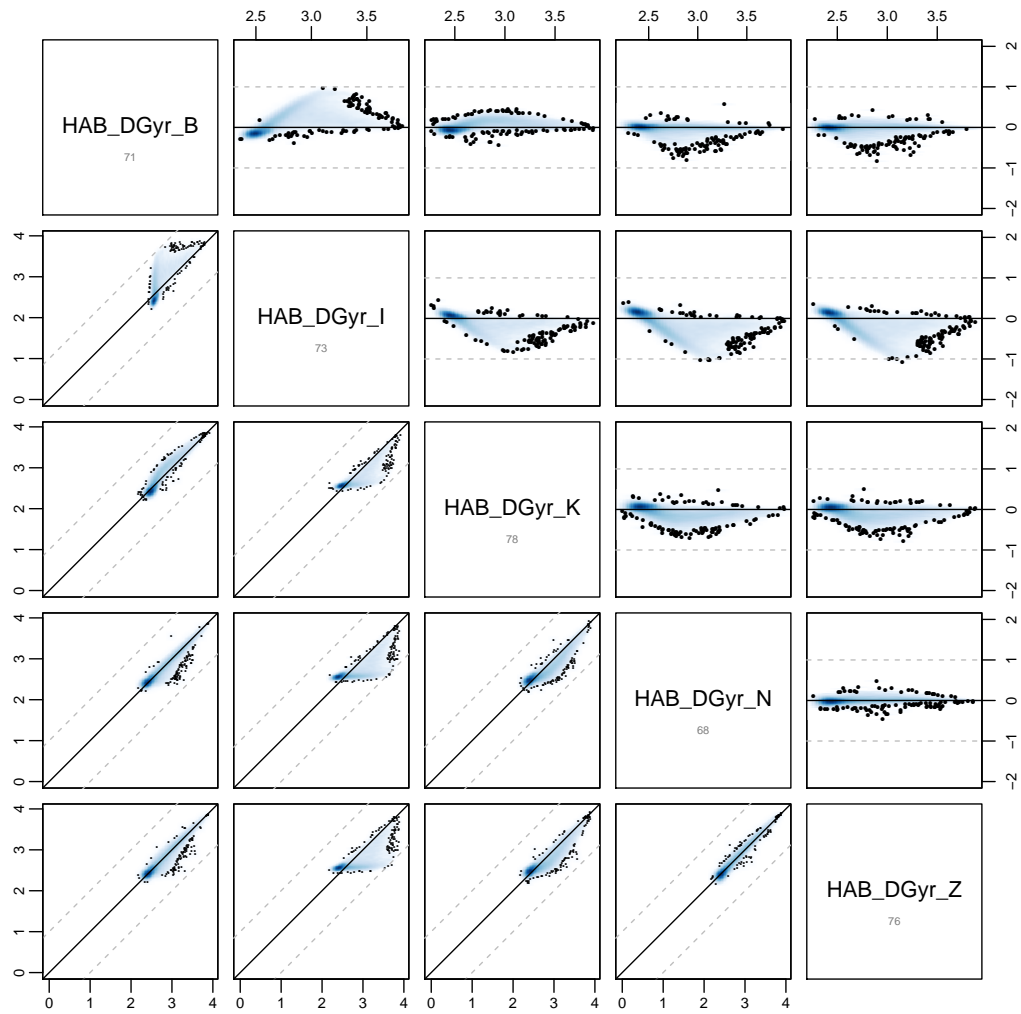
Pairwise plots for group HAB_BAmY



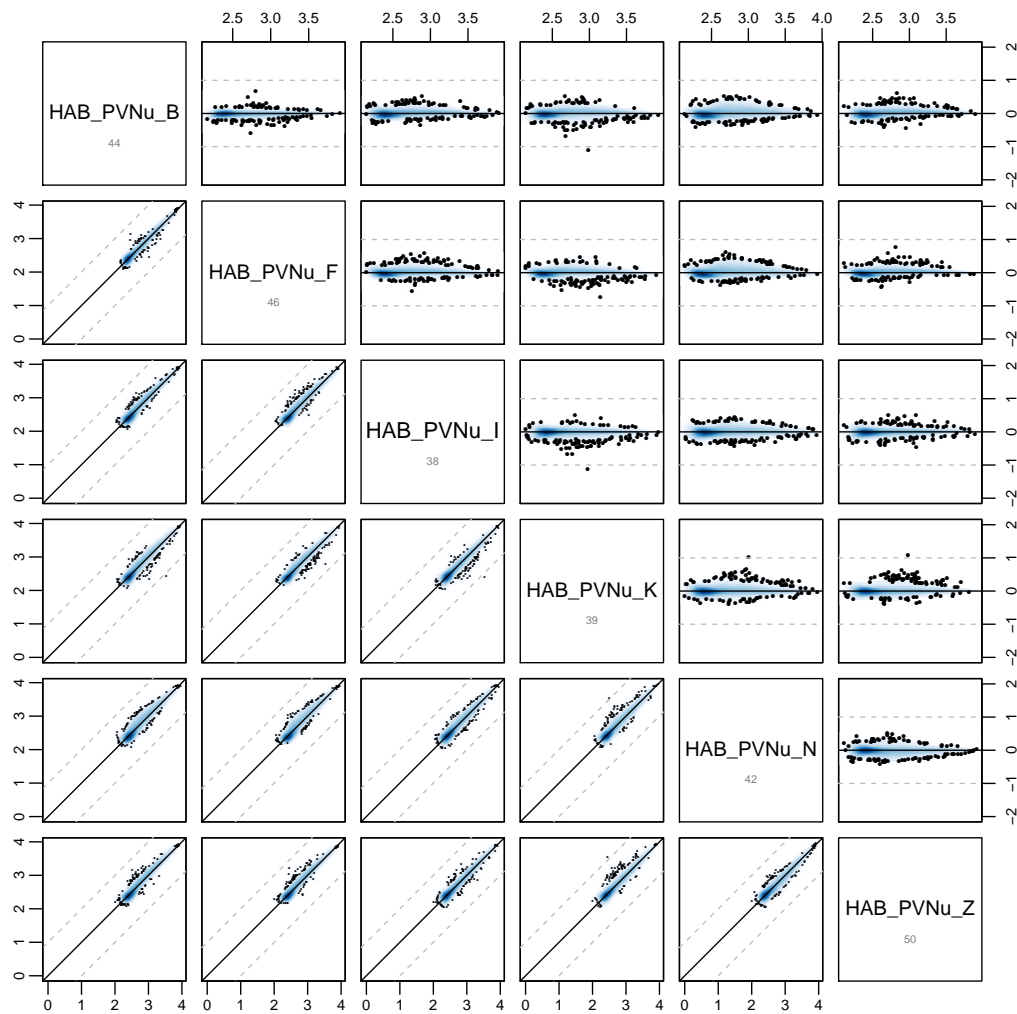
Pairwise plots for group HAB_Cing



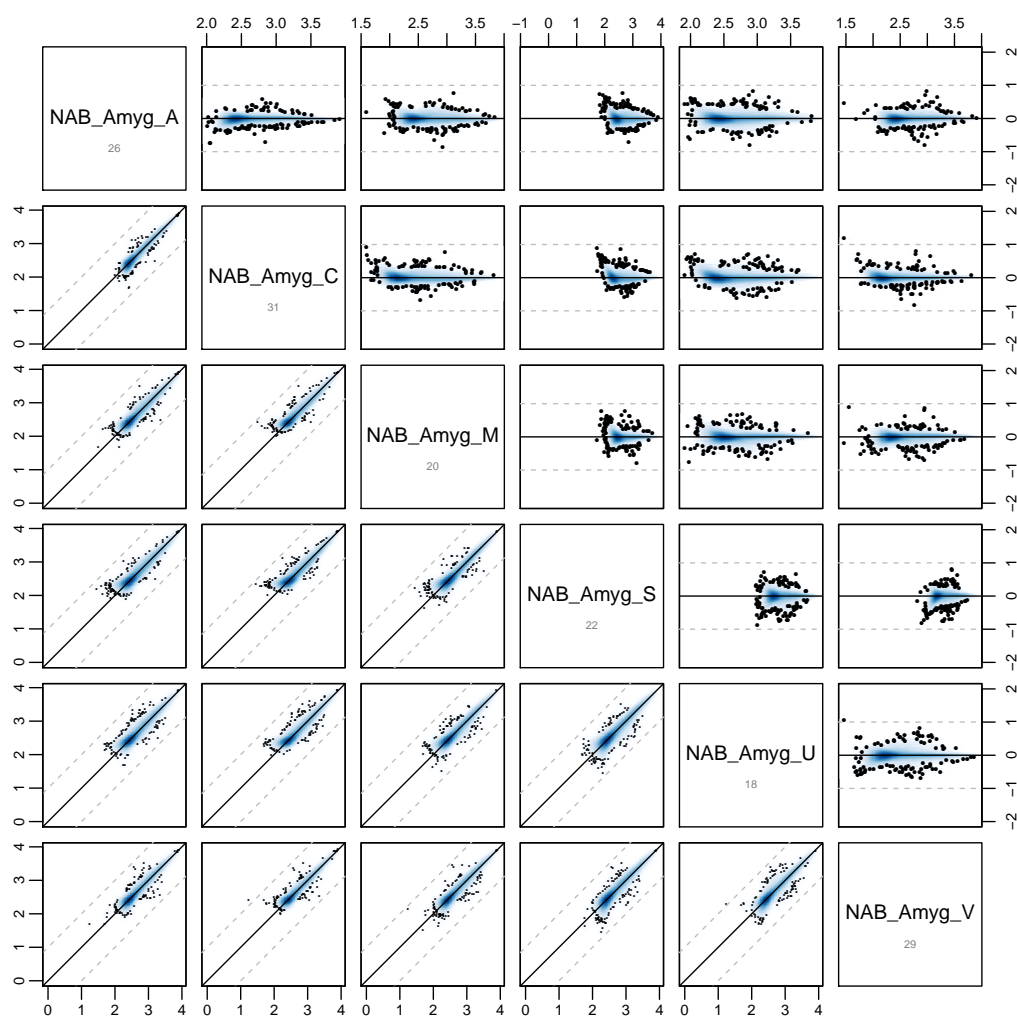
Pairwise plots for group HAB_DGyr



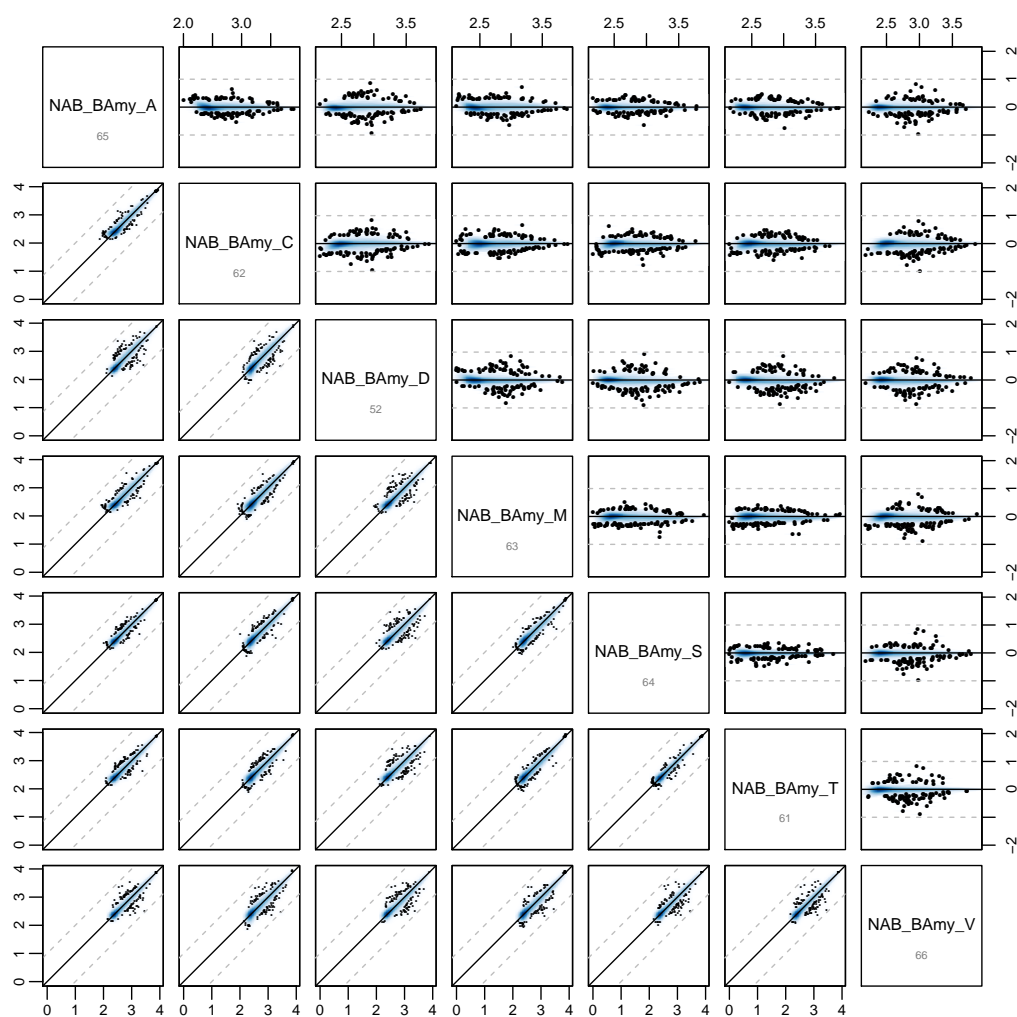
Pairwise plots for group HAB_PVNu



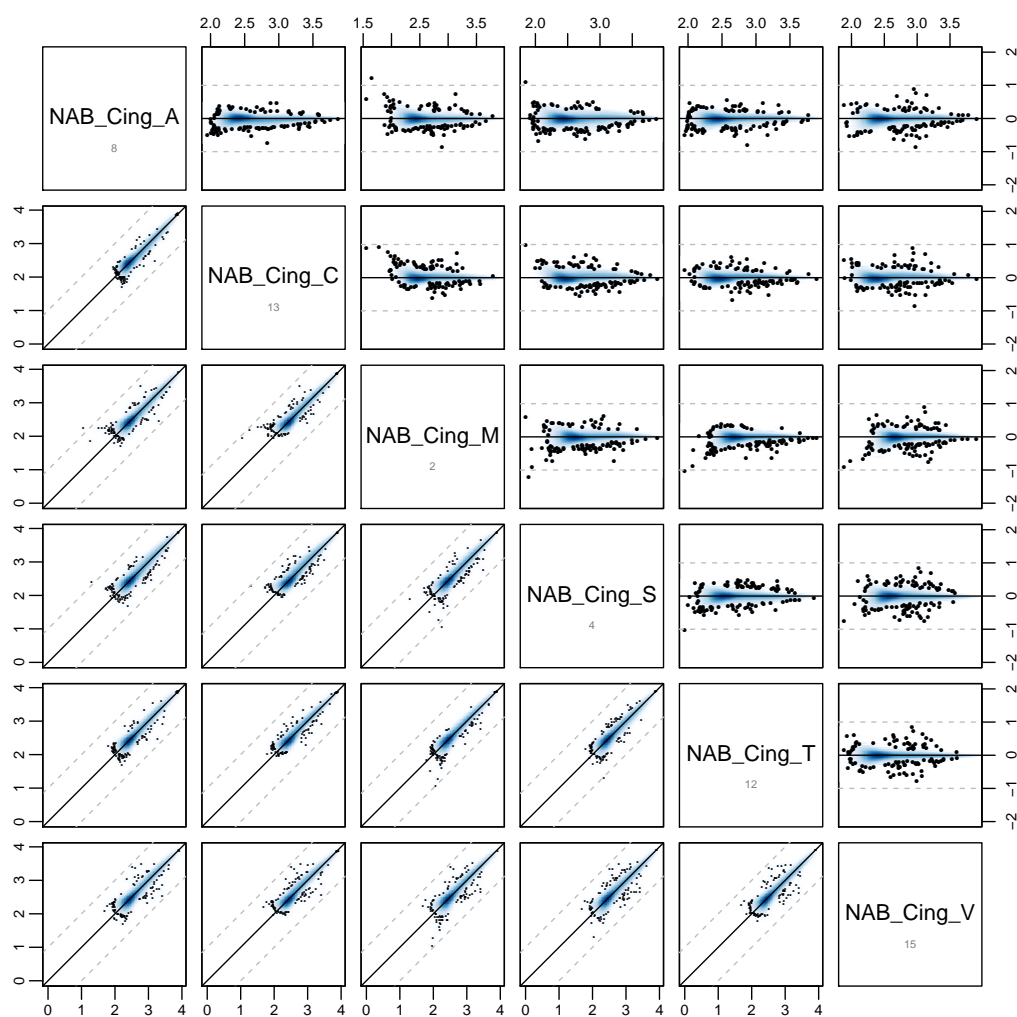
Pairwise plots for group NAB_Amyg



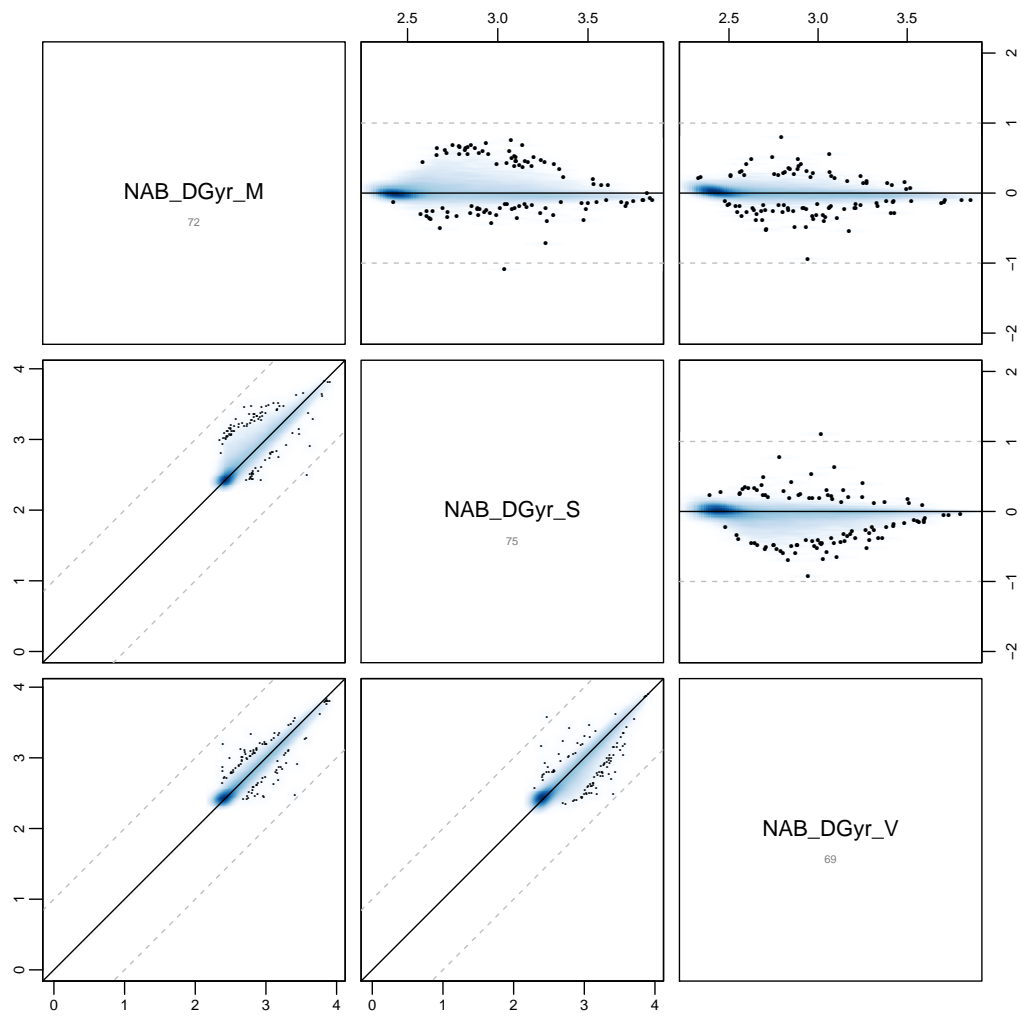
Pairwise plots for group NAB_BAmy



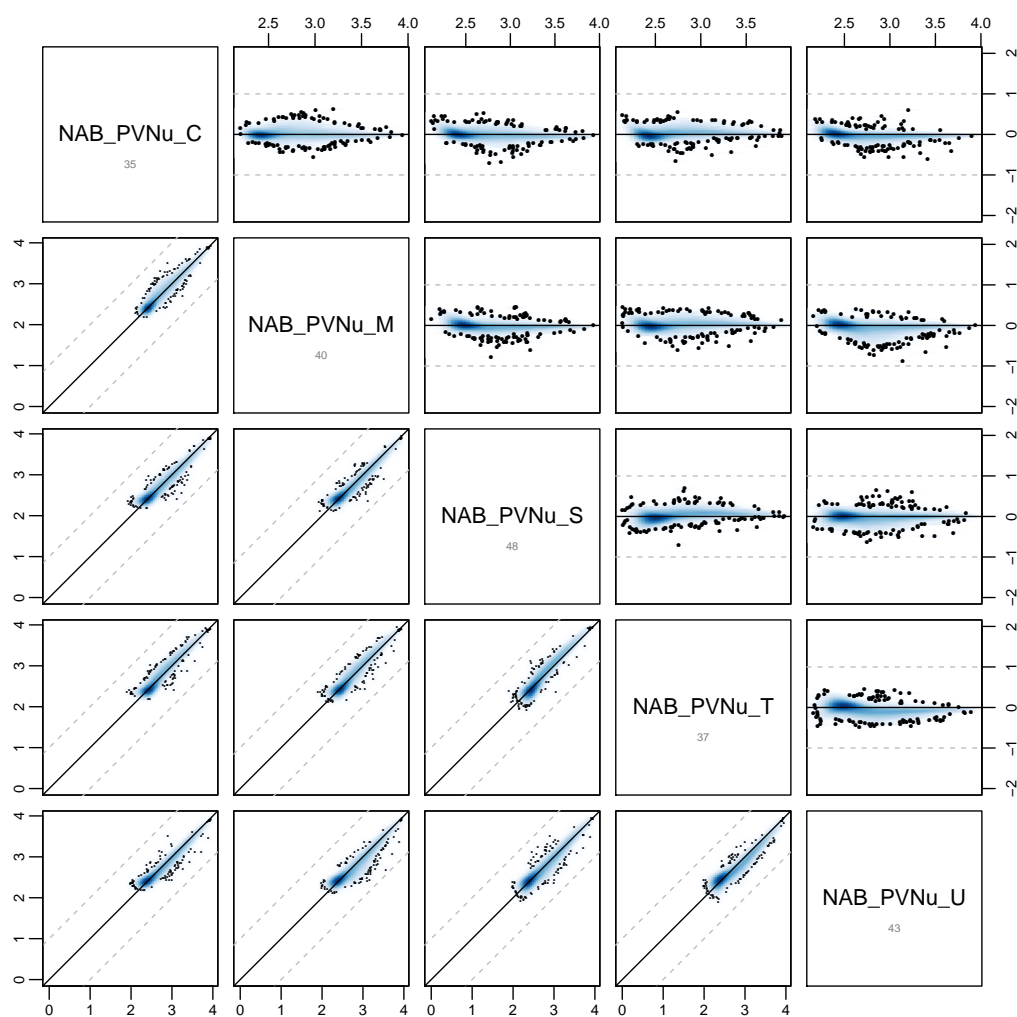
Pairwise plots for group NAB_Cing



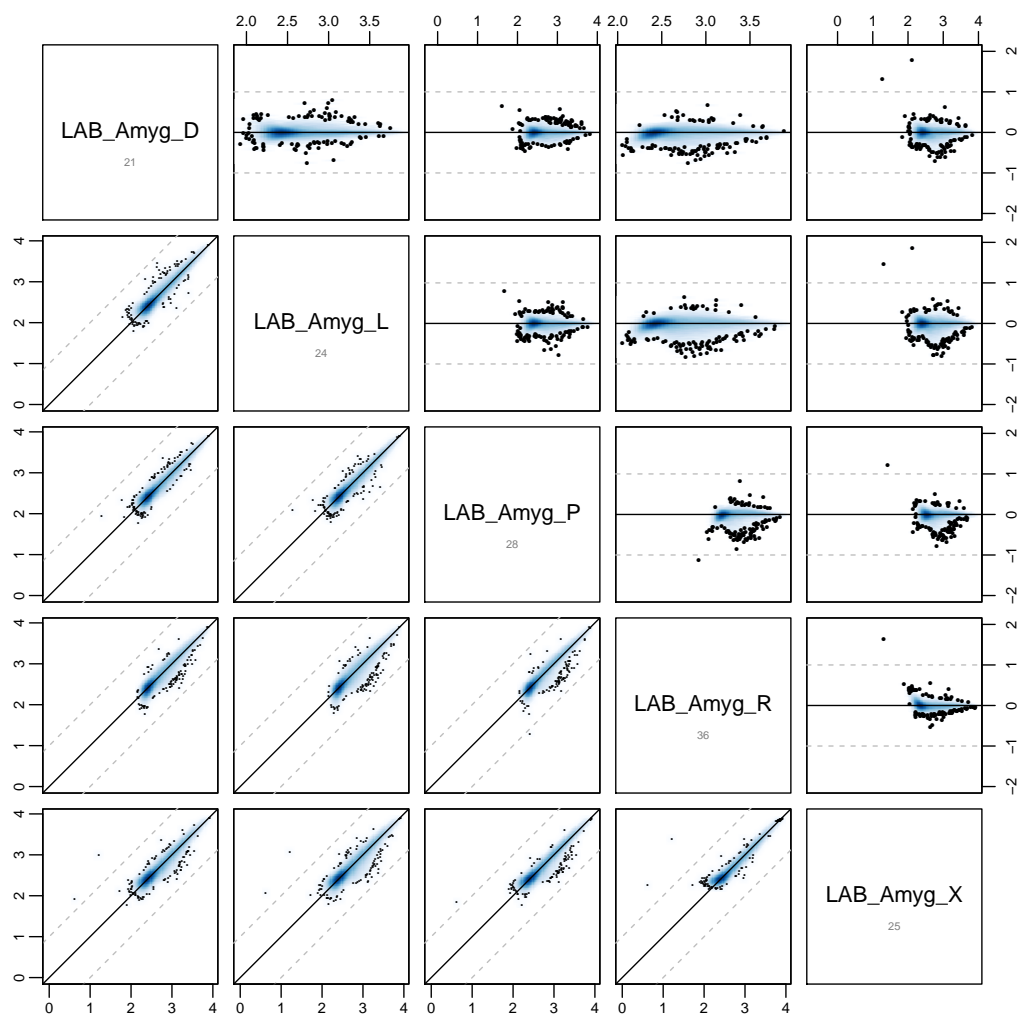
Pairwise plots for group NAB_DGyr



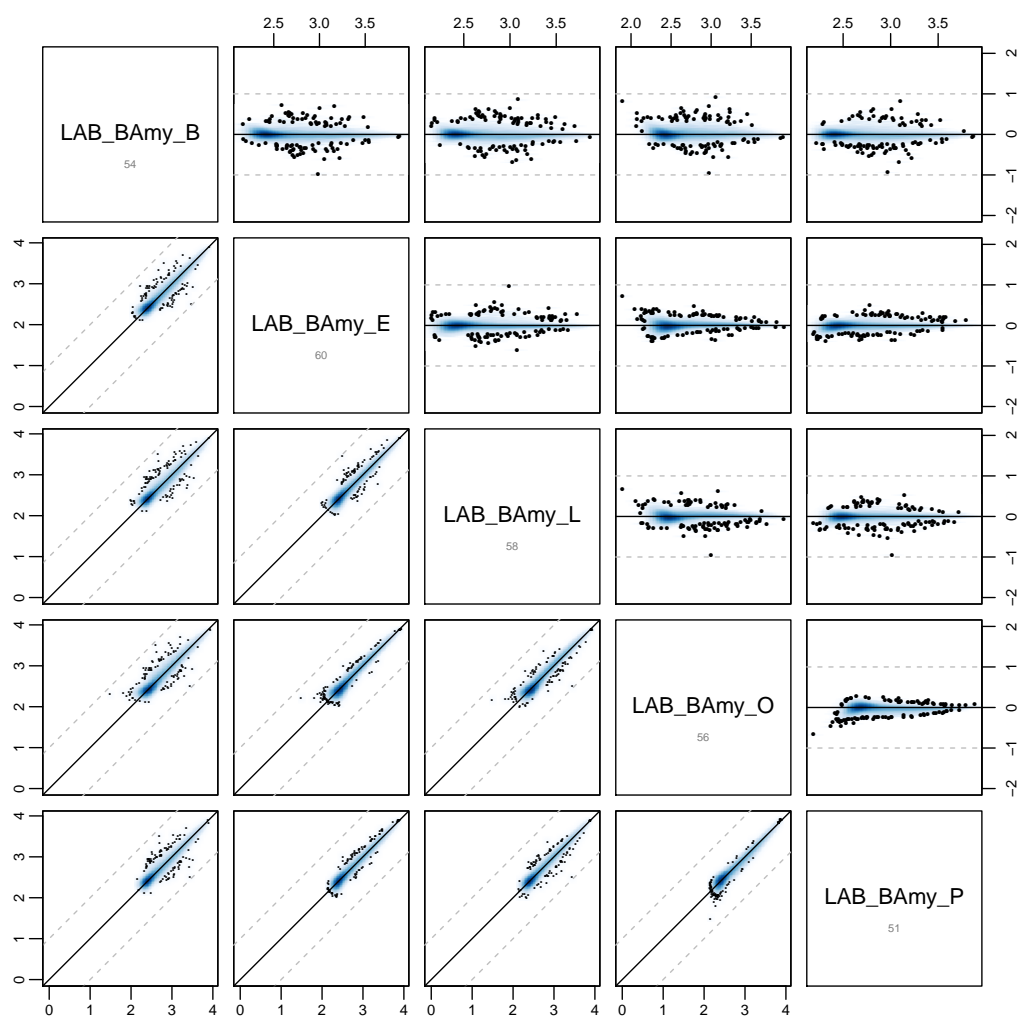
Pairwise plots for group NAB_PVNu



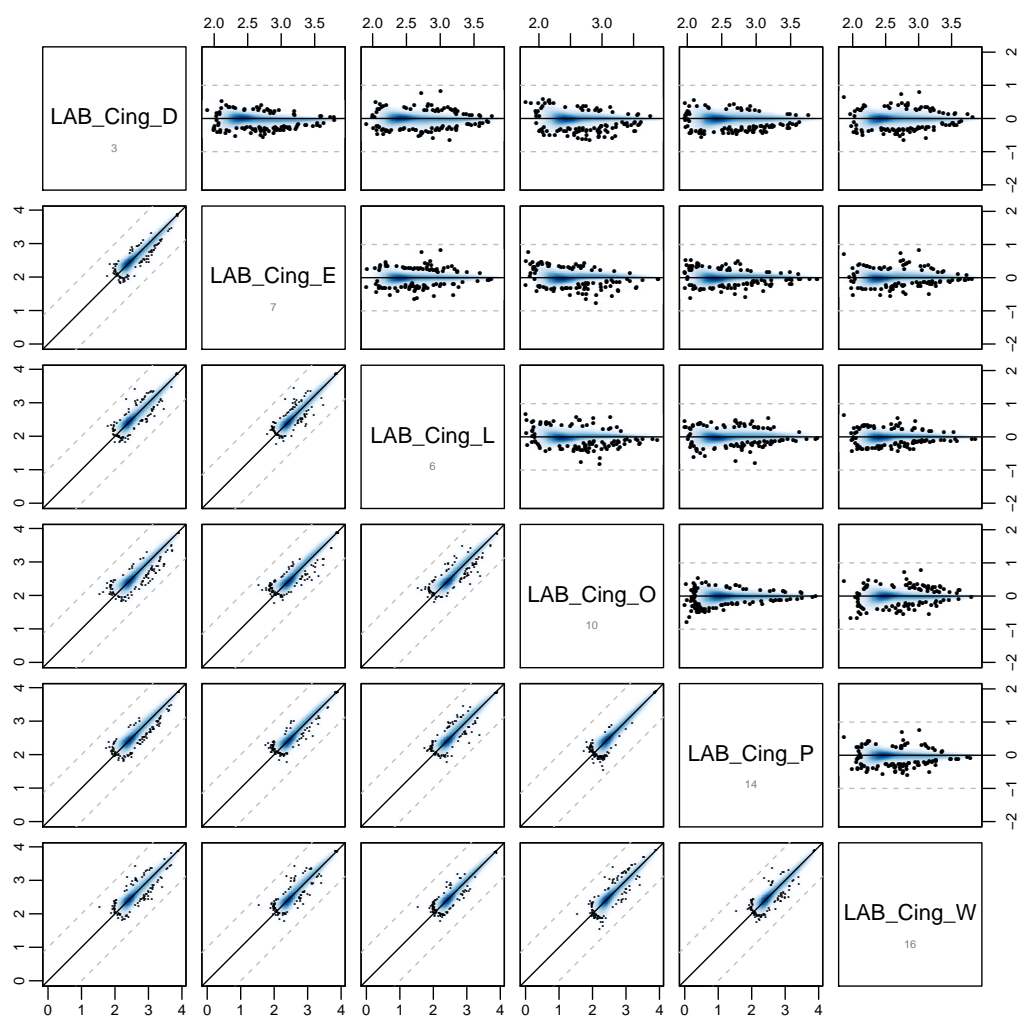
Pairwise plots for group LAB_Amyg



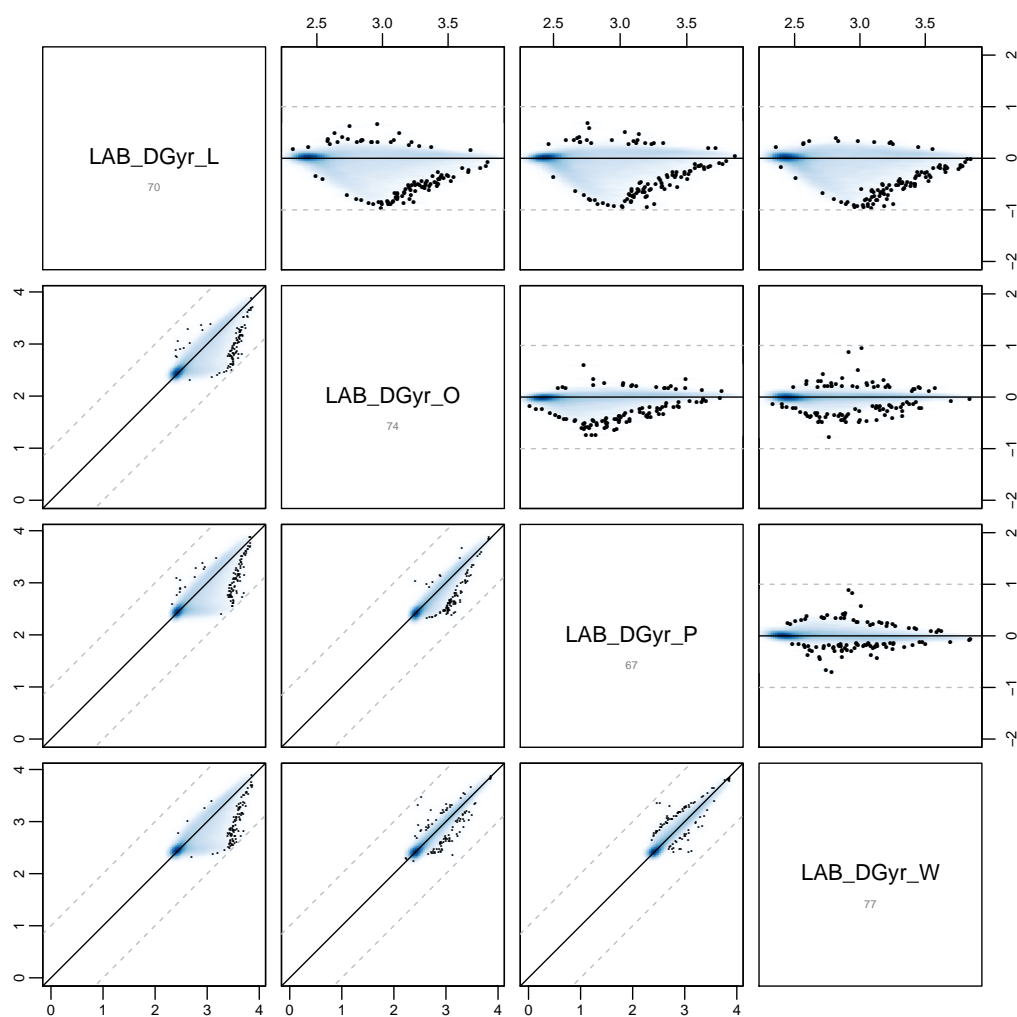
Pairwise plots for group LAB_BAmy



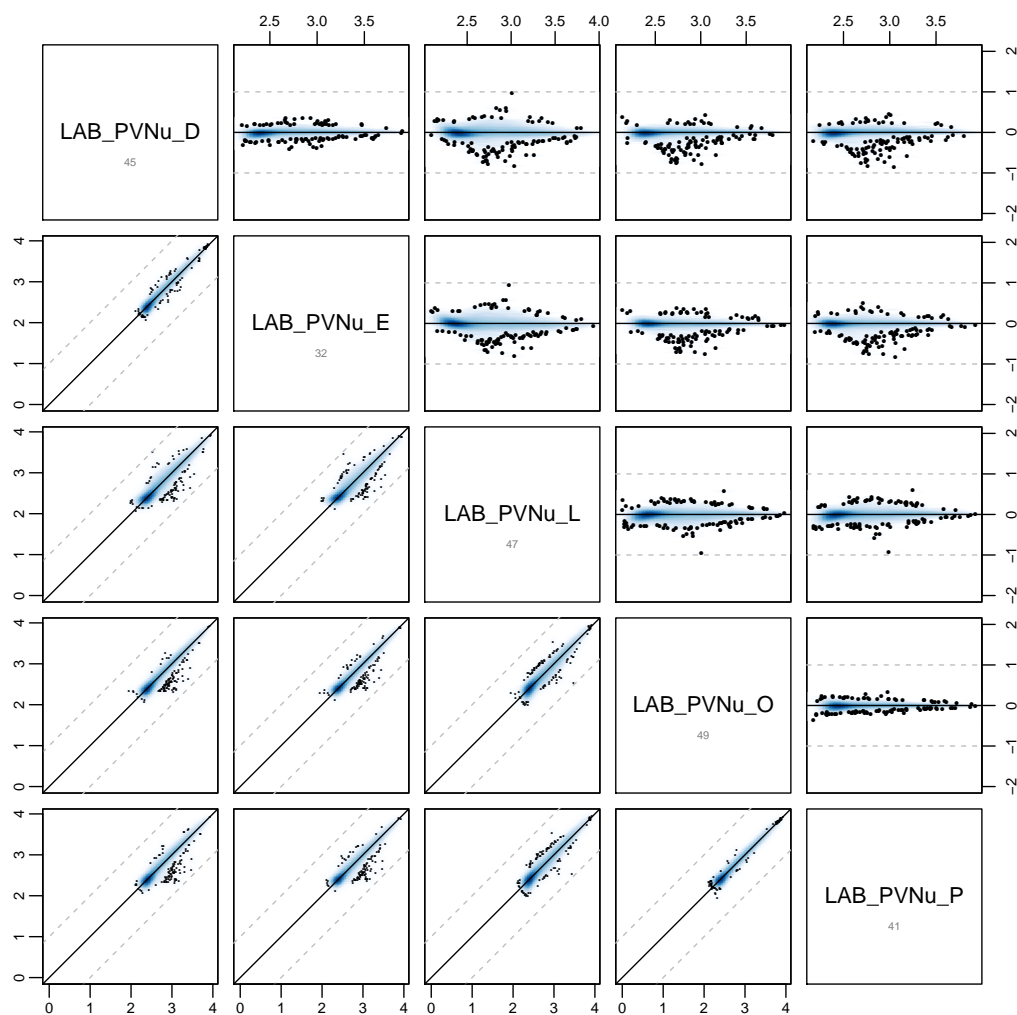
Pairwise plots for group LAB_Cing



Pairwise plots for group LAB_DGyr



Pairwise plots for group LAB_PVNu



2.3 Filtering

The 46657 probes found in all the samples are further filtered:

1. Accepting only genes with EntrezGene-ID² drops 0 probes, 46657 pass.
2. The sequences of 46657 probes could be aligned uniquely to the human genome with no more than two mismatches. Requiring unique alignment does not further narrow the probe selection (i. e., all those probes have EntrezGeneIDs)
3. Selecting only genes with a *detection p-value* of less than 1×10^{-04} . Filtering by detection to only clearly detected probes drops an additional 34486 probes, leaving 12171.

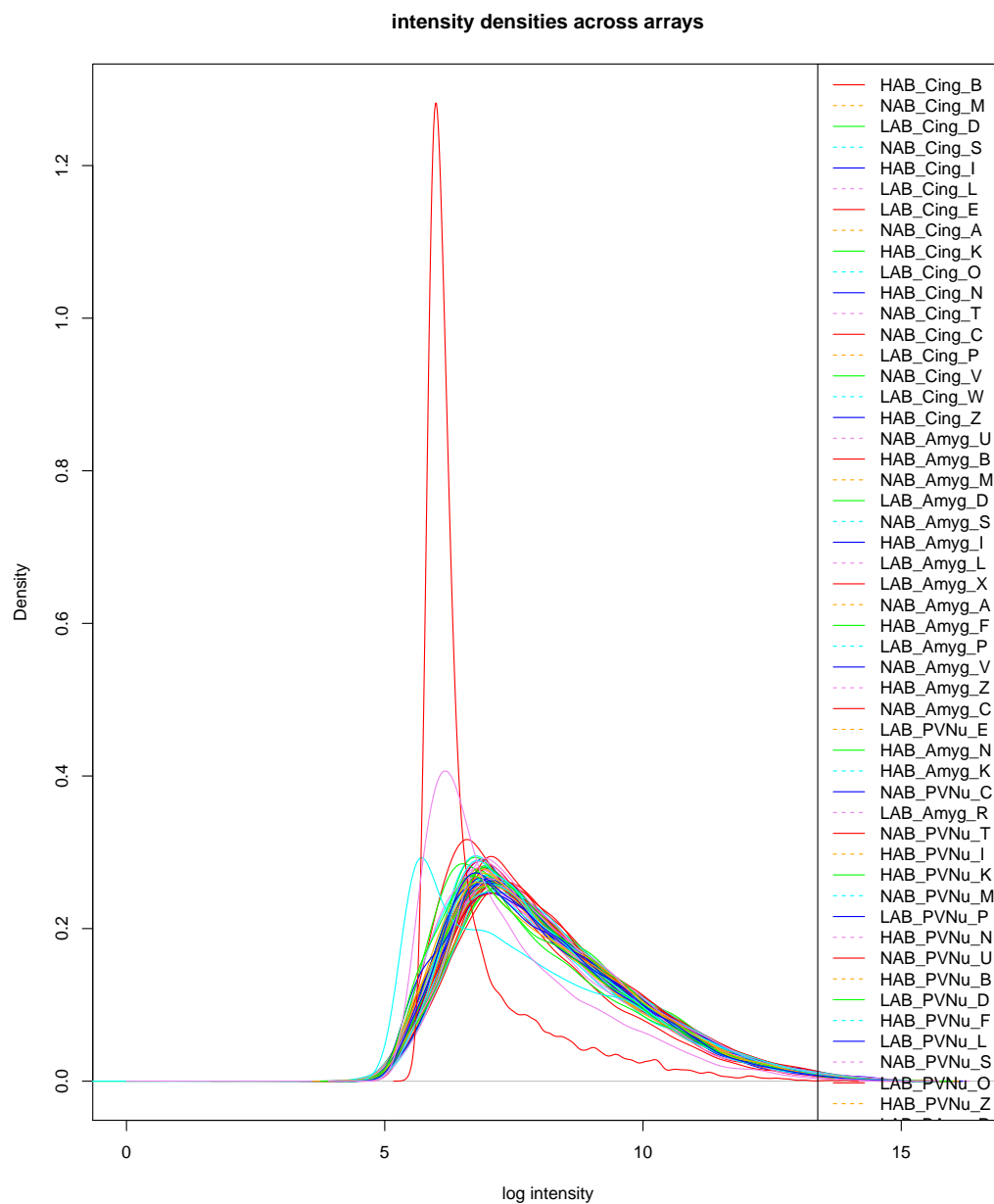
This selection can be depicted in the following Venn diagram. The 12171 probes shown in the intersection of the three circles pass all filter requirements and are considered for further processing. The color of the inscribed counts (and the background shading) indicates which of the above filter steps removes the corresponding section from the probe pool.



²According to ILLUMINA[®]'s annotation as provided by the BioConductor `illuminaHumanv4.db` annotation package.

2.4 Raw Intensity distribution across arrays (filtered)

The filtered normalized data show the following intensity distribution across arrays



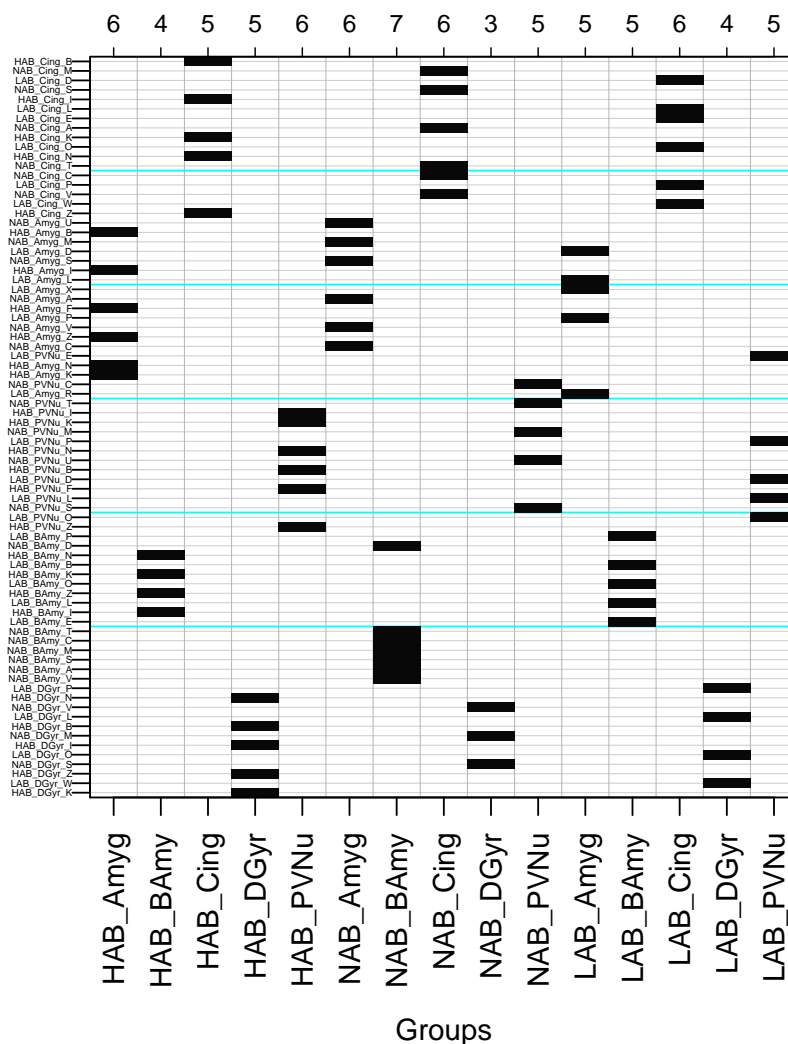
3 Differential Expression Analysis

For differential expression analysis, functions from the LIMMA package[6] can be used on the normalized transformed expression values. Significantly regulated genes are ranked using an empirical BAYES method³ [5], that uses information from the ensemble of all samples to estimate the sample variance for each gene. This approach aims at stabilizing the statistical analysis, especially for small array numbers [7].

The samples are split according to anxiety behaviour and brain region into the groups

HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—
 —NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—
 —LAB_PVNu HighAnx.Behav._Amygdala HighAnx.Behav._Basal Amygd. HighAnx.Behav._Cingulate
 HighAnx.Behav._Dorsal Gyr. HighAnx.Behav._ParaVentr.Nucl. NormAnx.Behav._Amygdala
 NormAnx.Behav._Basal Amygd. NormAnx.Behav._Cingulate NormAnx.Behav._Dorsal Gyr.
 NormAnx.Behav._ParaVentr.Nucl. LowAnx.Behav._Amygdala LowAnx.Behav._Basal Amygd.
 LowAnx.Behav._Cingulate LowAnx.Behav._Dorsal Gyr. LowAnx.Behav._ParaVentr.Nucl.

The resulting design matrix



³we use the implementation `eBayes()` from R package LIMMA.[6]

will be used for all of the subsequent analyses. All samples are included

Multiple testing is corrected for using the false discovery rate (FDR) approach[1] which leads to the values in the *adj.P.Val* column. Note that this is not to be interpreted as a significance measure (see page 140).

3.1 Combined Contrasts

First, we look at overall effects combining several contrasts. This is achieved by combining the (moderated) t -statistics into a (moderated) F -statistic, testing whether there is differential expression in any of the single contrasts for a given gene. This way genes which are involved in any of the contrasts show up. The single contrast results are shown in section 3.2 starting from page 50. We begin by looking for genes which are differentially expressed across all contrasts. Using the contrast matrix

	HN _a	HN _b	HN _c	HN _d	HN _p	LN _a	LN _b	LN _c	LN _d	LN _p	HL _a	HL _b	HL _c	HL _d	HL _p
HAB_Amyg	1	0	0	0	0	0	0	0	0	0	1	0	0	0	0
HAB_BAmy	0	1	0	0	0	0	0	0	0	0	0	1	0	0	0
HAB_Cing	0	0	1	0	0	0	0	0	0	0	0	0	1	0	0
HAB_DGyr	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0
HAB_PVNu	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1
NAB_Amyg	-1	0	0	0	0	-1	0	0	0	0	0	0	0	0	0
NAB_BAmy	0	-1	0	0	0	0	-1	0	0	0	0	0	0	0	0
NAB_Cing	0	0	-1	0	0	0	0	-1	0	0	0	0	0	0	0
NAB_DGyr	0	0	0	-1	0	0	0	0	-1	0	0	0	0	0	0
NAB_PVNu	0	0	0	0	-1	0	0	0	0	-1	0	0	0	0	0
LAB_Amyg	0	0	0	0	0	1	0	0	0	0	-1	0	0	0	0
LAB_BAmy	0	0	0	0	0	0	1	0	0	0	0	-1	0	0	0
LAB_Cing	0	0	0	0	0	0	0	1	0	0	0	0	-1	0	0
LAB_DGyr	0	0	0	0	0	0	0	0	1	0	0	0	0	-1	0
LAB_PVNu	0	0	0	0	0	0	0	0	0	1	0	0	0	0	-1

The statistics for the top 120 genes across the 15 contrasts (out of 975 genes having adjusted p -values below 0.05) are shown in table 2, the corresponding expression plots are shown in Figs. 4a-c on pages 47 through 49.

ILMN_Gene	Search_Key	A_A_Id	HN _a	HN _b	HN _c	HN _d	HN _p	LN _a	LN _b	LN _c	LN _d	LN _p	HL _a	HL _b	HL _c	HL _d
1 RAB25	NM_020387.1	50195	-7.5	-6.8	-5.4	-5.2	-9.1	1.1	-1.6	1	1.1	1.1	-7.9	-4.3	-5.5	-5.8
2 OR8B2	NM_001005468.1	6100440	6.9	6.4	7.3	3.2	7.1	-1	1.4	-1.1	1.1	-1	7.1	4.7	7.9	2.9
3 SDHAP3	NR_003263.2	1400524	-13	-20	-20	-13	-19	1.2	-2.3	1.1	1.1	1	-16	-8.7	-21	-13
6274		102480441	3.8	4.2	4.8	4.9	5.8	-1	1.4	-1	1.1	-1.1	3.9	3	4.8	4.6
6275		2810541	-18	-16	-19	-11	-19	-17	-14	-19	-11	-18	-1.1	-1.1	-1	-1
6276		107050626	-5.9	-4.1	-3.8	-5.3	-5.4	-1.2	-1.4	-1.1	-1.2	-1.1	-4.9	-3	-3.5	-4.5
6277		380692	3.5	3.1	5.9	1.5	3.2	1.1	1.1	-1.1	1	-1.1	3.1	2.7	6.6	1.5
4 NARG1	NM_057175.3	3140524	-5.9	-8.9	-7.1	-4.6	-6.7	1.4	-1.5	-1	1.1	1.1	-8.1	-6.1	-7	-5.2
6279		106020102	-3.9	-1.7	-2.6	-2.4	-3	-1.2	-1.1	1	-1.1	1	-3.2	-1.5	-2.7	-2.2
5 ST7	NM_018412.3	4570575	-2	-1.2	1	-1.1	-12	1.2	-1	-1	-1	-1.2	-2.4	-1.2	1	-1.1
6281		1090195	5.7	6.7	7	5.2	5.9	6.2	6.7	7.2	8.7	5.9	-1.1	1	-1	-1.7
6282		106400035	4.3	7.5	6.3	2.8	6.8	-1	1.5	1	1.1	1	4.5	5.2	6.2	2.6
6 EIF4B	NM_001417.2	5390494	1.2	-1.7	-1.2	-1.3	-1	9.6	3	7	4	8	-8.3	-5.3	-8.4	-5.2
6284		106760170	4	3.1	4.3	2.4	4.3	-1.3	1.3	-1.1	1.1	-1	5	2.4	4.6	2.2
7 ZNF680	NM_178558.2	1090280	1.1	-1.2	1.1	-1	-1	5.6	3.3	6.5	5.7	5.6	-5.1	-3.9	-5.8	-5.8
6286		105390397	2.6	2.2	3.2	2	2.3	-1	1.1	-1.1	-1	-1	2.6	1.9	3.4	2.1
6287		103840575	3	3	2.9	1.9	3.1	-1	1.1	1	-1.1	1	3.1	2.7	2.8	2

ILMN_Gene	Search_Key	A_A_Id	HN _a	HN _b	HN _c	HN _d	HN _p	LN _a	LN _b	LN _c	LN _d	LN _p	HL _a	HL _b	HL _c	HL _d
6288		103130746	9.4	3.9	9.4	2.5	5.4	7.6	4	9.5	4.1	5.4	1.2	-1	-1	-1.6
6289		104850273	-5.2	-2.9	-3.8	-5.2	-2.6	-4.9	-2.8	-3.5	-4.6	-2.2	-1	-1	-1.1	-1.1
8	SDHAP3	NR_003263.1	6350341	8	4.4	5.4	6.2	7.4	8.4	4.6	5.5	10	9.2	-1.1	-1.1	-1
6291		610086	-1.7	-1.5	-1.7	-2	-1.8	-4.7	-3.3	-5.7	-3.8	-4.2	2.8	2.2	3.4	1.9
6292		103130736	3.7	4	3.4	2.4	3.4	-1.1	1.1	-1.1	-1.1	1.1	4	3.5	3.6	2.8
9	C11ORF63	NM_199124.1	6550037	-3.2	-5.2	-5.1	-6.6	-6.5	-3.4	-5.3	-5.1	-6.3	-5.5	1.1	1	-1
10	LOC100132934	XM_001723077.1	2120390	4.9	4.3	4.2	3.3	4	1	-1	1	1.2	1.1	4.7	4.4	2.8
6295		101260021	-2.5	-3.4	-3	-2.5	-2.3	-1.1	-1.4	1	1.1	-1	-2.3	-2.4	-3.1	-2.8
11	TMEM103	NM_017713.1	4850064	4	4.5	5.5	5.1	5.4	4.4	4.3	5.4	7.4	5.9	-1.1	1	-1.5
6297		1770017	-1	-1.1	-1.2	-1.3	-1.2	-2.6	-1.9	-3.5	-3.1	-3.2	2.6	1.8	2.9	2.4
12	MUC6	XM_290540.6	2650292	-2.1	-1.8	-2	-2.6	-2.2	-1.9	-2.1	-2.2	-2.7	-2.7	-1.1	1.2	1.1
6299		104480102	-2.5	-1.6	-2.1	-2.2	-1.8	-2.6	-1.5	-2.1	-2.3	-1.7	1	-1.1	1	1.1
13	LOC730990	XM_001722060.1	2060170	-4.2	-4.1	-4.3	-6	-4.6	-1	-1.5	-1.2	-1	1.1	-4	-2.8	-3.7
6301		870685	-2.8	-2.1	-2	-2.2	-2.6	1	-1.1	1	-1	-1	-2.9	-1.9	-2	-2.2
14	SFRS13A	NM_054016.1	6110014	-2.8	-2.5	-2.3	-2.8	-3.2	-2.7	-2.5	-2.2	-2.3	-2.8	-1.1	-1	-1.2
15	KIR2DL5B	NM_001018081.1	5550017	-1.5	-1.3	-1.2	1	-4.7	1.2	1	1.2	1.1	1.4	-1.8	-1.3	-1.1
6304		103850064	2.2	1.9	1.9	1.9	2.2	2.3	1.9	1.9	2.2	2.2	-1	1	1	-1.2
6305		101340050	-3.1	-2	-2.5	-2	-2.7	-3.2	-2	-3	-1.9	-2.4	1	1	1.2	-1
6306		5390647	-1.9	-2.3	-4.4	-1.2	-1.4	-1.9	-2.2	-4.4	-1.4	-1.3	-1	-1	-1	1.2
6307		3060168	-2.1	-2.5	-2.3	-2.1	-2.1	-2	-2.3	-2.3	-2.1	-1.9	-1	-1.1	1	-1
16	HS.551438	Hs.551438	50438	-5	-6.3	-5.2	-4.3	-3.9	1	-1.4	-1	1.1	1.2	-5.1	-4.5	-4.5
17	DHX32	NM_018180.2	1980164	6.2	4.5	7.3	4.1	4.7	1.2	1.5	1.2	1	1.2	5.3	3	6
18	GSTZ1	NM_001513.2	7040044	3.1	2.5	4	1.4	2.1	1.2	1	1	1.1	1.1	2.6	2.4	3.9
19	FAM53A	NM_001013622.1	4060112	-2.2	-3.7	-8.5	-2.2	-1.3	-1.9	-3.3	-8.2	-2.5	-1.4	-1.1	-1.1	1.1
20	KLF6	NM_001008490.1	360110	-3.2	-1.7	-2.9	-4.2	-1.7	-3.2	-1.6	-2.6	-4.5	-1.8	1	-1.1	-1.1
21	LOC648704	XM_937786.1	4850047	-2.1	-2.4	-2.2	-2.3	-2.3	1.1	-1.1	1.1	1	-1	-2.3	-2.1	-2.5
6314		102230433	4	2.8	4.2	1.7	3.5	3.9	2.4	4.7	3	3.6	1	1.2	-1.1	-1.7
6315		100450079	-2.2	-2.2	-2.4	-2.5	-1.9	-2.2	-2.1	-2.4	-2.6	-1.9	-1	-1.1	-1	1
6316		2650546	-1.1	-1.1	1	-1.3	-1.2	-2.1	-1.8	-2.4	-3.8	-4.8	2	1.6	2.5	2.9
6317		102350528	-2.8	-1.8	-2	-2.7	-2.3	-3.2	-1.9	-2	-2.8	-2.4	1.2	1.1	1	1.1
22	UBE2K	NM_001111112.1	6220021	1.1	1.3	-1.1	-1.1	-1.1	-7.7	-4.5	-8.3	-3.8	-6.5	8.5	5.9	7.8
23	GLMN	NM_053274.1	2850609	1.9	1.7	2.7	1.4	2.4	1	1.1	-1.1	1	-1.1	1.9	1.6	2.9
6320		100380619	-4.7	-6.6	-7.8	-5.5	-5.7	-4.8	-6.2	-7.8	-4.2	-5.9	1	-1.1	-1	-1.3
6321		105910364	-2.1	-1.4	-1.7	-2.8	-1.4	-2.2	-1.6	-1.7	-3.1	-1.5	1	1.1	1	1.1
6322		106130025	2.3	2.2	1.9	2.1	2.3	1.1	1.1	-1	-1	-1	2.1	1.9	2	2.1
6323		100990672	-1.2	-1.3	-1.1	-1.3	-1.2	2.5	1.9	2.8	2.8	2.9	-3	-2.4	-3.1	-3.6
24	LOC732377	XM_001133069.1	1500097	3.7	3.3	3.3	1.6	3.5	3.5	2.8	3.3	2.3	3.4	1	1.2	-1
6325		106520398	-3.7	-3.4	-3.9	-2.8	-2.5	-3.7	-3.6	-3.7	-2.2	-2.5	1	1.1	-1.1	-1.3
6326		103840301	-1	-1	-1	-1.2	-1.1	2.8	1.5	2	1.8	2.2	-2.9	-1.5	-2	-2.1
6327		106450088	-2.7	-3.3	-3.1	-2.3	-4.1	1.4	-1.2	1.1	1.2	1	-3.8	-2.8	-3.6	-2.8
25	LOC400696	NM_207646.1	1660110	1.7	1.9	1.8	1.9	2.5	1.9	2	1.9	2.4	2.8	-1.1	-1	-1.3
6329		100050152	1.1	1.3	2.1	3.7	1.1	1.1	1.2	2.8	4.7	1	1	1.1	-1.3	-1.3
6330		103190068	1	1	1.1	-1.2	-1	-2.6	-1.9	-2.4	-2.5	-2.4	2.7	1.9	2.5	2.1
26	C3ORF57	NM_145035.2	4560600	-1	-1.2	1	-1.1	1.1	2.7	2	2.9	2.8	3.5	-2.8	-2.4	-2.9
27	LOC100130133	XR_037307.1	5390332	-3.2	-2.4	-2.6	-2.5	-1.3	-3.4	-2.4	-2.5	-2.3	-1.2	1.1	1	-1.1
6333		6040707	-2.8	-3	-2.5	-2.7	-2.9	1.2	-1.3	1	1	-1	-3.3	-2.3	-2.5	-2.8
6334		104780592	-2.1	-1.5	-1.5	-1.8	-2	-1.9	-1.6	-1.5	-1.9	-2.1	-1.1	1.1	1	1
28	IGFL1	NM_198541.1	6020605	1.8	1.1	1.3	1.3	3.5	1.8	1.5	1.6	1.3	3.8	-1	-1.4	-1.2
6336		102360148	1	-1.3	1	-1	-1.1	1.8	1.3	2.6	1.3	2.4	-1.8	-1.7	-2.6	-1.3
29	HS.131670	Hs.131670	270139	5.3	4.2	5.5	2.2	5.1	5.6	4.4	5.5	2.9	5.5	-1.1	-1	-1.3
30	OR10S1	NM_001004474.1	6110292	3.1	2.7	2.2	1.4	5.6	1.2	1.4	1.2	-1.4	1.5	2.6	1.9	2
6339		6290739	-2	-2.4	-6.1	-2.1	-1.3	-2.1	-2.2	-6.6	-2.1	-1.3	1	-1.1	1.1	-1
31	OGFOD1	NM_001031707.1	2510731	-3.4	-4	-3	-4.1	-2.7	1.1	-1.4	1.2	-1.2	1.3	-3.7	-2.9	-3.6
32	HS.439870	Hs.439870	6370497	1.2	-1.6	1.1	-1.2	-1.1	4.3	1.9	3.3	2.1	3	-3.7	-3.1	-2.5
33	TRIM49	NM_020358.2	450068	-1.8	-1.8	-1.9	-1.5	-2.2	-1.7	-1.8	-1.9	-1.5	-1.9	-1.1	-1	-1
34	LOC646588	XM_943454.1	2940468	5.6	5.3	11	2.4	5.9	6.2	5.5	9.3	3.5	5.8	-1.1	-1	-1.5
35	LOC645915	XM_933265.1	2650133	2.1	1.9	1.9	2.4	2.4	2	2	2.2	2.3	2.5	1.1	-1	-1.2
36	BCORL2	NM_173700.1	2570594	2.4	2.1	3	1.7	2	2.7	2.3	3	2.6	2.2	-1.1	-1.1	-1.5
37	GTF2I	XM_939506.1	4570736	-3.1	-2.9	-2.4	-3	-2.9	-3.2	-2.8	-2.6	-2	-2.7	1	-1	-1.5
6347		106550070	-1.6	-1.6	-1.4	-1	-1.8	1.5	1	1.4	1.4	1.7	-2.5	-1.7	-2	-1.5
38	SPDYE1	NM_001031618.1	770025	2.2	1.7	1.9	2.6	2.7	-1.1	1.1	-1.2	1	-1.1	2.3	1.5	2.3
6349		430670	4.4	4.4	5.7	2.5	3.2	-1.1	1.4	1	1	-1	4.7	3.3	5.6	2.4

ILMN_Gene	Search_Key	A_A_Id	HN _a	HN _b	HN _c	HN _d	HN _p	LN _a	LN _b	LN _c	LN _d	LN _p	HL _a	HL _b	HL _c	HL _d	
6350		104780484	1	1.4	1.1	-1.2	-1	-3.8	-2.5	-2.8	-2.6	-3.8	4	3.4	3.1	2.2	
6351		2760204	-1.2	-1.2	1	-1.1	-1	3.6	1.4	3.5	2.3	2.3	-4.3	-1.7	-3.4	-2.6	
6352		6900239	-2.6	-2.6	-2.9	-3.4	-3.7	-2	-2.7	-2.9	-2.7	-3.3	-1.3	1	1	-1.3	
6353		102030600	1.6	2.3	1.7	2.2	1.6	-1.2	1.1	1	1	-1.1	1.8	2	1.7	2.2	
6354		103800239	-1.1	-1	-1.2	-1.4	1.2	-2.3	-1.9	-2.3	-2.2	-2.3	2.2	1.9	2	1.6	
6355		102340121	1.4	1.5	2.3	1.1	1.7	1	1	-1	-1.1	-1	1.4	1.5	2.4	1.2	
39	HS.538100	Hs.538100	1500575	-1.9	-1.7	-1.8	-1.6	-1.9	1.2	-1.1	1.1	1.3	1.2	-2.2	-1.6	-1.9	-2.1
40	ZXDC	NM_001040653.1	5080121	1	1	1.1	-1	-1	2.5	1.6	1.7	2	3.1	-2.4	-1.6	-1.5	-2.1
41	CYC1	NM_001916.2	1770520	-1.1	-1.5	-1.2	-1.5	-1.2	4.1	2	4.7	3	4.2	-4.4	-3.1	-5.4	-4.6
6359		106770014	-2	-2.1	-2	-1.9	-1.9	-1.1	-1.3	-1.1	-1	-1	-1.9	-1.5	-1.8	-1.9	
42	RTN4RL2	NM_178570.1	60411	-1.2	-1.2	1	1	-1	3.4	1.3	3.3	1.4	1.5	-3.9	-1.5	-3.3	-1.4
43	LOC645550	XM_928570.1	5690403	1.1	-1.6	-1.1	-1.6	-1.1	3.1	1.5	2.2	1.5	2.2	-2.8	-2.4	-2.4	-2.4
44	SCRIB	NM_015356.3	2970176	3.3	2.7	3.4	1.8	3.3	3.4	2.4	3.4	3.2	3.3	-1	1.1	-1	-1.8
6363		101410064	1.8	1.5	1.7	2	1.6	1.7	1.4	1.6	2.5	1.5	1.1	1.1	1.1	-1.3	
45	ZMIZ1	NM_020338.2	2450131	-1.9	-2.5	-2.6	-3.8	-4	-1.1	-1.7	1	-1.3	-1.1	-1.7	-1.5	-2.6	-3
6365		102450601	-1.3	-1.3	-1.2	-1.3	-1.1	2.9	1.9	3.2	2.3	3.1	-3.7	-2.5	-3.8	-3	
6366		106980129	2.3	1.6	2.3	1.8	1.5	2.3	1.7	2.4	2.6	1.8	-1	-1.1	-1	-1.5	
6367		106110139	2.1	2.1	2	1.4	2.3	-1.4	-1.1	-1.6	-1.4	-1.8	2.8	2.4	3.2	2	
6368		106380458	-2	-2.7	-2.4	-1.8	-1.9	1	-1.4	-1	1	-1	-2	-1.9	-2.3	-1.8	
6369		102810239	-1.6	-2.1	-1.6	-2	-1.1	-1.9	-2.5	-1.6	-2	-1.2	1.2	1.2	1	1	
46	LOC653853	XM_936030.1	2470440	2	1.9	1.9	1.3	1.7	1	1.1	1.1	1	1	1.9	1.7	1.7	1.3
6371		103780671	1.7	1.5	1.9	2.4	2	1	-1	1.2	1	-1	1.7	1.5	1.6	2.4	
47	SDC3	XM_940667.1	1990551	-1.7	-2	-1.9	-1.9	-1.7	-1.9	-2	-1.8	-1.8	-1.7	1.2	1	-1	-1
6373		104920288	-1.1	1.2	1	-1.6	1.1	-3.2	-2.5	-3.1	-3.6	-3.1	3	3	3.2	2.3	
48	ALPI	NM_001631.2	2570162	1.2	1.2	1.3	-1.1	1.3	-2	-1.3	-1.6	-3.1	-1.8	2.4	1.6	2	2.9
6375		103990364	-1.3	1.1	1	-1.2	1	-4	-2	-3.4	-1.9	-2	3.1	2.1	3.4	1.6	
6376		102230086	19	15	21	3.3	26	1	-1.7	-1.4	-2.3	1.3	19	26	30	7.5	
6377		103780278	-1.1	1.1	1	-1.3	1.1	-2.6	-2.6	-2.7	-1.9	-1.4	2.5	2.8	2.8	1.5	
49	ST8SIA4	NM_005668.3	4230017	6.5	4.8	6	1.6	9.6	6.8	4.6	6.6	2.4	10	-1	1	-1.1	-1.5
50	LOC390251	XR_040181.1	3140341	1.1	-1	1.1	-1.4	-1.1	-3	-2.5	-3.5	-2.8	-4	3.2	2.5	3.8	2.1
6380		102480487	-2.3	-1.4	-1.9	-3.4	-1.5	-1.2	-1.2	-1.2	1	-1.1	-2	-1.1	-1.7	-3.4	
6381		104480458	-1.1	-1.2	-1.2	-6.7	-1.2	1.1	-1.1	-1.2	-5	-1.1	-1.2	-1.1	-1	-1.3	
6382		102760520	-1.9	-2.1	-2.1	-2	-2.1	1.1	-1.2	-1	1.1	-1.1	-2	-1.7	-2	-2.3	
6383		102680201	-1.7	-1.3	-1.5	-1.9	-1.5	-1.1	-1	1	-1.2	-1	-1.5	-1.3	-1.5	-1.6	
6384		101170242	1.3	1.9	1.5	-1.1	1.6	-3	-2.3	-2.8	-2.3	-2	3.9	4.5	4	2.2	
6385		6900167	-2.5	-2.8	-2.4	-1.6	-2.3	1.2	-1	1.4	1.8	1	-3	-2.7	-3.4	-3	
6386		100540373	-2.3	-2.7	-1.6	-2.5	-2	1.1	-1.2	1.2	-1.1	1.1	-2.5	-2.3	-1.9	-2.4	
6387		101780504	-2.1	-1.5	-2	-2.7	-1.5	-1	-1.1	1	-1.1	1.1	-2	-1.3	-2	-2.5	
51	HLA-DMA	NM_006120.2	540563	1.8	-1	1.3	-1.1	1.1	2.4	1.4	2.9	3.1	1.1	-1.3	-1.5	-2.3	-3.3
6389		2190438	1.9	1.3	1.8	1.1	1.9	-1.3	-1	-1.3	-1	-1.2	2.6	1.4	2.4	1.1	
52	PFKFB2	NM_001018053.1	7040181	-2.1	-1.9	-2.1	-1.8	-2.3	-2.3	-1.9	-2.1	-1.9	-2.3	1.1	-1.1	-1	1.1

Table 2: Top 120 genes (all arrays)

The normalised expression values for the 120 top genes are plotted in Figs. 4a-c.

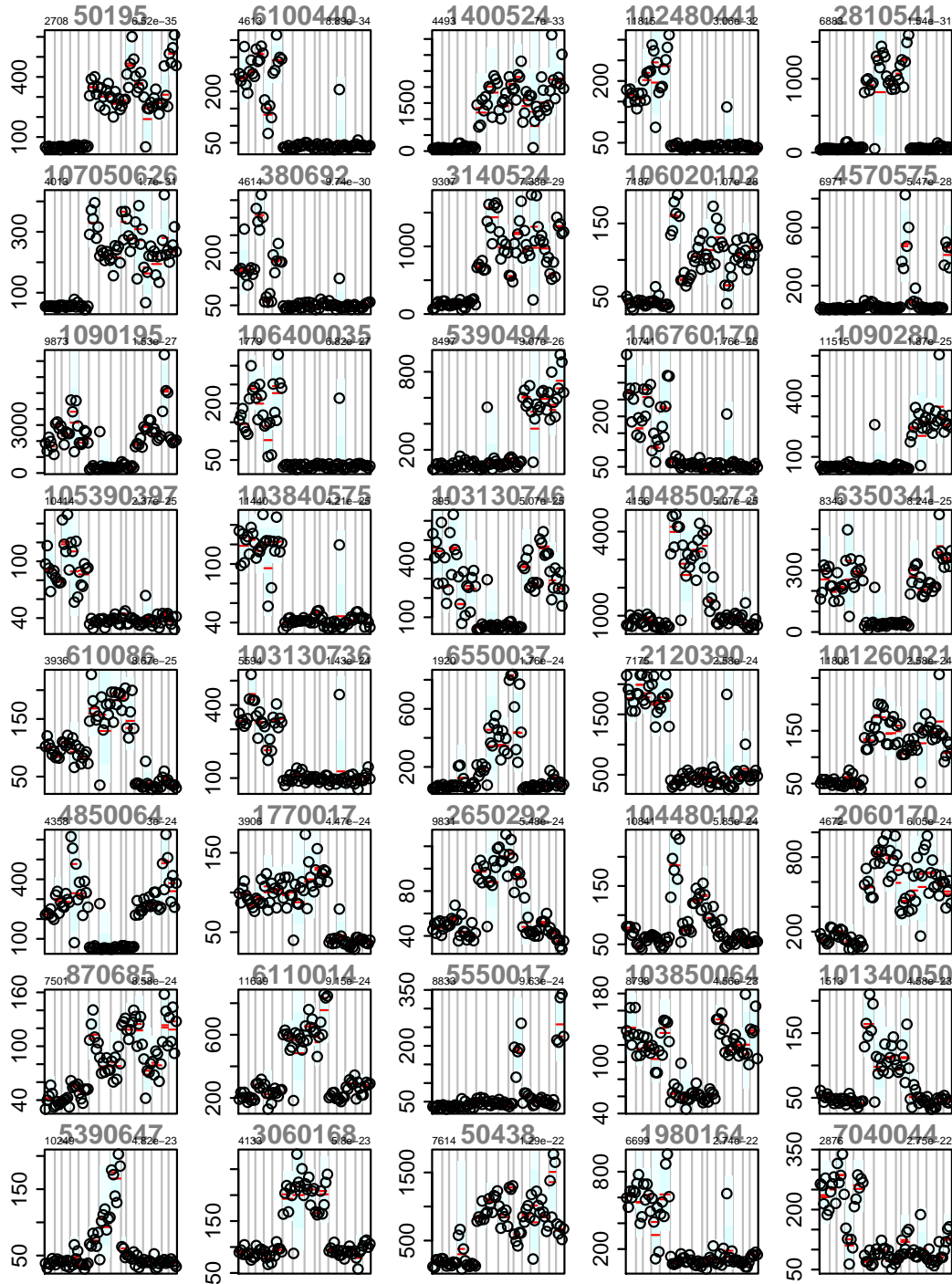


Figure 4a: The normalised expression values for the 40 top genes. Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

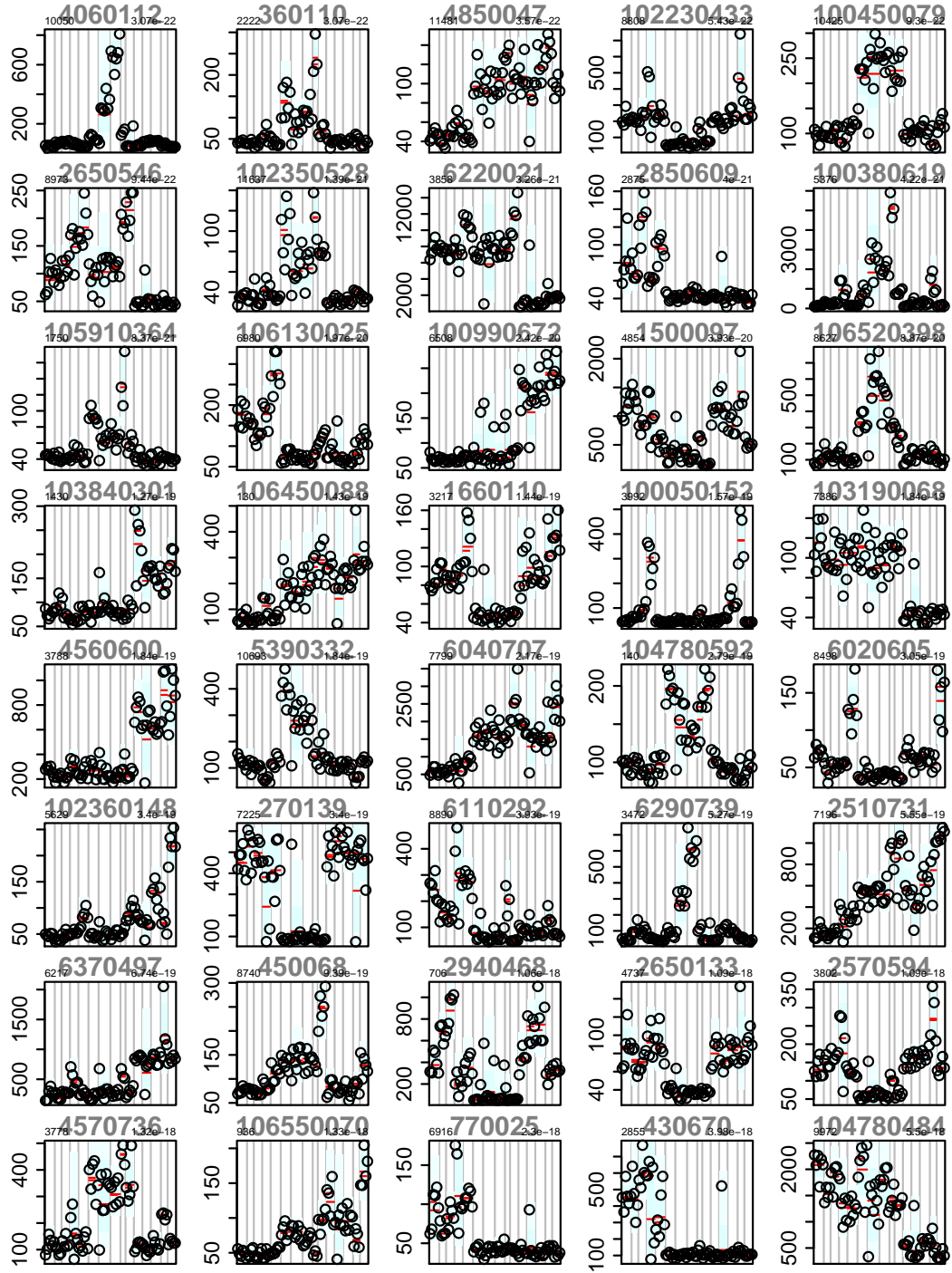


Figure 4b: Continued: normalised expression values for the top genes (41–80) for main contrasts. Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

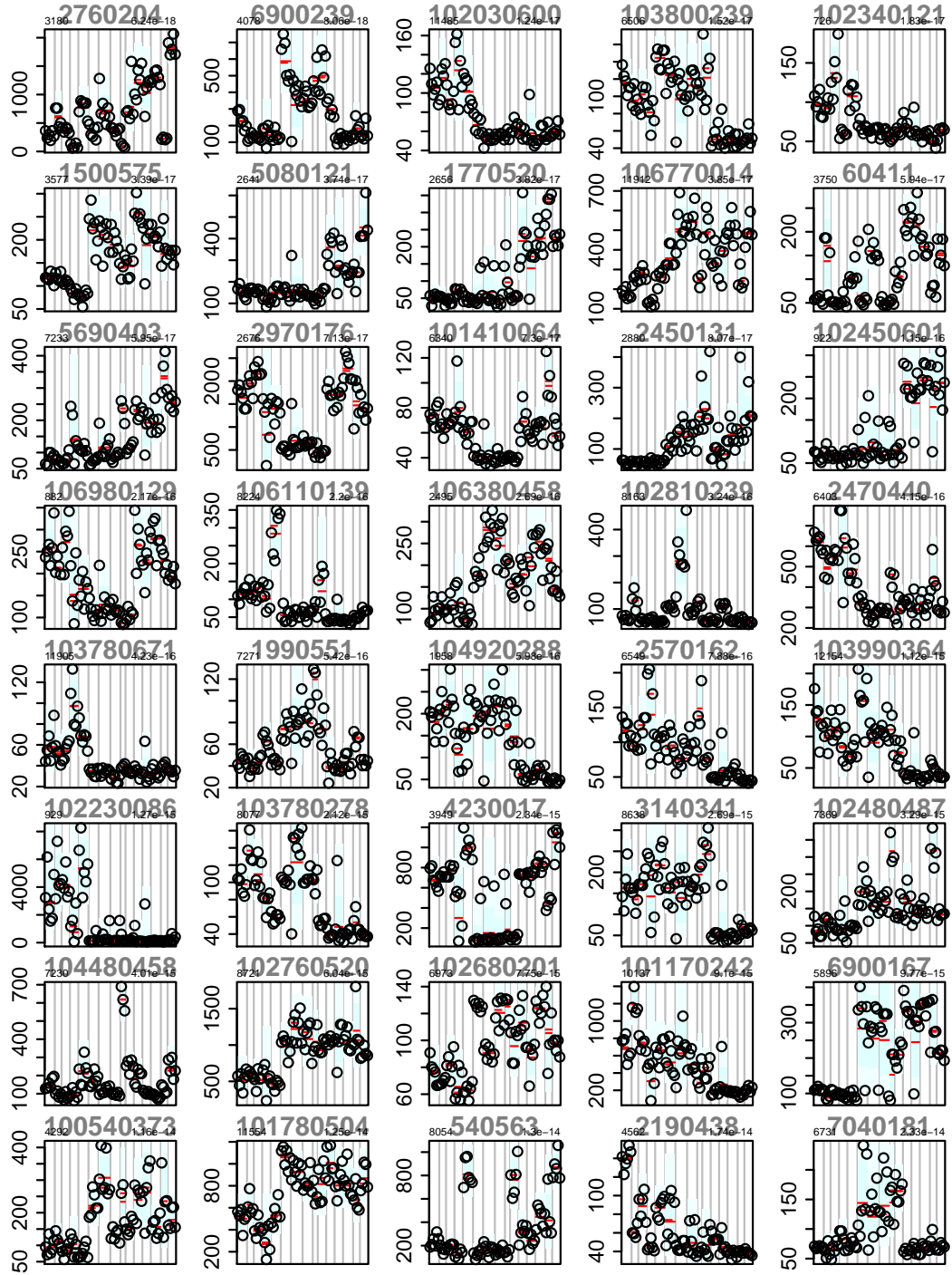


Figure 4c: Continued: normalised expression values for the top genes (81–120) for main contrasts. Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2 Single contrast analysis

3.2.1 Contrast HNa

Using the matrix representing the contrast defined by $\text{HAB_Amyg} - \text{NAB_Amyg}$

HNa	
HAB_Amyg	1
NAB_Amyg	-1

The statistics for the top 120 genes across the contrast (out of 237 genes having adjusted p -values below 0.05) are shown in table 3, the corresponding expression plots are shown in Figs. 5a-c on pages 53 through 55.

ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271		106020102	-3.9	-15	2.3e-23	1.79e-19	33.3
1 RAB25	NM_020387.1	50195	-7.5	-15	2.94e-23	1.79e-19	33.2
2 OR8B2	NM_001005468.1	6100440	6.9	14.5	1.67e-22	5.55e-19	32.2
6274		107050626	-5.9	-14.4	1.82e-22	5.55e-19	32.1
6275		2810541	-18	-12.6	1.61e-19	3.92e-16	28
3 SDHAP3	NR_003263.2	1400524	-13	-12.1	1.36e-18	2.76e-15	26.7
6277		104850273	-5.2	-11.8	3.12e-18	5.42e-15	26.1
6278		103130746	9.4	11.5	1.15e-17	1.75e-14	25.3
6279		380692	3.5	11.5	1.31e-17	1.77e-14	25.2
6280		104480102	-2.5	-11.4	1.73e-17	2.11e-14	25
6281		102480441	3.8	11.1	6.91e-17	7.65e-14	24.1
6282		870685	-2.8	-10.6	4.54e-16	4.6e-13	22.8
6283		101340050	-3.1	-10.5	6.91e-16	6.47e-13	22.5
4 LOC100132934	XM_001723077.1	2120390	4.9	10.4	1.06e-15	9.24e-13	22.2
5 NARG1	NM_057175.3	3140524	-5.9	-10.3	1.48e-15	1.2e-12	22
6 SDHAP3	NR_003263.1	6350341	8	10.2	2.38e-15	1.81e-12	21.7
6287		103840575	3	10.2	2.61e-15	1.87e-12	21.6
6288		106760170	4	10.1	2.97e-15	2.01e-12	21.5
7 SNAR-I	NR_024343.1	2370164	-2.5	-10	4.4e-15	2.78e-12	21.2
6290		105390397	2.6	10	4.57e-15	2.78e-12	21.2
8 GSTZ1	NM_001513.2	7040044	3.1	10	4.82e-15	2.8e-12	21.2
9 KLF6	NM_001008490.1	360110	-3.2	-10	5.11e-15	2.83e-12	21.1
6293		103130736	3.7	9.95	6.37e-15	3.37e-12	21
6294		1090195	5.7	9.76	1.36e-14	6.88e-12	20.5
10 LOC100130133	XR_037307.1	5390332	-3.2	-9.65	2.15e-14	1.05e-11	20.1
6296		102350528	-2.8	-9.63	2.37e-14	1.11e-11	20.1
6297		103850064	2.2	9.55	3.24e-14	1.44e-11	19.8
11 DHX32	NM_018180.2	1980164	6.2	9.55	3.31e-14	1.44e-11	19.8
12 SFRS13A	NM_054016.1	6110014	-2.8	-9.5	4.04e-14	1.7e-11	19.7
6300		102230433	4	9.09	2.23e-13	9.04e-11	18.5
6301		104780592	-2.1	-9.06	2.49e-13	9.76e-11	18.4
6302		106400035	4.3	9	3.2e-13	1.22e-10	18.2
6303		105910364	-2.1	-8.98	3.55e-13	1.31e-10	18.1
13 HS.551438	Hs.551438	50438	-5	-8.65	1.36e-12	4.88e-10	17.2
14 LOC730990	XM_001722060.1	2060170	-4.2	-8.64	1.43e-12	4.96e-10	17.1
15 LOC732377	XM_001133069.1	1500097	3.7	8.59	1.79e-12	6.04e-10	17
6307		106130025	2.3	8.57	1.95e-12	6.41e-10	16.9
6308		101260021	-2.5	-8.41	3.73e-12	1.19e-09	16.4
16 MUC6	XM_290540.6	2650292	-2.1	-8.25	7.45e-12	2.32e-09	15.9
6310		6040541	2.2	8.21	8.75e-12	2.66e-09	15.8

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6311			3060168	-2.1	-8.19	9.47e-12	2.81e-09	15.7
6312			106520398	-3.7	-8.17	1.02e-11	2.96e-09	15.7
6313			100450079	-2.2	-8.12	1.28e-11	3.63e-09	15.5
17	OR10S1	NM_001004474.1	6110292	3.1	7.88	3.56e-11	9.84e-09	14.8
18	TMEM103	NM_017713.1	4850064	4	7.78	5.21e-11	1.41e-08	14.5
19	HS.131670	Hs.131670	270139	5.3	7.75	6.1e-11	1.61e-08	14.4
20	GTF2I	XM_939506.1	4570736	-3.1	-7.71	7.2e-11	1.86e-08	14.2
21	LOC653853	XM_936030.1	2470440	2	7.6	1.11e-10	2.81e-08	13.9
6319			103360184	-2.2	-7.58	1.25e-10	3.11e-08	13.8
6320			6040707	-2.8	-7.45	2.1e-10	5.12e-08	13.4
6321			430670	4.4	7.44	2.2e-10	5.26e-08	13.4
22	LOC648704	XM_937786.1	4850047	-2.1	-7.44	2.25e-10	5.26e-08	13.4
6323			106770014	-2	-7.31	3.84e-10	8.82e-08	13
6324			106980129	2.3	7.27	4.51e-10	1.02e-07	12.9
23	OGFOD1	NM_001031707.1	2510731	-3.4	-7.25	4.78e-10	1.06e-07	12.8
6326			102480487	-2.3	-7.2	6.07e-10	1.32e-07	12.6
6327			101410064	1.8	7.15	7.34e-10	1.57e-07	12.5
6328			102680201	-1.7	-6.99	1.44e-09	3.01e-07	12
24	BCORL2	NM_173700.1	2570594	2.4	6.99	1.46e-09	3.01e-07	12
25	MTMR10	NM_017762.1	6900112	1.7	6.89	2.18e-09	4.36e-07	11.7
26	SCRIB	NM_015356.3	2970176	3.3	6.89	2.19e-09	4.36e-07	11.7
27	GLMN	NM_053274.1	2850609	1.9	6.87	2.39e-09	4.68e-07	11.6
6333			100380619	-4.7	-6.84	2.72e-09	5.26e-07	11.5
28	LOC645915	XM_933265.1	2650133	2.1	6.81	3.02e-09	5.73e-07	11.4
29	SPDYE1	NM_001031618.1	770025	2.2	6.72	4.41e-09	8.22e-07	11.1
30	LOC646588	XM_943454.1	2940468	5.6	6.72	4.46e-09	8.22e-07	11.1
31	TRIM49	NM_020358.2	450068	-1.8	-6.7	4.84e-09	8.79e-07	11.1
32	TNFRSF18	NM_148902.1	520066	2.2	6.67	5.33e-09	9.54e-07	11
6339			101780504	-2.1	-6.66	5.65e-09	9.97e-07	10.9
33	LOC100131209	XM_001725125.1	6380253	1.9	6.62	6.73e-09	1.17e-06	10.8
34	C11ORF63	NM_199124.1	6550037	-3.2	-6.58	7.8e-09	1.34e-06	10.7
35	HS.538100	Hs.538100	1500575	-1.9	-6.55	8.88e-09	1.5e-06	10.6
36	ESCO1	NM_052911.1	2340750	-1.6	-6.42	1.54e-08	2.56e-06	10.2
6344			5390647	-1.9	-6.38	1.8e-08	2.96e-06	10
37	ST8SIA4	NM_005668.3	4230017	6.5	6.36	1.93e-08	3.13e-06	9.99
6346			102230086	19	6.33	2.19e-08	3.5e-06	9.89
38	ST7	NM_018412.3	4570575	-2	-6.26	2.91e-08	4.61e-06	9.67
6348			3390324	-1.6	-6.22	3.45e-08	5.39e-06	9.54
6349			106450088	-2.7	-6.21	3.58e-08	5.51e-06	9.51
6350			105390722	-1.8	-6.18	3.97e-08	6.04e-06	9.43
6351			101690180	-1.6	-6.18	4.02e-08	6.04e-06	9.42
6352			100540373	-2.3	-6.15	4.49e-08	6.66e-06	9.34
6353			103800546	-1.9	-6.14	4.8e-08	7.04e-06	9.29
6354			6900239	-2.6	-6.11	5.44e-08	7.88e-06	9.19
39	DLG1	NM_004087.1	4210541	2.8	6.09	5.89e-08	8.43e-06	9.13
40	IGFL1	NM_198541.1	6020605	1.8	6.07	6.19e-08	8.76e-06	9.09
6357			2190438	1.9	6.06	6.64e-08	9.29e-06	9.03
6358			101580301	3.2	6.02	7.76e-08	1.06e-05	8.91
6359			106020113	-1.7	-6.02	7.76e-08	1.06e-05	8.91
6360			2630025	-4.5	-6.01	7.89e-08	1.07e-05	8.9
41	WWC1	NM_015238.1	1090575	-1.8	-5.96	9.81e-08	1.31e-05	8.73
42	MIR153-1	NR_029688.1	4610441	1.9	5.95	1.01e-07	1.34e-05	8.71
43	LOC642333	XM_939884.1	5390148	1.9	5.93	1.11e-07	1.46e-05	8.63
44	PTPN9	NM_002833.2	3930279	3.8	5.92	1.15e-07	1.49e-05	8.61
45	LOC400120	NM_203451.1	3440519	3.6	5.9	1.24e-07	1.59e-05	8.55
46	ZNF655	NM_001009956.1	6550390	2.5	5.88	1.36e-07	1.72e-05	8.48
47	CAPNS1	NM_001003962.1	5290500	2	5.83	1.68e-07	2.09e-05	8.32

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6368			106380458	-2	-5.83	1.69e-07	2.09e-05	8.31
48	PFKFB2	NM_001018053.1	7040181	-2.1	-5.82	1.7e-07	2.09e-05	8.31
49	SGCB	NM_000232.3	1190162	-2	-5.79	1.93e-07	2.34e-05	8.21
6371			101580368	-1.8	-5.75	2.3e-07	2.77e-05	8.07
6372			101500408	-1.6	-5.67	3.13e-07	3.73e-05	7.83
6373			100110411	-1.5	-5.6	4.07e-07	4.81e-05	7.62
6374			6900167	-2.5	-5.59	4.37e-07	5.11e-05	7.57
50	LOC400696	NM_207646.1	1660110	1.7	5.58	4.44e-07	5.15e-05	7.56
6376			1740324	1.9	5.57	4.74e-07	5.44e-05	7.5
6377			3520451	1.6	5.52	5.62e-07	6.39e-05	7.37
51	KCTD8	NM_198353.1	1980079	2.9	5.48	6.56e-07	7.39e-05	7.25
52	OR5P2	NM_153444.1	770280	2.6	5.46	7.05e-07	7.87e-05	7.19
53	TCEB3B	NM_016427.2	5220088	1.9	5.44	7.89e-07	8.73e-05	7.11
6381			102760520	-1.9	-5.39	9.36e-07	0.000103	6.97
54	CXORF30	XR_000668.1	360671	1.7	5.39	9.51e-07	0.000103	6.96
6383			103780671	1.7	5.39	9.58e-07	0.000103	6.95
55	DUSP11	NM_003584.1	670112	4.8	5.38	9.71e-07	0.000104	6.94
56	SRP54	XM_940545.1	1570279	1.6	5.34	1.16e-06	0.000122	6.81
6386			5220180	2.5	5.33	1.17e-06	0.000123	6.8
6387			4540494	-2.5	-5.26	1.59e-06	0.000165	6.56
6388			105570601	1.9	5.24	1.68e-06	0.000174	6.51
6389			102810239	-1.6	-5.16	2.26e-06	0.000231	6.28
57	SDC3	XM_940667.1	1990551	-1.7	-5.14	2.52e-06	0.000255	6.2

Table 3: Top 120 genes (all arrays)

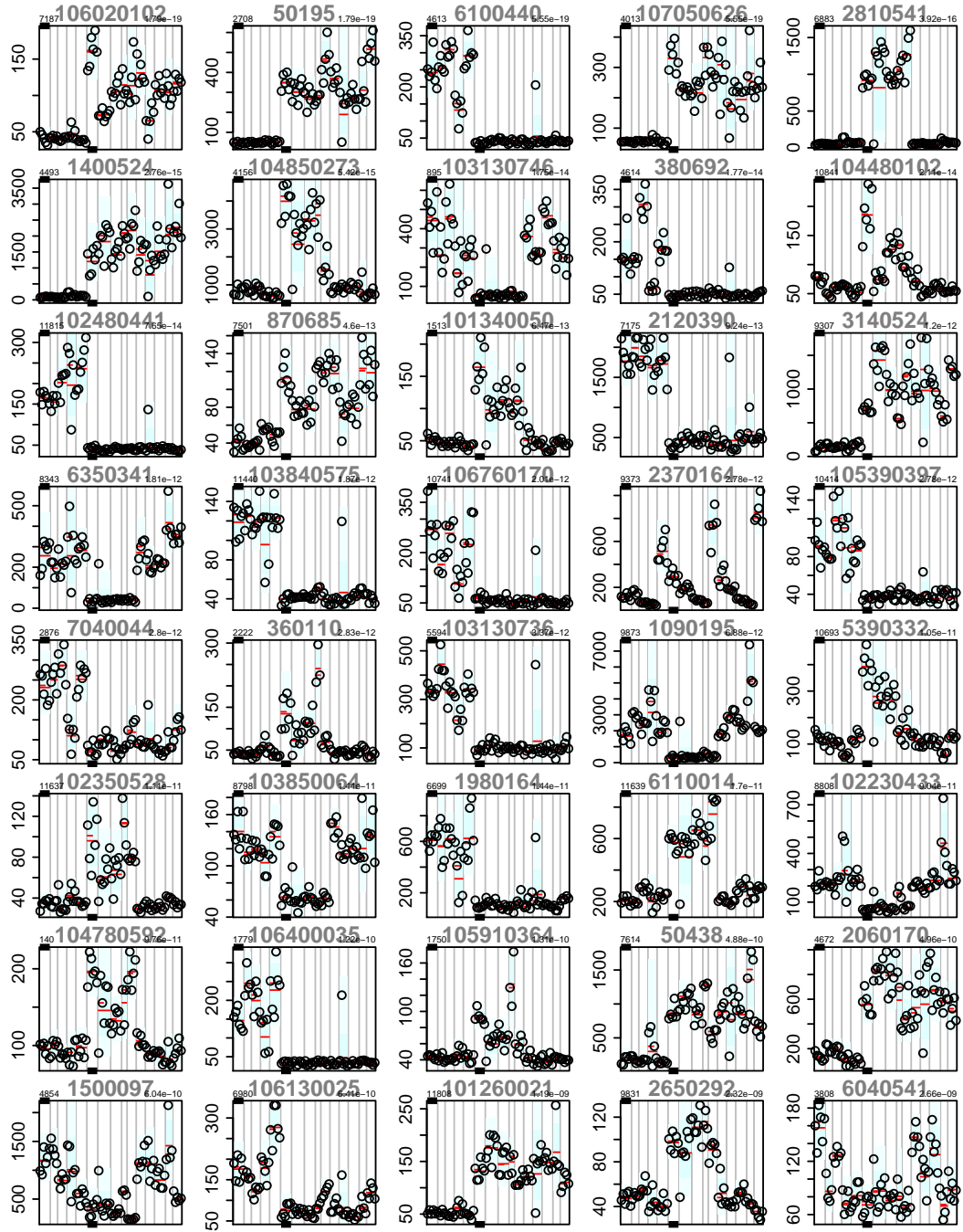


Figure 5a: Top 40 genes for contrast HNa (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

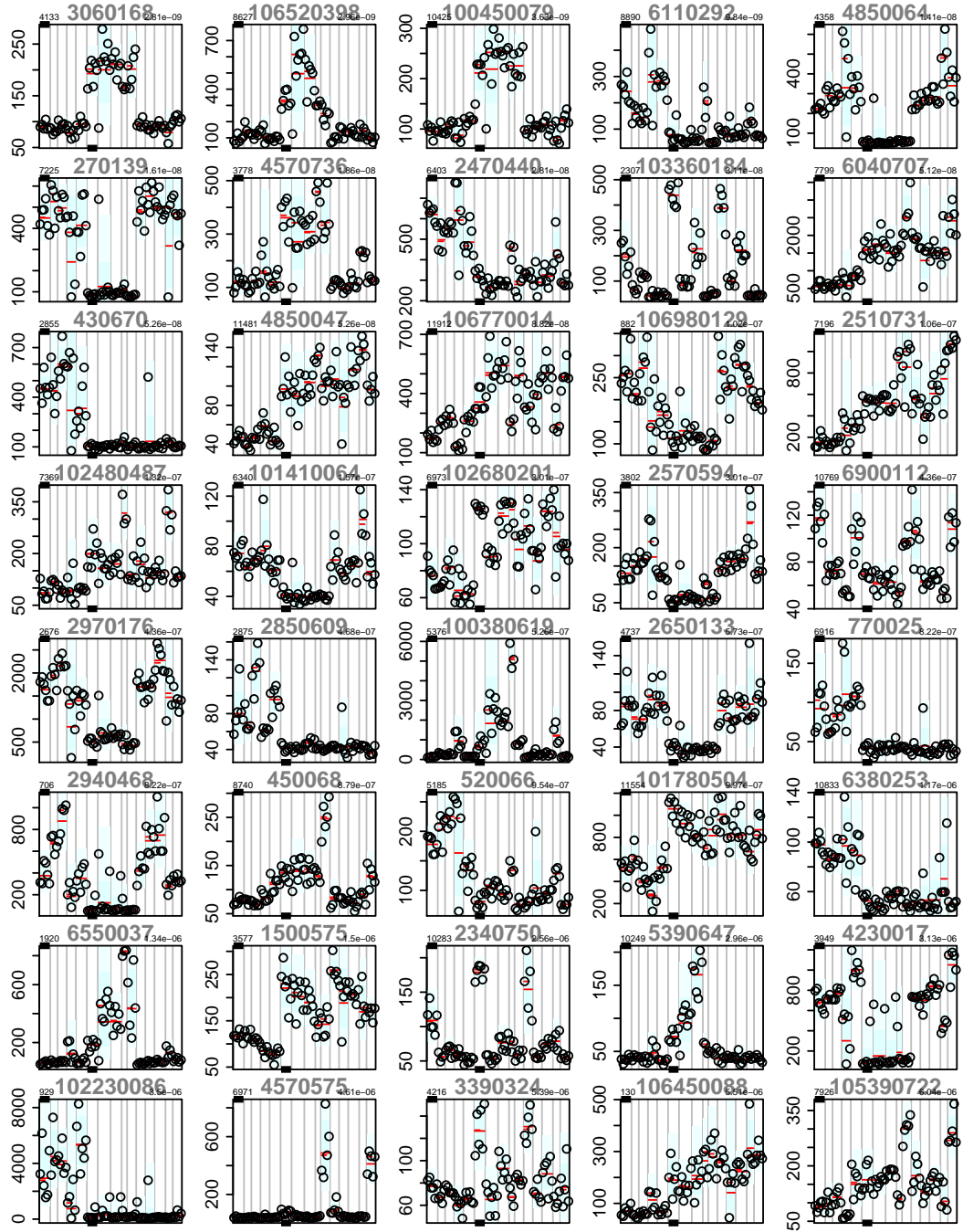


Figure 5b: Significant probes (41–80) for contrast HNa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

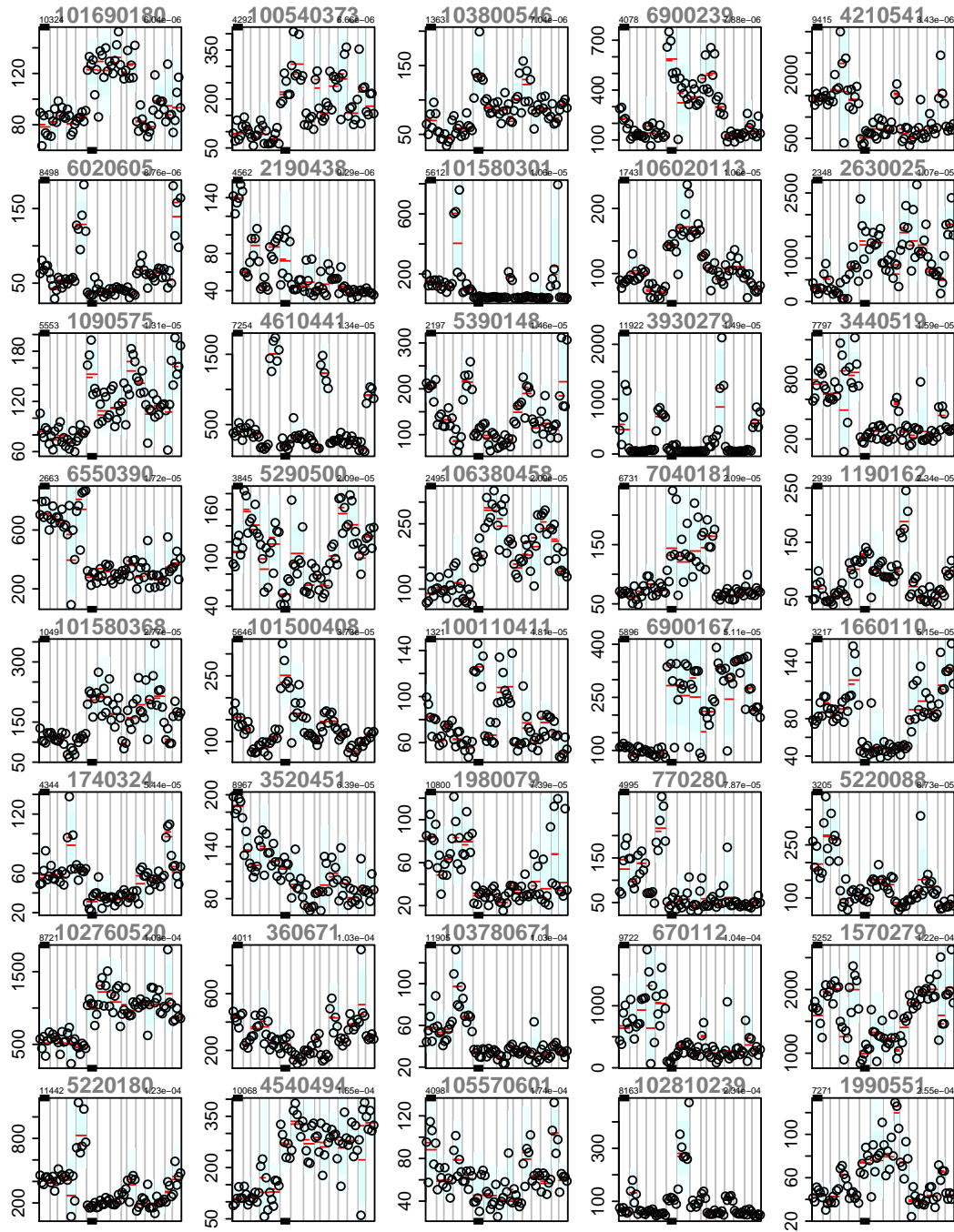


Figure 5c: Significant probes (81–120) for contrast HNa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.2 Contrast HNb

Using the matrix representing the contrast defined by HAB_BAmY - NAB_BAmY

HNb	
HAB_BAmY	1
NAB_BAmY	-1

The statistics for the top 120 genes across the contrast (out of 202 genes having adjusted p -values below 0.05) are shown in table 4, the corresponding expression plots are shown in Figs. 6a-c on pages 59 through 61.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	RAB25	NM_020387.1	50195	-6.8	-13.1	2.56e-20	2.76e-16	29.9
2	SDHAP3	NR_003263.2	1400524	-20	-12.9	4.75e-20	2.76e-16	29.5
3	OR8B2	NM_001005468.1	6100440	6.4	12.8	6.8e-20	2.76e-16	29.2
4	NARG1	NM_057175.3	3140524	-8.9	-11.7	4.73e-18	1.44e-14	26.4
6275			106400035	7.5	11.4	1.62e-17	3.95e-14	25.6
6276			2810541	-16	-11.2	3.88e-17	7.86e-14	25
6277			102480441	4.2	11	8.46e-17	1.47e-13	24.5
6278			107050626	-4.1	-10.5	7.21e-16	1.06e-12	23
6279			101260021	-3.4	-10.5	7.87e-16	1.06e-12	22.9
6280			1090195	6.7	9.75	1.4e-14	1.71e-11	20.9
6281			103130736	4	9.6	2.61e-14	2.81e-11	20.4
6282			380692	3.1	9.59	2.77e-14	2.81e-11	20.4
6283			103840575	3	9.26	1.09e-13	1.02e-10	19.4
6284			3060168	-2.5	-9.15	1.71e-13	1.49e-10	19
5	HS.551438	Hs.551438	50438	-6.3	-9.07	2.35e-13	1.91e-10	18.8
6	LOC100132934	XM_001723077.1	2120390	4.3	8.89	5.16e-13	3.92e-10	18.2
7	C11ORF63	NM_199124.1	6550037	-5.2	-8.65	1.4e-12	1e-09	17.5
6288			102030600	2.3	8.29	6.3e-12	4.26e-09	16.3
8	LOC648704	XM_937786.1	4850047	-2.4	-8.26	7.05e-12	4.52e-09	16.3
9	FAM53A	NM_001013622.1	4060112	-3.7	-8.02	1.96e-11	1.19e-08	15.5
6291			106380458	-2.7	-7.88	3.53e-11	2.05e-08	15
10	SFRS13A	NM_054016.1	6110014	-2.5	-7.81	4.64e-11	2.47e-08	14.8
11	LOC730990	XM_001722060.1	2060170	-4.1	-7.81	4.67e-11	2.47e-08	14.8
12	TMEM103	NM_017713.1	4850064	4.5	7.74	6.17e-11	3.13e-08	14.6
6295			100380619	-6.6	-7.7	7.48e-11	3.64e-08	14.5
6296			106760170	3.1	7.52	1.55e-10	7.25e-08	13.9
13	GSTZ1	NM_001513.2	7040044	2.5	7.49	1.79e-10	7.56e-08	13.8
6298			100450079	-2.2	-7.49	1.81e-10	7.56e-08	13.8
6299			5390647	-2.3	-7.49	1.82e-10	7.56e-08	13.8
6300			105390397	2.2	7.48	1.86e-10	7.56e-08	13.8
14	OGFOD1	NM_001031707.1	2510731	-4	-7.46	2.06e-10	8.1e-08	13.7
6302			102810239	-2.1	-7.44	2.21e-10	8.4e-08	13.6
6303			870685	-2.1	-7.29	4.06e-10	1.5e-07	13.2
6304			6040707	-3	-7.28	4.34e-10	1.55e-07	13.1
15	LOC732377	XM_001133069.1	1500097	3.3	7.24	5.07e-10	1.76e-07	13
16	DHX32	NM_018180.2	1980164	4.5	7.19	6.17e-10	2.09e-07	12.9
6307			106130025	2.2	7.16	7.17e-10	2.36e-07	12.7
6308			103850064	1.9	7.12	8.36e-10	2.68e-07	12.6
6309			104850273	-2.9	-7.07	1.05e-09	3.26e-07	12.4
6310			106520398	-3.4	-7.02	1.25e-09	3.8e-07	12.3
6311			430670	4.4	6.94	1.81e-09	5.36e-07	12
6312			106450088	-3.3	-6.78	3.47e-09	1.01e-06	11.5

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			106770014	-2.1	-6.76	3.71e-09	1.05e-06	11.5
17	SDHAP3	NR_003263.1	6350341	4.4	6.68	5.2e-09	1.42e-06	11.2
18	GTF2I	XM_939506.1	4570736	-2.9	-6.68	5.26e-09	1.42e-06	11.2
19	LOC653853	XM_936030.1	2470440	1.9	6.6	7.14e-09	1.89e-06	10.9
6317			100540373	-2.7	-6.59	7.47e-09	1.94e-06	10.9
20	LOC100130133	XR_037307.1	5390332	-2.4	-6.56	8.57e-09	2.17e-06	10.8
21	SDC3	XM_940667.1	1990551	-2	-6.5	1.1e-08	2.73e-06	10.6
6320			103130746	3.9	6.45	1.34e-08	3.25e-06	10.5
22	TRIM49	NM_020358.2	450068	-1.8	-6.43	1.45e-08	3.46e-06	10.4
23	OR10S1	NM_001004474.1	6110292	2.7	6.33	2.2e-08	5.14e-06	10.1
6323			102230433	2.8	6.25	2.97e-08	6.83e-06	9.83
24	LOC400696	NM_207646.1	1660110	1.9	6.21	3.61e-08	8.15e-06	9.67
25	HS.131670	Hs.131670	270139	4.2	6.16	4.31e-08	9.54e-06	9.53
26	MUC6	XM_290540.6	2650292	-1.8	-6.1	5.49e-08	1.19e-05	9.34
27	WBSCR22	NM_017528.2	6370538	2.3	6.07	6.24e-08	1.33e-05	9.24
28	LOC646588	XM_943454.1	2940468	5.3	6.01	8.14e-08	1.71e-05	9.03
29	SGCB	NM_000232.3	1190162	-2.1	-5.95	1.02e-07	2.11e-05	8.85
30	KRTCAP2	NM_173852.3	6110605	-2.9	-5.83	1.62e-07	3.29e-05	8.48
6331			101340050	-2	-5.83	1.67e-07	3.32e-05	8.46
6332			6900167	-2.8	-5.78	2.01e-07	3.94e-05	8.32
6333			101580368	-1.9	-5.75	2.32e-07	4.48e-05	8.2
31	HS.151285	Hs.151285	3440300	-3	-5.72	2.61e-07	4.97e-05	8.11
32	LOC100131209	XM_001725125.1	6380253	1.8	5.67	3.15e-07	5.9e-05	7.96
6336			4540494	-2.9	-5.66	3.24e-07	5.98e-05	7.94
33	LOC645915	XM_933265.1	2650133	1.9	5.65	3.37e-07	6.13e-05	7.9
6338			6900239	-2.6	-5.6	4.12e-07	7.37e-05	7.74
6339			102760520	-2.1	-5.58	4.48e-07	7.91e-05	7.68
6340			2100369	-2.5	-5.55	5.13e-07	8.91e-05	7.57
6341			6290739	-2.4	-5.53	5.54e-07	9.5e-05	7.51
6342			2370605	1.6	5.51	5.89e-07	9.96e-05	7.46
6343			106020102	-1.7	-5.49	6.32e-07	0.000105	7.4
34	ZMIZ1	NM_020338.2	2450131	-2.5	-5.47	6.82e-07	0.000112	7.34
35	LOC729815	XR_037436.1	2450450	-2.1	-5.47	6.89e-07	0.000112	7.34
6346			100050079	-1.8	-5.47	6.98e-07	0.000112	7.33
36	GLMN	NM_053274.1	2850609	1.7	5.45	7.47e-07	0.000118	7.27
6348			106020113	-1.6	-5.45	7.56e-07	0.000118	7.26
37	BCORL2	NM_173700.1	2570594	2.1	5.41	8.78e-07	0.000135	7.14
6350			102230086	15	5.35	1.11e-06	0.000167	6.95
38	SCRIB	NM_015356.3	2970176	2.7	5.35	1.12e-06	0.000167	6.95
6352			104480102	-1.6	-5.34	1.12e-06	0.000167	6.95
6353			103800546	-1.9	-5.31	1.26e-06	0.000185	6.85
39	VN1R2	NM_173856.1	4760286	-2	-5.27	1.51e-06	0.000218	6.71
6355			106980286	-2	-5.26	1.56e-06	0.000223	6.68
40	TNFRSF18	NM_148902.1	520066	2	5.22	1.81e-06	0.000256	6.57
6357			101690180	-1.5	-5.1	2.9e-06	0.000406	6.19
6358			102350528	-1.8	-4.98	4.64e-06	0.000642	5.81
6359			101660458	-1.7	-4.95	5.02e-06	0.000686	5.75
41	LOC440233	XM_496037.2	6660301	-2	-4.94	5.39e-06	0.000728	5.69
6361			104780332	1.6	4.93	5.58e-06	0.000746	5.67
6362			102320576	-1.8	-4.92	5.7e-06	0.000754	5.65
42	ST8SIA4	NM_005668.3	4230017	4.8	4.89	6.36e-06	0.000833	5.56
43	LRRC43	NM_152759.3	610735	-1.9	-4.88	6.73e-06	0.000872	5.52
44	PFKFB2	NM_001018053.1	7040181	-1.9	-4.87	6.95e-06	0.00089	5.49
45	TRIM36	NM_018700.3	1690402	-1.8	-4.84	7.66e-06	0.000971	5.41
6367			101410064	1.5	4.84	7.76e-06	0.000974	5.4
46	HS.245405	Hs.245405	6660440	-2	-4.82	8.27e-06	0.00103	5.35
6369			5570605	1.8	4.81	8.76e-06	0.00108	5.31

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
47	HS.514893	Hs.514893	1990524	-1.8	-4.78	9.52e-06	0.00116	5.24
48	HS.538100	Hs.538100	1500575	-1.7	-4.78	9.67e-06	0.00117	5.23
6372			102340121	1.5	4.78	9.83e-06	0.00117	5.21
6373			101580301	2.7	4.77	1.02e-05	0.00121	5.18
49	CXORF30	XR_000668.1	360671	1.7	4.74	1.13e-05	0.00132	5.1
6375			106110139	2.1	4.71	1.27e-05	0.00147	5.01
50	TCEB3B	NM_016427.2	5220088	1.8	4.69	1.37e-05	0.00156	4.95
6377			103840750	-2	-4.69	1.37e-05	0.00156	4.94
6378			4060301	-1.6	-4.64	1.64e-05	0.00185	4.8
51	FBXO22	NM_012170.2	3840128	-1.9	-4.61	1.78e-05	0.00199	4.74
52	TMEM17	NM_198276.1	5900750	-2	-4.58	2.05e-05	0.00227	4.63
53	LMLN	NM_033029.1	4540047	-7.8	-4.56	2.14e-05	0.00235	4.59
6382			103440278	-1.8	-4.52	2.49e-05	0.0027	4.47
54	ZNF655	NM_001009956.1	6550390	2.2	4.52	2.51e-05	0.0027	4.46
6384			3800288	-1.8	-4.5	2.73e-05	0.00291	4.4
55	KCNK7	NM_033347.1	1500142	-2.9	-4.48	2.92e-05	0.00309	4.34
6386			100520671	-1.8	-4.46	3.1e-05	0.00326	4.29
6387			2690017	-1.8	-4.45	3.24e-05	0.00337	4.26
6388			104780592	-1.5	-4.44	3.31e-05	0.00342	4.24
6389			2900537	-1.6	-4.44	3.35e-05	0.00343	4.23
6390			101090181	-1.6	-4.43	3.52e-05	0.00357	4.19

Table 4: Top 120 genes (all arrays)

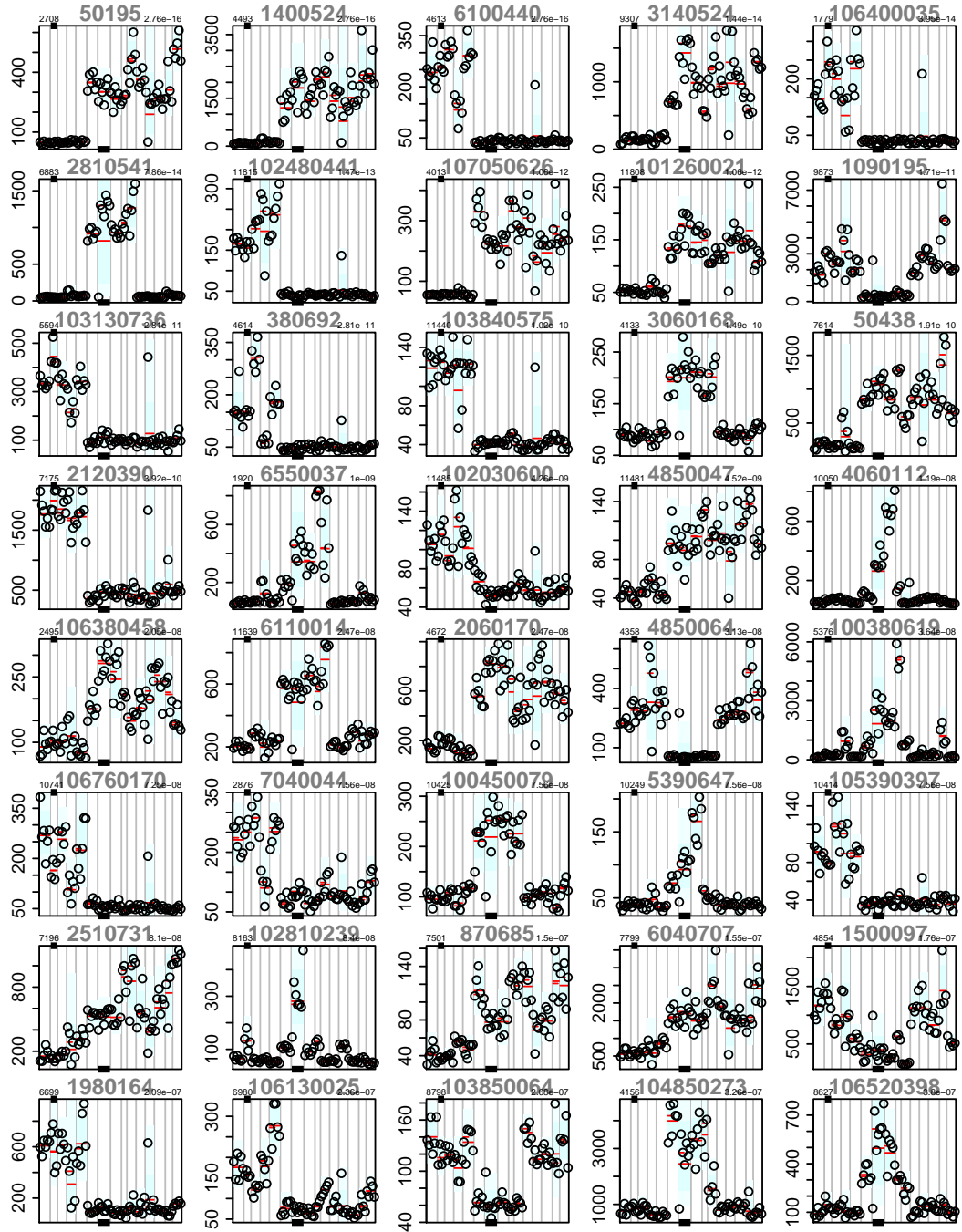


Figure 6a: Top 40 genes for contrast HNb (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

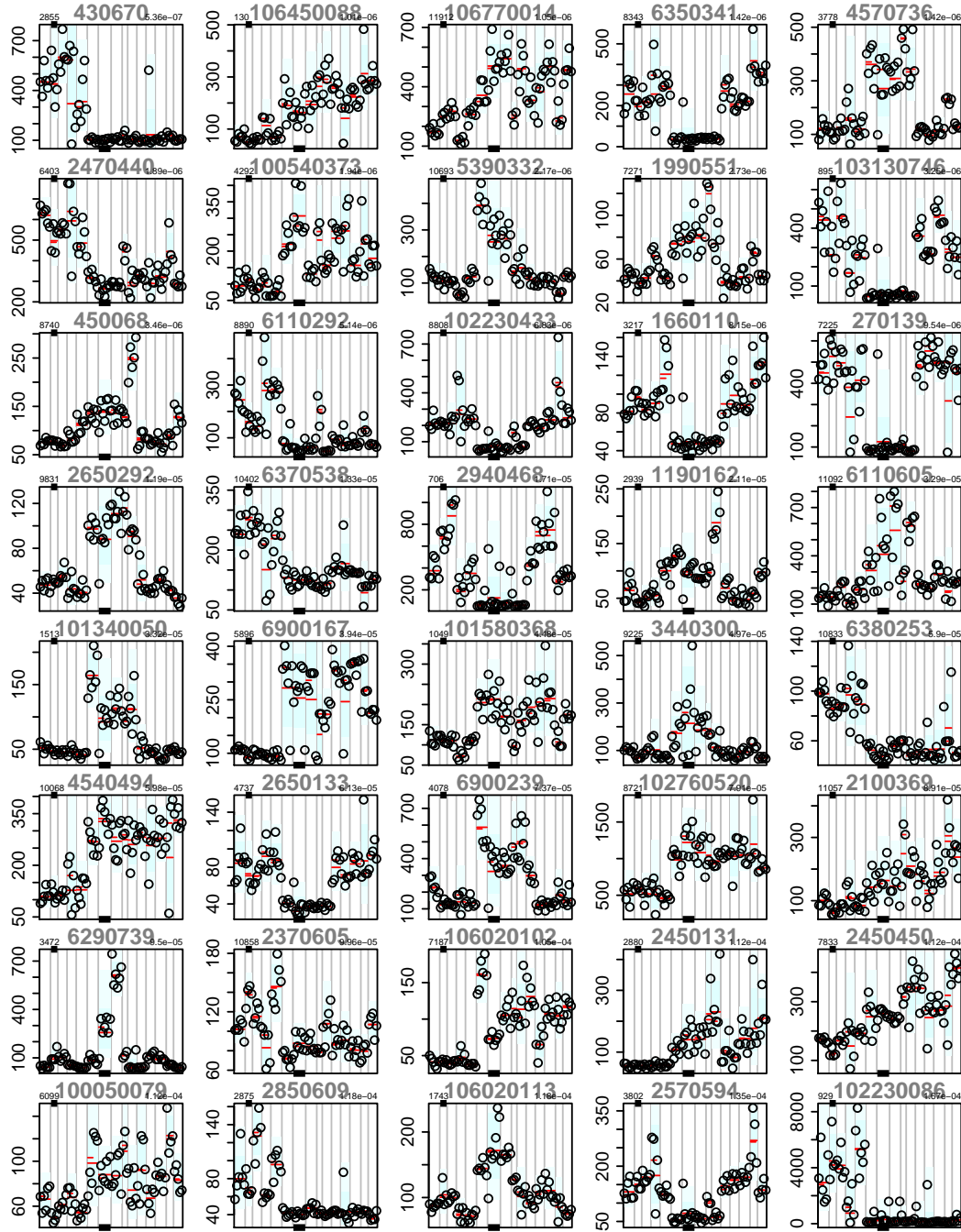


Figure 6b: Significant probes (41–80) for contrast HNB (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

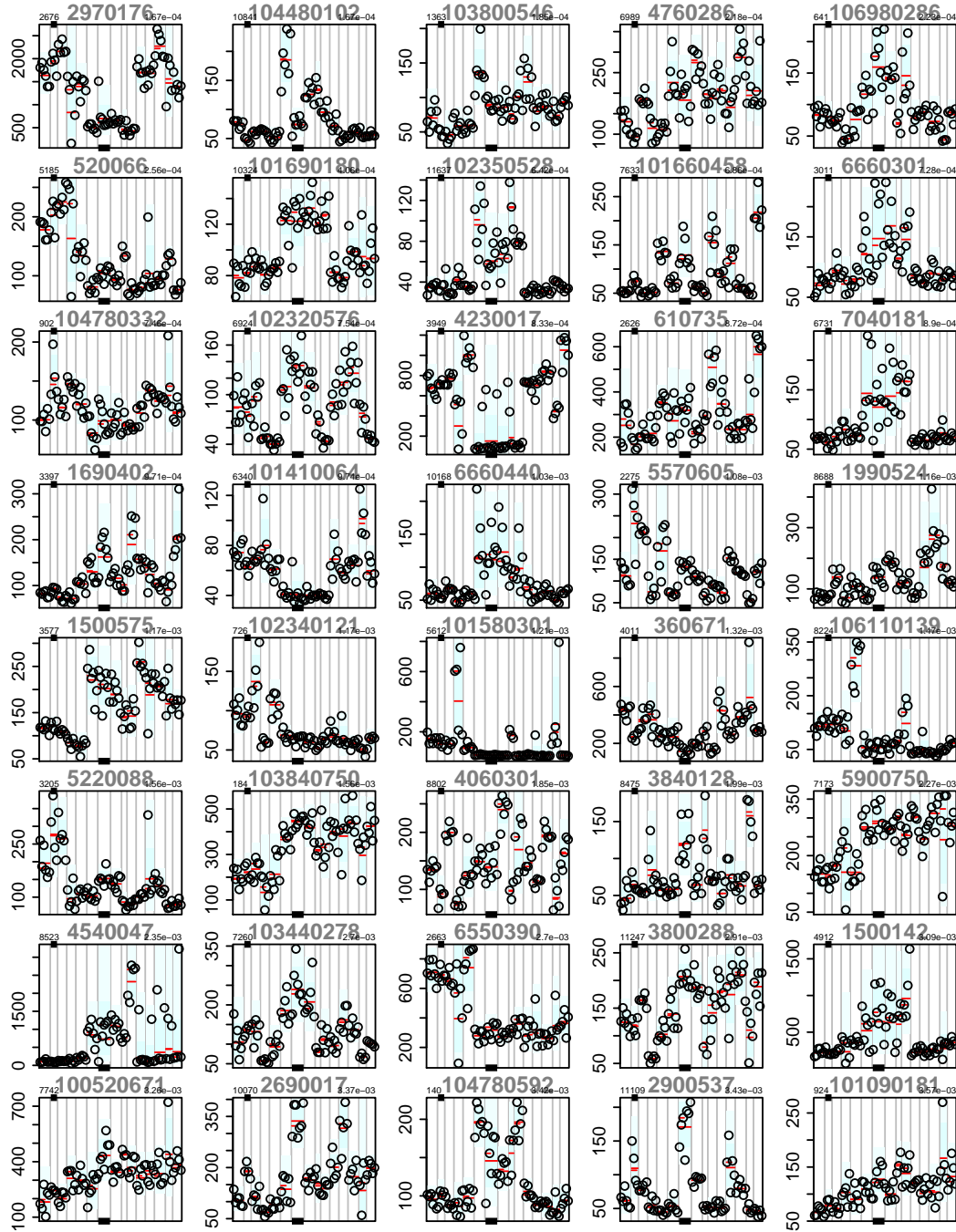


Figure 6c: Significant probes (81–120) for contrast HNb (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.3 Contrast HNc

Using the matrix representing the contrast defined by HAB_Cing - NAB_Cing

HNc	
HAB_Cing	1
NAB_Cing	-1

The statistics for the top 120 genes across the contrast (out of 214 genes having adjusted p -values below 0.05) are shown in table 5, the corresponding expression plots are shown in Figs. 7a-c on pages 65 through 67.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			380692	5.9	15.5	3.85e-24	4.69e-20	31.8
1	OR8B2	NM_001005468.1	6100440	7.3	14.2	3.95e-22	2.4e-18	29.4
6273			5390647	-4.4	-14	1.07e-21	4.33e-18	28.9
2	FAM53A	NM_001013622.1	4060112	-8.5	-13.5	5.66e-21	1.72e-17	28
3	SDHAP3	NR_003263.2	1400524	-20	-13.3	1.39e-20	3.39e-17	27.5
6276			102480441	4.8	12.3	4.8e-19	9.55e-16	25.5
6277			2810541	-19	-12.3	5.49e-19	9.55e-16	25.4
4	RAB25	NM_020387.1	50195	-5.4	-12	1.73e-18	2.63e-15	24.8
6279			6290739	-6.1	-11.7	5.41e-18	7.31e-15	24.1
5	GSTZ1	NM_001513.2	7040044	4	11.6	9.8e-18	1.15e-14	23.7
6281			105390397	3.2	11.5	1.04e-17	1.15e-14	23.7
6282			103130746	9.4	11	9.55e-17	9.69e-14	22.3
6	NARG1	NM_057175.3	3140524	-7.1	-10.9	1.25e-16	1.17e-13	22.2
6284			106400035	6.3	10.8	2.22e-16	1.93e-13	21.8
6285			107050626	-3.8	-10.4	9.83e-16	7.98e-13	20.9
6286			102340121	2.3	10.4	1.09e-15	8.17e-13	20.8
6287			1090195	7	10.4	1.14e-15	8.17e-13	20.8
6288			106020102	-2.6	-10.2	2.61e-15	1.71e-12	20.3
6289			106760170	4.3	10.2	2.67e-15	1.71e-12	20.3
7	GLMN	NM_053274.1	2850609	2.7	10	4.96e-15	3.02e-12	19.9
6291			101260021	-3	-9.92	6.96e-15	4.03e-12	19.6
8	DHX32	NM_018180.2	1980164	7.3	9.87	8.72e-15	4.82e-12	19.5
6293			104850273	-3.8	-9.28	9.96e-14	5.1e-11	17.9
6294			103840575	2.9	9.28	1.01e-13	5.1e-11	17.9
9	TMEM103	NM_017713.1	4850064	5.5	9.08	2.31e-13	1.13e-10	17.4
6296			102230433	4.2	9.01	3.05e-13	1.43e-10	17.2
10	LOC100132934	XM_001723077.1	2120390	4.2	9	3.22e-13	1.45e-10	17.1
11	LOC646588	XM_943454.1	2940468	11	8.9	4.92e-13	2.14e-10	16.8
6299			103130736	3.4	8.81	7.19e-13	3.02e-10	16.6
6300			104480102	-2.1	-8.77	8.31e-13	3.31e-10	16.5
12	C11ORF63	NM_199124.1	6550037	-5.1	-8.77	8.42e-13	3.31e-10	16.5
13	KLF6	NM_001008490.1	360110	-2.9	-8.71	1.05e-12	4.01e-10	16.3
6303			100380619	-7.8	-8.67	1.29e-12	4.76e-10	16.2
6304			100450079	-2.4	-8.6	1.72e-12	6.15e-10	16
6305			3060168	-2.3	-8.56	2.04e-12	7.09e-10	15.9
14	LOC730990	XM_001722060.1	2060170	-4.3	-8.41	3.75e-12	1.27e-09	15.5
15	HS.551438	Hs.551438	50438	-5.2	-8.4	4.01e-12	1.32e-09	15.4
6308			430670	5.7	8.34	5.02e-12	1.61e-09	15.3
16	BCORL2	NM_173700.1	2570594	3	8.28	6.58e-12	2.05e-09	15.1
6310			106520398	-3.9	-8.17	1.05e-11	3.19e-09	14.8
6311			101340050	-2.5	-7.96	2.53e-11	7.5e-09	14.2
17	SDHAP3	NR_003263.1	6350341	5.4	7.88	3.46e-11	1e-08	13.9

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
18	DEFA1	NM.004084.2	4540239	2.8	7.8	4.81e-11	1.36e-08	13.7
19	LOC648704	XM.937786.1	4850047	-2.2	-7.57	1.26e-10	3.49e-08	13
6315			100050152	2.1	7.54	1.45e-10	3.93e-08	12.9
20	HS.131670	Hs.131670	270139	5.5	7.52	1.55e-10	4.1e-08	12.9
21	LOC100130133	XR_037307.1	5390332	-2.6	-7.48	1.89e-10	4.9e-08	12.8
22	MUC6	XM.290540.6	2650292	-2	-7.46	2.06e-10	5.23e-08	12.7
23	LOC732377	XM.001133069.1	1500097	3.3	7.41	2.47e-10	6.14e-08	12.6
24	TRIM49	NM.020358.2	450068	-1.9	-7.41	2.53e-10	6.15e-08	12.6
25	SFRS13A	NM.054016.1	6110014	-2.3	-7.34	3.34e-10	7.97e-08	12.4
6322			103850064	1.9	7.23	5.4e-10	1.26e-07	12
6323			106380458	-2.4	-7.14	7.63e-10	1.75e-07	11.8
26	LOC653853	XM.936030.1	2470440	1.9	7.12	8.46e-10	1.91e-07	11.7
27	TNFRSF18	NM.148902.1	520066	2.4	7.07	1.04e-09	2.29e-07	11.6
6326			106980129	2.3	7.03	1.22e-09	2.65e-07	11.4
6327			870685	-2	-6.93	1.82e-09	3.88e-07	11.2
6328			102120270	-2.7	-6.93	1.86e-09	3.91e-07	11.1
6329			106450088	-3.1	-6.75	3.84e-09	7.92e-07	10.6
28	SCRIB	NM.015356.3	2970176	3.4	6.73	4.28e-09	8.68e-07	10.5
6331			106770014	-2	-6.55	8.78e-09	1.75e-06	10
6332			6900239	-2.9	-6.52	1e-08	1.97e-06	9.93
6333			101410064	1.7	6.44	1.4e-08	2.7e-06	9.68
29	OR5P2	NM.153444.1	770280	3.2	6.42	1.5e-08	2.85e-06	9.63
6335			103780671	1.9	6.36	1.92e-08	3.59e-06	9.45
30	C8ORF17	NM.020237.1	4260669	1.9	6.33	2.15e-08	3.97e-06	9.37
6337			6040707	-2.5	-6.3	2.49e-08	4.53e-06	9.26
31	CAPNS1	NM.001003962.1	5290500	2.1	6.27	2.82e-08	5.04e-06	9.18
6339			102230086	21	6.26	2.95e-08	5.21e-06	9.14
32	OGFOD1	NM.001031707.1	2510731	-3	-6.23	3.25e-08	5.65e-06	9.07
6341			106130025	1.9	6.19	3.8e-08	6.52e-06	8.96
6342			102350528	-2	-6.18	4.1e-08	6.94e-06	8.9
33	WBSCR22	NM.017528.2	6370538	2.2	6.08	6.15e-08	1.03e-05	8.61
34	ALOX15	XM.937556.1	1230722	2.5	5.98	9e-08	1.48e-05	8.33
35	SDC3	XM.940667.1	1990551	-1.9	-5.97	9.32e-08	1.51e-05	8.3
6346			101780504	-2	-5.96	9.97e-08	1.6e-05	8.25
6347			105910364	-1.7	-5.94	1.08e-07	1.71e-05	8.19
6348			102760520	-2.1	-5.92	1.14e-07	1.79e-05	8.15
6349			103520706	11	5.87	1.43e-07	2.21e-05	7.99
36	GTF2I	XM.939506.1	4570736	-2.4	-5.85	1.55e-07	2.37e-05	7.93
37	ST8SIA4	NM.005668.3	4230017	6	5.82	1.73e-07	2.61e-05	7.85
6352			5570605	1.9	5.75	2.3e-07	3.4e-05	7.64
38	ZMIZ1	NM.020338.2	2450131	-2.6	-5.75	2.32e-07	3.4e-05	7.63
6354			106020113	-1.7	-5.68	2.99e-07	4.33e-05	7.45
39	PFKFB2	NM.001018053.1	7040181	-2.1	-5.66	3.2e-07	4.57e-05	7.4
40	LOC645915	XM.933265.1	2650133	1.9	5.66	3.24e-07	4.57e-05	7.39
41	KRTCAP2	NM.173852.3	6110605	-2.7	-5.66	3.26e-07	4.57e-05	7.38
6358			103360184	-1.9	-5.56	4.87e-07	6.73e-05	7.09
42	LOC400696	NM.207646.1	1660110	1.8	5.54	5.27e-07	7.21e-05	7.03
6360			102030600	1.7	5.5	6.03e-07	8.16e-05	6.93
43	HS.538100	Hs.538100	1500575	-1.8	-5.49	6.48e-07	8.67e-05	6.87
6362			103800546	-1.9	-5.47	6.86e-07	9.07e-05	6.83
44	CXORF30	XR.000668.1	360671	1.8	5.42	8.47e-07	0.000111	6.68
45	SPDYE1	NM.001031618.1	770025	1.9	5.37	1.03e-06	0.000134	6.53
46	TCEB3B	NM.016427.2	5220088	1.9	5.34	1.14e-06	0.000146	6.45
47	ZNF655	NM.001009956.1	6550390	2.4	5.33	1.21e-06	0.000154	6.41
6367			102480487	-1.9	-5.3	1.34e-06	0.000168	6.33
48	OR10S1	NM.001004474.1	6110292	2.2	5.3	1.35e-06	0.000168	6.33
49	SRP54	XM.940545.1	1570279	1.6	5.24	1.66e-06	0.000204	6.18

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
50	LAMB3	NM_001017402.1	4590739	2	5.22	1.82e-06	0.000221	6.11
6371			2190438	1.8	5.14	2.48e-06	0.000299	5.88
6372			6900167	-2.4	-5.14	2.52e-06	0.000301	5.87
51	HS.538951	Hs.538951	1990020	2.2	5.13	2.55e-06	0.000301	5.86
6374			3520451	1.6	5.09	2.95e-06	0.000346	5.75
6375			101690180	-1.5	-5.08	3.15e-06	0.000365	5.7
52	LMLN	NM_033029.1	4540047	-9	-5.06	3.31e-06	0.00038	5.66
6377			6040541	1.7	5.06	3.38e-06	0.000384	5.65
53	KCTD8	NM_198353.1	1980079	2.8	5.05	3.51e-06	0.000395	5.62
54	SUMO1P3	NR_002190.1	4050358	-1.6	-5.04	3.58e-06	0.0004	5.6
55	LOC729660	XR_039044.1	4540577	-2.1	-5.04	3.7e-06	0.000409	5.58
6381			102680201	-1.5	-5.03	3.79e-06	0.000416	5.56
56	LOC400120	NM_203451.1	3440519	3.1	4.98	4.59e-06	0.000499	5.42
6383			106980286	-1.9	-4.97	4.65e-06	0.000501	5.41
6384			2630025	-3.7	-4.96	4.85e-06	0.000518	5.38
57	SGCB	NM_000232.3	1190162	-1.8	-4.96	4.99e-06	0.000528	5.36
6386			101580301	2.7	4.94	5.38e-06	0.000565	5.3
58	COL14A1	NM_021110.1	3800010	1.5	4.87	6.94e-06	0.000722	5.11
6388			104780592	-1.5	-4.81	8.65e-06	0.000887	4.95
59	DLG1	NM_004087.1	4210541	2.3	4.81	8.67e-06	0.000887	4.95
6390			100110411	-1.5	-4.8	9.15e-06	0.000928	4.91

Table 5: Top 120 genes (all arrays)

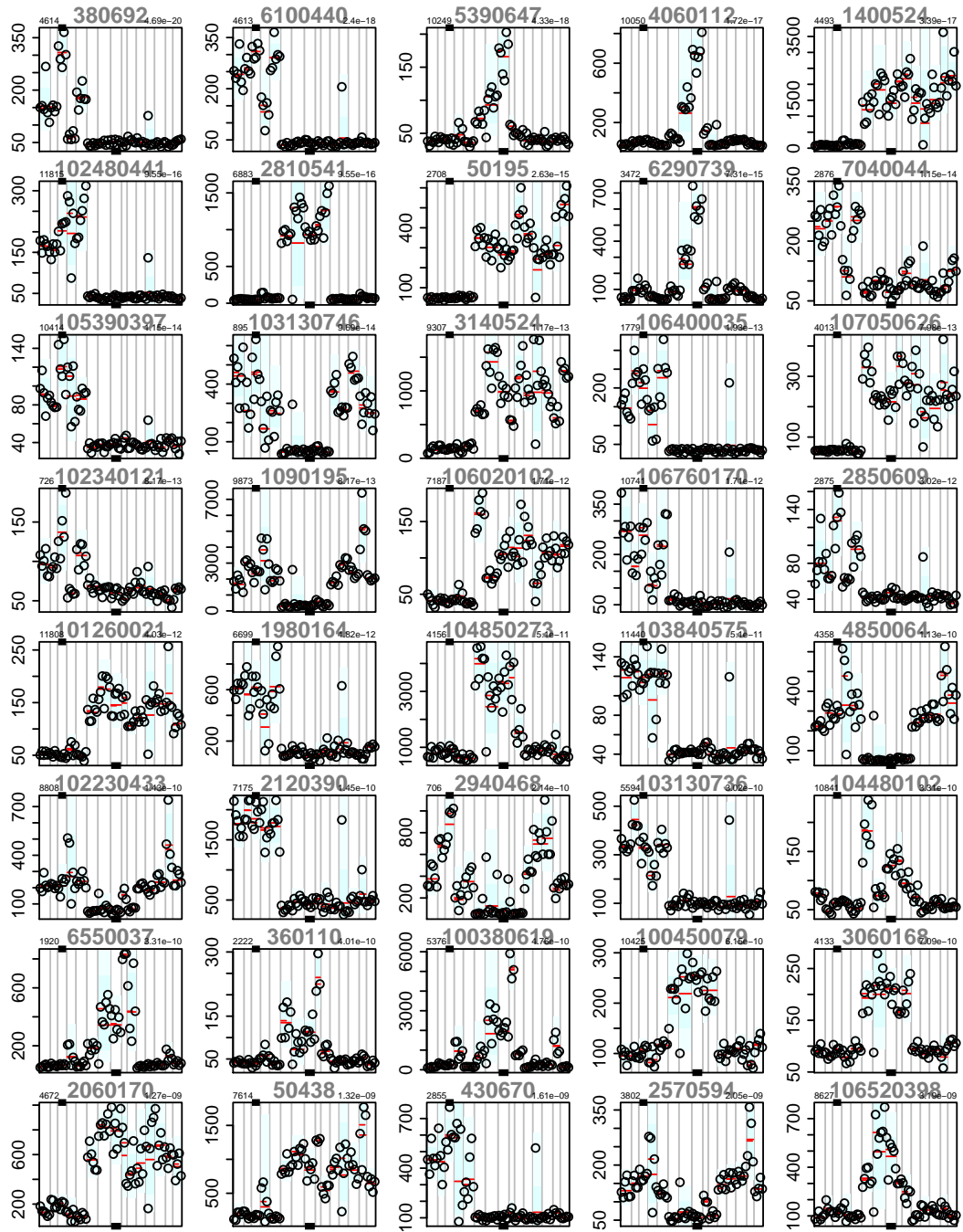


Figure 7a: Top 40 genes for contrast HNC (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

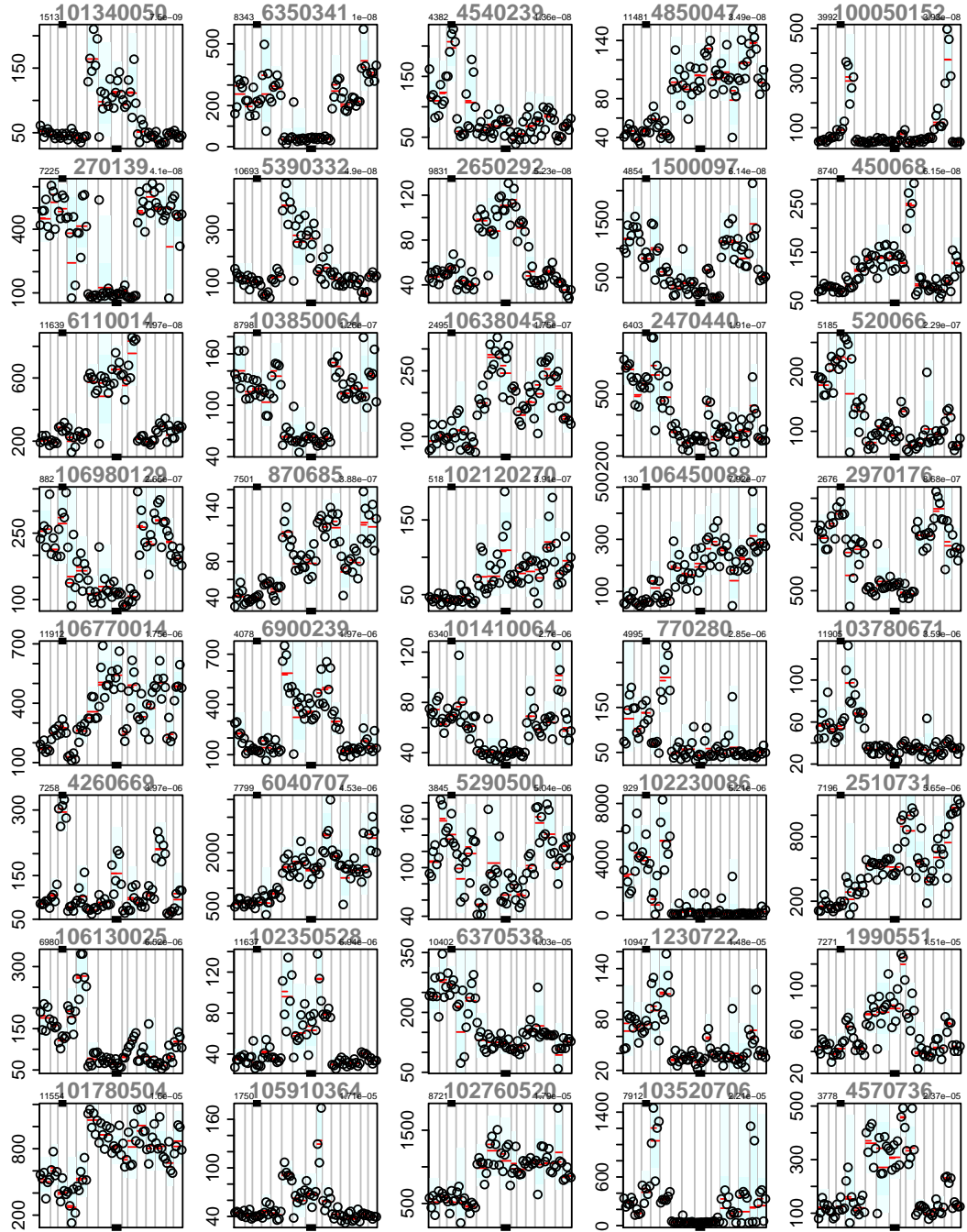


Figure 7b: Significant probes (41–80) for contrast HNC (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

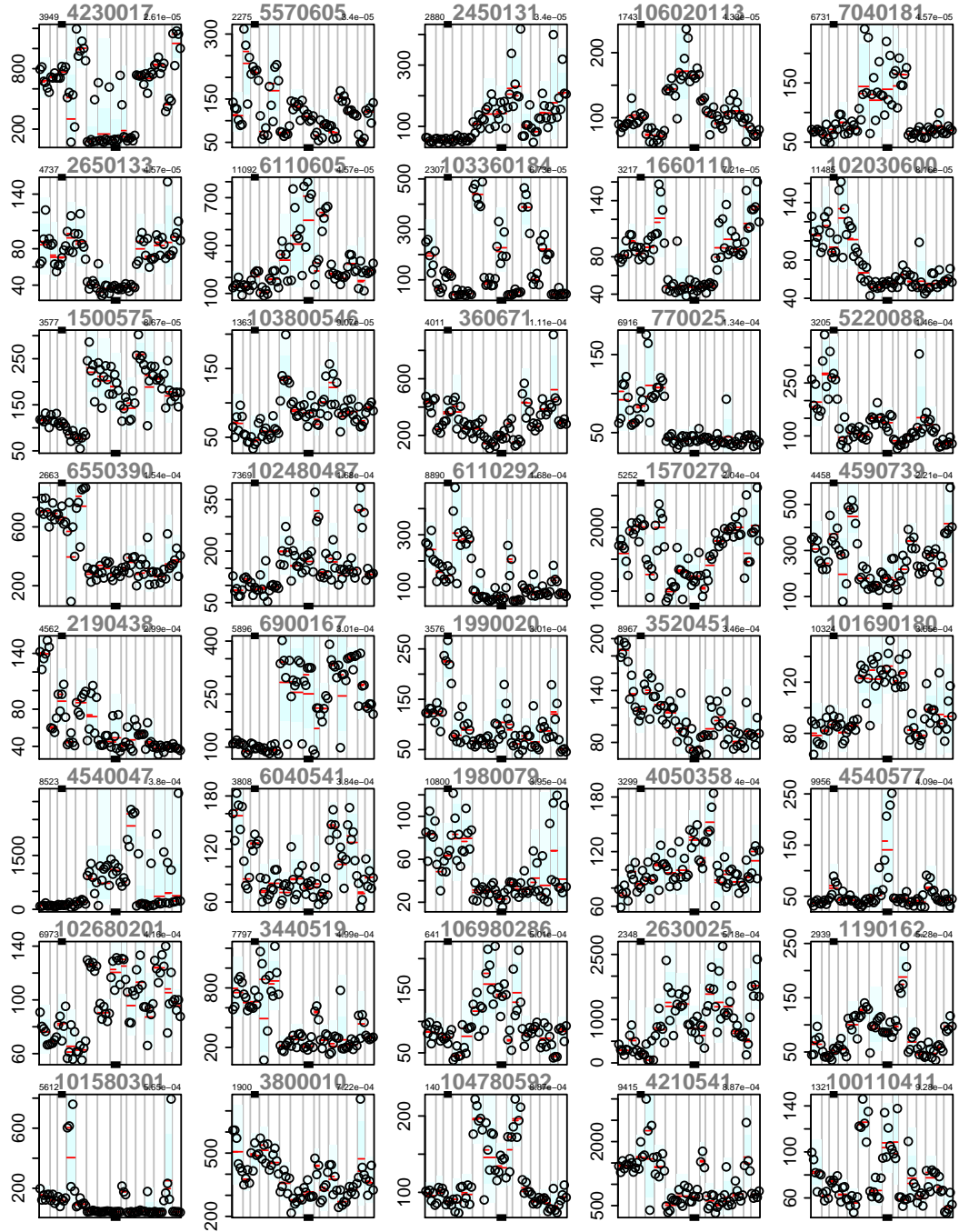


Figure 7c: Significant probes (81–120) for contrast HNC (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

3.2.4 Contrast HNd

Using the matrix representing the contrast defined by HAB_DGyr - NAB_DGyr

HNd	
HAB_DGyr	1
NAB_DGyr	-1

The statistics for the top 120 genes across the contrast (out of 1408 genes having adjusted p -values below 0.05) are shown in table 6, the corresponding expression plots are shown in Figs. 8a-c on pages 71 through 73.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			104480458	-6.7	-13.6	3.6e-21	4.38e-17	34.9
1	MTM1	NM_000252.1	2320537	-4.6	-12.4	4.26e-19	2.59e-15	31.3
6273			100050152	3.7	11	7.73e-17	3.13e-13	27.2
6274			107050626	-5.3	-10.7	2.86e-16	8.7e-13	26.1
6275			102480441	4.9	10.4	9.63e-16	2.34e-12	25.1
6276			105910364	-2.8	-10.1	3.74e-15	7.59e-12	24
2	KLF6	NM_001008490.1	360110	-4.2	-9.73	1.52e-14	2.65e-11	22.9
3	RAB25	NM_020387.1	50195	-5.2	-9.63	2.35e-14	3.57e-11	22.5
6279			104850273	-5.2	-9.45	4.9e-14	6.63e-11	21.9
4	SDHAP3	NR_003263.2	1400524	-13	-9.3	9.1e-14	1.11e-10	21.4
5	MUC6	XM_290540.6	2650292	-2.6	-8.78	8.2e-13	9.07e-10	19.6
6282			100520465	-2.5	-8.63	1.48e-12	1.5e-09	19.1
6	LOC730990	XM_001722060.1	2060170	-6	-8.56	2.04e-12	1.91e-09	18.8
7	C11ORF63	NM_199124.1	6550037	-6.6	-8.41	3.73e-12	3.24e-09	18.3
6285			2810541	-11	-8.38	4.26e-12	3.46e-09	18.2
6286			102480487	-3.4	-8.21	8.63e-12	6.57e-09	17.6
8	CES1	NM_001025195.1	2680056	-2.8	-7.79	5.02e-11	3.59e-08	16.1
6288			104480102	-2.2	-7.72	6.81e-11	4.6e-08	15.8
6289			106020102	-2.4	-7.59	1.17e-10	7.52e-08	15.4
9	SFRS13A	NM_054016.1	6110014	-2.8	-7.46	2.02e-10	1.23e-07	14.9
6291			100450079	-2.5	-7.34	3.39e-10	1.96e-07	14.5
6292			102350528	-2.7	-7.31	3.8e-10	2.09e-07	14.4
6293			1090195	5.2	7.3	3.95e-10	2.09e-07	14.3
10	TMEM103	NM_017713.1	4850064	5.1	7.22	5.51e-10	2.79e-07	14.1
6295			102680201	-1.9	-7.12	8.3e-10	4.04e-07	13.7
11	SDHAP3	NR_003263.1	6350341	6.2	7.1	9.23e-10	4.32e-07	13.6
12	NARG1	NM_057175.3	3140524	-4.6	-7.08	9.79e-10	4.41e-07	13.6
6298			103780671	2.4	7.07	1.03e-09	4.46e-07	13.5
6299			101780504	-2.7	-6.91	2.01e-09	8.19e-07	12.9
6300			102030600	2.2	6.91	2.02e-09	8.19e-07	12.9
13	OR8B2	NM_001005468.1	6100440	3.2	6.88	2.24e-09	8.79e-07	12.9
6302			100460538	-2.3	-6.84	2.64e-09	1e-06	12.7
14	ZMIZ1	NM_020338.2	2450131	-3.8	-6.76	3.68e-09	1.36e-06	12.4
6304			101260021	-2.5	-6.71	4.69e-09	1.68e-06	12.2
6305			870685	-2.2	-6.63	6.5e-09	2.26e-06	11.9
6306			103520706	25	6.6	7.1e-09	2.4e-06	11.9
15	OGFOD1	NM_001031707.1	2510731	-4.1	-6.57	8.16e-09	2.62e-06	11.7
6308			101410064	2	6.57	8.18e-09	2.62e-06	11.7
6309			3060168	-2.1	-6.54	9.12e-09	2.85e-06	11.6
16	LOC648704	XM_937786.1	4850047	-2.3	-6.53	9.77e-09	2.97e-06	11.6
17	FOXA2	NM_153675.1	3780731	-2.2	-6.44	1.4e-08	4.15e-06	11.3
18	SPDYE1	NM_001031618.1	770025	2.6	6.43	1.43e-08	4.15e-06	11.3

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
19	LOC645915	XM_933265.1	2650133	2.4	6.41	1.56e-08	4.43e-06	11.2
20	GIPC1	NM_005716.2	4850088	-2.5	-6.36	1.95e-08	5.39e-06	11
6315			3840348	-2.3	-6.33	2.2e-08	5.96e-06	10.9
6316			6900239	-3.4	-6.32	2.26e-08	5.97e-06	10.9
6317			100520072	-2.8	-6.27	2.85e-08	7.37e-06	10.7
21	LOC100132934	XM_001723077.1	2120390	3.3	6.17	4.27e-08	1.08e-05	10.3
22	HS.551438	Hs.551438	50438	-4.3	-6.16	4.46e-08	1.11e-05	10.3
6320			6550075	-3.3	-6.09	5.89e-08	1.43e-05	10
23	HS.348697	Hs.348697	6620706	-1.9	-6.04	7.12e-08	1.7e-05	9.87
6322			106130025	2.1	6.03	7.49e-08	1.75e-05	9.82
24	SLC38A4	NM_018018.2	2260181	-2.5	-6.02	7.84e-08	1.8e-05	9.78
6324			103850204	-2.6	-6.01	7.97e-08	1.8e-05	9.77
6325			103850064	1.9	5.98	8.89e-08	1.97e-05	9.68
6326			100380619	-5.5	-5.98	9.12e-08	1.98e-05	9.65
25	ENAH	NM_018212.4	3170132	2	5.93	1.1e-07	2.34e-05	9.5
26	LOC100130133	XR_037307.1	5390332	-2.5	-5.93	1.13e-07	2.36e-05	9.47
6329			101770315	-2.7	-5.92	1.14e-07	2.36e-05	9.46
27	GTF2I	XM_939506.1	4570736	-3	-5.91	1.22e-07	2.47e-05	9.4
28	LOC440386	XR_040492.1	6760093	-2.1	-5.89	1.28e-07	2.55e-05	9.36
6332			105390397	2	5.86	1.48e-07	2.9e-05	9.23
6333			104780592	-1.8	-5.84	1.59e-07	3.07e-05	9.17
29	DHX32	NM_018180.2	1980164	4.1	5.8	1.85e-07	3.51e-05	9.04
6335			102810239	-2	-5.78	2e-07	3.74e-05	8.98
6336			100110053	-2.1	-5.75	2.25e-07	4.15e-05	8.87
6337			103130075	1.7	5.75	2.3e-07	4.17e-05	8.85
6338			100110411	-1.7	-5.73	2.45e-07	4.38e-05	8.8
6339			6040707	-2.7	-5.67	3.08e-07	5.43e-05	8.6
6340			104280671	2	5.54	5.14e-07	8.86e-05	8.15
6341			1740324	2.2	5.54	5.17e-07	8.86e-05	8.15
6342			101770184	-2.4	-5.42	8.32e-07	0.000141	7.73
6343			102450037	-2	-5.4	9.04e-07	0.000151	7.66
6344			2690017	-2.2	-5.36	1.06e-06	0.000175	7.52
6345			103060358	-2.4	-5.34	1.15e-06	0.000186	7.46
6346			103130736	2.4	5.34	1.16e-06	0.000186	7.45
6347			100540373	-2.5	-5.3	1.34e-06	0.000211	7.32
6348			106020113	-1.8	-5.26	1.57e-06	0.000245	7.18
6349			106770014	-1.9	-5.22	1.83e-06	0.000282	7.05
30	SDC3	XM_940667.1	1990551	-1.9	-5.19	2.05e-06	0.000311	6.95
6351			102260025	-2.5	-5.18	2.1e-06	0.000314	6.93
6352			106520398	-2.8	-5.18	2.11e-06	0.000314	6.92
6353			106200097	-1.8	-5.13	2.53e-06	0.000372	6.77
6354			101340050	-2	-5.11	2.79e-06	0.000404	6.68
6355			103840750	-2.4	-5.1	2.88e-06	0.000412	6.66
31	RPS21	NM_001024.3	2690338	-2.8	-5.07	3.18e-06	0.000451	6.57
32	LOC400696	NM_207646.1	1660110	1.9	5.06	3.32e-06	0.000464	6.53
33	CRK	NM_016823.2	7040014	-2.4	-5.04	3.66e-06	0.000506	6.45
34	SSX4	XM_936387.1	6860037	-2	-5.02	3.88e-06	0.000528	6.4
6360			106760170	2.4	5.02	3.94e-06	0.000528	6.38
6361			104050746	-3	-5.02	3.95e-06	0.000528	6.38
35	KLK11	NM_144947.1	5700136	-2.5	-5.01	4.01e-06	0.00053	6.37
36	LOC728667	XM_001128080.2	2650600	-3.3	-5	4.29e-06	0.000561	6.31
6364			106400035	2.8	4.98	4.5e-06	0.000582	6.27
6365			102480292	-2	-4.95	5.02e-06	0.000643	6.17
37	SAA4	NM_006512.1	3710022	-2	-4.93	5.58e-06	0.000707	6.08
6367			106940324	-3.1	-4.89	6.46e-06	0.000811	5.95
6368			106220156	-2.2	-4.88	6.62e-06	0.000822	5.93
6369			101770270	-1.8	-4.87	6.82e-06	0.000839	5.91

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			101770722	-2.9	-4.87	6.91e-06	0.000841	5.89
38	LOC100134273	XM_001724343.1	4480128	-2.5	-4.86	7.05e-06	0.000849	5.88
39	ZMIZ2	NM_174929.2	630711	-1.7	-4.85	7.42e-06	0.000886	5.83
40	SNHG7	NR_003672.2	6760021	-1.9	-4.83	8e-06	0.000946	5.77
6374			102680458	-1.8	-4.8	8.94e-06	0.00105	5.67
6375			102970463	-1.9	-4.8	9.09e-06	0.00105	5.66
41	LOC729815	XR_037436.1	2450450	-2.1	-4.79	9.24e-06	0.00106	5.64
6377			4210270	-1.8	-4.77	1.01e-05	0.00114	5.56
42	C6ORF165	NM_178823.2	2850487	-1.7	-4.77	1.01e-05	0.00114	5.56
6379			102760520	-2	-4.76	1.03e-05	0.00115	5.55
6380			103130672	-2	-4.74	1.11e-05	0.00123	5.48
6381			100520487	-2.7	-4.74	1.12e-05	0.00123	5.47
6382			2630025	-4.4	-4.71	1.26e-05	0.00136	5.38
43	CR2	NM_001877.3	4810292	1.7	4.7	1.3e-05	0.0014	5.35
6384			102450494	-2.6	-4.7	1.33e-05	0.00141	5.33
6385			104590402	-2.1	-4.69	1.33e-05	0.00141	5.32
6386			105720253	-2.1	-4.68	1.38e-05	0.00145	5.29
44	MYO1C	NM_033375.3	3710605	-2.1	-4.68	1.42e-05	0.00148	5.27
6388			103840377	-1.8	-4.67	1.47e-05	0.00152	5.24
6389			100870152	-2.3	-4.66	1.51e-05	0.00154	5.22
6390			103840575	1.9	4.66	1.52e-05	0.00154	5.21

Table 6: Top 120 genes (all arrays)

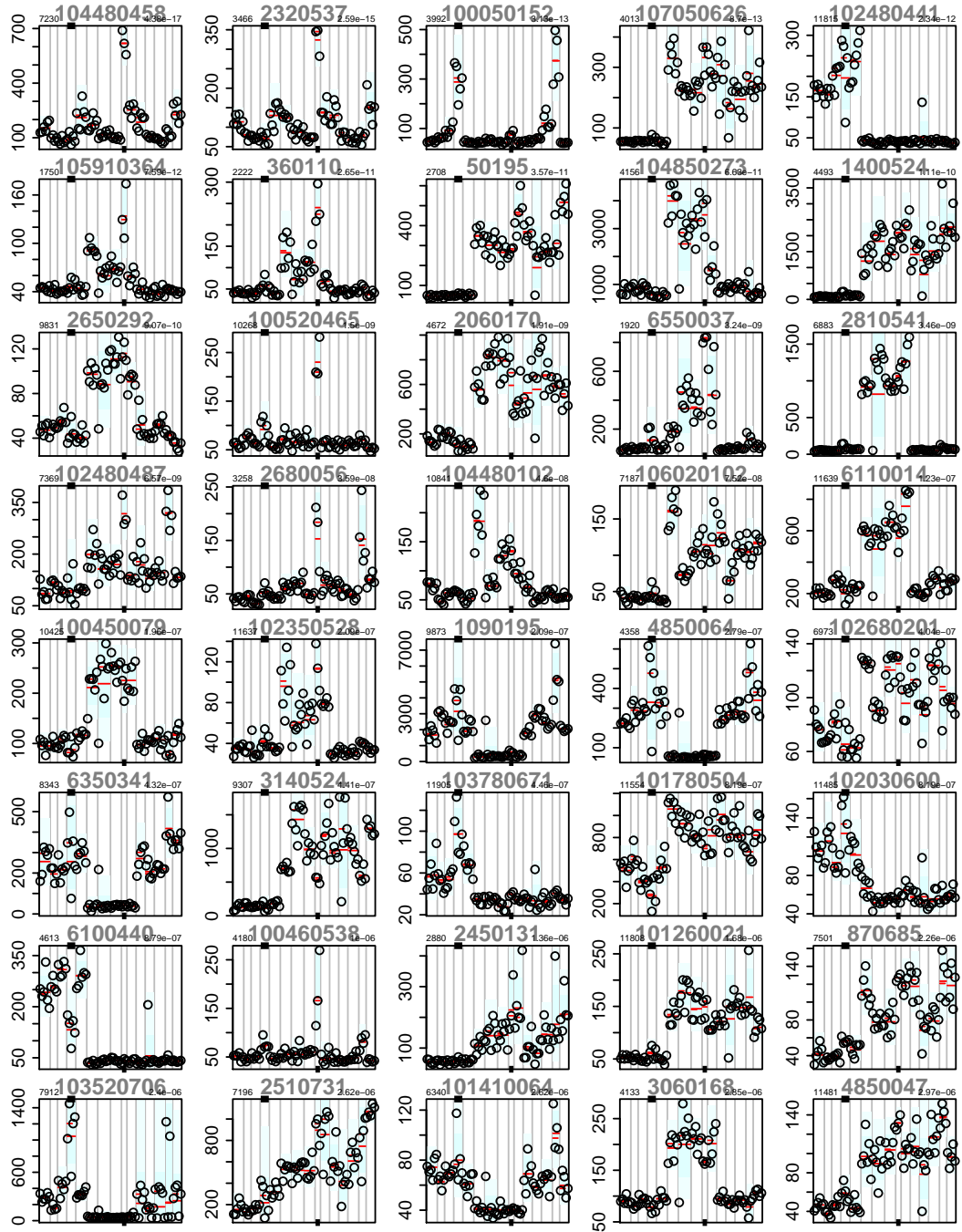


Figure 8a: Top 40 genes for contrast HN_d (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

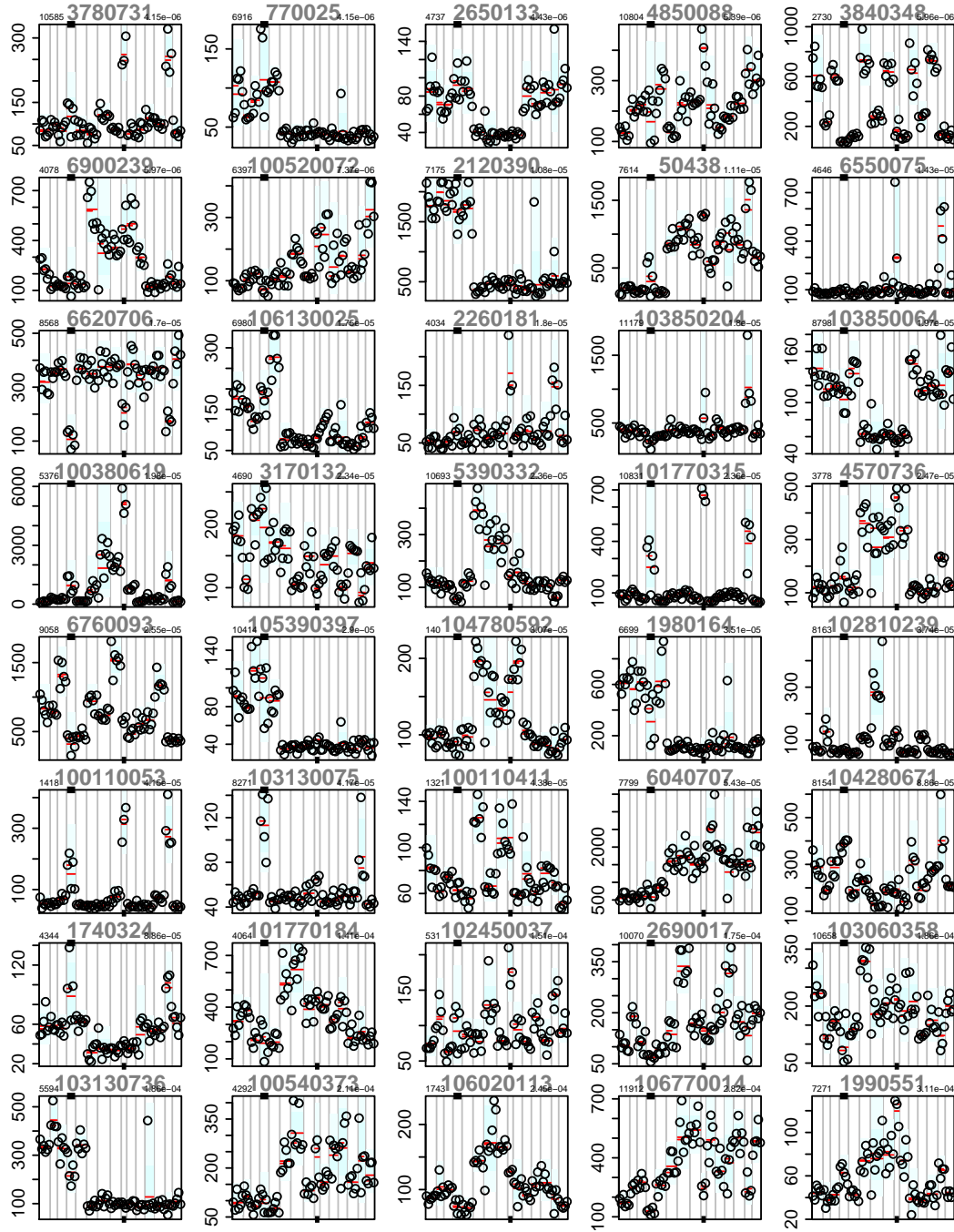


Figure 8b: Significant probes (41–80) for contrast HNd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

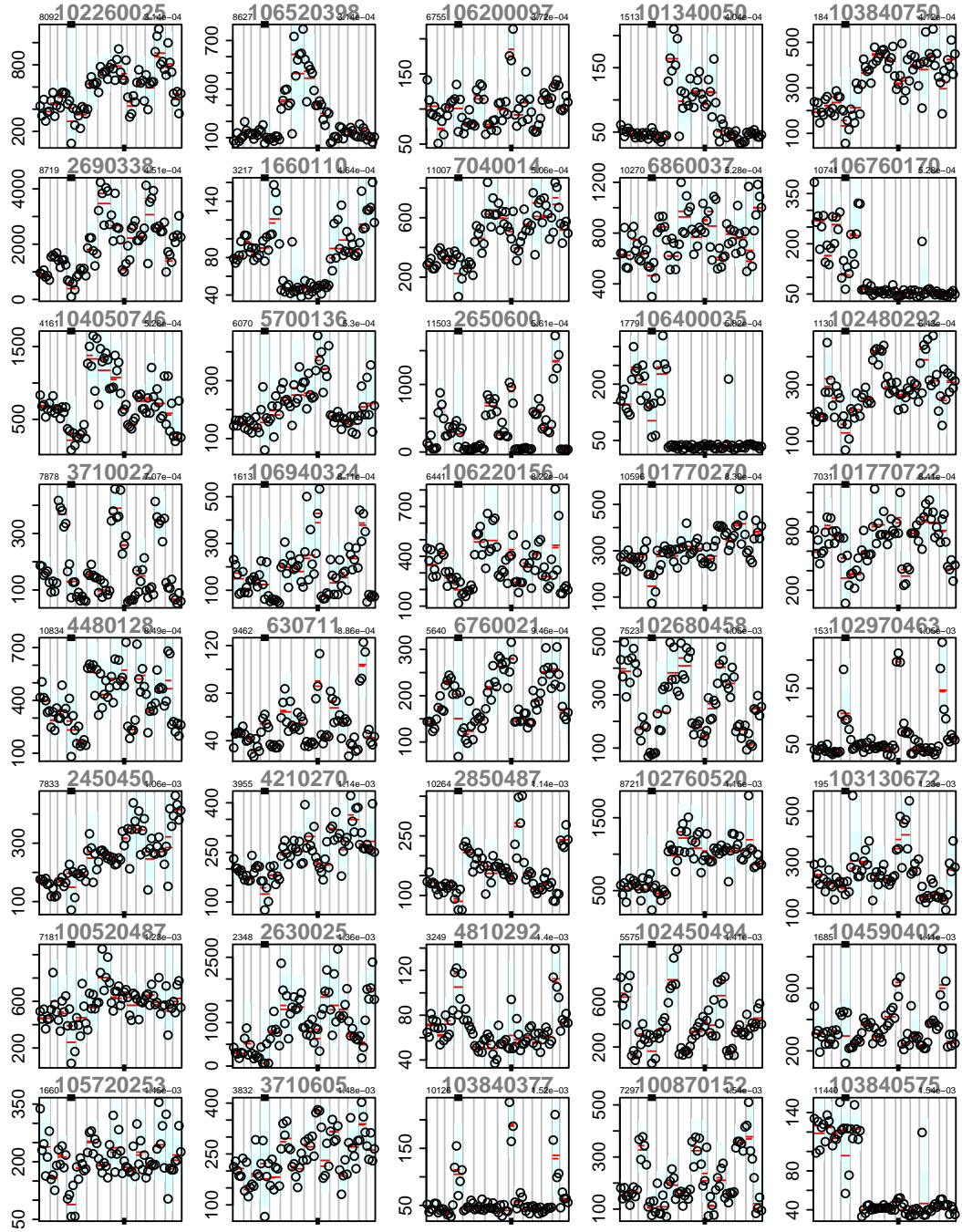


Figure 8c: Significant probes (81–120) for contrast HNd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

3.2.5 Contrast HNp

Using the matrix representing the contrast defined by HAB_PVNu - NAB_PVNu

HNp	
HAB_PVNu	1
NAB_PVNu	-1

The statistics for the top 120 genes across the contrast (out of 233 genes having adjusted p -values below 0.05) are shown in table 7, the corresponding expression plots are shown in Figs. 9a-c on pages 77 through 79.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	ST7	NM_018412.3	4570575	-12	-21.4	5.62e-32	6.85e-28	44.2
2	RAB25	NM_020387.1	50195	-9.1	-15.6	3.16e-24	1.93e-20	35.1
3	KIR2DL5B	NM_001018081.1	5550017	-4.7	-15.2	1.27e-23	5.17e-20	34.3
4	OR8B2	NM_001005468.1	6100440	7.1	14	9.2e-22	2.8e-18	31.8
6275			102480441	5.8	13.9	1.17e-21	2.84e-18	31.6
5	SDHAP3	NR_003263.2	1400524	-19	-13.1	2.92e-20	5.63e-17	29.6
6277			107050626	-5.4	-13	3.24e-20	5.63e-17	29.6
6	IGFL1	NM_198541.1	6020605	3.5	12.6	1.51e-19	2.29e-16	28.6
6279			2810541	-19	-12.3	5.01e-19	6.77e-16	27.8
7	C9ORF68	NM_001039395.1	5890332	-4.3	-11.7	6e-18	7.31e-15	26.1
6281			106020102	-3	-11.5	1.09e-17	1.21e-14	25.7
8	OR10S1	NM_001004474.1	6110292	5.6	11.4	2.04e-17	2.07e-14	25.3
6283			106400035	6.8	11.2	3.86e-17	3.61e-14	24.9
9	NARG1	NM_057175.3	3140524	-6.7	-10.6	5.39e-16	4.69e-13	23.1
6285			380692	3.2	10.2	2.14e-15	1.64e-12	22.1
6286			106760170	4.3	10.2	2.16e-15	1.64e-12	22.1
10	SFRS13A	NM_054016.1	6110014	-3.2	-10.2	2.7e-15	1.93e-12	21.9
11	C11ORF63	NM_199124.1	6550037	-6.5	-10.1	3.2e-15	2.17e-12	21.8
6289			103840575	3.1	10	4.83e-15	3.09e-12	21.5
6290			870685	-2.6	-9.55	3.3e-14	2.01e-11	20.1
6291			1090195	5.9	9.5	4.09e-14	2.37e-11	20
12	SDHAP3	NR_003263.1	6350341	7.4	9.4	5.96e-14	3.29e-11	19.7
13	TMEM103	NM_017713.1	4850064	5.4	9.02	2.92e-13	1.54e-10	18.6
6294			103850064	2.2	8.99	3.4e-13	1.72e-10	18.4
14	LOC400696	NM_207646.1	1660110	2.5	8.96	3.85e-13	1.87e-10	18.4
15	TRIM49	NM_020358.2	450068	-2.2	-8.93	4.21e-13	1.97e-10	18.3
16	GLMN	NM_053274.1	2850609	2.4	8.83	6.63e-13	2.99e-10	18
6298			103130736	3.4	8.8	7.25e-13	3.15e-10	17.9
17	LOC730990	XM_001722060.1	2060170	-4.6	-8.74	9.61e-13	4.03e-10	17.7
18	MUC6	XM_290540.6	2650292	-2.2	-8.72	1.01e-12	4.11e-10	17.6
6301			101340050	-2.7	-8.67	1.25e-12	4.78e-10	17.5
19	LOC100132934	XM_001723077.1	2120390	4	8.67	1.26e-12	4.78e-10	17.5
20	ZMIZ1	NM_020338.2	2450131	-4	-8.48	2.86e-12	1.05e-09	16.9
6304			104780592	-2	-8.41	3.73e-12	1.34e-09	16.7
6305			105390397	2.3	8.37	4.41e-12	1.53e-09	16.6
6306			106450088	-4.1	-8.35	4.87e-12	1.65e-09	16.5
6307			103130746	5.4	8.25	7.43e-12	2.44e-09	16.2
6308			6900239	-3.7	-8.05	1.71e-11	5.47e-09	15.5
21	LOC648704	XM_937786.1	4850047	-2.3	-8.04	1.81e-11	5.65e-09	15.5
6310			106130025	2.3	8.01	2e-11	6.07e-09	15.4
22	OR5P2	NM_153444.1	770280	4.2	7.99	2.18e-11	6.48e-09	15.3
23	SPDYE1	NM_001031618.1	770025	2.7	7.96	2.5e-11	7.25e-09	15.2

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			102230433	3.5	7.87	3.63e-11	1.01e-08	15
6314			3060168	-2.1	-7.87	3.67e-11	1.01e-08	15
24	LOC732377	XM_001133069.1	1500097	3.5	7.85	3.97e-11	1.07e-08	14.9
25	LCN10	NM_001001712.1	4610576	-1.9	-7.78	5.32e-11	1.41e-08	14.7
26	DHX32	NM_018180.2	1980164	4.7	7.75	6.01e-11	1.56e-08	14.6
27	LOC645915	XM_933265.1	2650133	2.4	7.6	1.13e-10	2.86e-08	14.1
6319			101260021	-2.3	-7.44	2.2e-10	5.47e-08	13.6
6320			102350528	-2.3	-7.33	3.44e-10	8.27e-08	13.3
6321			104480102	-1.8	-7.33	3.47e-10	8.27e-08	13.2
28	ST8SIA4	NM_005668.3	4230017	9.6	7.33	3.53e-10	8.27e-08	13.2
6323			6040707	-2.9	-7.3	3.88e-10	8.75e-08	13.2
6324			100380619	-5.7	-7.3	3.88e-10	8.75e-08	13.2
29	HS.131670	Hs.131670	270139	5.1	7.24	5.16e-10	1.14e-07	12.9
30	DEFB114	NM_001037499.1	6620411	2.1	7.1	9.18e-10	1.99e-07	12.5
31	HS.551438	Hs.551438	50438	-3.9	-7	1.38e-09	2.94e-07	12.2
32	MTERFD3	NM_025198.3	3360671	3.8	6.91	2.01e-09	4.22e-07	11.9
33	GTF2I	XM_939506.1	4570736	-2.9	-6.87	2.32e-09	4.79e-07	11.8
34	ALOX15	XM_937556.1	1230722	2.9	6.81	3.03e-09	6.14e-07	11.6
6331			102230086	26	6.69	4.91e-09	9.8e-07	11.2
6332			105390722	-2	-6.66	5.57e-09	1.09e-06	11.1
35	LOC646588	XM_943454.1	2940468	5.9	6.59	7.47e-09	1.44e-06	10.9
36	SCRIB	NM_015356.3	2970176	3.3	6.57	8.33e-09	1.57e-06	10.8
6335			104850273	-2.6	-6.56	8.39e-09	1.57e-06	10.8
6336			102340121	1.7	6.46	1.28e-08	2.35e-06	10.5
6337			103780671	2	6.44	1.37e-08	2.48e-06	10.4
6338			100450079	-1.9	-6.42	1.5e-08	2.68e-06	10.3
37	KRTCAP2	NM_173852.3	6110605	-3.1	-6.34	2.08e-08	3.67e-06	10.1
6340			100520072	-2.4	-6.34	2.13e-08	3.71e-06	10
38	ZNF175	NM_007147.2	6940458	-2.5	-6.24	3.12e-08	5.35e-06	9.75
6342			104610411	2	6.24	3.22e-08	5.4e-06	9.73
39	GSTZ1	NM_001513.2	7040044	2.1	6.23	3.24e-08	5.4e-06	9.72
6344			106770014	-1.9	-6.2	3.7e-08	6.08e-06	9.62
40	WWC1	NM_015238.1	1090575	-1.9	-6.19	3.8e-08	6.17e-06	9.6
41	PFKFB2	NM_001018053.1	7040181	-2.3	-6.16	4.37e-08	6.99e-06	9.49
42	HS.538100	Hs.538100	1500575	-1.9	-6.11	5.39e-08	8.51e-06	9.32
6348			5570605	2	6.09	5.84e-08	9.12e-06	9.26
6349			102760520	-2.1	-6.06	6.52e-08	1e-05	9.17
43	HS.533844	Hs.533844	6620102	-1.7	-6.05	6.86e-08	1.04e-05	9.13
44	LOC100131209	XM_001725125.1	6380253	1.8	5.95	1.01e-07	1.51e-05	8.83
45	LOC653853	XM_936030.1	2470440	1.7	5.94	1.07e-07	1.59e-05	8.78
6353			106450725	-1.7	-5.81	1.78e-07	2.62e-05	8.38
6354			106550070	-1.8	-5.74	2.36e-07	3.41e-05	8.16
6355			106660487	-1.7	-5.67	3.15e-07	4.49e-05	7.93
46	LOC100129407	XM_001715870.1	2570047	4	5.67	3.17e-07	4.49e-05	7.92
6357			100870373	1.9	5.64	3.52e-07	4.92e-05	7.84
6358			6200278	3.3	5.63	3.69e-07	5.1e-05	7.8
47	LMLN	NM_033029.1	4540047	-11	-5.62	3.79e-07	5.19e-05	7.78
6360			102680201	-1.5	-5.6	4.2e-07	5.68e-05	7.7
6361			2100369	-2.5	-5.58	4.39e-07	5.87e-05	7.67
6362			101770184	-2.1	-5.57	4.58e-07	6.06e-05	7.63
48	OGFOD1	NM_001031707.1	2510731	-2.7	-5.55	5.06e-07	6.63e-05	7.55
6364			430670	3.2	5.54	5.23e-07	6.77e-05	7.53
49	TRIM36	NM_018700.3	1690402	-1.8	-5.39	9.53e-07	0.00012	7.05
6366			106110139	2.3	5.39	9.56e-07	0.00012	7.05
6367			2190438	1.9	5.38	9.7e-07	0.00012	7.04
6368			106520398	-2.5	-5.38	9.76e-07	0.00012	7.03
50	PTPN9	NM_002833.2	3930279	3.6	5.38	9.77e-07	0.00012	7.03

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			2650278	3.9	5.38	9.99e-07	0.000122	7.01
51	SDC3	XM_940667.1	1990551	-1.7	-5.36	1.05e-06	0.000127	6.97
6372			101850632	2	5.35	1.09e-06	0.00013	6.95
6373			106380458	-1.9	-5.33	1.21e-06	0.000143	6.86
52	BCORL2	NM_173700.1	2570594	2	5.27	1.52e-06	0.000178	6.68
53	LAMB3	NM_001017402.1	4590739	2.1	5.25	1.65e-06	0.000191	6.62
54	WBSCR22	NM_017528.2	6370538	2	5.17	2.17e-06	0.000249	6.4
6377			101410064	1.6	5.17	2.2e-06	0.00025	6.39
55	LOC400120	NM_203451.1	3440519	3.2	5.14	2.45e-06	0.000276	6.3
56	SGCB	NM_000232.3	1190162	-1.9	-5.14	2.48e-06	0.000277	6.29
6380			106980286	-1.9	-5.14	2.5e-06	0.000277	6.29
6381			102810286	1.8	5.13	2.57e-06	0.000281	6.26
6382			101690180	-1.5	-5.12	2.71e-06	0.000295	6.22
6383			106130600	1.8	5.09	3.04e-06	0.000327	6.13
57	LOC732434	XM_001724202.1	2340735	-1.5	-5.06	3.31e-06	0.000354	6.06
58	LOC642672	XM_943423.1	1580609	1.8	5.05	3.44e-06	0.000364	6.03
59	DEFA1	NM_004084.2	4540239	1.9	4.92	5.77e-06	0.000606	5.62
6387			100540373	-2	-4.9	6.22e-06	0.000647	5.56
60	RPS21	NM_001024.3	2690338	-2.3	-4.85	7.43e-06	0.000766	5.42
61	CAPNS1	NM_001003962.1	5290500	1.8	4.84	7.69e-06	0.000787	5.39
62	TAC4	NM_170685.1	2510259	2.6	4.83	7.94e-06	0.000805	5.36

Table 7: Top 120 genes (all arrays)

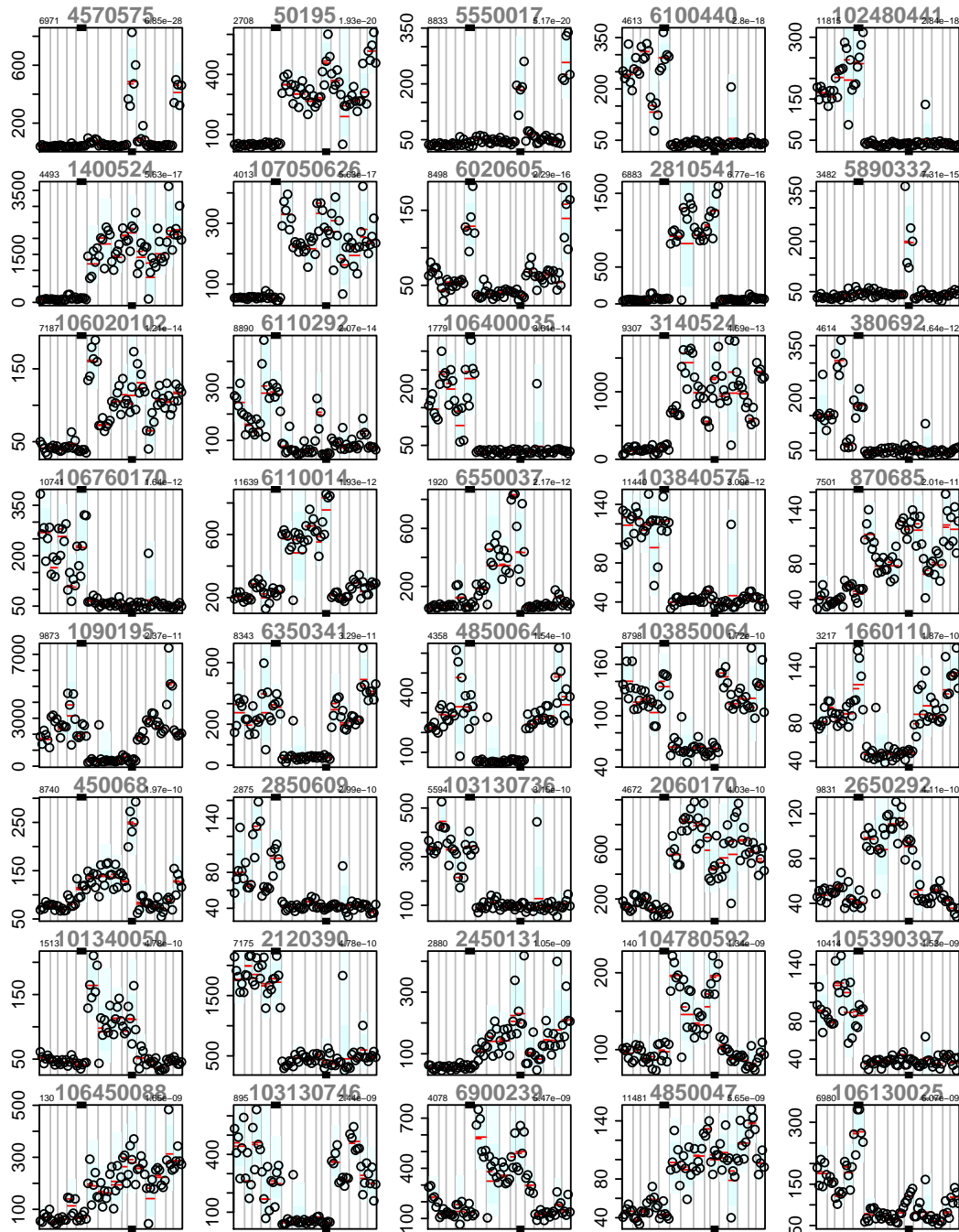


Figure 9a: Top 40 genes for contrast HNp (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

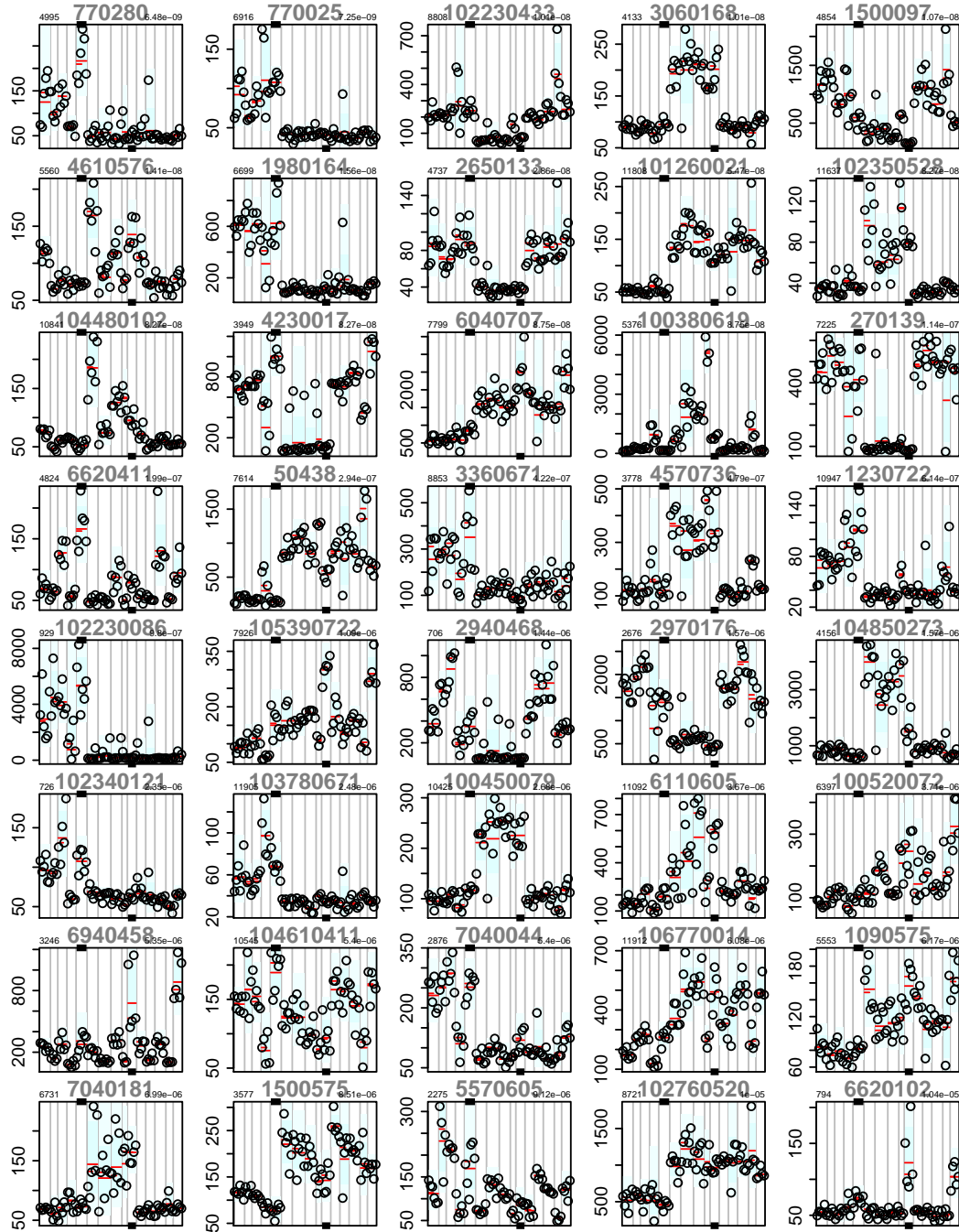


Figure 9b: Significant probes (41–80) for contrast HNp (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

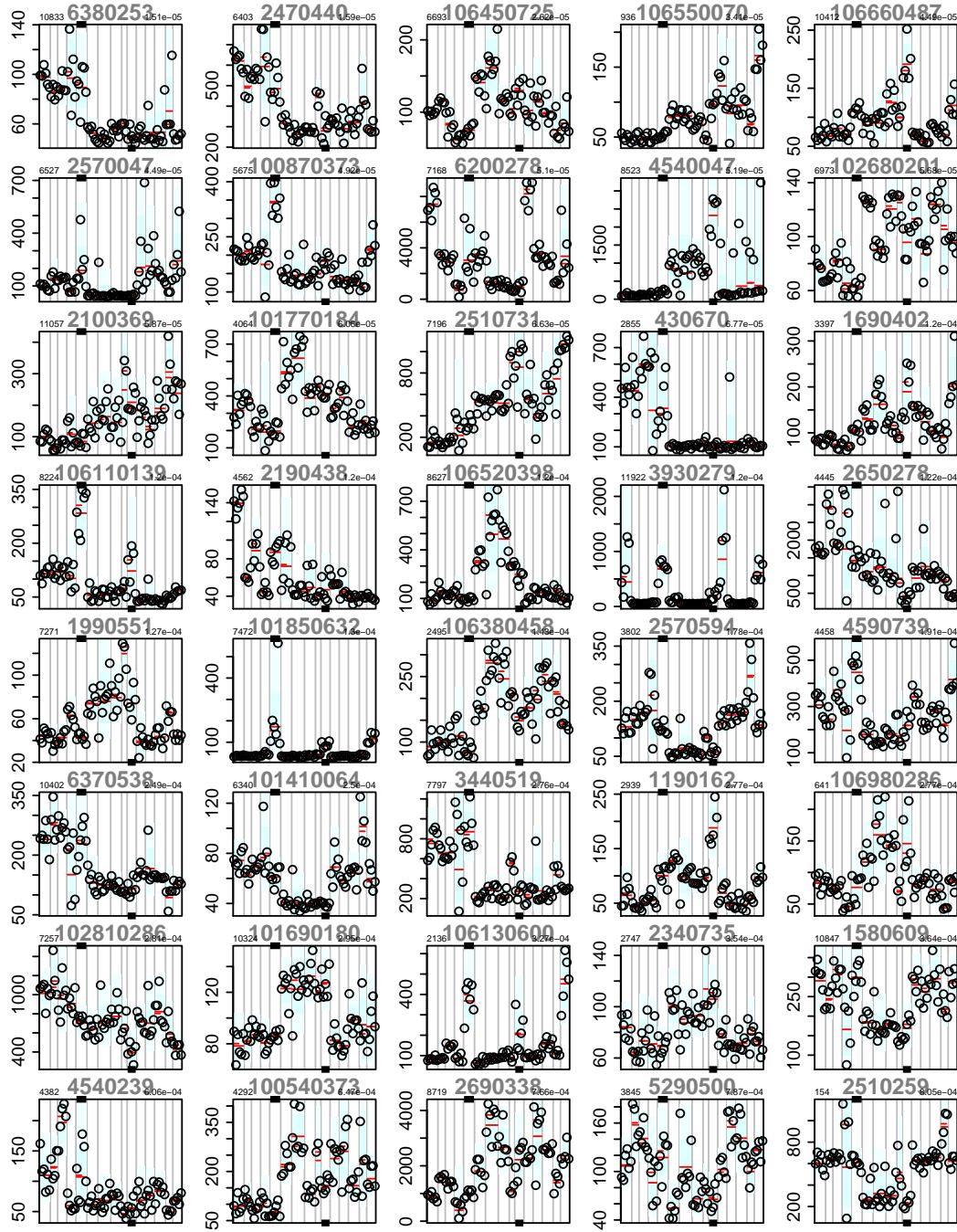


Figure 9c: Significant probes (81–120) for contrast HNp (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.6 Contrast LNa

Using the matrix representing the contrast defined by LAB_Amyg - NAB_Amyg

LNa	
NAB_Amyg	-1
LAB_Amyg	1

The statistics for the top 120 genes across the contrast (out of 240 genes having adjusted p -values below 0.05) are shown in table 8, the corresponding expression plots are shown in Figs. 10a-c on pages 83 through 85.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			2810541	-17	-11.8	3.98e-18	4.85e-14	26.7
6272			104480102	-2.6	-11.4	1.94e-17	1.18e-13	25.6
1	EIF4B	NM_001417.2	5390494	9.6	11.2	4.23e-17	1.72e-13	25
6274			104850273	-4.9	-11	9.31e-17	2.83e-13	24.5
6275			610086	-4.7	-10.6	3.74e-16	9.12e-13	23.5
6276			102350528	-3.2	-10.6	5.06e-16	1.03e-12	23.3
6277			101340050	-3.2	-10.1	4.01e-15	6.97e-12	21.8
2	SDHAP3	NR_003263.1	6350341	8.4	9.98	5.64e-15	8.37e-12	21.6
6279			103130746	7.6	9.95	6.19e-15	8.37e-12	21.5
6280			103840301	2.8	9.74	1.48e-14	1.63e-11	20.9
3	LOC100130133	XR_037307.1	5390332	-3.4	-9.73	1.54e-14	1.63e-11	20.9
6282			1090195	6.2	9.72	1.61e-14	1.63e-11	20.8
4	KLF6	NM_001008490.1	360110	-3.2	-9.65	2.19e-14	2.05e-11	20.6
5	ZNF680	NM_178558.2	1090280	5.6	9.6	2.7e-14	2.34e-11	20.5
6285			103850064	2.3	9.53	3.6e-14	2.92e-11	20.2
6	HS.439870	Hs.439870	6370497	4.3	9.01	3.04e-13	2.31e-10	18.7
6287			105910364	-2.2	-8.91	4.6e-13	3.29e-10	18.4
7	RTN4RL2	NM_178570.1	60411	3.4	8.85	5.93e-13	4.01e-10	18.2
8	SFRS13A	NM_054016.1	6110014	-2.7	-8.62	1.56e-12	9.99e-10	17.5
6290			102230433	3.9	8.57	1.95e-12	1.18e-09	17.3
9	UBE2K	NM_001111112.1	6220021	-7.7	-8.55	2.06e-12	1.19e-09	17.2
6292			103990364	-4	-8.52	2.43e-12	1.34e-09	17.1
6293			1770017	-2.6	-8.4	3.97e-12	2.03e-09	16.8
10	PTPN9	NM_002833.2	3930279	7.4	8.4	4.01e-12	2.03e-09	16.7
11	LOC645550	XM_928570.1	5690403	3.1	8.36	4.7e-12	2.29e-09	16.6
6296			2760204	3.6	8.25	7.25e-12	3.39e-09	16.3
6297			103190068	-2.6	-8.1	1.38e-11	6.22e-09	15.8
12	LOC732377	XM_001133069.1	1500097	3.5	7.91	3.12e-11	1.36e-08	15.2
6299			106520398	-3.7	-7.89	3.37e-11	1.4e-08	15.1
13	TMEM103	NM_017713.1	4850064	4.4	7.88	3.45e-11	1.4e-08	15.1
14	HS.131670	Hs.131670	270139	5.6	7.66	8.75e-11	3.44e-08	14.4
6302			104780484	-3.8	-7.62	1.03e-10	3.9e-08	14.3
15	BCORL2	NM_173700.1	2570594	2.7	7.56	1.32e-10	4.87e-08	14.1
16	GTF2I	XM_939506.1	4570736	-3.2	-7.51	1.64e-10	5.8e-08	13.9
6305			100450079	-2.2	-7.51	1.67e-10	5.8e-08	13.9
17	ZXDC	NM_001040653.1	5080121	2.5	7.45	2.12e-10	7.17e-08	13.7
6307			104780592	-1.9	-7.41	2.47e-10	8.11e-08	13.6
6308			3060168	-2	-7.33	3.56e-10	1.14e-07	13.3
6309			103800239	-2.3	-7.12	8.38e-10	2.61e-07	12.7
6310			106980129	2.3	7.07	1.02e-09	3.1e-07	12.5
6311			6040541	2	6.99	1.43e-09	4.24e-07	12.2
18	C3ORF57	NM_145035.2	4560600	2.7	6.91	2.05e-09	5.93e-07	12

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			103780278	-2.6	-6.87	2.34e-09	6.63e-07	11.9
19	MUC6	XM_290540.6	2650292	-1.9	-6.84	2.68e-09	7.4e-07	11.7
20	LOC100133443	XM_001716638.1	2640717	2.3	6.84	2.74e-09	7.4e-07	11.7
21	LOC646588	XM_943454.1	2940468	6.2	6.81	3.03e-09	8.01e-07	11.7
22	SCRIB	NM_015356.3	2970176	3.4	6.78	3.46e-09	8.97e-07	11.5
6318			100380619	-4.8	-6.59	7.47e-09	1.89e-06	10.9
23	C11ORF63	NM_199124.1	6550037	-3.4	-6.54	9.19e-09	2.28e-06	10.8
6320			102810239	-1.9	-6.49	1.13e-08	2.74e-06	10.6
6321			100990672	2.5	6.46	1.28e-08	3.05e-06	10.5
24	HLA-DMA	NM_006120.2	540563	2.4	6.45	1.36e-08	3.19e-06	10.5
25	CYC1	NM_001916.2	1770520	4.1	6.39	1.7e-08	3.91e-06	10.3
6324			106550154	2.3	6.36	1.91e-08	4.31e-06	10.2
26	SDC3	XM_940667.1	1990551	-1.9	-6.36	1.95e-08	4.31e-06	10.2
6326			104920288	-3.2	-6.35	1.99e-08	4.33e-06	10.2
27	SRP54	XM_940545.1	1570279	1.8	6.34	2.1e-08	4.48e-06	10.1
6328			106510441	-1.9	-6.31	2.36e-08	4.95e-06	10
28	PFKFB2	NM_001018053.1	7040181	-2.3	-6.3	2.45e-08	5.05e-06	10
6330			100110411	-1.6	-6.25	2.98e-08	6.05e-06	9.85
29	ST8SIA4	NM_005668.3	4230017	6.8	6.22	3.47e-08	6.93e-06	9.73
30	LOC400696	NM_207646.1	1660110	1.9	6.21	3.59e-08	7.05e-06	9.71
6333			5390600	-2.6	-6.13	4.88e-08	9.42e-06	9.46
6334			101500408	-1.7	-6.12	5.24e-08	9.96e-06	9.41
31	CKAP2L	NM_152515.2	6380324	2.1	6.06	6.57e-08	1.23e-05	9.23
32	IGFL1	NM_198541.1	6020605	1.8	6.02	7.58e-08	1.4e-05	9.11
33	LOC645915	XM_933265.1	2650133	2	6.01	8.14e-08	1.48e-05	9.06
6338			102450601	2.9	5.96	9.66e-08	1.73e-05	8.92
6339			101410064	1.7	5.96	9.86e-08	1.74e-05	8.91
34	LOC100129407	XM_001715870.1	2570047	4.2	5.94	1.04e-07	1.82e-05	8.86
6341			102450048	1.9	5.87	1.42e-07	2.43e-05	8.62
6342			5390647	-1.9	-5.85	1.51e-07	2.56e-05	8.57
6343			60204	-5.1	-5.85	1.55e-07	2.58e-05	8.55
6344			104120092	1.6	5.75	2.29e-07	3.77e-05	8.24
35	LOC647391	XM_936466.1	2710603	1.6	5.74	2.36e-07	3.82e-05	8.21
6346			102360148	1.8	5.72	2.52e-07	4.02e-05	8.16
6347			100510176	1.8	5.72	2.54e-07	4.02e-05	8.15
6348			670433	-2.3	-5.72	2.58e-07	4.03e-05	8.14
36	TRIM49	NM_020358.2	450068	-1.7	-5.71	2.66e-07	4.1e-05	8.12
6350			100070184	3.7	5.7	2.8e-07	4.26e-05	8.08
6351			2510452	1.6	5.68	3e-07	4.51e-05	8.02
6352			5890632	-2.2	-5.63	3.61e-07	5.3e-05	7.87
37	LOC390251	XR_040181.1	3140341	-3	-5.63	3.61e-07	5.3e-05	7.87
6354			2650546	-2.1	-5.62	3.89e-07	5.63e-05	7.82
6355			101170242	-3	-5.55	5.11e-07	7.32e-05	7.6
38	PLEC1	NM_201379.1	4780273	-2.7	-5.48	6.61e-07	9.36e-05	7.39
6357			103610551	11	5.46	7.25e-07	0.000101	7.32
39	ALPI	NM_001631.2	2570162	-2	-5.45	7.31e-07	0.000101	7.31
6359			104200402	-2.7	-5.37	1.04e-06	0.00014	7.03
6360			103440278	-1.9	-5.36	1.04e-06	0.00014	7.03
40	MTMR10	NM_017762.1	6900112	1.5	5.29	1.39e-06	0.000186	6.8
41	CAPNS1	NM_001003962.1	5290500	1.9	5.21	1.87e-06	0.000248	6.56
6363			101690180	-1.5	-5.18	2.13e-06	0.000279	6.46
6364			105670064	1.8	5.18	2.16e-06	0.00028	6.44
42	CXORF30	XR_000668.1	360671	1.7	5.16	2.3e-06	0.000294	6.39
6366			103440168	-2.1	-5.14	2.48e-06	0.000314	6.33
6367			107040195	2.5	5.13	2.57e-06	0.000323	6.3
43	ACOT9	NM_001037171.1	5220497	2.7	5.13	2.61e-06	0.000325	6.29
6369			7100463	1.9	5.11	2.78e-06	0.000342	6.24

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
44	F2RL1	NM_005242.3	1050068	1.7	5.09	2.96e-06	0.000361	6.19
45	LCN10	NM_001001712.1	4610576	-1.5	-5.09	3.03e-06	0.000365	6.17
6372			100510161	2.1	5.08	3.15e-06	0.000376	6.14
46	LOC157627	NR_024281.1	4850546	2.8	5.07	3.19e-06	0.000378	6.13
6374			106020113	-1.6	-5.06	3.33e-06	0.000389	6.1
47	LOC642333	XM_939884.1	5390148	1.8	5.06	3.36e-06	0.000389	6.09
6376			6660128	2.7	5.06	3.41e-06	0.000391	6.08
48	LOC644714	XM_934516.1	5390097	1.8	5.05	3.52e-06	0.0004	6.05
49	SGCB	NM_000232.3	1190162	-1.8	-5.02	3.96e-06	0.000446	5.96
6379			101240056	-2	-5	4.16e-06	0.000464	5.92
6380			102510671	-2.4	-5	4.28e-06	0.000473	5.9
50	LOC100134170	XM_001721704.1	5570022	1.6	4.98	4.51e-06	0.000494	5.85
6382			103800465	-1.7	-4.98	4.55e-06	0.000494	5.85
51	HS.566864	Hs.566864	1230372	2	4.97	4.81e-06	0.000518	5.8
6384			5050039	-2.6	-4.93	5.56e-06	0.000593	5.69
52	BID	NM_197967.1	1190022	-4.2	-4.91	5.88e-06	0.000622	5.64
53	LOC644884	XM_927971.1	5290520	1.8	4.91	5.93e-06	0.000622	5.63
6387			102350114	-1.8	-4.89	6.38e-06	0.000664	5.58
54	CXORF59	NM_173695.1	1990347	-1.9	-4.79	9.29e-06	0.000959	5.27
55	FBLN7	NM_153214.1	5670154	-3.8	-4.77	1e-05	0.00102	5.22
56	HSF5	NM_001080439.1	110176	2.9	4.77	1.02e-05	0.00104	5.2

Table 8: Top 120 genes (all arrays)

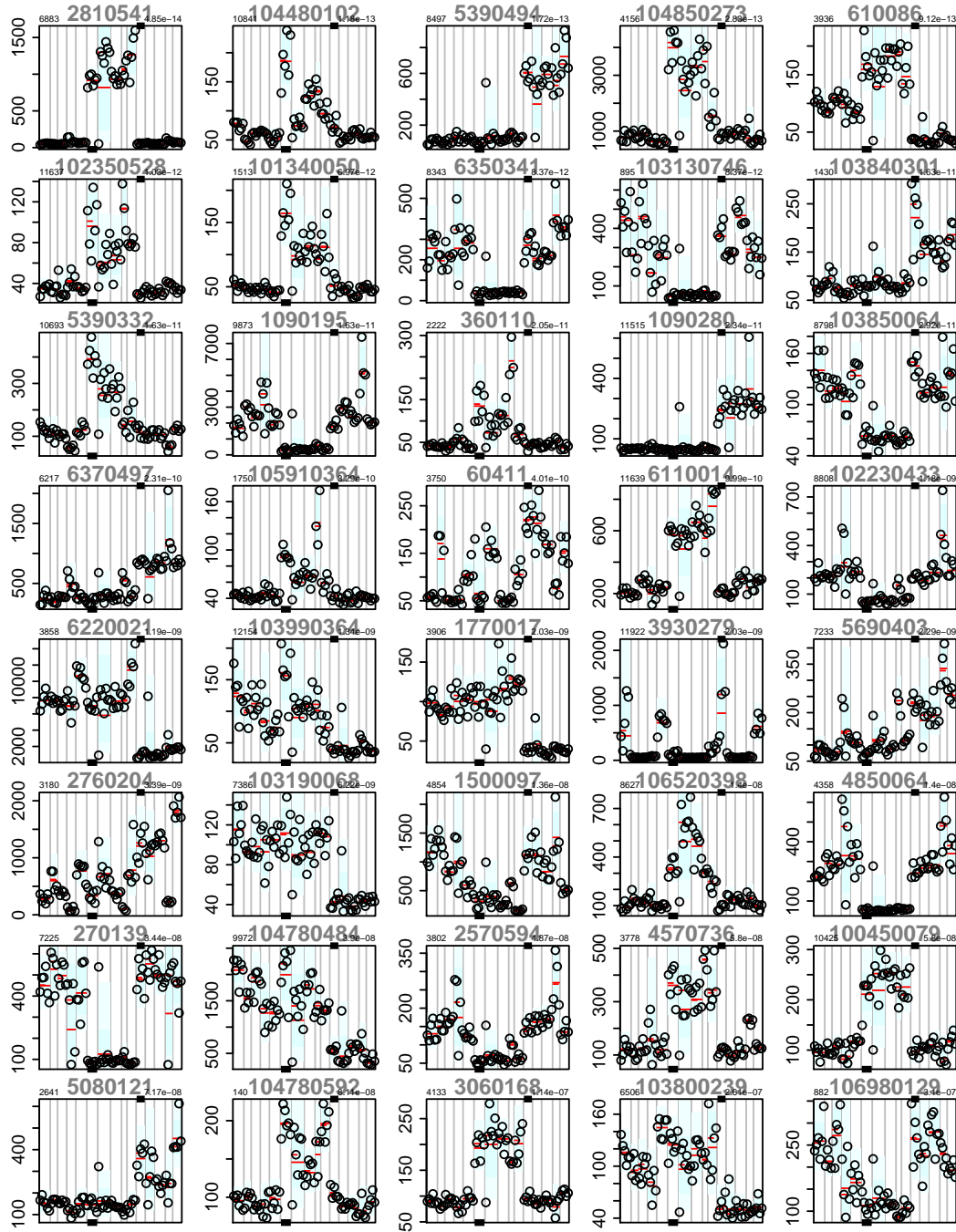


Figure 10a: Top 40 genes for contrast LNa (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

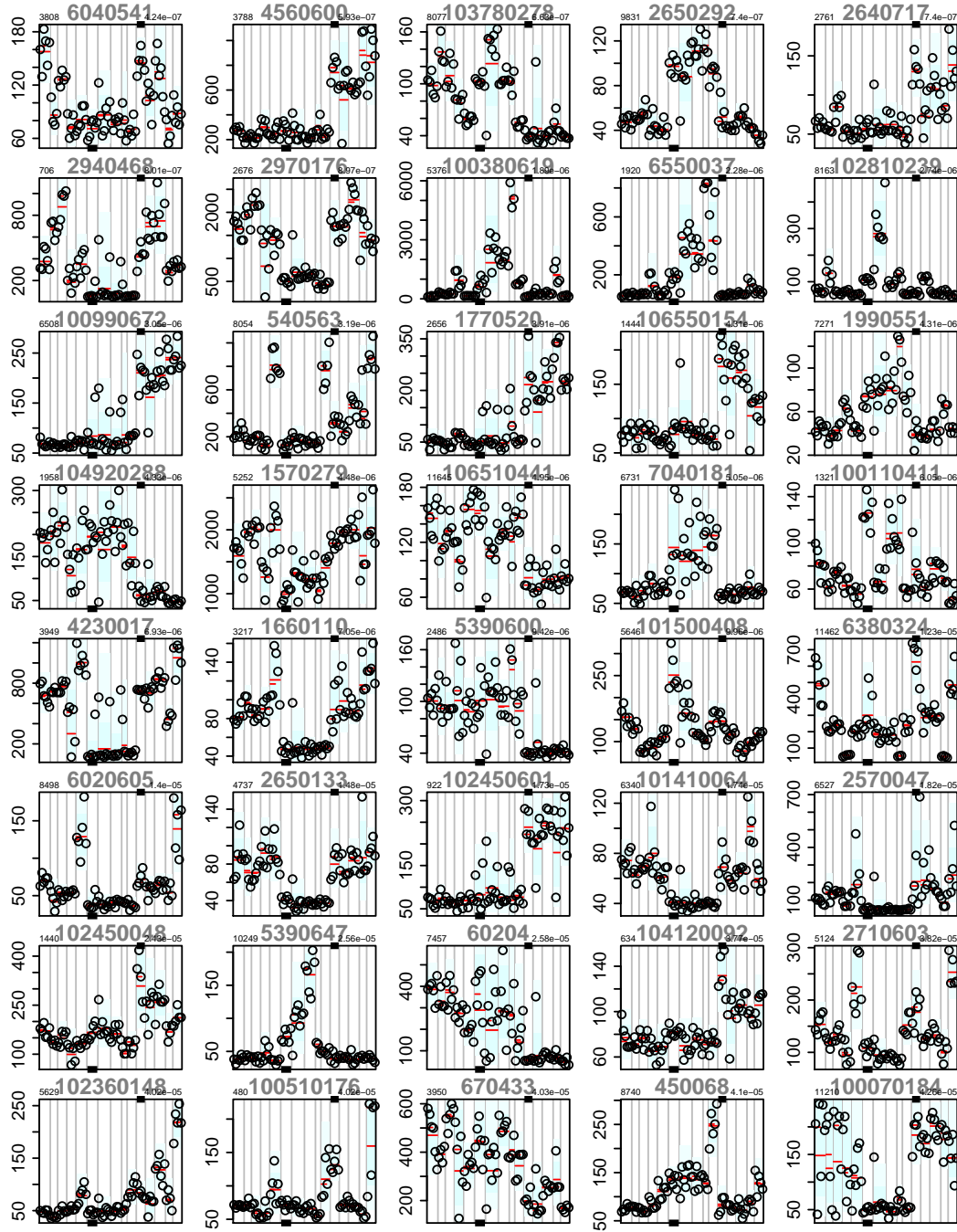


Figure 10b: Significant probes (41–80) for contrast LNa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

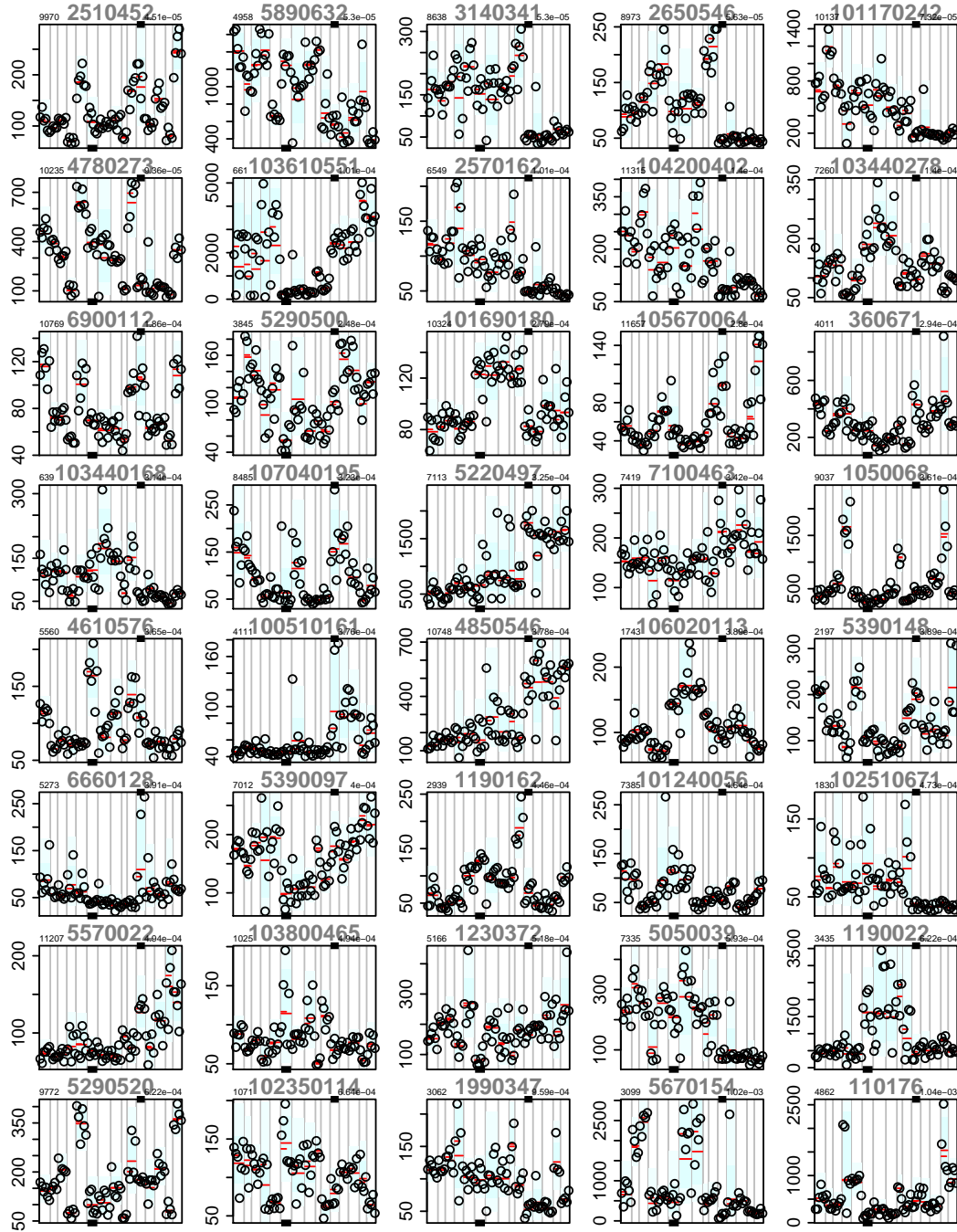


Figure 10c: Significant probes (81–120) for contrast LNa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.7 Contrast LNb

Using the matrix representing the contrast defined by LAB_BAmY - NAB_BAmY

LNb	
NAB_BAmY	-1
LAB_BAmY	1

The statistics for the top 120 genes across the contrast (out of 122 genes having adjusted p -values below 0.05) are shown in table 9, the corresponding expression plots are shown in Figs. 11a-c on pages 89 through 91.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			2810541	-14	-11.5	1.42e-17	1.72e-13	21.8
6272			1090195	6.7	10.4	8.57e-16	5.21e-12	19.5
6273			102810239	-2.5	-9.61	2.51e-14	1.02e-10	17.5
1	C11ORF63	NM_199124.1	6550037	-5.3	-9.32	8.39e-14	2.55e-10	16.8
6275			3060168	-2.3	-9.08	2.32e-13	5.65e-10	16.2
6276			610086	-3.3	-8.5	2.55e-12	5.18e-09	14.7
2	MUC6	XM_290540.6	2650292	-2.1	-8.36	4.68e-12	8.13e-09	14.3
3	SFRS13A	NM_054016.1	6110014	-2.5	-8.3	6.12e-12	9.31e-09	14.1
4	TMEM103	NM_017713.1	4850064	4.3	8.09	1.46e-11	1.97e-08	13.6
6280			106520398	-3.6	-7.99	2.21e-11	2.7e-08	13.3
6281			100380619	-6.2	-7.95	2.61e-11	2.88e-08	13.2
6282			5390647	-2.2	-7.93	2.85e-11	2.89e-08	13.2
5	FAM53A	NM_001013622.1	4060112	-3.3	-7.73	6.45e-11	6.04e-08	12.6
6284			100450079	-2.1	-7.49	1.76e-10	1.53e-07	12
6285			103850064	1.9	7.44	2.24e-10	1.8e-07	11.8
6	SDHAP3	NR_003263.1	6350341	4.6	7.42	2.37e-10	1.8e-07	11.8
6287			104850273	-2.8	-7.24	5.1e-10	3.65e-07	11.3
7	SDC3	XM_940667.1	1990551	-2	-7.08	9.7e-10	6.56e-07	10.9
8	LOC100130133	XR_037307.1	5390332	-2.4	-7.06	1.1e-09	7.02e-07	10.8
6290			103130746	4	6.98	1.5e-09	9.15e-07	10.6
9	LOC400696	NM_207646.1	1660110	2	6.95	1.67e-09	9.68e-07	10.5
10	GTF2I	XM_939506.1	4570736	-2.8	-6.94	1.8e-09	9.94e-07	10.4
6293			103780278	-2.6	-6.89	2.17e-09	1.15e-06	10.3
11	ZNF680	NM_178558.2	1090280	3.3	6.83	2.77e-09	1.4e-06	10.2
12	HS.131670	Hs.131670	270139	4.4	6.81	2.99e-09	1.46e-06	10.1
13	TRIM49	NM_020358.2	450068	-1.8	-6.73	4.19e-09	1.96e-06	9.88
14	LOC732377	XM_001133069.1	1500097	2.8	6.65	5.96e-09	2.69e-06	9.64
15	LOC646588	XM_943454.1	2940468	5.5	6.59	7.62e-09	3.31e-06	9.47
16	UBE2K	NM_001111112.1	6220021	-4.5	-6.47	1.21e-08	5.09e-06	9.16
6300			101340050	-2	-6.41	1.6e-08	6.5e-06	8.97
17	BCORL2	NM_173700.1	2570594	2.3	6.39	1.74e-08	6.82e-06	8.92
6302			6900239	-2.7	-6.27	2.8e-08	1.07e-05	8.59
18	LOC645915	XM_933265.1	2650133	2	6.17	4.23e-08	1.56e-05	8.31
6304			104780592	-1.6	-6.04	7.17e-08	2.57e-05	7.95
6305			101690180	-1.6	-6.01	8.12e-08	2.82e-05	7.87
6306			102350528	-1.9	-5.95	1.03e-07	3.47e-05	7.71
19	HS.151285	Hs.151285	3440300	-2.9	-5.92	1.16e-07	3.82e-05	7.62
20	LOC100129407	XM_001715870.1	2570047	4	5.9	1.26e-07	4.05e-05	7.56
6309			1770017	-1.9	-5.83	1.67e-07	5.2e-05	7.37
21	CXORF30	XR_000668.1	360671	1.8	5.8	1.89e-07	5.75e-05	7.29
6311			102230433	2.4	5.74	2.39e-07	7.08e-05	7.13
22	EIF4B	NM_001417.2	5390494	3	5.69	2.84e-07	8.23e-05	7

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			105910364	-1.6	-5.67	3.11e-07	8.79e-05	6.94
6314			103440168	-2.2	-5.63	3.63e-07	9.84e-05	6.84
6315			103800239	-1.9	-5.63	3.64e-07	9.84e-05	6.83
6316			104780484	-2.5	-5.51	5.97e-07	0.000158	6.49
6317			5050039	-2.8	-5.48	6.69e-07	0.000173	6.41
23	SGCB	NM_000232.3	1190162	-1.9	-5.46	7.25e-07	0.00018	6.36
24	PLEC1	NM_201379.1	4780273	-2.6	-5.46	7.27e-07	0.00018	6.35
6320			101340161	-1.8	-5.45	7.41e-07	0.00018	6.34
6321			6290739	-2.2	-5.39	9.42e-07	0.000225	6.17
6322			106020113	-1.6	-5.31	1.27e-06	0.000296	5.97
6323			103190068	-1.9	-5.31	1.29e-06	0.000296	5.95
25	LOC100128585	XR_039418.1	6660687	2.7	5.23	1.78e-06	0.000402	5.73
6325			104920288	-2.5	-5.16	2.29e-06	0.000506	5.56
26	ST8SIA4	NM_005668.3	4230017	4.6	5.14	2.47e-06	0.000538	5.5
27	CCDC4	XM_941085.1	6650397	-1.7	-5.12	2.72e-06	0.000581	5.43
28	LOC440233	XM_496037.2	6660301	-2	-5.05	3.49e-06	0.000732	5.26
29	SCRIB	NM_015356.3	2970176	2.4	5.03	3.84e-06	0.000793	5.19
30	C3ORF57	NM_145035.2	4560600	2	5.01	4.03e-06	0.000818	5.16
31	LOC390251	XR_040181.1	3140341	-2.5	-4.94	5.28e-06	0.00105	4.97
6332			106980286	-1.8	-4.87	7.01e-06	0.00138	4.77
32	PFKFB2	NM_001018053.1	7040181	-1.9	-4.83	8.07e-06	0.00156	4.67
6334			106980129	1.7	4.77	9.98e-06	0.0019	4.52
6335			104480102	-1.5	-4.76	1.03e-05	0.00194	4.5
6336			6200278	2.6	4.73	1.16e-05	0.00214	4.42
33	HS.245405	Hs.245405	6660440	-1.9	-4.69	1.33e-05	0.00242	4.32
6338			2650546	-1.8	-4.69	1.35e-05	0.00242	4.31
6339			2900537	-1.5	-4.66	1.52e-05	0.00268	4.23
6340			104920138	-1.7	-4.62	1.74e-05	0.00303	4.13
6341			100990672	1.9	4.56	2.17e-05	0.00372	3.97
34	SRP54	XM_940545.1	1570279	1.5	4.55	2.28e-05	0.00385	3.94
35	LOC100133479	XM_001718115.1	4200707	-1.7	-4.5	2.7e-05	0.00449	3.82
36	KCNK7	NM_033347.1	1500142	-2.7	-4.5	2.73e-05	0.00449	3.81
6345			5890632	-1.8	-4.49	2.77e-05	0.00449	3.8
6346			5390600	-1.9	-4.48	2.94e-05	0.0047	3.76
6347			106660487	-1.5	-4.47	3.03e-05	0.00479	3.74
6348			5390551	-2.6	-4.45	3.29e-05	0.00508	3.68
6349			101170242	-2.3	-4.45	3.3e-05	0.00508	3.68
6350			100070184	2.7	4.39	4.09e-05	0.00622	3.53
6351			103990364	-2	-4.34	4.89e-05	0.00734	3.4
37	MIR1226	NR_031595.1	540167	-1.8	-4.33	4.96e-05	0.00737	3.39
6353			106510441	-1.5	-4.32	5.11e-05	0.0075	3.37
38	KRTCAP2	NM_173852.3	6110605	-2.1	-4.31	5.36e-05	0.00776	3.34
39	LOC100131512	XM_001722891.1	380095	-1.6	-4.3	5.46e-05	0.00782	3.32
40	ABLIM1	NM_006720.3	2570112	-1.6	-4.28	5.86e-05	0.00829	3.27
6357			101410064	1.4	4.27	6.09e-05	0.00852	3.25
41	ZXDC	NM_001040653.1	5080121	1.6	4.24	6.84e-05	0.00945	3.16
42	HS.439870	Hs.439870	6370497	1.9	4.23	7.21e-05	0.00985	3.13
43	OR4K14	NM_001004712.1	4810735	-1.7	-4.19	8.29e-05	0.0112	3.03
44	HUWE1	NM_031407.3	6980332	-2	-4.07	0.000123	0.0162	2.75
6362			540079	-1.4	-4.07	0.000123	0.0162	2.75
45	BID	NM_197967.1	1190022	-3.2	-4.07	0.000124	0.0162	2.74
46	KLF6	NM_001008490.1	360110	-1.6	-4.06	0.000127	0.0165	2.72
6365			101500408	-1.4	-4.05	0.000132	0.0168	2.7
6366			106550154	1.7	4.05	0.000132	0.0168	2.7
6367			670433	-1.7	-4.04	0.000138	0.0173	2.67
47	LOC642672	XM_943423.1	1580609	1.6	4.04	0.00014	0.0173	2.66
48	IGFL1	NM_198541.1	6020605	1.5	4.02	0.000146	0.018	2.63

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			2030114	-2	-4.01	0.000155	0.0189	2.58
6371			104780332	1.4	3.95	0.000189	0.0228	2.44
49	HS.481464	Hs.481464	2760068	-1.6	-3.9	0.000221	0.0261	2.33
50	CKAP2L	NM_152515.2	6380324	1.6	3.9	0.000221	0.0261	2.33
51	SDHAP3	NR_003263.2	1400524	-2.3	-3.89	0.000228	0.0263	2.31
6375			3800093	-2.1	-3.89	0.000228	0.0263	2.31
52	HS.460114	Hs.460114	4230020	-1.5	-3.89	0.000229	0.0263	2.31
6377			103990735	-2.7	-3.88	0.000238	0.0271	2.28
53	FBLN7	NM_153214.1	5670154	-2.9	-3.86	0.000252	0.0282	2.24
54	LOC283157	XM_939588.1	6760333	-1.6	-3.86	0.000253	0.0282	2.24
55	SMAD1	NM_001003688.1	3170131	-1.6	-3.86	0.000255	0.0282	2.23
56	STXBP6	NM_014178.6	2370092	-1.4	-3.86	0.000257	0.0282	2.23
6382			103610551	5	3.85	0.000266	0.0289	2.2
57	PDE5A	NM_001083.3	5290044	-1.5	-3.82	0.000294	0.0316	2.13
6384			102450601	1.9	3.8	0.000314	0.0335	2.08
6385			106450725	-1.4	-3.78	0.00033	0.0349	2.05
58	LOC650761	XM_939844.1	6760681	-2	-3.76	0.000357	0.0375	1.99
6387			104120092	1.3	3.75	0.000365	0.038	1.98
6388			104200167	1.9	3.73	0.000385	0.0397	1.94
6389			103840301	1.5	3.73	0.000395	0.0403	1.92
59	MAPK7	NM_002749.2	4810010	-1.8	-3.69	0.000446	0.0452	1.84

Table 9: Top 120 genes (all arrays)

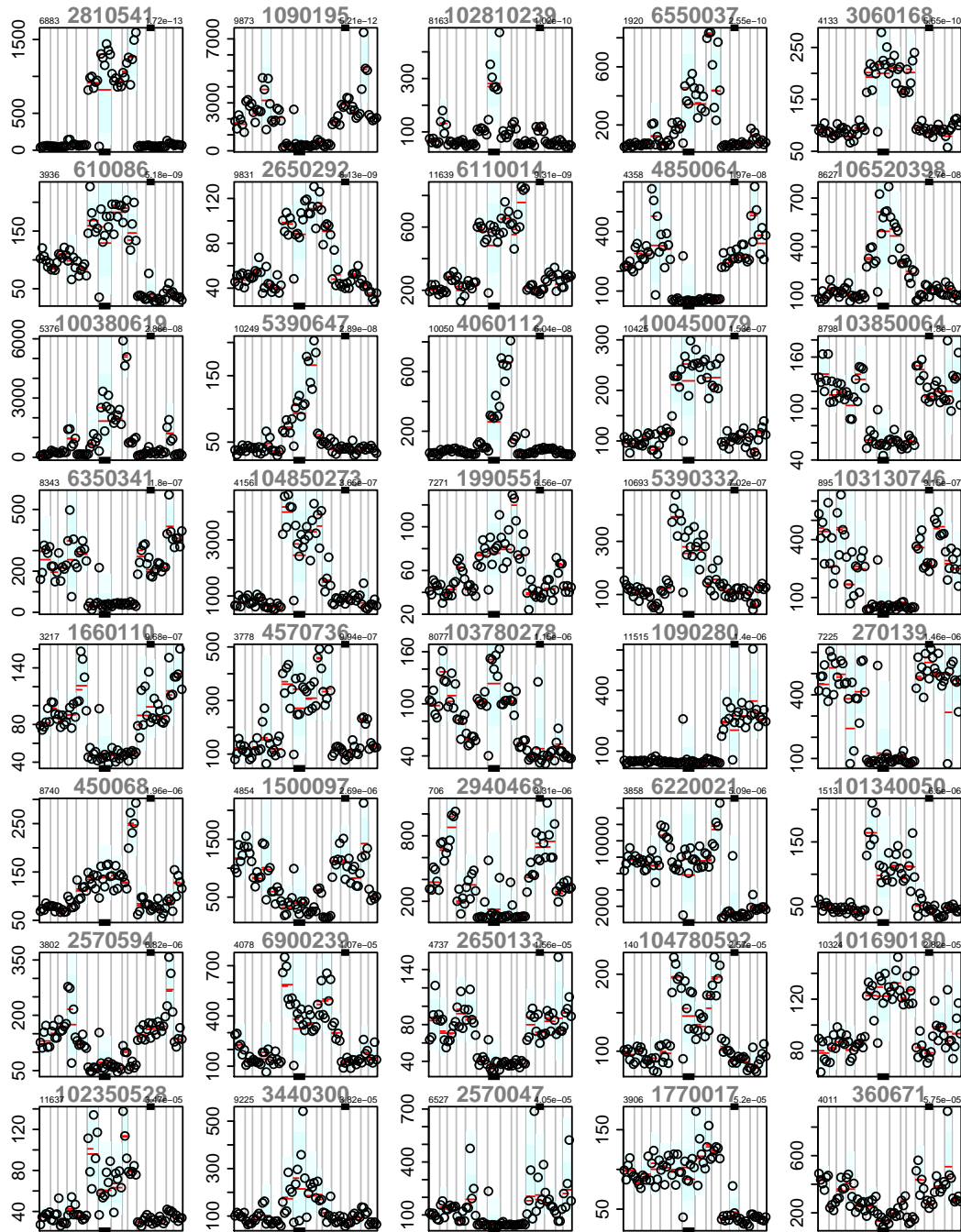


Figure 11a: Top 40 genes for contrast LNb (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

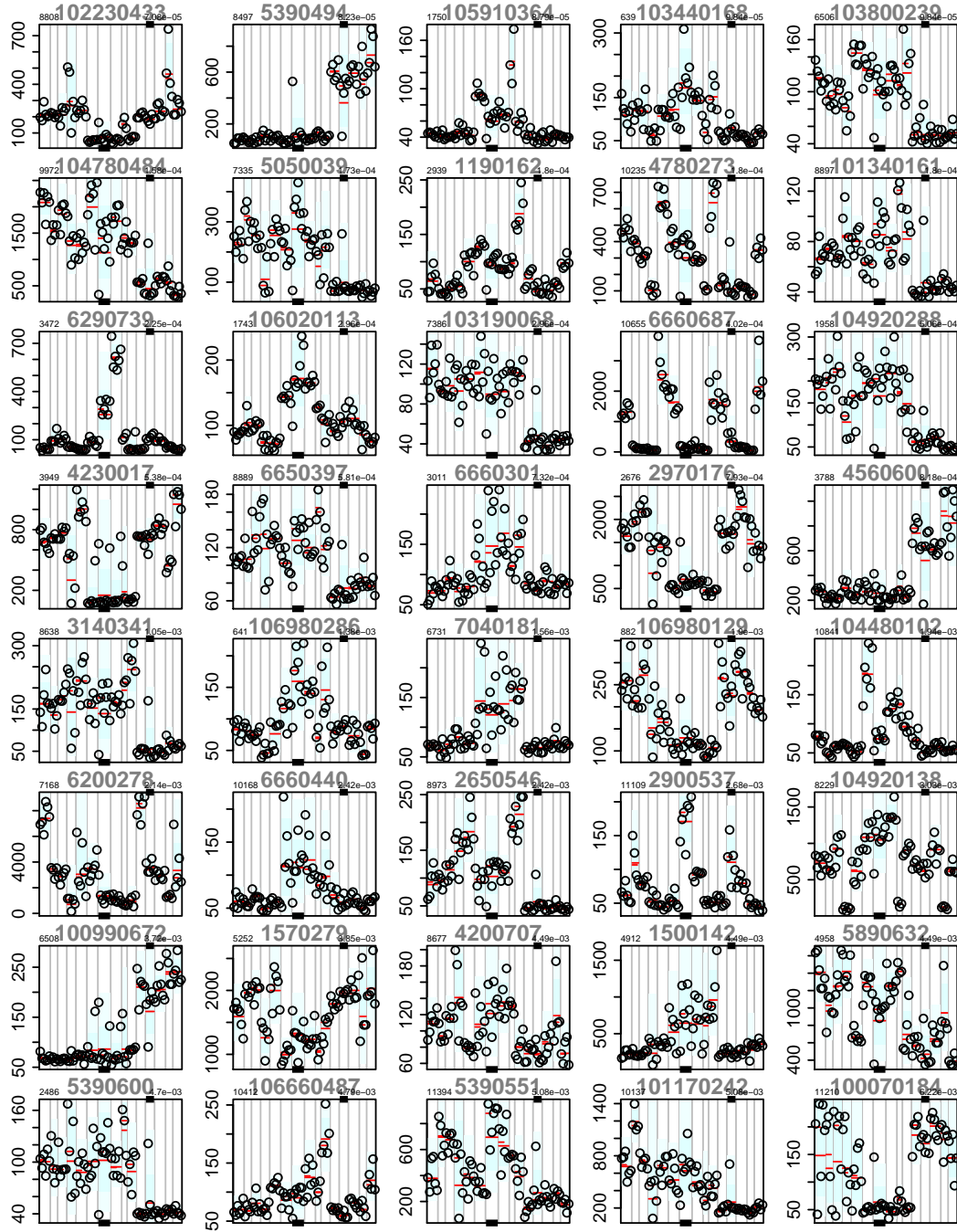


Figure 11b: Significant probes (41–80) for contrast LNB (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

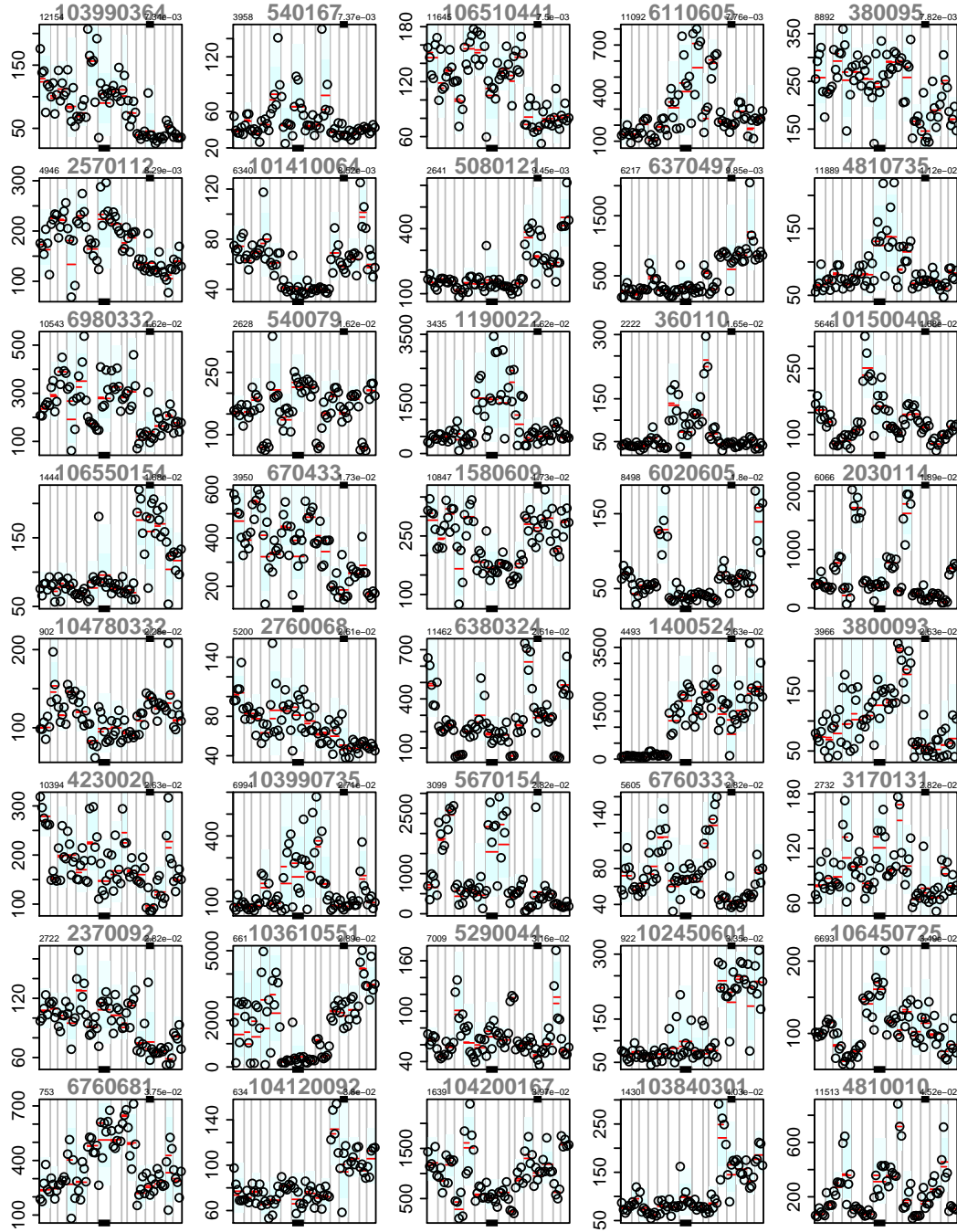


Figure 11c: Significant probes (81–120) for contrast LNb (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.8 Contrast LNC

Using the matrix representing the contrast defined by LAB_Cing - NAB_Cing

LNC	
NAB_Cing	-1
LAB_Cing	1

The statistics for the top 120 genes across the contrast (out of 241 genes having adjusted p -values below 0.05) are shown in table 10, the corresponding expression plots are shown in Figs. 12a-c on pages 95 through 97.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			5390647	-4.4	-14.6	1.04e-22	1.27e-18	32.1
1	FAM53A	NM_001013622.1	4060112	-8.2	-13.9	1.43e-21	8.71e-18	30.6
6273			6290739	-6.6	-12.9	5.44e-20	2.05e-16	28.4
6274			2810541	-19	-12.8	6.73e-20	2.05e-16	28.3
6275			610086	-5.7	-12.6	1.93e-19	4.7e-16	27.6
6276			1770017	-3.5	-11.7	6.61e-18	1.34e-14	25.4
6277			103130746	9.5	11.6	8.97e-18	1.56e-14	25.2
6278			100050152	2.8	11.1	6.68e-17	1.02e-13	23.9
6279			1090195	7.2	11	7.52e-17	1.02e-13	23.8
2	ZNF680	NM_178558.2	1090280	6.5	11	9.05e-17	1.1e-13	23.7
6281			101340050	-3	-10.2	2.15e-15	2.38e-12	21.5
3	EIF4B	NM_001417.2	5390494	7	10.1	3.19e-15	3.11e-12	21.3
6283			102230433	4.7	10.1	3.32e-15	3.11e-12	21.2
6284			102360148	2.6	9.81	1.1e-14	9.55e-12	20.4
4	TMEM103	NM_017713.1	4850064	5.4	9.47	4.46e-14	3.62e-11	19.4
6286			104480102	-2.1	-9.35	7.48e-14	5.69e-11	19.1
5	UBE2K	NM_001111112.1	6220021	-8.3	-9.27	1.03e-13	7.37e-11	18.8
6	C11ORF63	NM_199124.1	6550037	-5.1	-9.2	1.38e-13	9.28e-11	18.6
7	RTN4RL2	NM_178570.1	60411	3.3	9.19	1.45e-13	9.28e-11	18.6
6290			100380619	-7.8	-9.06	2.45e-13	1.49e-10	18.2
6291			3060168	-2.3	-9.02	2.97e-13	1.72e-10	18.1
6292			104850273	-3.5	-8.96	3.74e-13	2.07e-10	17.9
8	MUC6	XM_290540.6	2650292	-2.2	-8.8	7.39e-13	3.91e-10	17.4
6294			100450079	-2.4	-8.75	9.04e-13	4.59e-10	17.3
9	LOC646588	XM_943454.1	2940468	9.3	8.71	1.07e-12	5.23e-10	17.2
10	BCORL2	NM_173700.1	2570594	3	8.69	1.18e-12	5.51e-10	17.1
6297			2760204	3.5	8.44	3.31e-12	1.49e-09	16.4
11	SDHAP3	NR_003263.1	6350341	5.5	8.38	4.35e-12	1.89e-09	16.2
12	HLA-DMA	NM_006120.2	540563	2.9	8.26	7.13e-12	2.99e-09	15.8
13	KLF6	NM_001008490.1	360110	-2.6	-8.2	9.21e-12	3.74e-09	15.6
6301			106520398	-3.7	-8.16	1.07e-11	4.21e-09	15.5
14	HS.131670	Hs.131670	270139	5.5	7.93	2.89e-11	1.1e-08	14.8
6303			103990364	-3.4	-7.86	3.8e-11	1.4e-08	14.6
15	LOC732377	XM_001133069.1	1500097	3.3	7.84	4.19e-11	1.5e-08	14.5
6305			103190068	-2.4	-7.64	9.56e-11	3.29e-08	13.9
6306			106980129	2.4	7.64	9.72e-11	3.29e-08	13.9
16	HS.439870	Hs.439870	6370497	3.3	7.63	1.01e-10	3.32e-08	13.9
6308			100990672	2.8	7.61	1.08e-10	3.45e-08	13.8
17	C3ORF57	NM_145035.2	4560600	2.9	7.57	1.26e-10	3.91e-08	13.7
6310			103850064	1.9	7.57	1.29e-10	3.91e-08	13.7
18	LOC100130133	XR_037307.1	5390332	-2.5	-7.56	1.32e-10	3.91e-08	13.7
6312			2030114	-3.5	-7.51	1.62e-10	4.7e-08	13.5

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
19	LOC645915	XM.933265.1	2650133	2.2	7.49	1.81e-10	5.11e-08	13.4
20	SFRS13A	NM.054016.1	6110014	-2.2	-7.41	2.49e-10	6.89e-08	13.2
6315			103780278	-2.7	-7.38	2.87e-10	7.76e-08	13.1
21	CYC1	NM.001916.2	1770520	4.7	7.36	3.09e-10	8.19e-08	13
22	TRIM49	NM.020358.2	450068	-1.9	-7.34	3.33e-10	8.61e-08	13
6318			103800239	-2.3	-7.22	5.61e-10	1.42e-07	12.6
23	SCRIB	NM.015356.3	2970176	3.4	7.16	6.97e-10	1.73e-07	12.4
6320			2650546	-2.4	-7.07	1.04e-09	2.52e-07	12.1
24	P2RY14	NM.014879.3	1340364	-2.5	-6.99	1.44e-09	3.43e-07	11.9
6322			6900239	-2.9	-6.94	1.75e-09	4.09e-07	11.7
6323			102450601	3.2	6.91	1.99e-09	4.58e-07	11.6
6324			102350528	-2	-6.75	3.89e-09	8.76e-07	11.1
25	LOC390251	XR.040181.1	3140341	-3.5	-6.74	4.12e-09	9.12e-07	11.1
6326			100070184	4.3	6.66	5.57e-09	1.2e-06	10.9
26	GTF2I	XM.939506.1	4570736	-2.6	-6.66	5.61e-09	1.2e-06	10.8
6328			105910364	-1.7	-6.65	5.97e-09	1.25e-06	10.8
6329			103840301	2	6.61	6.83e-09	1.41e-06	10.7
27	CAPNS1	NM.001003962.1	5290500	2.1	6.6	7.19e-09	1.46e-06	10.7
6331			106550154	2.2	6.55	9.04e-09	1.8e-06	10.5
28	CXORF30	XR.000668.1	360671	2	6.54	9.43e-09	1.85e-06	10.5
29	ST8SIA4	NM.005668.3	4230017	6.6	6.39	1.68e-08	3.25e-06	10
6334			104920288	-3.1	-6.37	1.86e-08	3.54e-06	9.93
30	LOC400696	NM.207646.1	1660110	1.9	6.33	2.2e-08	4.12e-06	9.81
6336			103440168	-2.3	-6.29	2.54e-08	4.69e-06	9.69
6337			104780484	-2.8	-6.25	3e-08	5.46e-06	9.57
31	LOC645550	XM.928570.1	5690403	2.2	6.15	4.51e-08	8.08e-06	9.26
32	SDC3	XM.940667.1	1990551	-1.8	-6.12	5.24e-08	9.24e-06	9.14
6340			104210019	-1.7	-6.04	7.16e-08	1.24e-05	8.9
6341			5050039	-3	-6	8.21e-08	1.41e-05	8.8
6342			5390600	-2.4	-5.92	1.13e-07	1.91e-05	8.55
33	CCNG2	NM.004354.1	130215	-2.4	-5.82	1.74e-07	2.91e-05	8.22
34	PFKFB2	NM.001018053.1	7040181	-2.1	-5.76	2.19e-07	3.61e-05	8.04
6345			101410064	1.6	5.67	3.18e-07	5.17e-05	7.75
35	GTF2E2	NM.002095.3	1570538	-2.6	-5.64	3.58e-07	5.74e-05	7.66
36	LOC653428	XM.927368.1	580095	1.7	5.58	4.43e-07	7.01e-05	7.5
6348			106980372	-3.7	-5.51	5.83e-07	9.09e-05	7.28
37	RPS4Y1	NM.001008.3	6100687	-2.7	-5.49	6.28e-07	9.67e-05	7.23
6350			103610551	9.7	5.48	6.64e-07	0.0001	7.18
38	ZNF180	NM.013256.1	3840494	2.7	5.48	6.67e-07	0.0001	7.18
39	SRP54	XM.940545.1	1570279	1.6	5.47	6.99e-07	0.000104	7.14
6353			106980286	-1.9	-5.42	8.38e-07	0.000123	7
6354			5890632	-2	-5.4	9.01e-07	0.000131	6.95
6355			104780592	-1.5	-5.39	9.29e-07	0.000133	6.92
6356			104120463	2.1	5.39	9.58e-07	0.000136	6.9
6357			101170242	-2.8	-5.37	1.03e-06	0.000144	6.84
40	AP1S2	NM.003916.3	940706	-2.6	-5.36	1.04e-06	0.000144	6.83
6359			6040541	1.7	5.36	1.08e-06	0.000147	6.81
41	GTPBP8	NM.014170.2	6620176	1.6	5.35	1.1e-06	0.000149	6.79
6361			106510441	-1.7	-5.34	1.15e-06	0.000154	6.75
42	CDKAL1	NM.017774.1	2230020	1.6	5.28	1.46e-06	0.000193	6.57
43	LCN10	NM.001001712.1	4610576	-1.5	-5.25	1.63e-06	0.000209	6.49
44	LOC728475	XM.001127527.2	4480411	2.2	5.25	1.63e-06	0.000209	6.49
45	LOC100129407	XM.001715870.1	2570047	3.4	5.25	1.63e-06	0.000209	6.49
46	SGCB	NM.000232.3	1190162	-1.8	-5.24	1.71e-06	0.000217	6.45
47	OR4K14	NM.001004712.1	4810735	-1.9	-5.22	1.81e-06	0.000227	6.4
48	SMAGP	NM.001031628.1	6220253	2	5.21	1.89e-06	0.000235	6.37
49	LOC100134170	XM.001721704.1	5570022	1.6	5.21	1.93e-06	0.000237	6.35

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			4010239	-2.3	-5.17	2.18e-06	0.000265	6.26
6371			101500408	-1.5	-5.13	2.58e-06	0.000311	6.13
6372			102810239	-1.6	-5.12	2.65e-06	0.000317	6.11
50	LOC729660	XR_039044.1	4540577	-2.1	-5.1	2.85e-06	0.000337	6.05
6374			101980600	7.6	5.1	2.88e-06	0.000337	6.04
51	LOC729454	XM_001130287.2	1660142	-1.9	-5.08	3.12e-06	0.000362	5.98
52	SLC39A4	NM_017767.1	1400286	-1.8	-5.03	3.75e-06	0.000429	5.84
53	SUMO1P3	NR_002190.1	4050358	-1.5	-5.03	3.77e-06	0.000429	5.83
54	TMPO	NM_003276.1	1990204	1.7	5	4.23e-06	0.000476	5.74
6379			3800093	-2.6	-4.99	4.38e-06	0.000489	5.72
6380			104200402	-2.4	-4.97	4.66e-06	0.000515	5.67
55	OSBPL3	NM_145322.1	6040181	3	4.96	4.95e-06	0.000543	5.62
56	LOC643763	XM_928976.1	6520044	2.8	4.95	5.08e-06	0.000552	5.6
6383			100510161	2	4.95	5.18e-06	0.000558	5.58
6384			103290286	-2.5	-4.93	5.55e-06	0.000592	5.53
57	HS.245405	Hs.245405	6660440	-1.9	-4.91	5.88e-06	0.000622	5.49
58	LOC440233	XM_496037.2	6660301	-1.9	-4.91	5.99e-06	0.000629	5.47
6387			101340161	-1.7	-4.9	6.28e-06	0.000653	5.43
6388			5390551	-2.8	-4.88	6.62e-06	0.000683	5.39
59	CXORF59	NM_173695.1	1990347	-1.8	-4.85	7.57e-06	0.000774	5.29
6390			6200278	2.7	4.84	7.82e-06	0.000789	5.26

Table 10: Top 120 genes (all arrays)

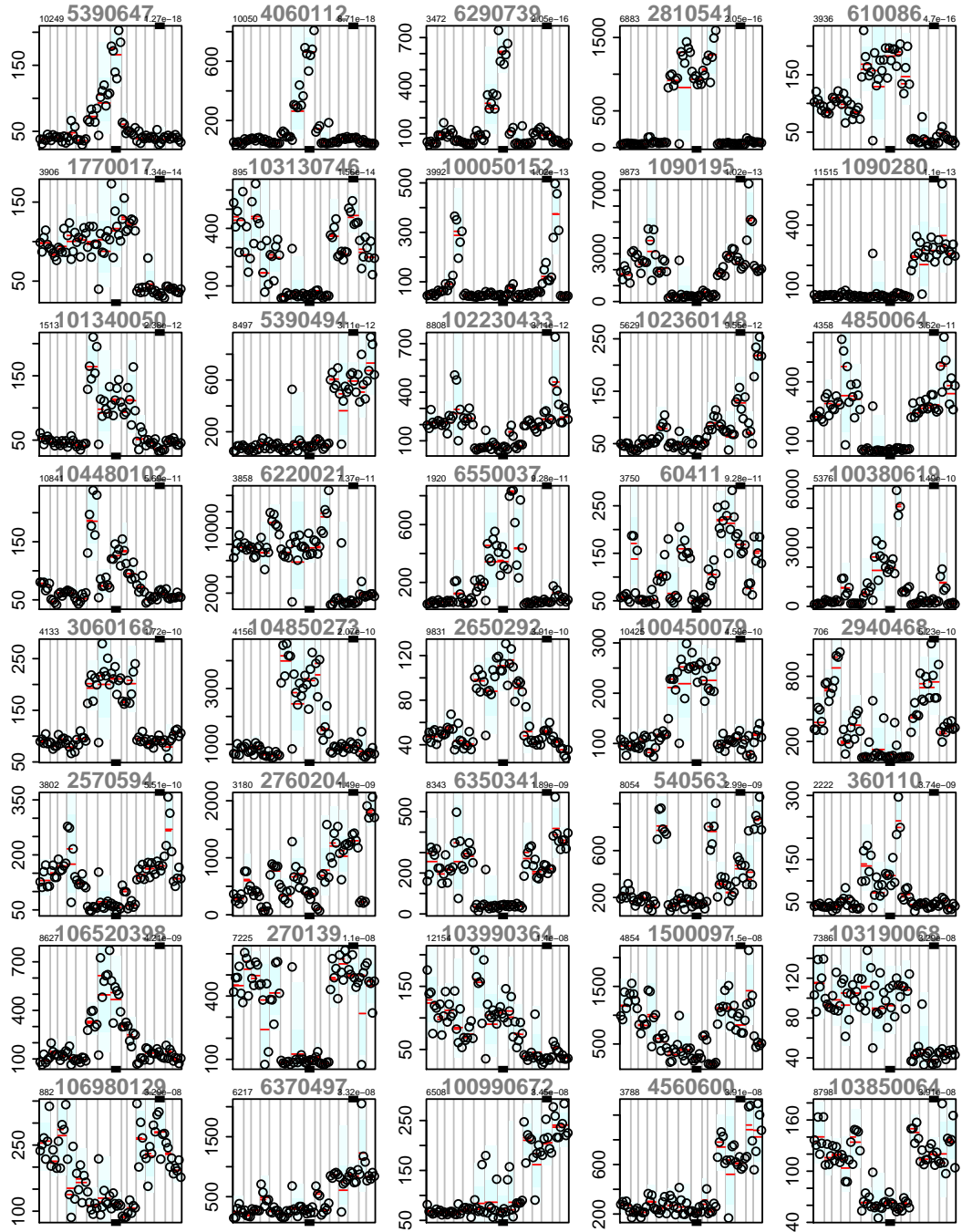


Figure 12a: Top 40 genes for contrast LNC (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

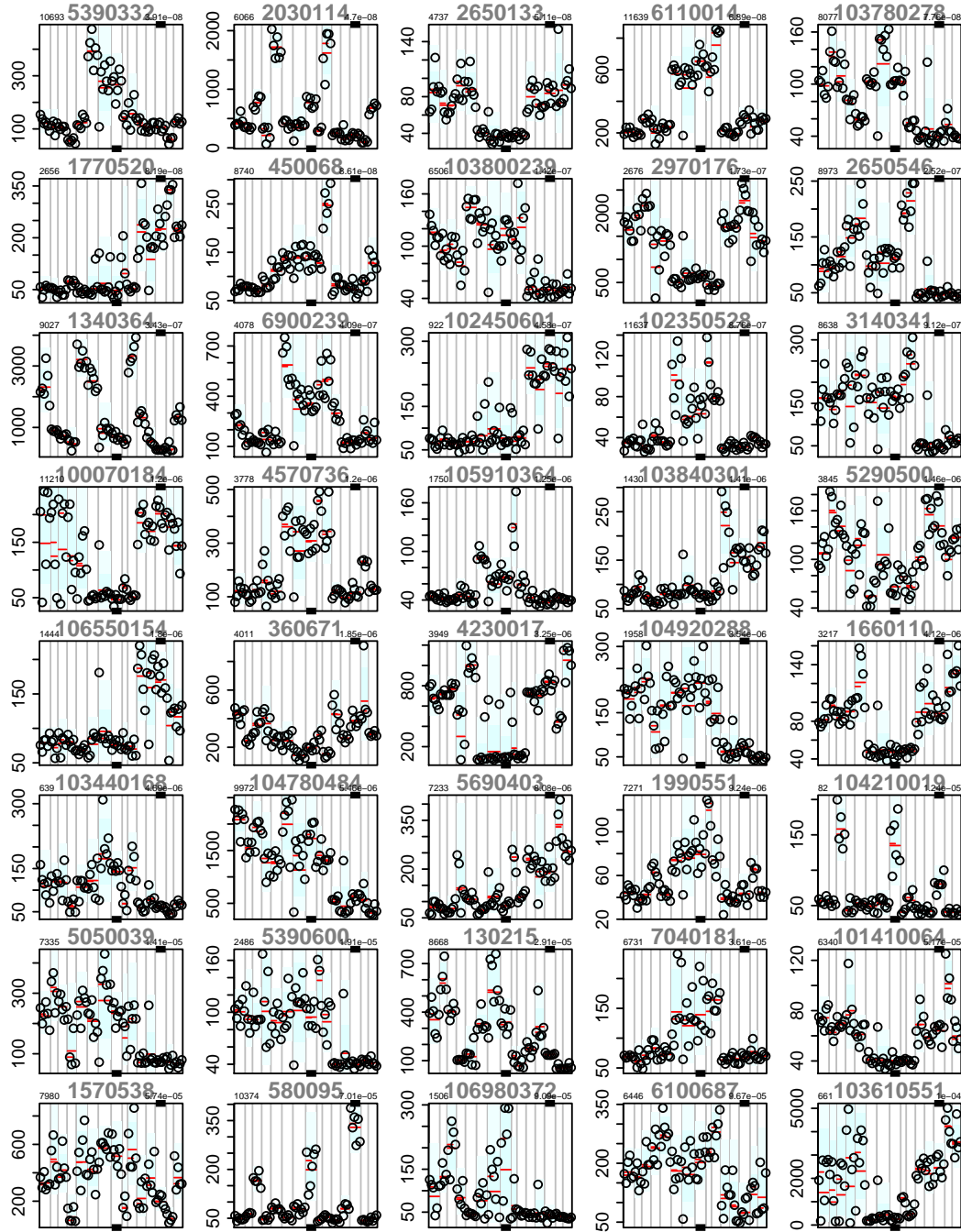


Figure 12b: Significant probes (41–80) for contrast LNC (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

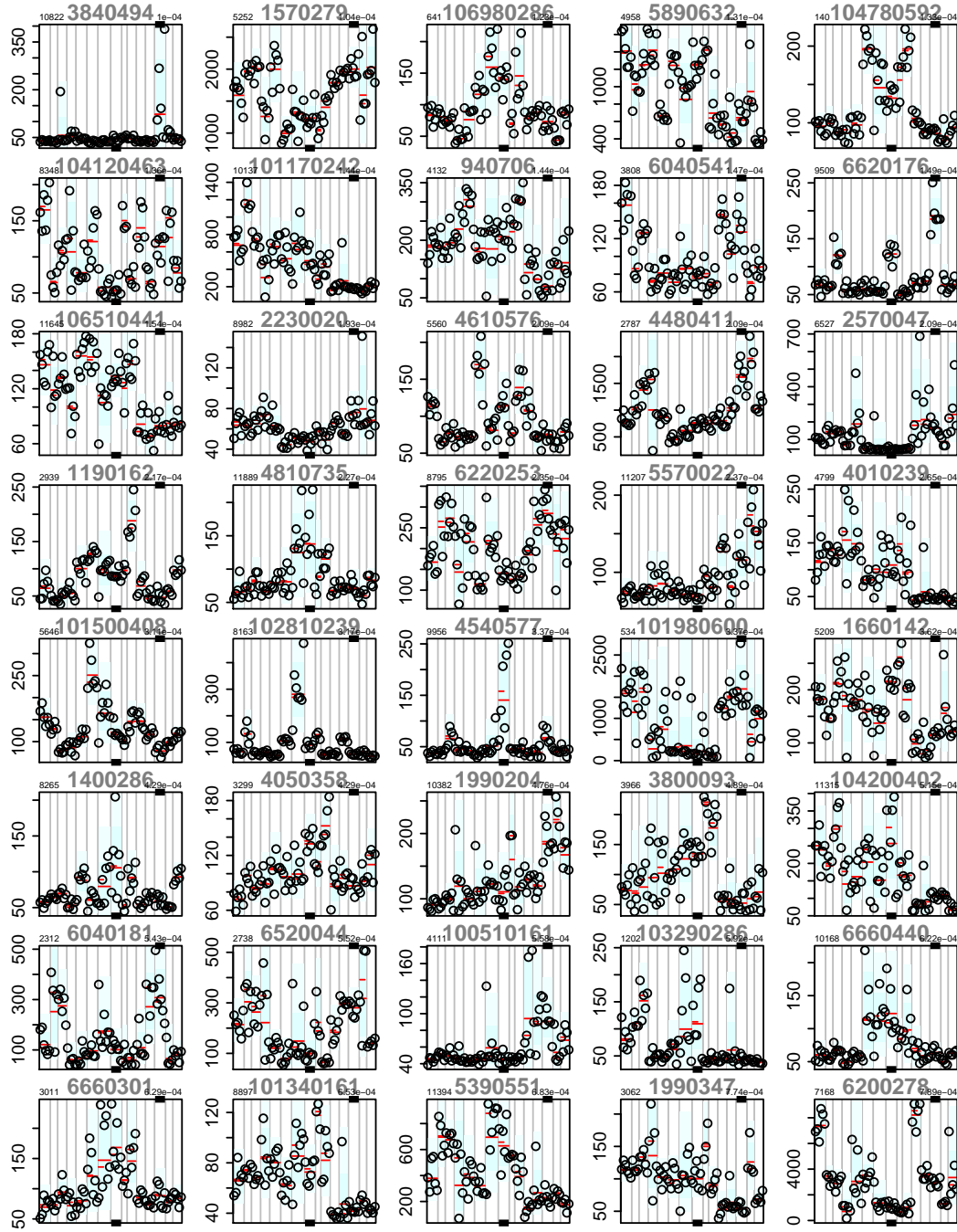


Figure 12c: Significant probes (81–120) for contrast LNC (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

3.2.9 Contrast LNd

Using the matrix representing the contrast defined by LAB_DGyr - NAB_DGyr

LNd	
NAB_DGyr	-1
LAB_DGyr	1

The statistics for the top 120 genes across the contrast (where 115 genes have adjusted p -values below 0.05) are shown in table 11, the corresponding expression plots are shown in Figs. 13a-c on pages 101 through 103.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			100050152	4.7	12.7	1.31e-19	1.59e-15	19.2
1	MTM1	NM_000252.1	2320537	-4.3	-11.4	1.89e-17	1.15e-13	17.2
6273			104480458	-5	-11.1	6.8e-17	2.76e-13	16.7
6274			100520465	-3.3	-10.6	4.05e-16	1.23e-12	15.9
6275			105910364	-3.1	-10.5	6.44e-16	1.57e-12	15.7
2	KLF6	NM_001008490.1	360110	-4.5	-9.8	1.18e-14	2.39e-11	14.4
6277			1090195	8.7	9.11	2.03e-13	3.53e-10	13.1
3	SDHAP3	NR_003263.1	6350341	10	8.61	1.66e-12	2.53e-09	12.1
4	TMEM103	NM_017713.1	4850064	7.4	8.5	2.63e-12	3.31e-09	11.8
5	MUC6	XM_290540.6	2650292	-2.7	-8.48	2.84e-12	3.31e-09	11.8
6281			101410064	2.5	8.47	2.99e-12	3.31e-09	11.8
6282			104850273	-4.6	-8.38	4.36e-12	4.43e-09	11.6
6283			2650546	-3.8	-8.21	8.66e-12	8.11e-09	11.2
6284			104480102	-2.3	-8.19	9.64e-12	8.38e-09	11.2
6285			1770017	-3.1	-7.96	2.46e-11	2e-08	10.7
6	C11ORF63	NM_199124.1	6550037	-6.3	-7.91	3.12e-11	2.37e-08	10.6
6287			2810541	-11	-7.87	3.59e-11	2.57e-08	10.5
7	ZNF680	NM_178558.2	1090280	5.7	7.7	7.37e-11	4.98e-08	10.1
6289			610086	-3.8	-7.38	2.85e-10	1.76e-07	9.44
6290			100450079	-2.6	-7.38	2.89e-10	1.76e-07	9.43
6291			102350528	-2.8	-7.34	3.36e-10	1.95e-07	9.35
8	ALPI	NM_001631.2	2570162	-3.1	-7.23	5.23e-10	2.89e-07	9.12
6293			103850064	2.2	7.07	1.02e-09	5.39e-07	8.76
9	LOC400696	NM_207646.1	1660110	2.4	6.75	3.9e-09	1.98e-06	8.04
6295			103130672	-2.6	-6.44	1.38e-08	6.28e-06	7.35
10	HLA-DMA	NM_006120.2	540563	3.1	6.44	1.38e-08	6.28e-06	7.34
6297			106980129	2.6	6.44	1.39e-08	6.28e-06	7.34
6298			105570692	-3.5	-6.18	4.01e-08	1.74e-05	6.75
6299			103190068	-2.5	-6.17	4.17e-08	1.75e-05	6.73
6300			3060168	-2.1	-6.1	5.55e-08	2.25e-05	6.57
6301			101340161	-2.4	-6.05	6.95e-08	2.65e-05	6.45
6302			104780592	-1.9	-6.05	6.96e-08	2.65e-05	6.45
6303			1740324	2.4	5.93	1.11e-07	4.08e-05	6.18
6304			100460538	-2.1	-5.9	1.25e-07	4.49e-05	6.11
6305			5390600	-3.1	-5.83	1.63e-07	5.56e-05	5.96
11	SFRS13A	NM_054016.1	6110014	-2.3	-5.83	1.65e-07	5.56e-05	5.96
12	LOC645915	XM_933265.1	2650133	2.3	5.74	2.38e-07	7.83e-05	5.75
6308			100990672	2.8	5.72	2.53e-07	8.05e-05	5.71
13	ERMN	NM_020711.1	4010253	-1.9	-5.72	2.58e-07	8.05e-05	5.7
6310			102810239	-2	-5.7	2.73e-07	8.31e-05	5.67
14	BCORL2	NM_173700.1	2570594	2.6	5.68	3.01e-07	8.93e-05	5.62
6312			104280671	2.1	5.65	3.42e-07	9.91e-05	5.54

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
15	C3ORF57	NM_145035.2	4560600	2.8	5.64	3.59e-07	0.000102	5.51
6314			104920288	-3.6	-5.57	4.58e-07	0.000127	5.38
6315			103130746	4.1	5.5	6.16e-07	0.000167	5.21
16	EIF4B	NM_001417.2	5390494	4	5.45	7.35e-07	0.000194	5.11
6317			102230433	3	5.37	1.01e-06	0.00026	4.92
17	SAA4	NM_006512.1	3710022	-2.2	-5.35	1.1e-06	0.000279	4.87
6319			103800239	-2.2	-5.29	1.37e-06	0.00034	4.75
6320			100510059	1.9	5.26	1.53e-06	0.000366	4.68
6321			1090088	-2.1	-5.26	1.53e-06	0.000366	4.68
18	PPOX	NM_000309.2	3120609	-2	-5.24	1.66e-06	0.000389	4.63
19	LOC100130133	XR_037307.1	5390332	-2.3	-5.2	1.93e-06	0.000444	4.55
6324			3800093	-3.6	-5.13	2.62e-06	0.00059	4.37
20	CR2	NM_001877.3	4810292	1.8	5.06	3.32e-06	0.000729	4.23
21	SCRIB	NM_015356.3	2970176	3.2	5.06	3.36e-06	0.000729	4.23
6327			4010239	-2.9	-5	4.16e-06	0.000881	4.1
6328			4760008	-1.6	-5	4.2e-06	0.000881	4.1
22	LOC100131335	XM_001718069.1	6980368	-2.3	-4.95	5.11e-06	0.00105	3.98
6330			2030114	-3	-4.93	5.53e-06	0.00112	3.93
6331			6900239	-2.7	-4.88	6.78e-06	0.00135	3.82
6332			100380619	-4.2	-4.83	8.1e-06	0.00159	3.71
23	LOC728475	XM_001127527.2	4480411	2.5	4.79	9.3e-06	0.0018	3.63
24	CCDC4	XM_941085.1	6650397	-1.9	-4.68	1.38e-05	0.00262	3.4
25	IL26	NM_018402.1	6550008	-5.7	-4.65	1.54e-05	0.00288	3.33
26	SDC3	XM_940667.1	1990551	-1.8	-4.63	1.7e-05	0.00309	3.27
27	LOC283157	XM_939588.1	6760333	-2	-4.63	1.71e-05	0.00309	3.27
6338			101340050	-1.9	-4.62	1.72e-05	0.00309	3.27
28	ZXDC	NM_001040653.1	5080121	2	4.61	1.82e-05	0.0032	3.24
6340			104200717	1.9	4.6	1.91e-05	0.00333	3.21
6341			100110411	-1.6	-4.52	2.51e-05	0.0043	3.04
6342			104200167	2.6	4.51	2.66e-05	0.00449	3.01
29	CXORF30	XR_000668.1	360671	1.8	4.48	2.89e-05	0.00482	2.96
30	FAM53A	NM_001013622.1	4060112	-2.5	-4.48	2.95e-05	0.00486	2.95
31	LOC440386	XR_040492.1	6760093	-1.8	-4.46	3.11e-05	0.00505	2.92
6346			103840301	1.8	4.43	3.49e-05	0.00558	2.85
32	LOC651293	XM_946211.1	2480411	-2.6	-4.4	3.87e-05	0.00611	2.79
33	UBE2K	NM_001111112.1	6220021	-3.8	-4.39	4.04e-05	0.0063	2.76
34	COL23A1	NM_173465.2	2350441	1.8	4.38	4.12e-05	0.00635	2.75
6350			105570601	2	4.3	5.53e-05	0.00842	2.58
6351			4480594	-2.5	-4.27	6.18e-05	0.00929	2.51
6352			2940500	-1.5	-4.26	6.44e-05	0.00945	2.49
35	LOC390251	XR_040181.1	3140341	-2.8	-4.26	6.44e-05	0.00945	2.49
6354			104780484	-2.6	-4.25	6.56e-05	0.0095	2.48
6355			2760204	2.3	4.24	6.98e-05	0.00999	2.44
6356			3360736	1.7	4.2	7.84e-05	0.0111	2.37
36	LOC645039	XM_928095.1	1780138	2.1	4.19	8.13e-05	0.0114	2.35
6358			2230497	1.9	4.16	8.94e-05	0.0124	2.29
6359			103850204	2	4.15	9.25e-05	0.0125	2.27
37	LOC732377	XM_001133069.1	1500097	2.3	4.15	9.31e-05	0.0125	2.27
38	ATXN1	NM_000332.2	5080154	1.6	4.15	9.37e-05	0.0125	2.26
39	LOC100129323	XM_001720515.1	4050273	4.4	4.12	0.000105	0.014	2.19
6363			106550292	-2.9	-4.09	0.000116	0.0152	2.14
6364			102940348	-1.9	-4.08	0.000119	0.0154	2.12
40	NKX2-1	NM_003317.3	4060497	1.8	4.07	0.000123	0.0157	2.1
6366			106350722	-2	-4.07	0.000126	0.016	2.09
6367			2510114	2.1	4.01	0.000151	0.0188	1.98
41	LOC100134170	XM_001721704.1	5570022	1.7	4.01	0.000151	0.0188	1.98
42	LOC652993	XR_018000.1	5360497	-1.7	-3.99	0.000162	0.0199	1.94

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
43	CYC1	NM_001916.2	1770520	3	3.97	0.000173	0.0211	1.9
44	STXBP6	NM_014178.6	2370092	-1.6	-3.96	0.00018	0.0216	1.88
6372			104560161	5.4	3.91	0.000216	0.0256	1.76
45	LOC222967	NM_173565.1	3060113	1.9	3.91	0.000216	0.0256	1.76
46	C20ORF51	NM_022099.3	2900369	1.8	3.87	0.000247	0.029	1.68
6375			60204	-3.8	-3.83	0.000284	0.0329	1.6
6376			104780332	1.5	3.79	0.000316	0.0363	1.54
47	HS.131670	Hs.131670	270139	2.9	3.78	0.000332	0.0377	1.51
48	PFKFB2	NM_001018053.1	7040181	-1.9	-3.77	0.000345	0.0389	1.49
6379			5890184	-4.8	-3.76	0.000351	0.0392	1.48
49	HS.278303	Hs.278303	3780687	-1.7	-3.76	0.000356	0.0394	1.47
6381			6290739	-2.1	-3.75	0.000371	0.0407	1.44
50	LOC646588	XM_943454.1	2940468	3.5	3.74	0.000382	0.0416	1.42
51	HS.439870	Hs.439870	6370497	2.1	3.71	0.000423	0.0456	1.36
6384			106380082	-1.8	-3.69	0.000439	0.0469	1.34
6385			102450601	2.3	3.69	0.000449	0.0476	1.33
6386			670520	1.7	3.66	0.000497	0.0521	1.27
6387			106520398	-2.2	-3.65	0.000516	0.0537	1.24
52	C6ORF165	NM_178823.2	2850487	-1.5	-3.63	0.000536	0.0552	1.22
53	GSTCD	NM_024751.1	5360487	-1.7	-3.61	0.000577	0.059	1.18
6390			106020113	-1.5	-3.61	0.000586	0.0594	1.17

Table 11: Top 120 genes (all arrays)

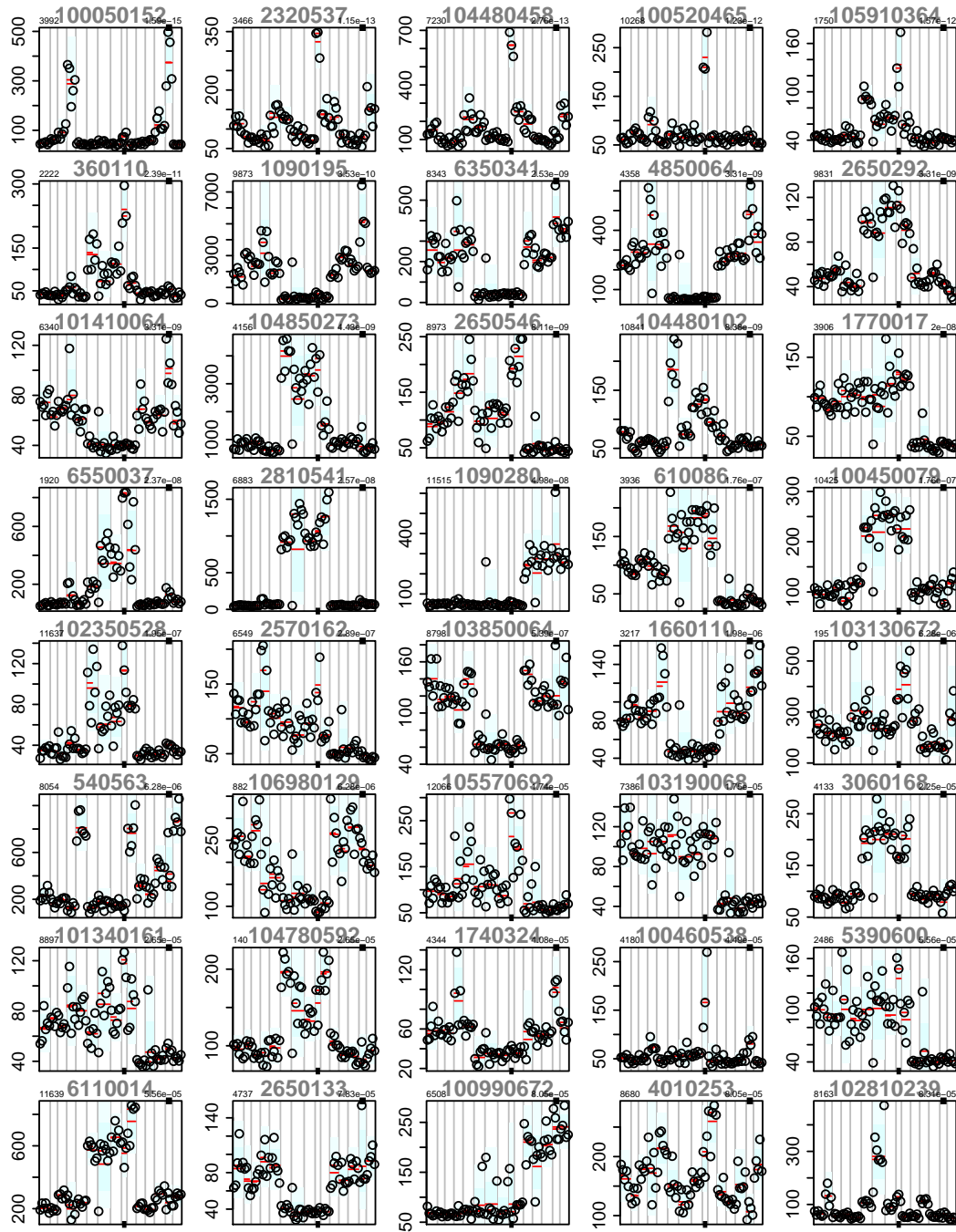


Figure 13a: Top 40 genes for contrast LNd (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

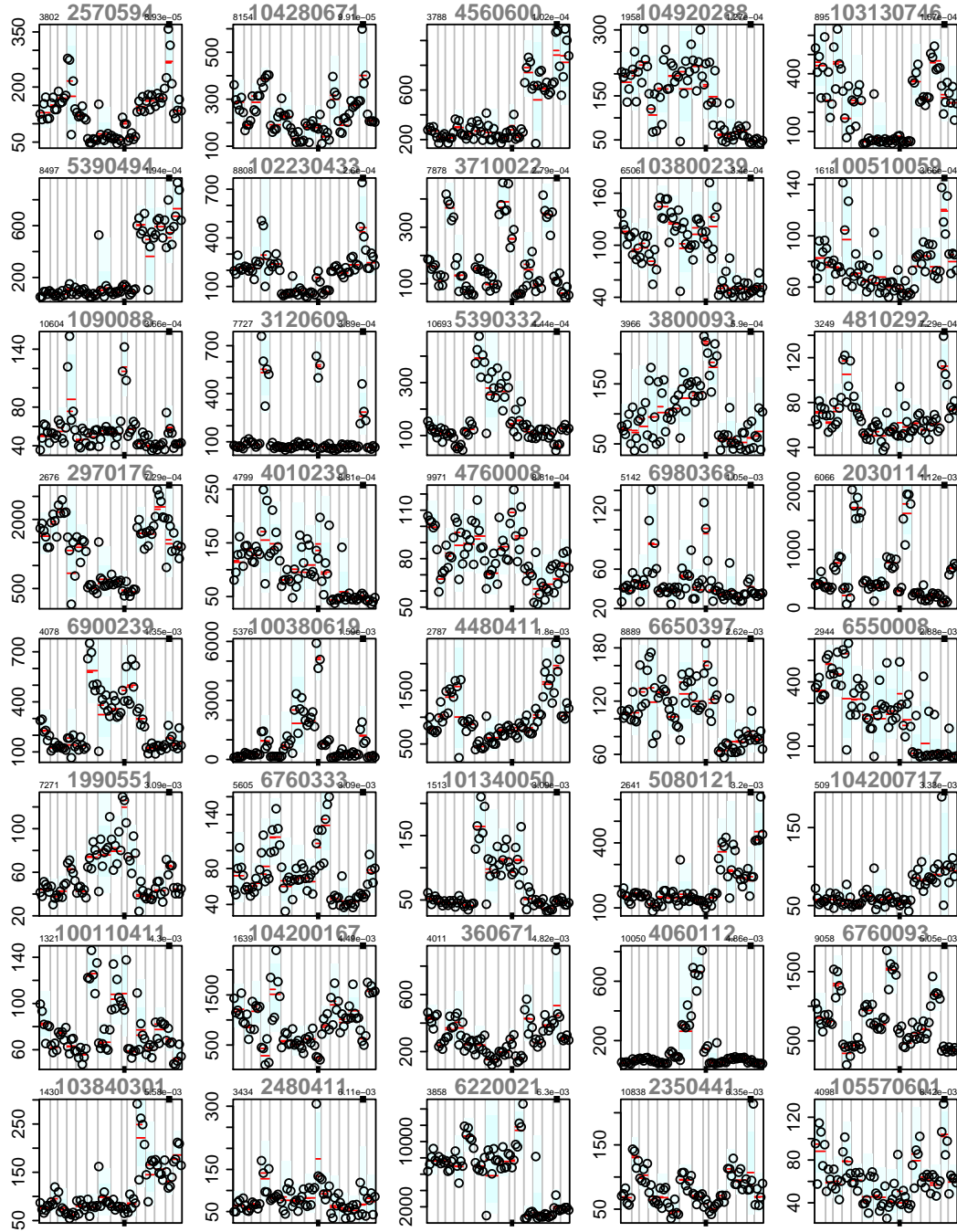


Figure 13b: Significant probes (41–80) for contrast LNd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

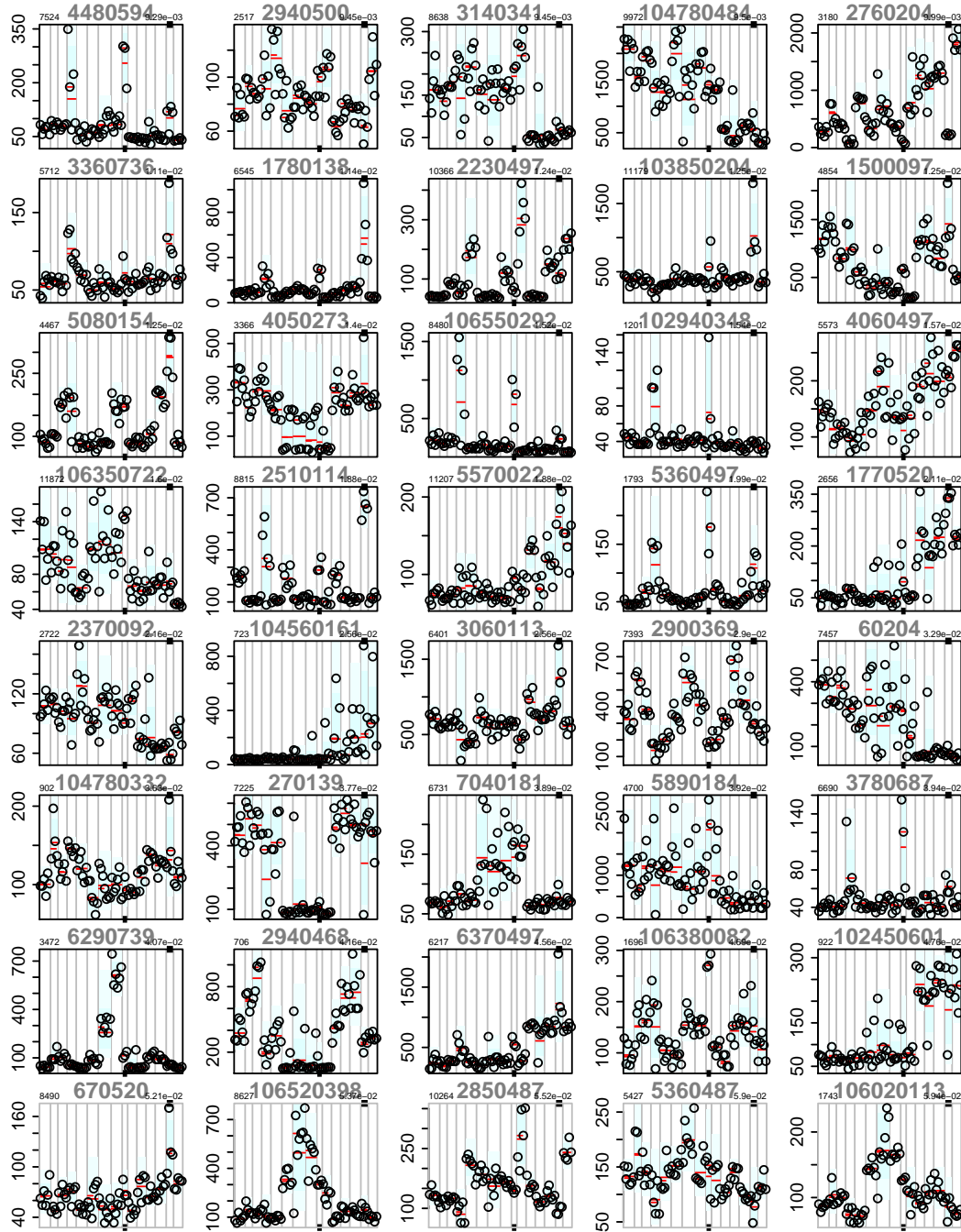


Figure 13c: Significant probes (81–120) for contrast LNd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.10 Contrast LNp

Using the matrix representing the contrast defined by LAB_PVNu - NAB_PVNu

LNp	
NAB_PVNu	-1
LAB_PVNu	1

The statistics for the top 120 genes across the contrast (out of 226 genes having adjusted p -values below 0.05) are shown in table 12, the corresponding expression plots are shown in Figs. 14a-c on pages 107 through 109.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	IGFL1	NM_198541.1	6020605	3.8	12.8	6.98e-20	8.5e-16	28.8
6272			2650546	-4.8	-11.7	4.94e-18	3.01e-14	26
6273			2810541	-18	-11.6	8.01e-18	3.25e-14	25.7
2	C9ORF68	NM_001039395.1	5890332	-4	-10.6	4.05e-16	1.23e-12	23
3	MUC6	XM_290540.6	2650292	-2.7	-10.4	9.19e-16	2.24e-12	22.5
4	SDHAP3	NR_003263.1	6350341	9.2	9.96	6.03e-15	1.22e-11	21.2
5	EIF4B	NM_001417.2	5390494	8	9.84	9.83e-15	1.71e-11	20.8
6278			1770017	-3.2	-9.78	1.25e-14	1.9e-11	20.7
6279			610086	-4.2	-9.5	3.98e-14	5.02e-11	19.8
6	LOC400696	NM_207646.1	1660110	2.8	9.49	4.13e-14	5.02e-11	19.8
7	ZNF680	NM_178558.2	1090280	5.6	9.2	1.42e-13	1.57e-10	18.9
8	TMEM103	NM_017713.1	4850064	5.9	9.09	2.24e-13	2.27e-10	18.6
6283			1090195	5.9	9.01	3.11e-13	2.91e-10	18.4
6284			105570368	-2.5	-8.89	5.1e-13	4.43e-10	18
9	ZXDC	NM_001040653.1	5080121	3.1	8.87	5.54e-13	4.49e-10	17.9
10	C11ORF63	NM_199124.1	6550037	-5.5	-8.85	6.05e-13	4.6e-10	17.9
11	SFRS13A	NM_054016.1	6110014	-2.8	-8.63	1.47e-12	9.98e-10	17.2
6288			103850064	2.2	8.63	1.48e-12	9.98e-10	17.2
6289			104780592	-2.1	-8.43	3.52e-12	2.26e-09	16.6
6290			102360148	2.4	8.35	4.87e-12	2.96e-09	16.3
12	C3ORF57	NM_145035.2	4560600	3.5	8.21	8.75e-12	5.07e-09	15.9
13	LOC100133443	XM_001716638.1	2640717	2.8	8.2	9.17e-12	5.08e-09	15.9
6293			103130746	5.4	7.93	2.88e-11	1.52e-08	15
14	LOC645915	XM_933265.1	2650133	2.5	7.73	6.62e-11	3.31e-08	14.4
6295			102230433	3.6	7.72	6.8e-11	3.31e-08	14.4
15	UBE2K	NM_001111112.1	6220021	-6.5	-7.47	1.94e-10	9.09e-08	13.6
6297			102350528	-2.4	-7.41	2.55e-10	1.15e-07	13.4
6298			101340050	-2.4	-7.38	2.88e-10	1.25e-07	13.3
6299			104780484	-3.8	-7.33	3.56e-10	1.49e-07	13.1
16	LOC732377	XM_001133069.1	1500097	3.4	7.28	4.26e-10	1.73e-07	13
17	HS.131670	Hs.131670	270139	5.5	7.26	4.65e-10	1.83e-07	12.9
18	ST8SIA4	NM_005668.3	4230017	10	7.16	7.12e-10	2.7e-07	12.6
6303			100380619	-5.9	-7.15	7.33e-10	2.7e-07	12.6
19	TRIM49	NM_020358.2	450068	-1.9	-7.14	7.72e-10	2.76e-07	12.5
6305			100990672	2.9	7.12	8.28e-10	2.8e-07	12.5
6306			6900239	-3.3	-7.12	8.29e-10	2.8e-07	12.5
6307			103840301	2.2	7.01	1.33e-09	4.37e-07	12.1
6308			103190068	-2.4	-6.96	1.66e-09	5.33e-07	11.9
20	LOC390251	XR_040181.1	3140341	-4	-6.78	3.37e-09	1.05e-06	11.4
6310			103800239	-2.3	-6.72	4.48e-09	1.36e-06	11.2
6311			106130600	2.2	6.57	8.32e-09	2.47e-06	10.7
21	HS.439870	Hs.439870	6370497	3	6.49	1.16e-08	3.36e-06	10.4

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
22	LOC100129407	XM.001715870.1	2570047	5.1	6.42	1.49e-08	4.22e-06	10.2
23	LCN10	NM.001001712.1	4610576	-1.8	-6.4	1.68e-08	4.64e-06	10.2
6315			3060168	-1.9	-6.39	1.74e-08	4.7e-06	10.1
24	P2RY14	NM.014879.3	1340364	-2.5	-6.29	2.53e-08	6.69e-06	9.84
25	SCRIB	NM.015356.3	2970176	3.3	6.28	2.67e-08	6.93e-06	9.79
26	LOC646588	XM.943454.1	2940468	5.8	6.25	3.1e-08	7.85e-06	9.68
27	CYC1	NM.001916.2	1770520	4.2	6.23	3.33e-08	8.28e-06	9.62
28	GTF2I	XM.939506.1	4570736	-2.7	-6.17	4.22e-08	1.01e-05	9.44
29	PFKFB2	NM.001018053.1	7040181	-2.3	-6.17	4.25e-08	1.01e-05	9.43
6322			104480102	-1.7	-6.1	5.62e-08	1.32e-05	9.22
6323			102450601	3.1	6.01	8.15e-08	1.87e-05	8.93
30	G3BP2	NM.012297.3	7100156	-2.3	-5.97	9.41e-08	2.12e-05	8.81
6325			100450079	-1.9	-5.96	9.87e-08	2.18e-05	8.78
6326			105570692	-2.7	-5.93	1.11e-07	2.42e-05	8.68
6327			104920288	-3.1	-5.92	1.15e-07	2.45e-05	8.66
6328			101580465	1.6	5.92	1.17e-07	2.45e-05	8.65
31	CXORF30	XR.000668.1	360671	1.9	5.9	1.25e-07	2.58e-05	8.59
6330			6200278	3.6	5.82	1.75e-07	3.56e-05	8.33
6331			6840088	1.9	5.78	2.02e-07	4.04e-05	8.22
32	BCORL2	NM.173700.1	2570594	2.2	5.67	3.07e-07	6.03e-05	7.89
33	CKAP2L	NM.152515.2	6380324	2	5.66	3.22e-07	6.2e-05	7.85
6334			101340161	-1.9	-5.66	3.27e-07	6.2e-05	7.84
34	LOC647391	XM.936466.1	2710603	1.7	5.66	3.31e-07	6.2e-05	7.83
35	LOC645550	XM.928570.1	5690403	2.2	5.52	5.62e-07	0.000104	7.41
6337			103440168	-2.2	-5.46	7.09e-07	0.000129	7.23
6338			5050039	-3	-5.45	7.43e-07	0.000133	7.19
36	LOC157627	NR.024281.1	4850546	3.2	5.44	7.88e-07	0.000139	7.15
37	HS.278817	Hs.278817	6940632	1.5	5.37	1.01e-06	0.000176	6.95
6341			106510441	-1.8	-5.35	1.11e-06	0.000191	6.88
38	CAPNS1	NM.001003962.1	5290500	1.9	5.28	1.47e-06	0.000248	6.66
6343			106520398	-2.5	-5.26	1.57e-06	0.000259	6.61
39	LOC100134170	XM.001721704.1	5570022	1.7	5.26	1.57e-06	0.000259	6.6
6345			104850273	-2.2	-5.23	1.78e-06	0.000289	6.51
6346			2760204	2.3	5.19	2.01e-06	0.000322	6.41
40	NKX2-1	NM.003317.3	4060497	1.9	5.19	2.08e-06	0.000328	6.38
41	LILRA3	NM.006865.2	6110037	2.5	5.17	2.2e-06	0.000343	6.34
6349			106550070	1.7	5.16	2.32e-06	0.000357	6.3
42	SGCB	NM.000232.3	1190162	-1.9	-5.12	2.67e-06	0.000406	6.19
6351			104200717	1.8	5.1	2.84e-06	0.000426	6.14
6352			104610411	1.8	5.07	3.24e-06	0.000481	6.03
43	LOC100129323	XM.001720515.1	4050273	4.5	5.05	3.45e-06	0.000506	5.98
6354			103140403	1.9	4.97	4.7e-06	0.000681	5.74
6355			101780341	-2.1	-4.94	5.25e-06	0.000746	5.65
44	SDC3	XM.940667.1	1990551	-1.7	-4.94	5.27e-06	0.000746	5.65
6357			670433	-2.1	-4.86	7.23e-06	0.00101	5.4
6358			4810593	1.6	4.84	7.87e-06	0.00109	5.33
6359			101770184	-2	-4.82	8.38e-06	0.00115	5.28
6360			6900435	1.6	4.81	8.78e-06	0.00119	5.25
6361			104150273	-1.9	-4.79	9.29e-06	0.00124	5.2
6362			2030114	-2.4	-4.79	9.49e-06	0.00125	5.18
45	LOC732434	XM.001724202.1	2340735	-1.5	-4.76	1.04e-05	0.00136	5.11
6364			102510671	-2.4	-4.75	1.06e-05	0.00138	5.09
6365			5390600	-2.1	-4.74	1.13e-05	0.00143	5.04
6366			105890195	-1.9	-4.74	1.13e-05	0.00143	5.04
46	TAC4	NM.170685.1	2510259	2.7	4.74	1.14e-05	0.00143	5.04
47	PTPN9	NM.002833.2	3930279	3.2	4.73	1.16e-05	0.00144	5.03
6369			106980129	1.8	4.73	1.19e-05	0.00146	5.01

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
48	KRTCAP2	NM_173852.3	6110605	-2.4	-4.72	1.22e-05	0.00148	4.99
6371			101410064	1.5	4.7	1.31e-05	0.00158	4.93
6372			6980193	1.6	4.68	1.42e-05	0.00169	4.87
49	HSP90AA1	NM_005348.2	7050332	1.7	4.67	1.45e-05	0.00172	4.85
6374			106660487	-1.6	-4.66	1.51e-05	0.00176	4.82
6375			4010239	-2.3	-4.66	1.53e-05	0.00178	4.8
6376			101980600	7.6	4.65	1.58e-05	0.00182	4.78
50	KLF6	NM_001008490.1	360110	-1.8	-4.63	1.7e-05	0.00192	4.72
6378			102450048	1.7	4.63	1.71e-05	0.00192	4.72
51	RPS4Y1	NM_001008.3	6100687	-2.5	-4.56	2.17e-05	0.00241	4.53
52	PHF17	NM_199320.1	6220411	1.7	4.56	2.18e-05	0.00241	4.52
53	TPX2	NM_012112.4	6290358	2	4.55	2.28e-05	0.00248	4.49
6382			103840025	1.6	4.55	2.28e-05	0.00248	4.49
54	LOC642672	XM_943423.1	1580609	1.7	4.54	2.38e-05	0.00256	4.46
55	LOC644714	XM_934516.1	5390097	1.8	4.52	2.48e-05	0.00263	4.42
56	LAMB3	NM_001017402.1	4590739	1.9	4.52	2.49e-05	0.00263	4.42
57	HS.520591	Hs.520591	730008	1.6	4.48	2.97e-05	0.00311	4.28
6387			104120092	1.5	4.47	3.07e-05	0.00319	4.25
6388			3800093	-2.5	-4.44	3.32e-05	0.00342	4.19
6389			670520	1.7	4.44	3.35e-05	0.00342	4.19
58	ALPI	NM_001631.2	2570162	-1.8	-4.43	3.44e-05	0.00349	4.16

Table 12: Top 120 genes (all arrays)

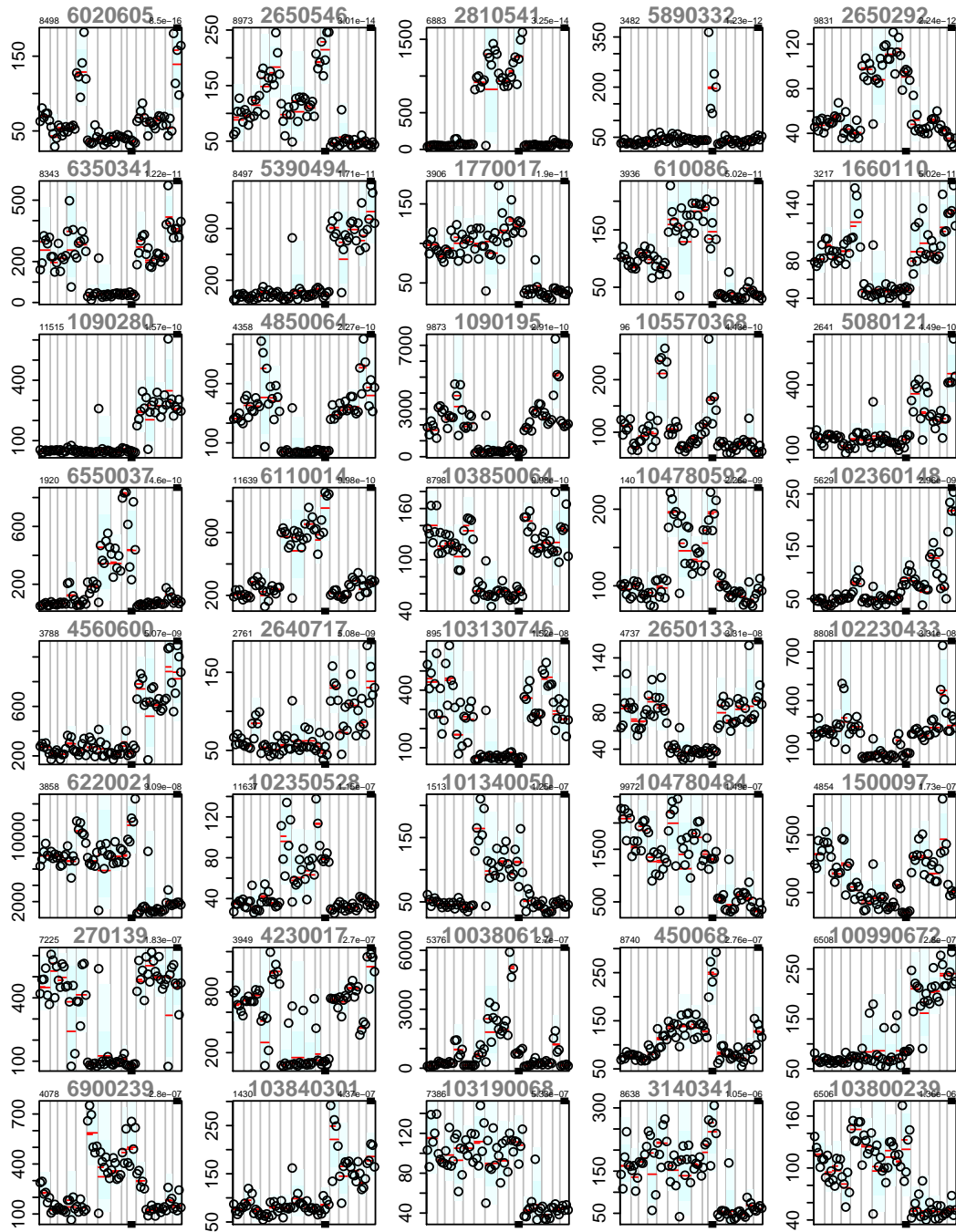


Figure 14a: Top 40 genes for contrast LNP (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

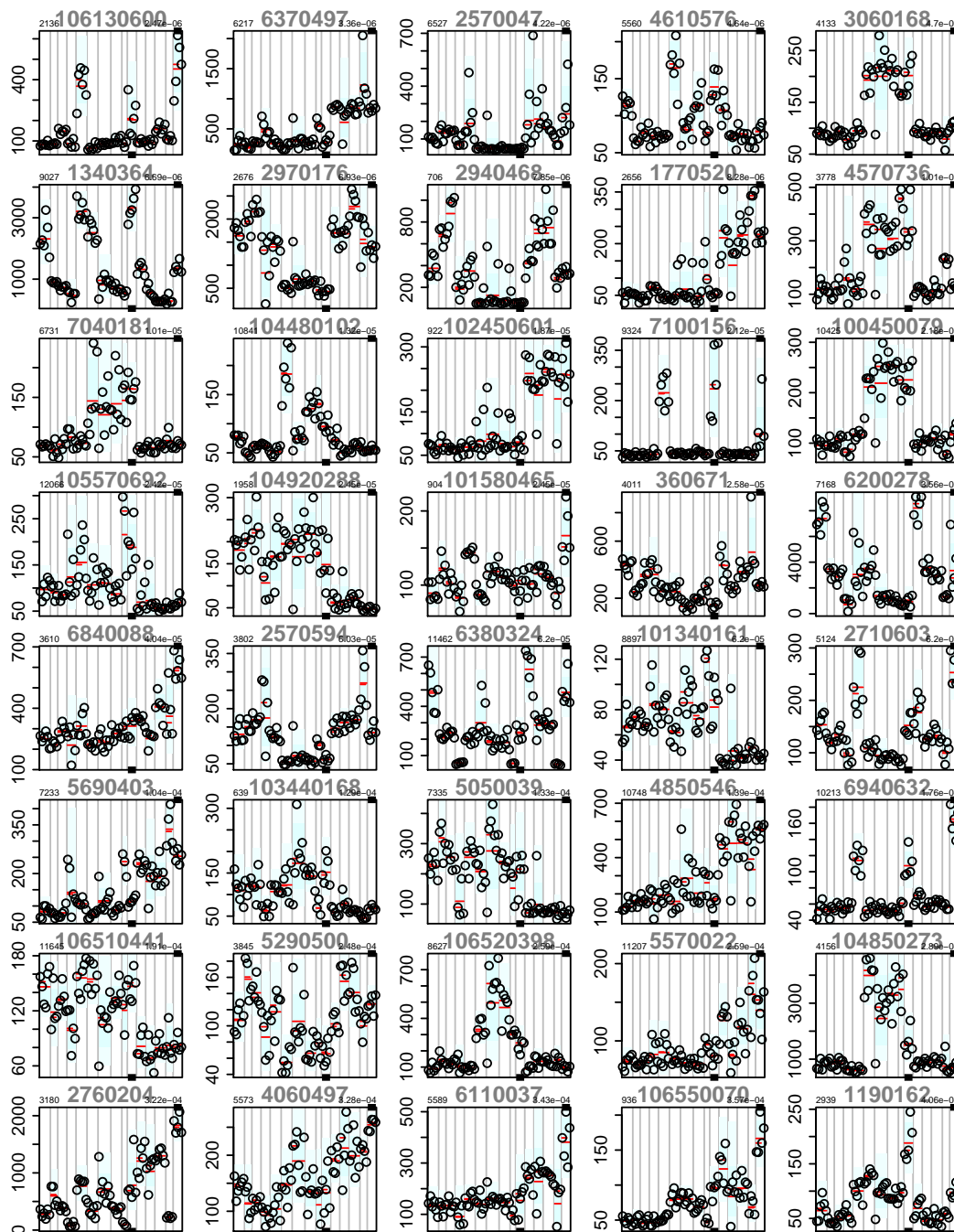


Figure 14b: Significant probes (41–80) for contrast LNP (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

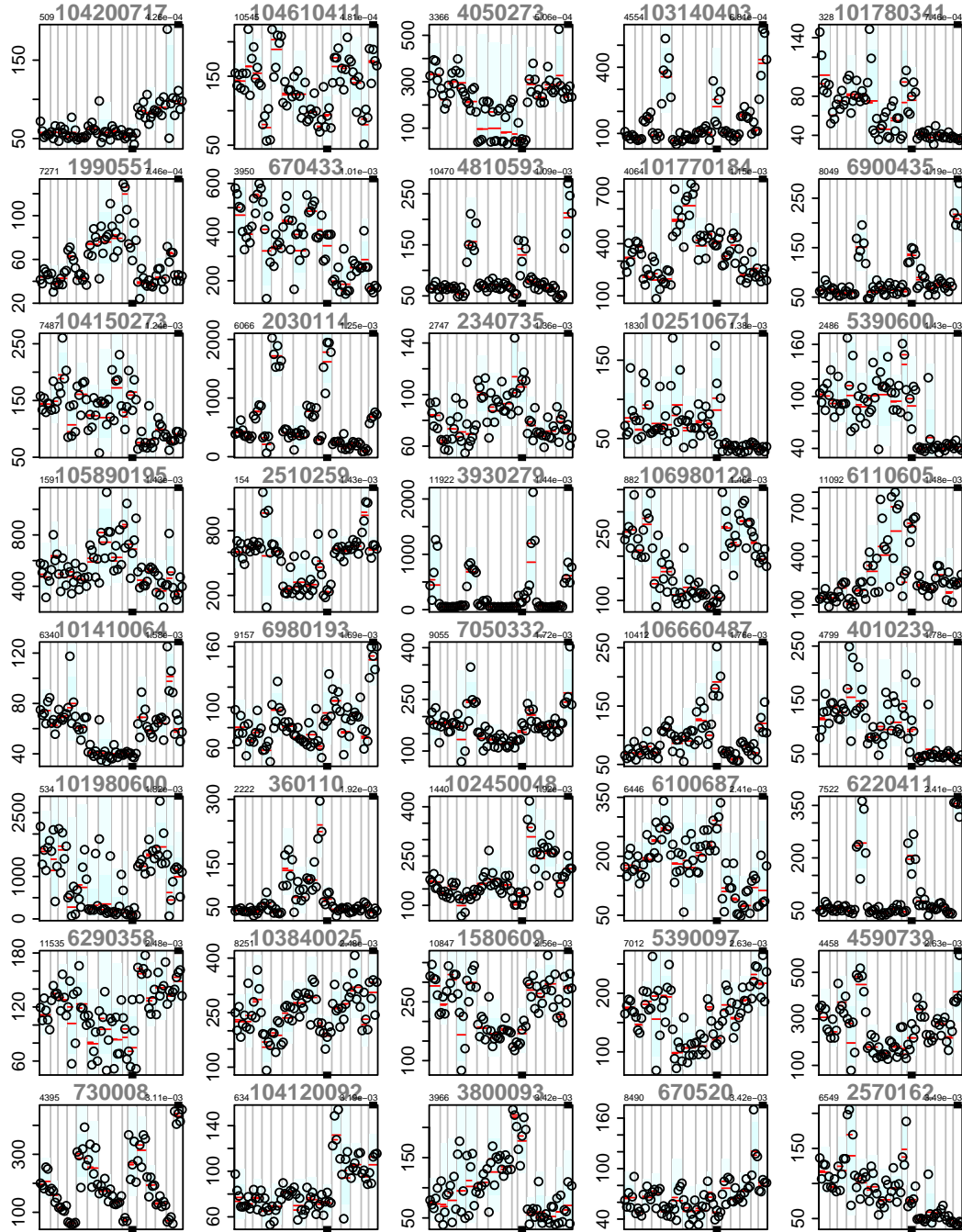


Figure 14c: Significant probes (81–120) for contrast LNP (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.11 Contrast HLa

Using the matrix representing the contrast defined by HAB_Amyg - LAB_Amyg

HLa	
HAB_Amyg	1
LAB_Amyg	-1

The statistics for the top 120 genes across the contrast (out of 291 genes having adjusted p -values below 0.05) are shown in table 13, the corresponding expression plots are shown in Figs. 15a-c on pages 113 through 115.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	RAB25	NM_020387.1	50195	-7.9	-14.7	8.22e-23	1e-18	35.6
2	OR8B2	NM_001005468.1	6100440	7.1	14	1.04e-21	6.31e-18	33.9
6273			107050626	-4.9	-12.3	5.66e-19	1.91e-15	29.5
6274			106020102	-3.2	-12.2	6.71e-19	1.91e-15	29.3
3	SDHAP3	NR_003263.2	1400524	-16	-12.2	7.83e-19	1.91e-15	29.2
4	NARG1	NM_057175.3	3140524	-8.1	-11.6	7.52e-18	1.52e-14	27.6
6277			106760170	5	11.2	3.7e-17	6.42e-14	26.4
6278			102480441	3.9	10.8	1.82e-16	2.77e-13	25.2
6279			870685	-2.9	-10.5	6.41e-16	8.66e-13	24.3
5	EIF4B	NM_001417.2	5390494	-8.3	-10.5	7.6e-16	9.25e-13	24.1
6281			103840575	3.1	10.1	3.49e-15	3.86e-12	23
6282			103840301	-2.9	-9.95	6.19e-15	6.28e-12	22.5
6283			103130736	4	9.92	7.05e-15	6.6e-12	22.4
6	RTN4RL2	NM_178570.1	60411	-3.9	-9.88	8.36e-15	7.17e-12	22.3
6285			380692	3.1	9.87	8.84e-15	7.17e-12	22.3
7	LOC100132934	XM_001723077.1	2120390	4.7	9.65	2.18e-14	1.66e-11	21.6
6287			105390397	2.6	9.58	2.94e-14	2.1e-11	21.3
8	SNAR-I	NR_024343.1	2370164	-2.5	-9.43	5.34e-14	3.61e-11	20.9
6289			2760204	-4.3	-9.33	8.19e-14	5.25e-11	20.6
9	ZNF680	NM_178558.2	1090280	-5.1	-9.09	2.24e-13	1.36e-10	19.8
6291			106550070	-2.5	-8.97	3.62e-13	2.1e-10	19.4
10	UBE2K	NM_001111112.1	6220021	8.5	8.92	4.49e-13	2.48e-10	19.2
6293			106400035	4.5	8.76	8.86e-13	4.69e-10	18.7
11	HS.551438	Hs.551438	50438	-5.1	-8.36	4.74e-12	2.4e-09	17.4
6295			103190068	2.7	8.34	5.11e-12	2.49e-09	17.3
12	DHX32	NM_018180.2	1980164	5.3	8.29	6.16e-12	2.88e-09	17.1
6297			1770017	2.6	8.28	6.4e-12	2.88e-09	17.1
6298			2190438	2.6	8.22	8.32e-12	3.54e-09	16.9
6299			6040707	-3.3	-8.22	8.44e-12	3.54e-09	16.9
13	LOC648704	XM_937786.1	4850047	-2.3	-8.07	1.58e-11	6.39e-09	16.4
14	HS.439870	Hs.439870	6370497	-3.7	-8.02	1.91e-11	7.48e-09	16.2
15	GSTZ1	NM_001513.2	7040044	2.6	7.99	2.2e-11	8.38e-09	16.1
16	LOC730990	XM_001722060.1	2060170	-4	-7.96	2.48e-11	9.16e-09	16
6304			104780484	4	7.87	3.68e-11	1.28e-08	15.7
6305			106450088	-3.8	-7.87	3.68e-11	1.28e-08	15.7
17	HS.538100	Hs.538100	1500575	-2.2	-7.83	4.32e-11	1.44e-08	15.6
6307			100990672	-3	-7.83	4.36e-11	1.44e-08	15.6
18	ST7	NM_018412.3	4570575	-2.4	-7.5	1.7e-10	5.44e-08	14.5
19	LOC645550	XM_928570.1	5690403	-2.8	-7.46	2.03e-10	6.33e-08	14.3
6310			430670	4.7	7.44	2.25e-10	6.84e-08	14.2
20	OGFOD1	NM_001031707.1	2510731	-3.7	-7.38	2.82e-10	8.38e-08	14.1
6312			102450601	-3.7	-7.32	3.58e-10	1.04e-07	13.9

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			101260021	-2.3	-7.28	4.27e-10	1.21e-07	13.7
6314			106130025	2.1	7.27	4.55e-10	1.26e-07	13.7
6315			102480324	2.8	7.26	4.65e-10	1.26e-07	13.7
6316			610086	2.8	7.13	7.94e-10	2.1e-07	13.2
21	ZXDC	NM_001040653.1	5080121	-2.4	-7.11	8.63e-10	2.23e-07	13.2
6318			103990364	3.1	7.06	1.06e-09	2.7e-07	13
22	ALPI	NM_001631.2	2570162	2.4	7.04	1.18e-09	2.93e-07	12.9
23	C3ORF57	NM_145035.2	4560600	-2.8	-6.95	1.68e-09	4.05e-07	12.6
24	SPDYE1	NM_001031618.1	770025	2.3	6.95	1.7e-09	4.05e-07	12.6
25	LOC653853	XM_936030.1	2470440	1.9	6.93	1.88e-09	4.39e-07	12.5
6323			60204	6.8	6.88	2.25e-09	5.17e-07	12.4
6324			101170242	3.9	6.86	2.47e-09	5.57e-07	12.3
6325			105670059	-3	-6.79	3.35e-09	7.41e-07	12
26	CYC1	NM_001916.2	1770520	-4.4	-6.69	5.08e-09	1.1e-06	11.7
6327			5340195	-2.2	-6.67	5.33e-09	1.14e-06	11.7
6328			106110139	2.8	6.59	7.48e-09	1.57e-06	11.4
6329			105390722	-2	-6.54	9.36e-09	1.92e-06	11.2
27	ACOT9	NM_001037171.1	5220497	-3.5	-6.53	9.62e-09	1.92e-06	11.2
6331			5890632	2.5	6.53	9.63e-09	1.92e-06	11.2
6332			104120092	-1.7	-6.53	9.77e-09	1.92e-06	11.2
6333			103800239	2.2	6.52	9.97e-09	1.93e-06	11.1
28	LOC100131209	XM_001725125.1	6380253	1.9	6.49	1.12e-08	2.11e-06	11.1
6335			103780278	2.5	6.49	1.13e-08	2.11e-06	11
29	TNFRSF18	NM_148902.1	520066	2.2	6.48	1.18e-08	2.17e-06	11
6337			101780341	2.5	6.48	1.2e-08	2.17e-06	11
6338			103130204	-6.9	-6.45	1.36e-08	2.44e-06	10.9
6339			100540373	-2.5	-6.41	1.6e-08	2.83e-06	10.8
6340			100130082	1.7	6.37	1.89e-08	3.29e-06	10.6
6341			102030600	1.8	6.34	2.11e-08	3.58e-06	10.5
30	OR10S1	NM_001004474.1	6110292	2.6	6.34	2.11e-08	3.58e-06	10.5
6343			6900673	2.7	6.33	2.19e-08	3.62e-06	10.5
6344			6900167	-3	-6.33	2.2e-08	3.62e-06	10.5
31	GLMN	NM_053274.1	2850609	1.9	6.32	2.25e-08	3.65e-06	10.5
6346			3390324	-1.7	-6.29	2.55e-08	4.08e-06	10.4
6347			106770014	-1.9	-6.25	3.05e-08	4.81e-06	10.2
6348			104200402	3.2	6.23	3.28e-08	5.11e-06	10.2
6349			102850064	-9.5	-6.21	3.57e-08	5.5e-06	10.1
6350			106550154	-2.2	-6.19	3.8e-08	5.79e-06	10
32	PLEC1	NM_201379.1	4780273	3.1	6.17	4.12e-08	6.19e-06	9.97
6352			670433	2.4	6.13	4.97e-08	7.37e-06	9.82
6353			5390600	2.6	6.11	5.26e-08	7.69e-06	9.77
6354			103360184	-2	-6.11	5.31e-08	7.69e-06	9.76
33	LOC100133443	XM_001716638.1	2640717	-2.1	-6.07	6.32e-08	9.05e-06	9.62
34	FBLN7	NM_153214.1	5670154	5.4	6.01	8e-08	1.13e-05	9.42
6357			102230086	19	6	8.28e-08	1.16e-05	9.4
6358			2630025	-4.8	-5.99	8.59e-08	1.19e-05	9.37
35	LOC157627	NR_024281.1	4850546	-3.4	-5.97	9.61e-08	1.31e-05	9.27
36	LOC390251	XR_040181.1	3140341	3.2	5.96	9.77e-08	1.32e-05	9.26
6361			101780504	-2	-5.95	1.04e-07	1.38e-05	9.21
6362			104920288	3	5.93	1.11e-07	1.47e-05	9.15
37	CXORF59	NM_173695.1	1990347	2.2	5.93	1.12e-07	1.47e-05	9.14
6364			100510176	-1.9	-5.9	1.26e-07	1.63e-05	9.05
38	DLG1	NM_004087.1	4210541	2.8	5.88	1.33e-07	1.71e-05	9
39	LOC137107	XM_070233.3	1780338	-24	-5.83	1.67e-07	2.11e-05	8.82
6367			106510441	1.8	5.76	2.18e-07	2.74e-05	8.59
6368			102760520	-2	-5.74	2.37e-07	2.95e-05	8.52
6369			3520451	1.7	5.74	2.42e-07	2.97e-05	8.51

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6370			4010239	2.6	5.72	2.52e-07	3.06e-05	8.47
6371			101580301	3.2	5.7	2.72e-07	3.28e-05	8.41
40	KIR2DL5B	NM_001018081.1	5550017	-1.8	-5.67	3.18e-07	3.79e-05	8.28
6373			106380458	-2	-5.63	3.72e-07	4.38e-05	8.15
6374			102450048	-1.8	-5.62	3.74e-07	4.38e-05	8.14
41	RPS21	NM_001024.3	2690338	-2.6	-5.6	4.16e-07	4.82e-05	8.06
42	LOC400120	NM_203451.1	3440519	3.5	5.59	4.33e-07	4.97e-05	8.02
6377			102360148	-1.8	-5.58	4.48e-07	5.1e-05	7.99
6378			2510452	-1.6	-5.57	4.74e-07	5.34e-05	7.95
43	LOC100134170	XM_001721704.1	5570022	-1.7	-5.56	4.89e-07	5.46e-05	7.92
6380			103990215	2.6	5.55	5.11e-07	5.65e-05	7.88
6381			101850056	-1.9	-5.54	5.17e-07	5.67e-05	7.88
44	LOC387804	XM_370648.3	7100452	8	5.54	5.25e-07	5.7e-05	7.86
6383			101090181	-1.8	-5.52	5.69e-07	6.13e-05	7.79
6384			102480487	-2	-5.49	6.47e-07	6.9e-05	7.69
45	LOC729815	XR_037436.1	2450450	-2	-5.46	7.3e-07	7.73e-05	7.59
46	ZNF655	NM_001009956.1	6550390	2.5	5.45	7.41e-07	7.77e-05	7.58
6387			2850731	-6.3	-5.44	7.78e-07	8.09e-05	7.53
6388			103780687	1.7	5.43	7.99e-07	8.25e-05	7.51
47	TRIM36	NM_018700.3	1690402	-1.8	-5.41	8.76e-07	8.96e-05	7.44
6390			5890048	-3.2	-5.39	9.44e-07	9.58e-05	7.37

Table 13: Top 120 genes (all arrays)

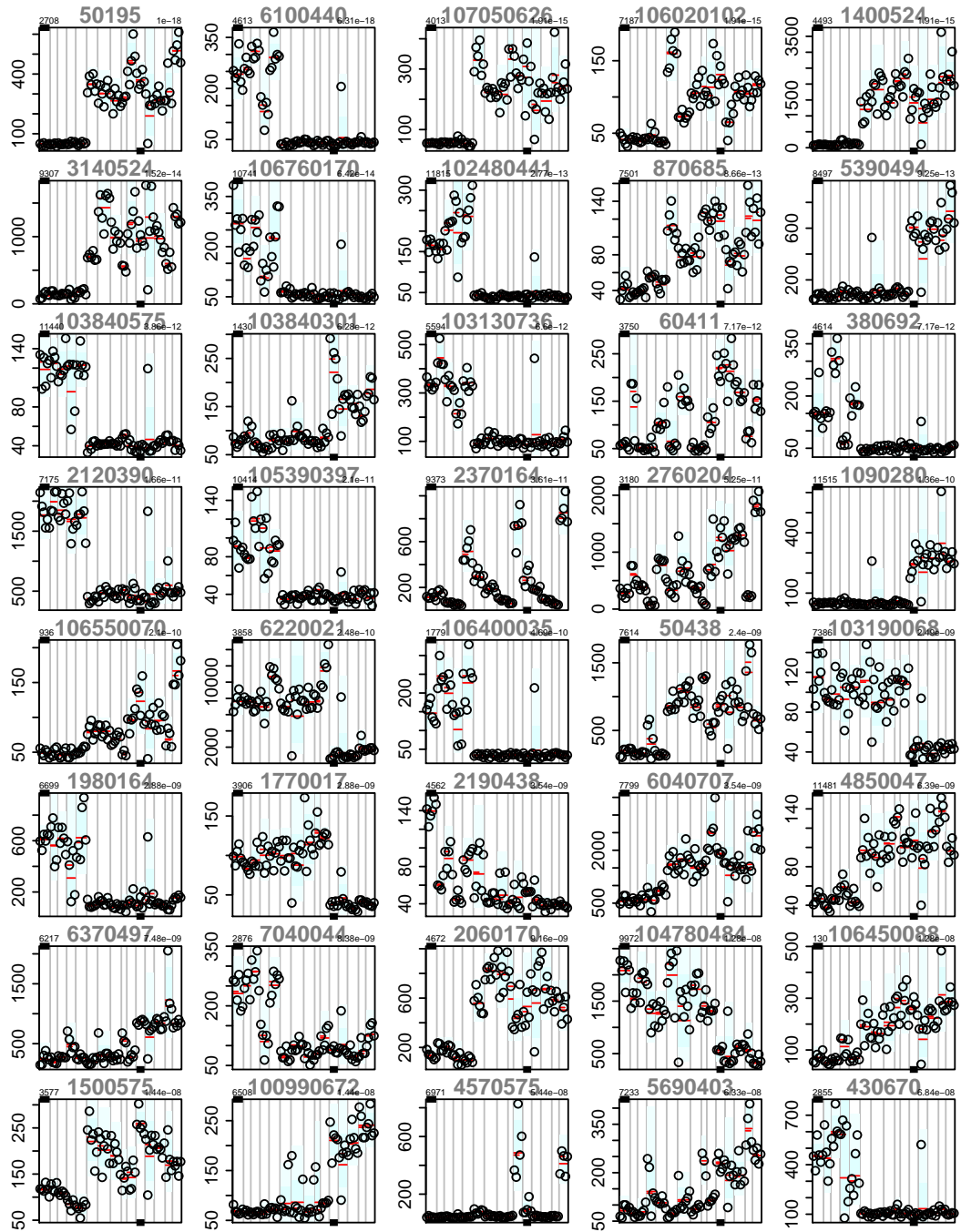


Figure 15a: Top 40 genes for contrast HLa (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

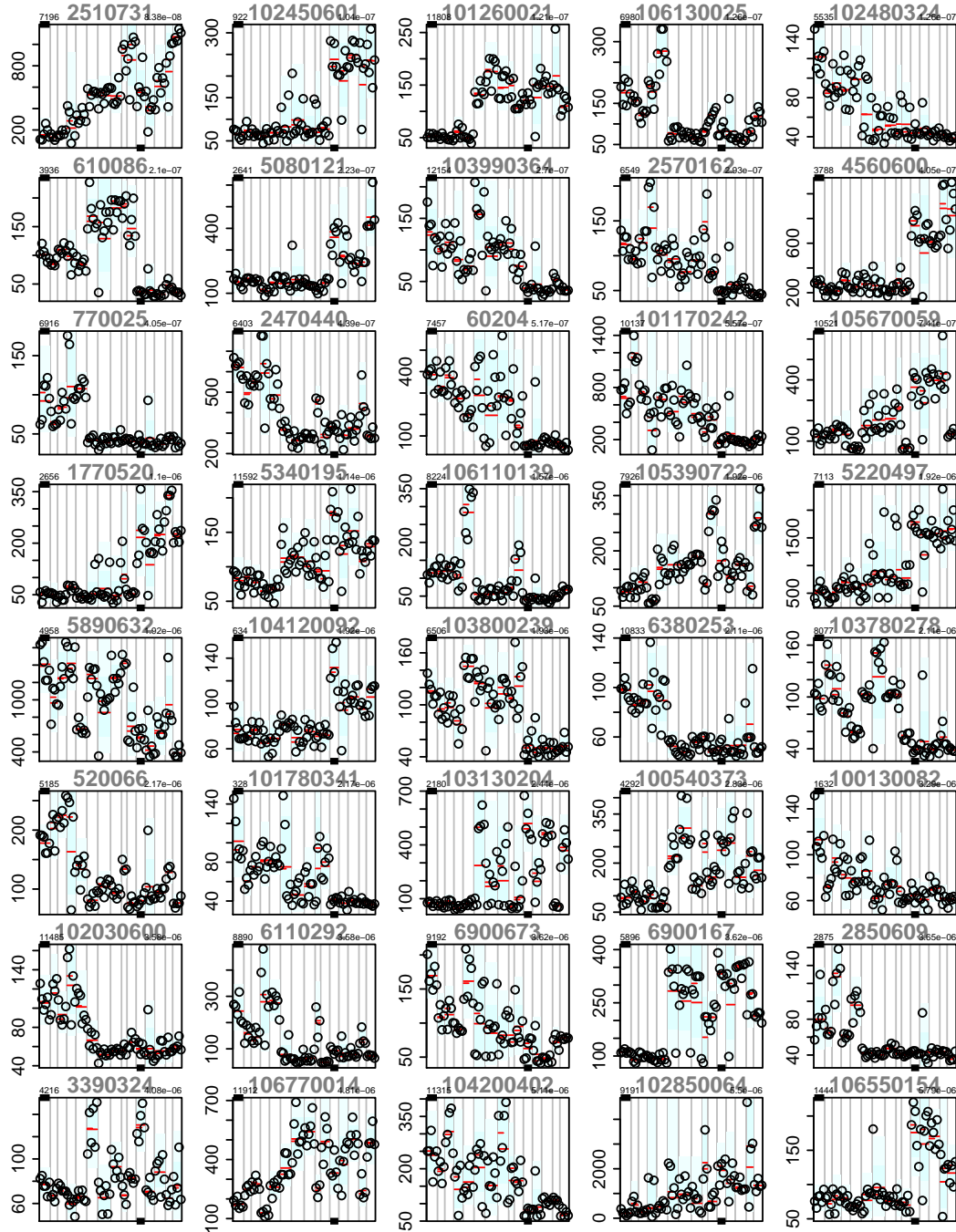


Figure 15b: Significant probes (41–80) for contrast HLa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

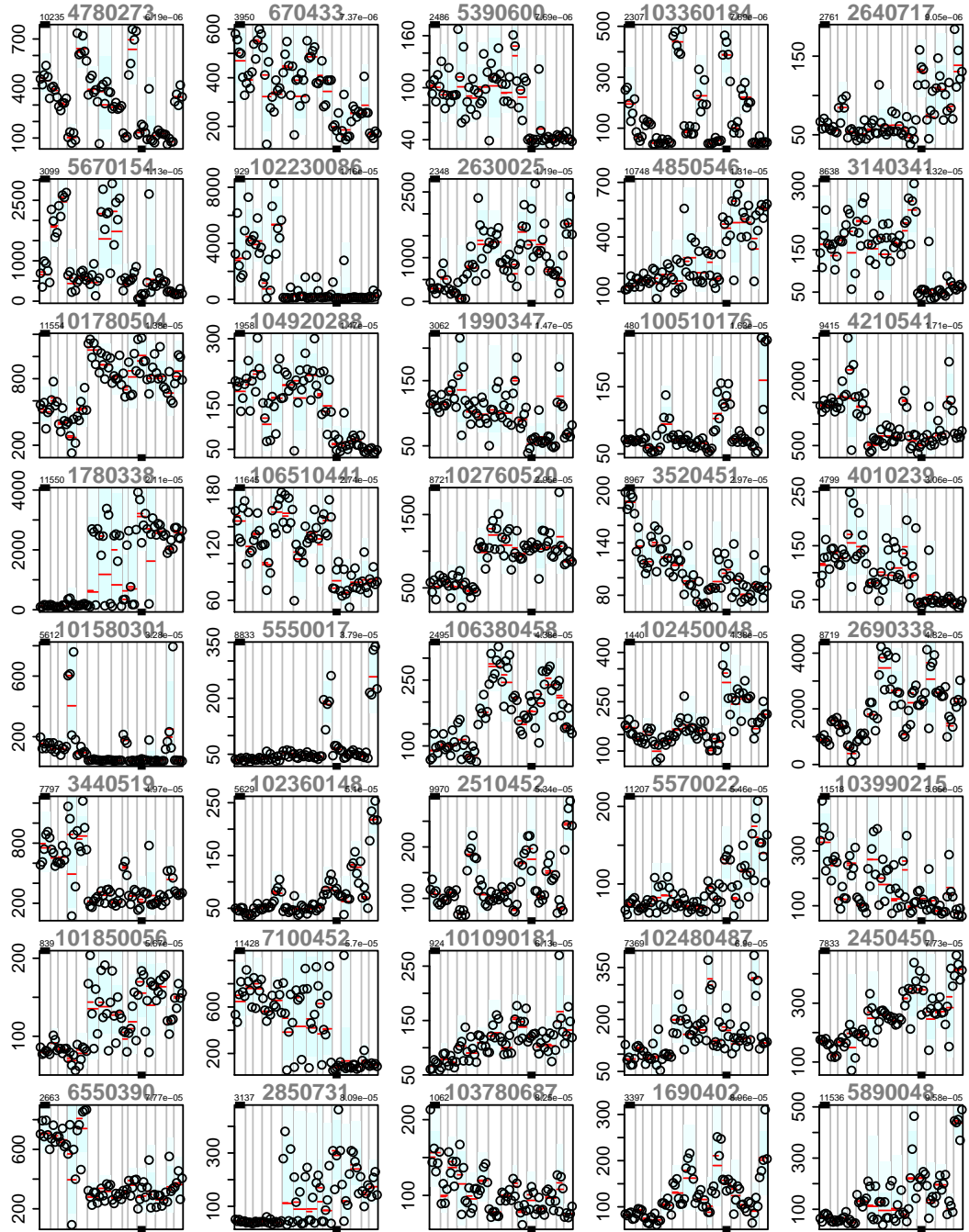


Figure 15c: Significant probes (81–120) for contrast HLa (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.12 Contrast HLb

Using the matrix representing the contrast defined by HAB_BAmY - LAB_BAmY

HLb	
HAB_BAmY	1
LAB_BAmY	-1

The statistics for the top 120 genes across the contrast (where 117 genes have adjusted p -values below 0.05) are shown in table 14, the corresponding expression plots are shown in Figs. 16a-c on pages 119 through 121.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	OR8B2	NM_001005468.1	6100440	4.7	9.98	5.5e-15	6.69e-11	13.6
2	RAB25	NM_020387.1	50195	-4.3	-9.26	1.08e-13	6.58e-10	12.3
3	NARG1	NM_057175.3	3140524	-6.1	-9.07	2.41e-13	9.77e-10	11.9
6274			106400035	5.2	8.7	1.12e-12	2.87e-09	11.3
4	SDHAP3	NR_003263.2	1400524	-8.7	-8.69	1.18e-12	2.87e-09	11.2
5	LOC100132934	XM_001723077.1	2120390	4.4	8.4	4.01e-12	8.13e-09	10.7
6277			103130736	3.5	8.13	1.24e-11	2.15e-08	10.2
6278			380692	2.7	7.9	3.26e-11	4.96e-08	9.71
6279			103840575	2.7	7.86	3.73e-11	5.04e-08	9.65
6280			102480441	3	7.73	6.46e-11	7.87e-08	9.39
6281			107050626	-3	-7.62	1.03e-10	1.14e-07	9.17
6	EIF4B	NM_001417.2	5390494	-5.3	-7.42	2.4e-10	2.43e-07	8.76
6283			101260021	-2.4	-7.12	8.51e-10	7.97e-07	8.14
7	HS.551438	Hs.551438	50438	-4.5	-6.96	1.64e-09	1.43e-06	7.82
8	ZNF680	NM_178558.2	1090280	-3.9	-6.85	2.57e-09	2.08e-06	7.59
6286			101170242	4.5	6.8	3.12e-09	2.37e-06	7.5
9	GSTZ1	NM_001513.2	7040044	2.4	6.72	4.5e-09	3.22e-06	7.31
10	UBE2K	NM_001111112.1	6220021	5.9	6.69	4.97e-09	3.26e-06	7.26
6289			103780278	2.8	6.69	5.09e-09	3.26e-06	7.25
6290			102030600	2	6.61	6.96e-09	4.24e-06	7.09
11	LOC648704	XM_937786.1	4850047	-2.1	-6.57	8.21e-09	4.76e-06	7.01
6292			104780484	3.4	6.37	1.88e-08	1.04e-05	6.58
12	HS.439870	Hs.439870	6370497	-3.1	-6.26	2.96e-08	1.57e-05	6.35
13	PLEC1	NM_201379.1	4780273	3.4	6.03	7.54e-08	3.83e-05	5.87
6295			102230086	26	5.99	8.78e-08	4.28e-05	5.79
14	HS.514893	Hs.514893	1990524	-2.3	-5.96	9.64e-08	4.51e-05	5.74
6297			105390397	1.9	5.89	1.31e-07	5.89e-05	5.58
15	LOC645550	XM_928570.1	5690403	-2.4	-5.84	1.61e-07	6.98e-05	5.47
6299			106130025	1.9	5.72	2.54e-07	0.000107	5.23
6300			870685	-1.9	-5.7	2.81e-07	0.000114	5.17
6301			100990672	-2.4	-5.68	2.99e-07	0.000117	5.14
6302			106760170	2.4	5.57	4.57e-07	0.000174	4.92
6303			106450088	-2.8	-5.55	4.96e-07	0.000183	4.87
6304			106550154	-2.2	-5.51	5.85e-07	0.000204	4.78
16	C3ORF57	NM_145035.2	4560600	-2.4	-5.51	5.85e-07	0.000204	4.78
17	OGFOD1	NM_001031707.1	2510731	-2.9	-5.38	9.83e-07	0.000332	4.51
6307			104920288	3	5.32	1.23e-06	0.000404	4.39
18	LOC730990	XM_001722060.1	2060170	-2.8	-5.31	1.26e-06	0.000405	4.37
6309			5050039	3.1	5.27	1.52e-06	0.000474	4.27
19	LOC653853	XM_936030.1	2470440	1.7	5.25	1.61e-06	0.000489	4.24
6311			6900167	-2.7	-5.19	2.02e-06	0.000599	4.12
6312			430670	3.3	5.18	2.16e-06	0.000625	4.08

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			100540373	-2.3	-5.16	2.3e-06	0.000651	4.05
6314			6040707	-2.3	-5.08	3.11e-06	0.00086	3.89
6315			106110139	2.4	5.05	3.5e-06	0.000947	3.82
6316			102450048	-1.8	-5.04	3.59e-06	0.000951	3.81
20	LOC157627	NR_024281.1	4850546	-3.1	-4.96	4.89e-06	0.00127	3.64
6318			103190068	1.9	4.94	5.33e-06	0.00134	3.59
21	DHX32	NM_018180.2	1980164	3	4.94	5.39e-06	0.00134	3.59
6320			610086	2.2	4.91	5.95e-06	0.00142	3.53
22	ACOT9	NM_001037171.1	5220497	-2.9	-4.91	5.97e-06	0.00142	3.53
23	TNFRSF18	NM_148902.1	520066	1.9	4.88	6.78e-06	0.00159	3.46
6323			106510441	1.7	4.86	7.14e-06	0.00164	3.43
6324			103800239	1.9	4.82	8.44e-06	0.0019	3.34
24	NKX2-1	NM_003317.3	4060497	-1.9	-4.77	9.99e-06	0.00221	3.25
6326			106380458	-1.9	-4.76	1.03e-05	0.00224	3.23
25	LOC729815	XR_037436.1	2450450	-2	-4.74	1.1e-05	0.00235	3.2
6328			670433	2.1	4.73	1.16e-05	0.00243	3.17
6329			2370605	1.5	4.72	1.2e-05	0.00245	3.15
6330			102450601	-2.5	-4.72	1.21e-05	0.00245	3.14
6331			5890632	2.1	4.71	1.23e-05	0.00245	3.13
6332			60204	4.3	4.71	1.25e-05	0.00245	3.13
6333			1770017	1.8	4.67	1.46e-05	0.00282	3.04
26	SNORA81	NR_002989.1	6040121	-1.8	-4.66	1.53e-05	0.00291	3.02
6335			101580368	-1.7	-4.65	1.56e-05	0.00293	3
27	CYC1	NM_001916.2	1770520	-3.1	-4.58	2e-05	0.00369	2.87
6337			102360148	-1.7	-4.56	2.2e-05	0.004	2.82
6338			4010239	2.3	4.49	2.81e-05	0.00503	2.68
6339			102510156	5.6	4.47	3.02e-05	0.00533	2.64
28	C14ORF139	NM_024633.2	5220333	2.6	4.46	3.17e-05	0.00551	2.61
6341			105670059	-2.2	-4.43	3.47e-05	0.00596	2.56
6342			106550070	-1.7	-4.42	3.57e-05	0.00599	2.55
29	TCEB3B	NM_016427.2	5220088	1.8	4.42	3.59e-05	0.00599	2.55
30	IL26	NM_018402.1	6550008	4.3	4.4	3.83e-05	0.00629	2.51
31	LOC137107	XM_070233.3	1780338	-14	-4.39	4.04e-05	0.00655	2.48
32	LOC100131209	XM_001725125.1	6380253	1.6	4.38	4.18e-05	0.00669	2.46
33	LOC645527	XM_928547.1	2630451	1.5	4.37	4.27e-05	0.00676	2.45
6348			104150273	1.8	4.37	4.34e-05	0.00678	2.44
34	GLMN	NM_053274.1	2850609	1.6	4.34	4.78e-05	0.00737	2.39
6350			102340121	1.5	4.25	6.58e-05	0.01	2.21
6351			103990364	2.1	4.25	6.72e-05	0.0101	2.2
35	ZNF655	NM_001009956.1	6550390	2.2	4.21	7.66e-05	0.0114	2.13
36	LOC390251	XR_040181.1	3140341	2.5	4.2	7.86e-05	0.0115	2.11
37	CXORF59	NM_173695.1	1990347	1.8	4.2	7.91e-05	0.0115	2.11
38	VN1R2	NM_173856.1	4760286	-1.8	-4.19	8.28e-05	0.0119	2.08
39	LOC387804	XM_370648.3	7100452	5.6	4.15	9.47e-05	0.0134	2.01
6357			4540494	-2.3	-4.1	0.000113	0.0159	1.91
6358			106400010	6.7	4.04	0.000137	0.019	1.8
6359			103800546	-1.7	-4.01	0.00015	0.0205	1.75
6360			102760520	-1.7	-3.98	0.000166	0.0224	1.69
40	FBLN7	NM_153214.1	5670154	3.5	3.98	0.000167	0.0224	1.69
6362			106020102	-1.5	-3.97	0.000172	0.0228	1.67
6363			6900673	2	3.97	0.000175	0.023	1.66
41	CENPK	NM_022145.2	5700086	1.8	3.92	0.000205	0.0265	1.58
6365			4210270	-1.5	-3.92	0.000208	0.0266	1.57
42	LOC100128585	XR_039418.1	6660687	-2.3	-3.91	0.000215	0.0273	1.55
6367			102810286	1.6	3.89	0.000233	0.029	1.51
6368			5390551	2.6	3.89	0.000233	0.029	1.5
43	HS.538100	Hs.538100	1500575	-1.6	-3.86	0.000256	0.0315	1.45

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
44	TERT	NM_198253.2	4810180	-1.6	-3.85	0.000264	0.0322	1.43
6371			104280487	-2.4	-3.82	0.000286	0.0344	1.39
45	ABLIM1	NM_006720.3	2570112	1.7	3.81	0.000304	0.0362	1.36
6373			103990215	2.1	3.8	0.000315	0.0372	1.34
6374			5700064	1.6	3.79	0.000325	0.038	1.32
46	RANBP1	NM_002882.2	7000735	1.7	3.78	0.000335	0.0388	1.3
47	CCNG2	NM_004354.1	130215	2	3.77	0.000348	0.0397	1.28
48	HS.460114	Hs.460114	4230020	1.6	3.76	0.000349	0.0397	1.28
49	OR10S1	NM_001004474.1	6110292	1.9	3.76	0.000355	0.04	1.27
6379			104200402	2.1	3.72	0.000406	0.0452	1.2
50	HUWE1	NM_031407.3	6980332	2.1	3.72	0.00041	0.0452	1.19
6381			106770014	-1.5	-3.71	0.000412	0.0452	1.19
6382			100520072	-1.8	-3.7	0.000437	0.0475	1.15
6383			2690017	-1.7	-3.69	0.00045	0.048	1.14
51	WBSCR22	NM_017528.2	6370538	1.7	3.69	0.00045	0.048	1.14
6385			106980372	2.8	3.68	0.000459	0.0486	1.13
52	DLG1	NM_004087.1	4210541	2.1	3.68	0.000464	0.0487	1.12
6387			105860647	-2	-3.67	0.000474	0.0493	1.11
6388			103780671	1.5	3.66	0.000489	0.0504	1.09
53	ZXDC	NM_001040653.1	5080121	-1.6	-3.65	0.000514	0.0526	1.06
6390			5890048	-2.4	-3.63	0.00055	0.0557	1.02

Table 14: Top 120 genes (all arrays)

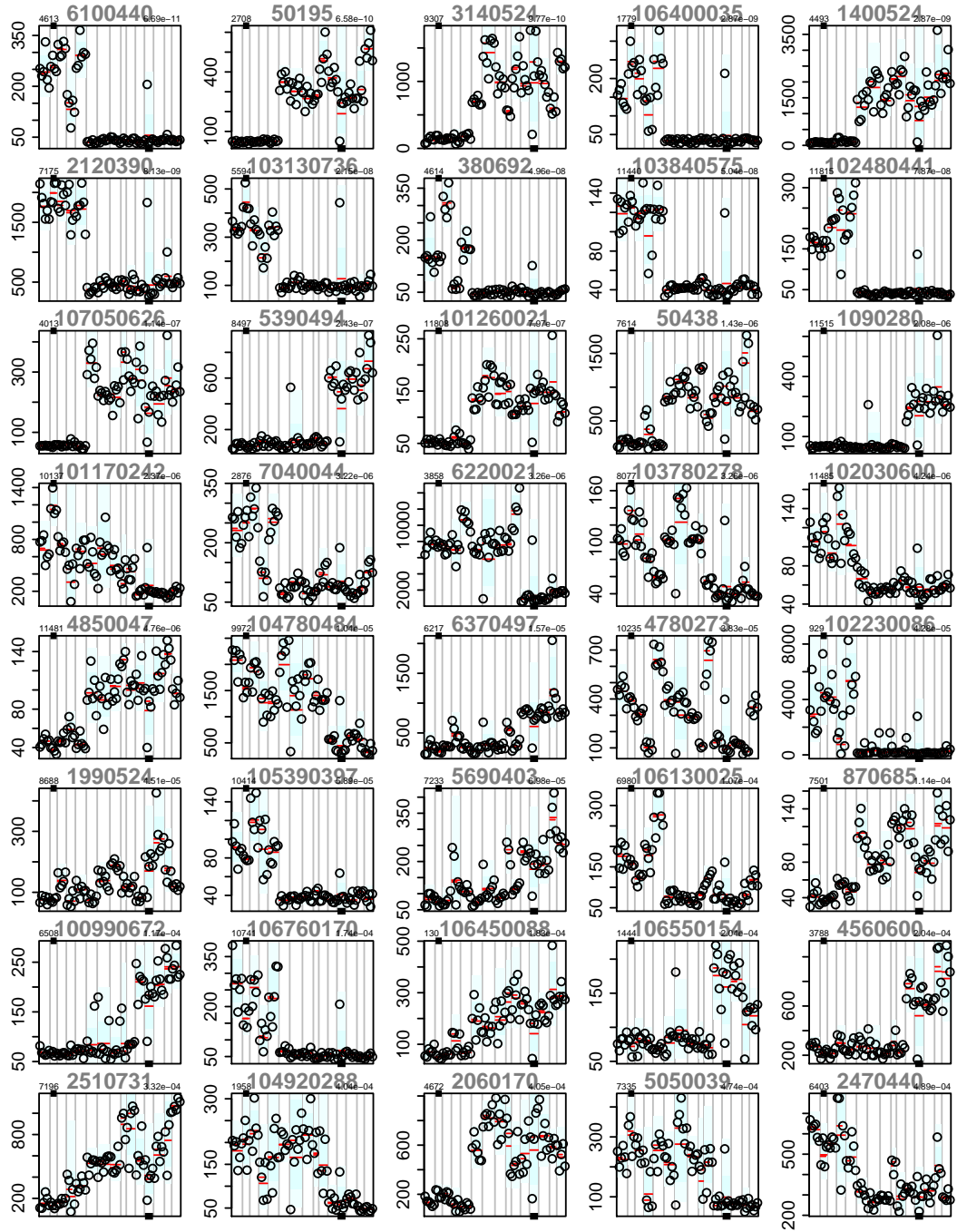


Figure 16a: Top 40 genes for contrast HLb (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

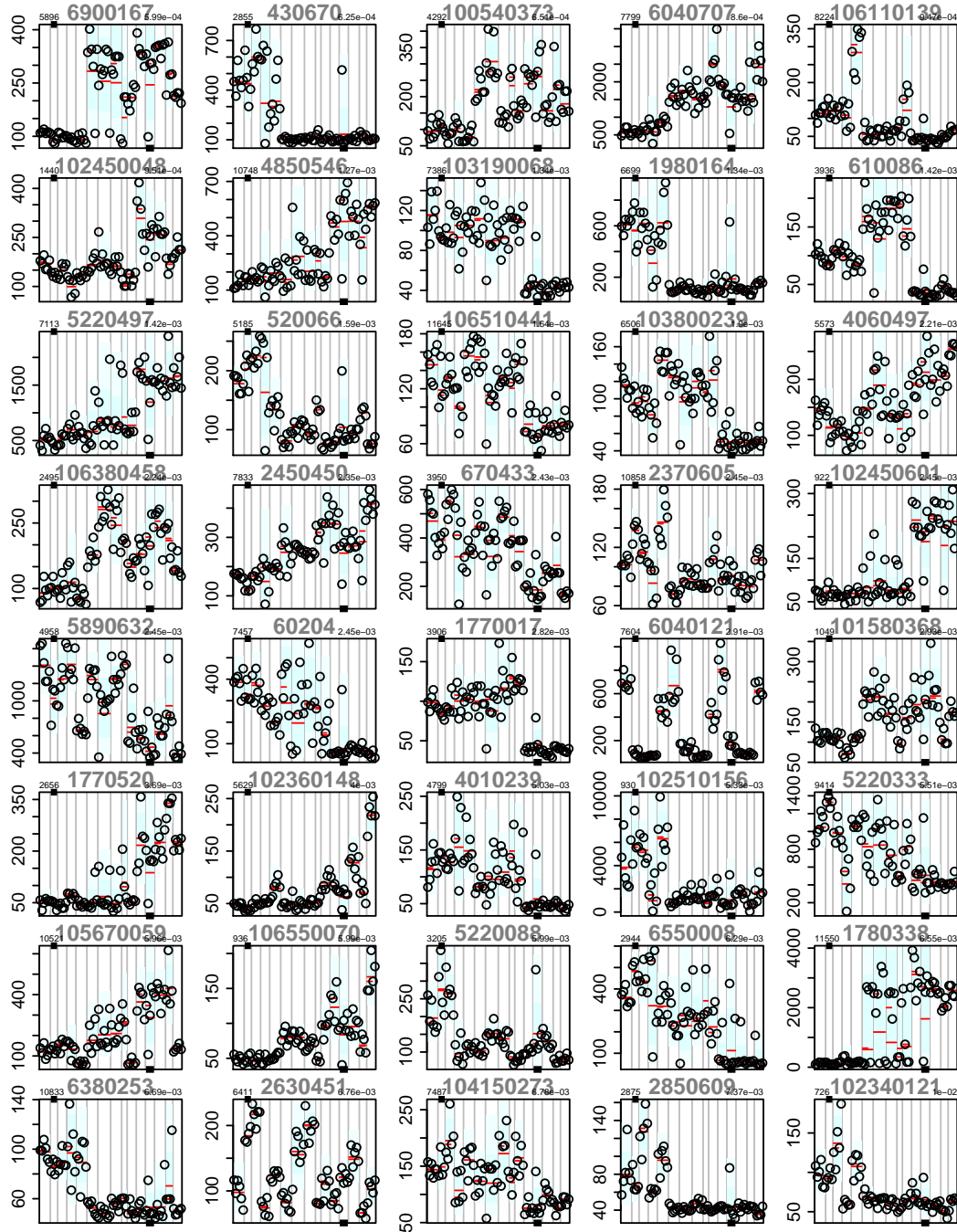


Figure 16b: Significant probes (41–80) for contrast HLb (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

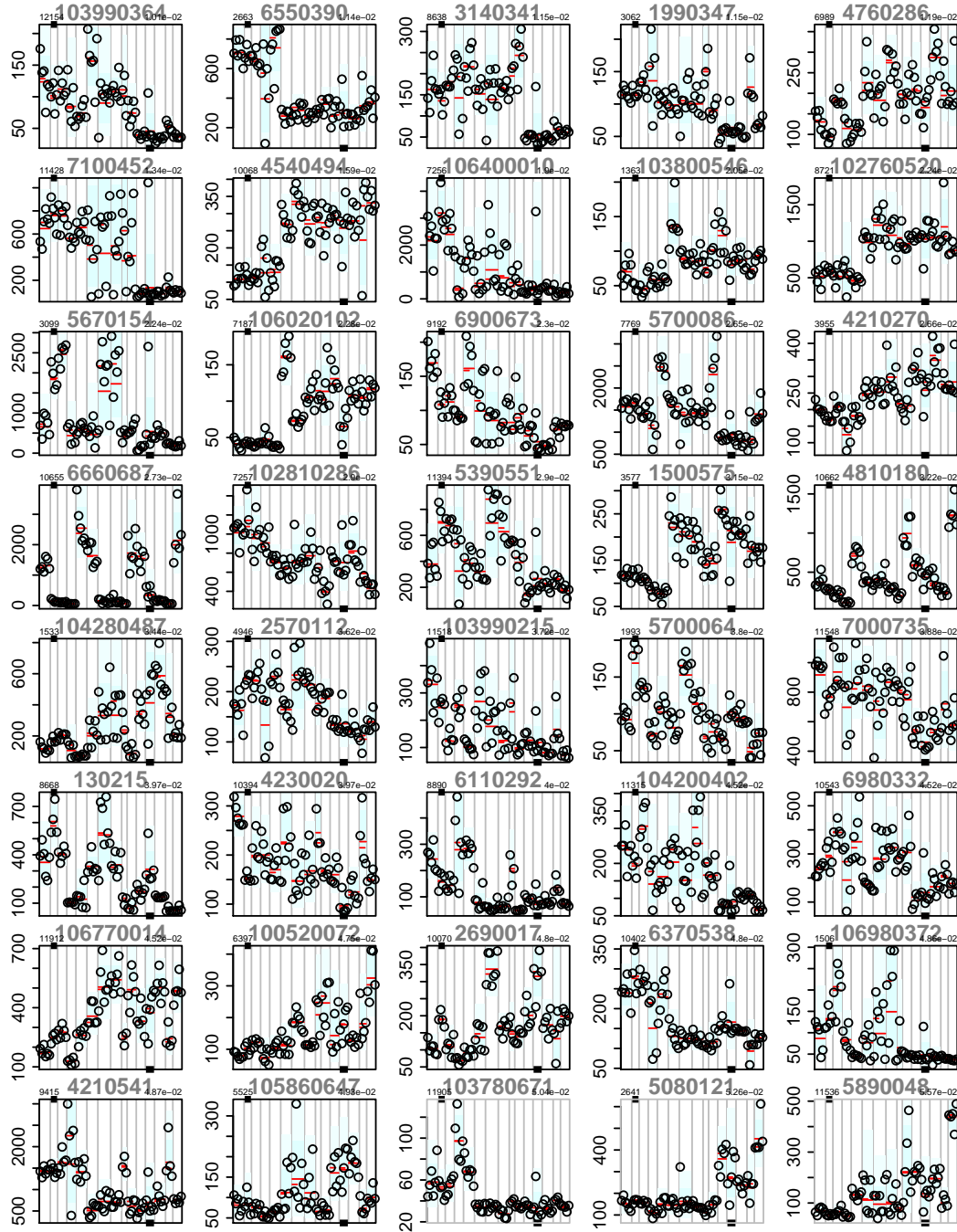


Figure 16c: Significant probes (81–120) for contrast HLb (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

3.2.13 Contrast HLc

Using the matrix representing the contrast defined by HAB_Cing - LAB_Cing

HLc	
HAB_Cing	1
LAB_Cing	-1

The statistics for the top 120 genes across the contrast (out of 254 genes having adjusted p -values below 0.05) are shown in table 15, the corresponding expression plots are shown in Figs. 17a-c on pages 125 through 127.

ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271		380692	6.6	16.6	1.2e-25	1.46e-21	35.6
1 OR8B2	NM_001005468.1	6100440	7.9	14.7	6.72e-23	4.09e-19	32.2
2 SDHAP3	NR_003263.2	1400524	-21	-13.6	3.99e-21	1.62e-17	29.9
6274		102480441	4.8	12.4	4.03e-19	1.23e-15	27.1
6275		105390397	3.4	12.3	5.47e-19	1.33e-15	26.9
3 RAB25	NM_020387.1	50195	-5.5	-12.1	1.14e-18	2.3e-15	26.4
4 GSTZ1	NM_001513.2	7040044	3.9	11.4	1.9e-17	3.3e-14	24.6
5 GLMN	NM_053274.1	2850609	2.9	11	9.21e-17	1.4e-13	23.6
6 NARG1	NM_057175.3	3140524	-7	-10.8	1.94e-16	2.63e-13	23.1
6280		102340121	2.4	10.7	2.45e-16	2.98e-13	22.9
6281		106400035	6.2	10.7	3.02e-16	3.34e-13	22.8
6282		106760170	4.6	10.7	3.42e-16	3.47e-13	22.7
7 EIF4B	NM_001417.2	5390494	-8.4	-10.5	6.56e-16	6.14e-13	22.3
6284		106020102	-2.7	-10.4	9.38e-16	8.15e-13	22
6285		101260021	-3.1	-10.1	4.04e-15	3.28e-12	21
8 ZNF680	NM_178558.2	1090280	-5.8	-9.83	1.05e-14	7.95e-12	20.4
6287		107050626	-3.5	-9.58	2.89e-14	2.07e-11	19.7
6288		102360148	-2.6	-9.31	8.99e-14	6.08e-11	18.9
6289		1770017	2.9	9.22	1.26e-13	8.08e-11	18.6
6290		103130736	3.6	9.17	1.59e-13	9.69e-11	18.5
6291		103840575	2.8	9.09	2.23e-13	1.29e-10	18.2
9 DHX32	NM_018180.2	1980164	6	8.92	4.45e-13	2.46e-10	17.8
10 LOC100132934	XM_001723077.1	2120390	4.1	8.84	6.23e-13	3.3e-10	17.5
11 LOC648704	XM_937786.1	4850047	-2.5	-8.75	8.98e-13	4.38e-10	17.3
12 RTN4RL2	NM_178570.1	60411	-3.3	-8.75	9.01e-13	4.38e-10	17.3
13 UBE2K	NM_001111112.1	6220021	7.8	8.61	1.67e-12	7.81e-10	16.8
6297		610086	3.4	8.5	2.61e-12	1.17e-09	16.5
14 HS.551438	Hs.551438	50438	-5.2	-8.39	4.07e-12	1.77e-09	16.2
6299		430670	5.6	8.33	5.38e-12	2.26e-09	16
6300		100990672	-3.1	-8.03	1.89e-11	7.65e-09	15.1
6301		2760204	-3.4	-7.88	3.45e-11	1.36e-08	14.6
6302		103190068	2.5	7.79	5.19e-11	1.97e-08	14.3
15 CYC1	NM_001916.2	1770520	-5.4	-7.65	8.97e-11	3.31e-08	13.9
6304		102120270	-3	-7.6	1.14e-10	4.07e-08	13.7
6305		106450088	-3.6	-7.58	1.23e-10	4.28e-08	13.7
6306		2190438	2.4	7.57	1.29e-10	4.37e-08	13.6
6307		103990364	3.4	7.55	1.37e-10	4.51e-08	13.6
6308		104210019	2	7.54	1.44e-10	4.62e-08	13.6
16 LOC730990	XM_001722060.1	2060170	-3.7	-7.51	1.62e-10	5.04e-08	13.5
6310		102450601	-3.8	-7.44	2.16e-10	6.57e-08	13.3
6311		106110139	3.2	7.42	2.39e-10	7.1e-08	13.2
6312		103780278	2.8	7.35	3.28e-10	9.49e-08	12.9

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
17	C3ORF57	NM_145035.2	4560600	-2.9	-7.21	5.87e-10	1.66e-07	12.5
18	LOC653428	XM_927368.1	580095	-2	-7.17	6.76e-10	1.87e-07	12.4
19	OGFOD1	NM_001031707.1	2510731	-3.6	-7.13	8.07e-10	2.18e-07	12.3
6316			2030114	3.5	7.12	8.25e-10	2.18e-07	12.3
20	TNFRSF18	NM_148902.1	520066	2.4	7.09	9.67e-10	2.5e-07	12.1
6318			2650546	2.5	7.08	9.86e-10	2.5e-07	12.1
6319			101170242	4	7.05	1.11e-09	2.75e-07	12
6320			870685	-2	-7.05	1.14e-09	2.76e-07	12
6321			6900167	-3.4	-7.03	1.2e-09	2.86e-07	12
6322			106380458	-2.3	-6.96	1.66e-09	3.85e-07	11.7
21	P2RY14	NM_014879.3	1340364	2.6	6.95	1.68e-09	3.85e-07	11.7
6324			102230086	30	6.93	1.88e-09	4.24e-07	11.6
22	LOC390251	XR_040181.1	3140341	3.8	6.92	1.93e-09	4.27e-07	11.6
23	HS.439870	Hs.439870	6370497	-3.1	-6.87	2.33e-09	5.07e-07	11.5
6327			106550070	-2	-6.83	2.78e-09	5.93e-07	11.3
24	SPDYE1	NM_001031618.1	770025	2.3	6.75	3.88e-09	8.14e-07	11.1
6329			103840301	-2	-6.68	5.3e-09	1.09e-06	10.9
6330			106130025	2	6.66	5.63e-09	1.14e-06	10.8
25	CCNG2	NM_004354.1	130215	2.9	6.63	6.41e-09	1.28e-06	10.7
26	CXORF59	NM_173695.1	1990347	2.3	6.53	9.57e-09	1.88e-06	10.4
27	LOC645550	XM_928570.1	5690403	-2.4	-6.51	1.04e-08	2.01e-06	10.3
28	MALT1	NM_006785.2	6040408	2.6	6.43	1.43e-08	2.71e-06	10.1
29	DEFA1	NM_004084.2	4540239	2.4	6.43	1.47e-08	2.75e-06	10.1
6336			106980372	4.9	6.42	1.5e-08	2.77e-06	10.1
6337			104780484	3.1	6.39	1.71e-08	3.11e-06	9.97
30	HS.538100	Hs.538100	1500575	-1.9	-6.38	1.75e-08	3.13e-06	9.95
6339			6040707	-2.5	-6.36	1.91e-08	3.38e-06	9.88
6340			103290286	3.5	6.36	1.97e-08	3.42e-06	9.86
31	HS.538951	Hs.538951	1990020	2.6	6.33	2.17e-08	3.72e-06	9.79
6342			104920288	3.2	6.32	2.32e-08	3.92e-06	9.74
6343			5050039	3.3	6.18	3.99e-08	6.66e-06	9.32
6344			101580368	-1.9	-6.15	4.6e-08	7.56e-06	9.22
6345			103130204	-6.2	-6.09	5.87e-08	9.53e-06	9.03
32	OR5P2	NM_153444.1	770280	3	6.05	6.87e-08	1.1e-05	8.91
33	HLA-DMA	NM_006120.2	540563	-2.3	-6.03	7.51e-08	1.19e-05	8.84
6348			6660181	-6.4	-6.01	7.9e-08	1.23e-05	8.8
6349			106550154	-2.2	-5.99	8.55e-08	1.32e-05	8.74
6350			101780504	-2	-5.98	9.18e-08	1.4e-05	8.69
34	IL26	NM_018402.1	6550008	5.9	5.97	9.46e-08	1.42e-05	8.66
6352			105670059	-2.6	-5.88	1.33e-07	1.98e-05	8.4
35	LOC653853	XM_936030.1	2470440	1.7	5.88	1.35e-07	1.98e-05	8.39
36	LOC387804	XM_370648.3	7100452	9.1	5.88	1.37e-07	1.98e-05	8.38
6355			106770014	-1.8	-5.85	1.5e-07	2.15e-05	8.31
6356			4010239	2.7	5.83	1.64e-07	2.32e-05	8.24
37	ZMIZ1	NM_020338.2	2450131	-2.6	-5.81	1.81e-07	2.53e-05	8.17
38	TMPO	NM_003276.1	1990204	-1.9	-5.8	1.85e-07	2.56e-05	8.15
39	ACOT9	NM_001037171.1	5220497	-3	-5.76	2.23e-07	3.05e-05	8
6360			5340195	-2	-5.74	2.33e-07	3.16e-05	7.97
40	ALPI	NM_001631.2	2570162	2	5.73	2.46e-07	3.28e-05	7.93
41	PLGLB1	NM_001032392.2	6020706	2.2	5.71	2.63e-07	3.48e-05	7.88
6363			5390600	2.4	5.71	2.7e-07	3.54e-05	7.86
6364			102480324	2.2	5.7	2.78e-07	3.57e-05	7.83
6365			104200402	2.9	5.7	2.78e-07	3.57e-05	7.83
42	TCEB3B	NM_016427.2	5220088	2	5.68	2.98e-07	3.78e-05	7.78
6367			102760520	-2	-5.68	3.01e-07	3.78e-05	7.77
43	FBLN7	NM_153214.1	5670154	4.9	5.67	3.17e-07	3.93e-05	7.73
6369			101850056	-2	-5.66	3.2e-07	3.93e-05	7.73

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6370			103800239	2	5.62	3.82e-07	4.61e-05	7.59
44	ZNF655	NM_001009956.1	6550390	2.6	5.62	3.85e-07	4.61e-05	7.58
6372			103800546	-1.9	-5.62	3.86e-07	4.61e-05	7.58
6373			60204	4.7	5.6	4.07e-07	4.81e-05	7.54
45	LOC137107	XM_070233.3	1780338	-21	-5.58	4.55e-07	5.33e-05	7.45
46	HS.514893	Hs.514893	1990524	-2	-5.54	5.22e-07	6.05e-05	7.35
6376			6900673	2.4	5.51	5.99e-07	6.88e-05	7.24
6377			102030600	1.7	5.48	6.54e-07	7.44e-05	7.17
6378			104150273	2	5.45	7.39e-07	8.33e-05	7.08
6379			2100369	-2.4	-5.43	7.93e-07	8.77e-05	7.03
6380			670433	2.2	5.43	7.98e-07	8.77e-05	7.02
47	CCDC4	XM_941085.1	6650397	1.8	5.43	8e-07	8.77e-05	7.02
6382			102680201	-1.5	-5.39	9.26e-07	0.000101	6.91
48	GTPBP8	NM_014170.2	6620176	-1.6	-5.36	1.06e-06	0.000114	6.8
6384			103360184	-1.8	-5.33	1.18e-06	0.000126	6.72
6385			105860647	-2.5	-5.26	1.55e-06	0.000164	6.51
6386			2850731	-5.9	-5.24	1.67e-06	0.000175	6.45
6387			4210270	-1.7	-5.23	1.78e-06	0.000185	6.4
49	LOC157627	NR_024281.1	4850546	-2.9	-5.22	1.82e-06	0.000188	6.38
6389			102450048	-1.7	-5.21	1.87e-06	0.000189	6.36
50	LOC100131209	XM_001725125.1	6380253	1.7	5.21	1.87e-06	0.000189	6.36

Table 15: Top 120 genes (all arrays)

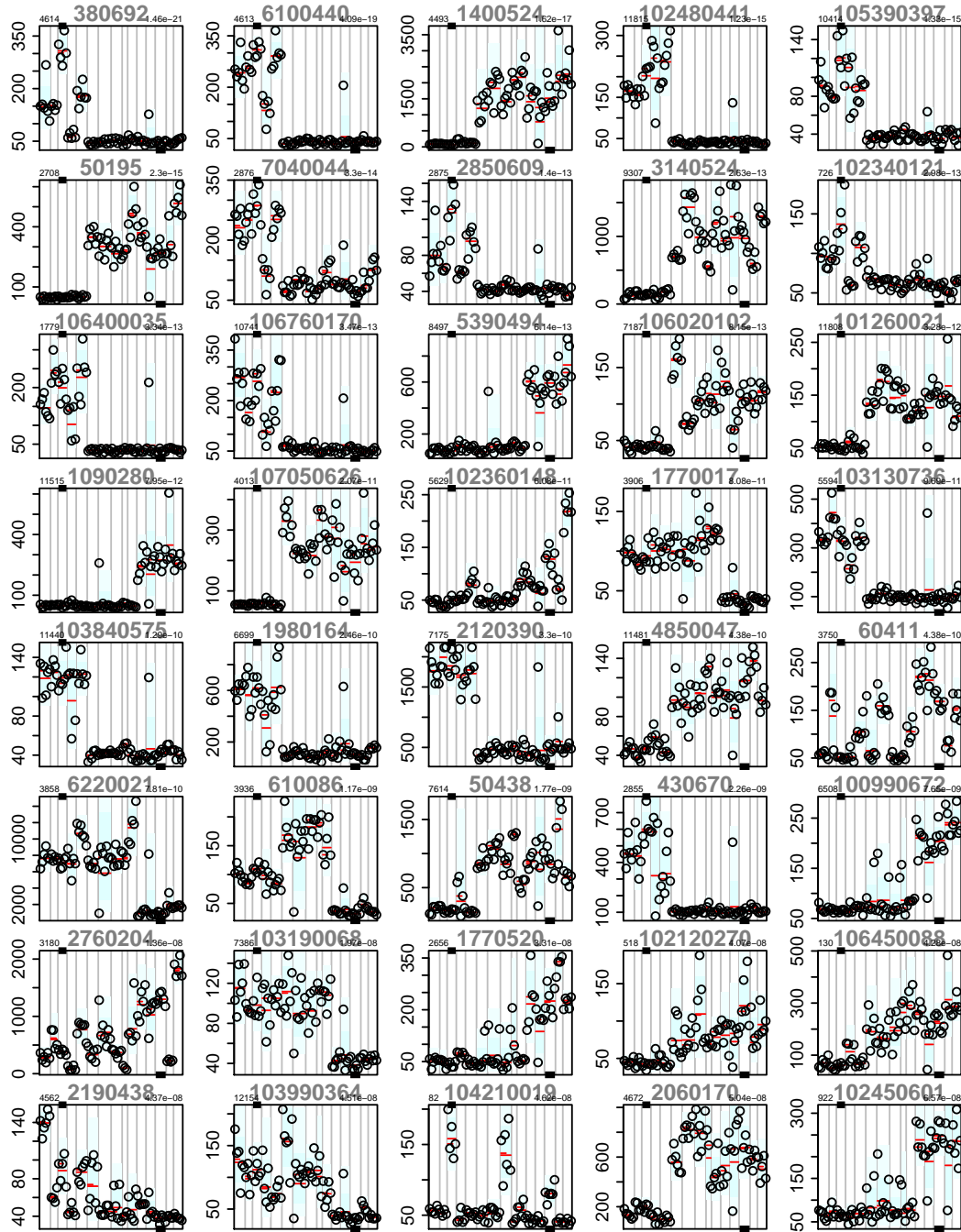


Figure 17a: Top 40 genes for contrast HLc (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

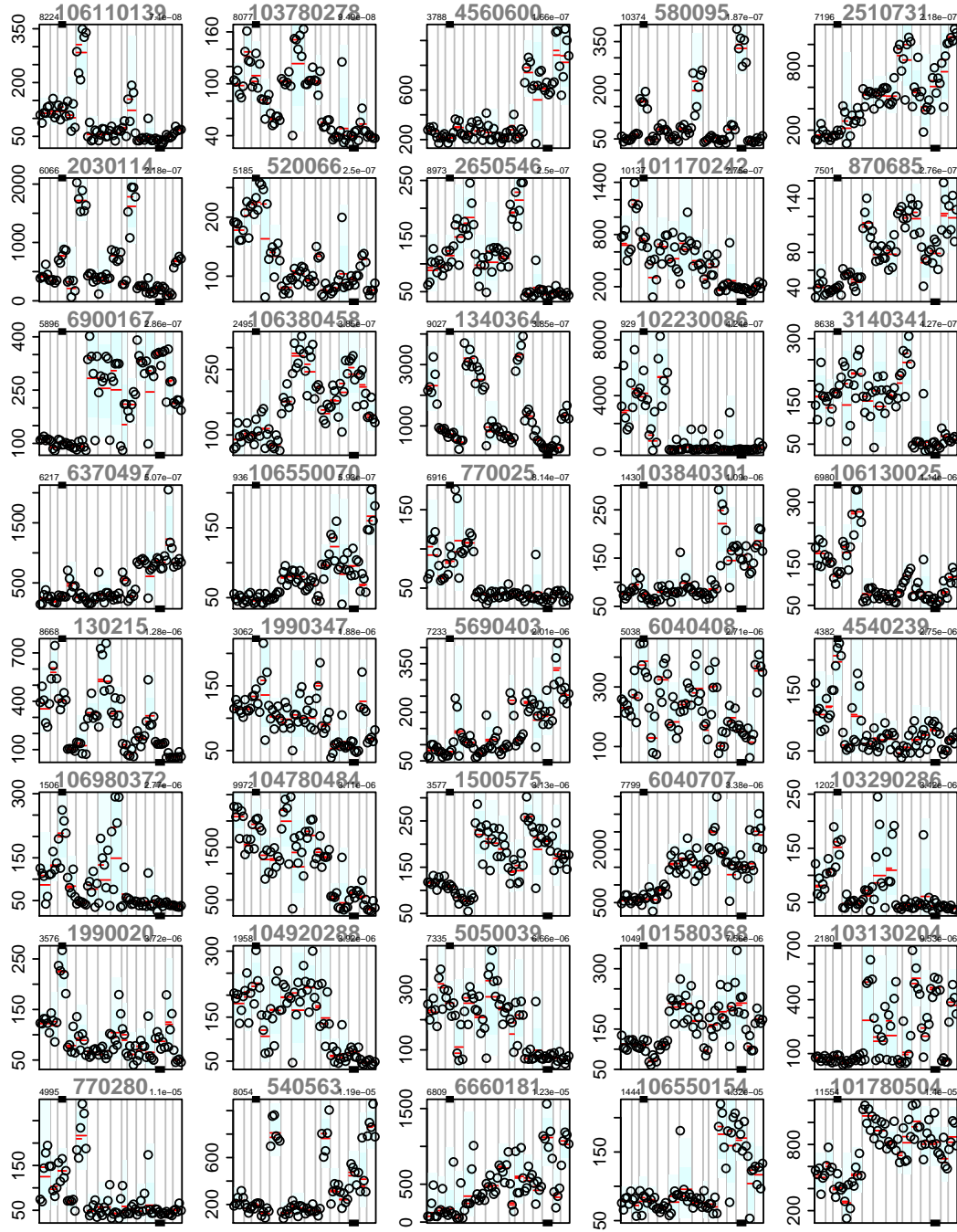


Figure 17b: Significant probes (41–80) for contrast HLc (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

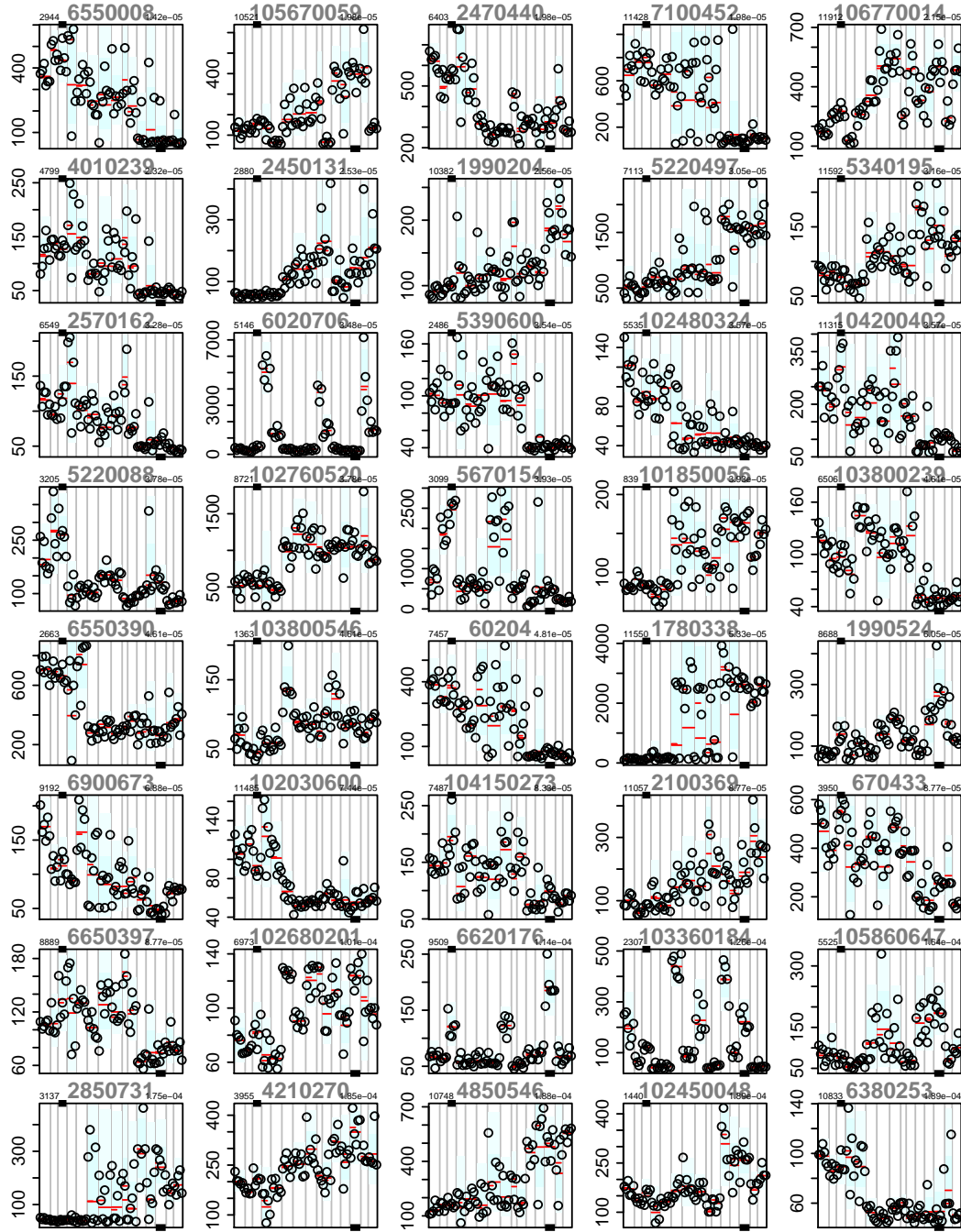


Figure 17c: Significant probes (81–120) for contrast HLc (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

3.2.14 Contrast HLd

Using the matrix representing the contrast defined by HAB_DGyr - LAB_DGyr

HLd	
HAB_DGyr	1
LAB_DGyr	-1

The statistics for the top 120 genes across the contrast (out of 2971 genes having adjusted p -values below 0.05) are shown in table 16, the corresponding expression plots are shown in Figs. 18a-c on pages 131 through 133.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6271			103850204	-5	-11.3	2.96e-17	1.83e-13	28.8
1	RAB25	NM_020387.1	50195	-5.8	-11.3	3e-17	1.83e-13	28.8
6273			102480441	4.6	10.9	1.11e-16	4.5e-13	27.7
6274			107050626	-4.5	-10.5	7.88e-16	2.4e-12	26
2	SDHAP3	NR_003263.2	1400524	-13	-10.4	1.09e-15	2.66e-12	25.8
3	LOC730990	XM_001722060.1	2060170	-5.9	-9.18	1.54e-13	3.13e-10	21.5
6277			102480487	-3.4	-9	3.18e-13	5.53e-10	20.9
4	ZNF680	NM_178558.2	1090280	-5.8	-8.84	6.35e-13	9.66e-10	20.3
6279			6550075	-4.7	-8.64	1.46e-12	1.98e-09	19.6
5	CES1	NM_001025195.1	2680056	-2.8	-8.46	3.08e-12	3.74e-09	18.9
6	NARG1	NM_057175.3	3140524	-5.2	-8.28	6.4e-12	7.08e-09	18.3
6282			101260021	-2.8	-8.24	7.75e-12	7.86e-09	18.1
6283			100990672	-3.6	-8.06	1.65e-11	1.55e-08	17.5
6284			100870152	-3.6	-7.95	2.63e-11	2.29e-08	17.1
7	HLA-DMA	NM_006120.2	540563	-3.3	-7.93	2.84e-11	2.3e-08	17
8	ALPI	NM_001631.2	2570162	2.9	7.78	5.4e-11	4.11e-08	16.4
6287			103780671	2.4	7.53	1.52e-10	1.09e-07	15.5
6288			2650546	2.9	7.51	1.67e-10	1.11e-07	15.4
9	LOC648704	XM_937786.1	4850047	-2.4	-7.5	1.73e-10	1.11e-07	15.4
6290			106020102	-2.2	-7.47	1.96e-10	1.19e-07	15.3
6291			102030600	2.2	7.36	3.08e-10	1.79e-07	14.9
6292			4210270	-2.2	-7.35	3.25e-10	1.8e-07	14.8
10	EIF4B	NM_001417.2	5390494	-5.2	-7.32	3.63e-10	1.92e-07	14.7
11	LOC728667	XM_001128080.2	2650600	-5.1	-7.3	3.93e-10	1.99e-07	14.7
12	LOC222967	NM_173565.1	3060113	-2.9	-7.25	4.85e-10	2.36e-07	14.5
13	CRK	NM_016823.2	7040014	-3.1	-7.16	7.06e-10	3.3e-07	14.2
14	LILRB1	NM_001081637.1	6840435	-2.1	-7.06	1.08e-09	4.87e-07	13.8
15	ENAH	NM_018212.4	3170132	2.1	7.01	1.31e-09	5.7e-07	13.6
16	HS.551438	Hs.551438	50438	-4.5	-6.98	1.53e-09	6.42e-07	13.5
6300			101780504	-2.5	-6.94	1.74e-09	6.77e-07	13.4
6301			870685	-2.2	-6.94	1.76e-09	6.77e-07	13.3
6302			1770017	2.4	6.94	1.78e-09	6.77e-07	13.3
17	FOXA2	NM_153675.1	3780731	-2.2	-6.86	2.47e-09	9.1e-07	13
18	HCP5	NM_006674.2	780600	-2.2	-6.84	2.64e-09	9.46e-07	13
19	OR8B2	NM_001005468.1	6100440	2.9	6.81	2.99e-09	1.04e-06	12.9
20	ZMIZ2	NM_174929.2	630711	-1.9	-6.79	3.24e-09	1.1e-06	12.8
21	HS.514893	Hs.514893	1990524	-2.5	-6.76	3.74e-09	1.23e-06	12.7
22	C3ORF57	NM_145035.2	4560600	-3	-6.73	4.28e-09	1.37e-06	12.6
23	SPDYE1	NM_001031618.1	770025	2.5	6.71	4.59e-09	1.43e-06	12.5
6310			106130025	2.1	6.68	5.1e-09	1.52e-06	12.4
24	RPS21	NM_001024.3	2690338	-3.5	-6.68	5.12e-09	1.52e-06	12.4
6312			103130736	2.8	6.63	6.29e-09	1.82e-06	12.2

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
6313			6400020	-1.9	-6.55	8.96e-09	2.54e-06	11.9
25	HS.538100	Hs.538100	1500575	-2.1	-6.53	9.84e-09	2.72e-06	11.8
6315			105390397	2.1	6.47	1.22e-08	3.31e-06	11.6
6316			105670059	-3.2	-6.46	1.27e-08	3.37e-06	11.6
6317			101340369	-3.9	-6.38	1.75e-08	4.51e-06	11.3
26	LOC645039	XM_928095.1	1780138	-2.8	-6.38	1.78e-08	4.51e-06	11.3
6319			103840301	-2.1	-6.37	1.86e-08	4.62e-06	11.3
27	C20ORF51	NM_022099.3	2900369	-2.3	-6.36	1.9e-08	4.62e-06	11.2
6321			102260025	-2.8	-6.36	1.95e-08	4.66e-06	11.2
6322			6040707	-2.8	-6.31	2.35e-08	5.49e-06	11
28	CYC1	NM_001916.2	1770520	-4.6	-6.26	2.93e-08	6.72e-06	10.9
6324			103170309	-2	-6.24	3.15e-08	7.11e-06	10.8
29	OGFOD1	NM_001031707.1	2510731	-3.4	-6.23	3.35e-08	7.42e-06	10.7
30	LOC100133979	XR_037040.1	380538	-2.5	-6.2	3.76e-08	8.16e-06	10.6
31	DHX32	NM_018180.2	1980164	4	6.19	3.89e-08	8.16e-06	10.6
32	LOC642420	XM_930795.1	5050309	-3.5	-6.19	3.89e-08	8.16e-06	10.6
6329			102760520	-2.3	-6.17	4.2e-08	8.67e-06	10.5
33	TERT	NM_198253.2	4810180	-2.2	-6.12	5.22e-08	1.06e-05	10.3
34	LOC100133390	XM_001723357.1	7040692	-4.2	-6.09	5.81e-08	1.16e-05	10.2
35	ZMIZ1	NM_020338.2	2450131	-3	-6.07	6.23e-08	1.22e-05	10.2
36	LOC100134170	XM_001721704.1	5570022	-1.9	-6.05	6.77e-08	1.31e-05	10.1
37	NKX2-1	NM_003317.3	4060497	-2.2	-6.01	8.12e-08	1.54e-05	9.94
6335			4010239	3.1	5.95	1.02e-07	1.9e-05	9.74
38	GAGE12B	NM_001127345.1	460707	-2.1	-5.91	1.18e-07	2.17e-05	9.61
39	LOC100132934	XM_001723077.1	2120390	2.8	5.9	1.27e-07	2.31e-05	9.54
6338			100520072	-2.4	-5.86	1.45e-07	2.59e-05	9.43
6339			2100369	-2.8	-5.82	1.7e-07	2.98e-05	9.28
6340			105550131	-2	-5.82	1.72e-07	2.98e-05	9.28
40	ERCC-00071	ERCC-00071	4230037	2.6	5.81	1.82e-07	3.12e-05	9.22
6342			100110053	-2	-5.77	2.14e-07	3.62e-05	9.08
6343			2100121	-2.5	-5.72	2.56e-07	4.27e-05	8.92
6344			102680201	-1.6	-5.7	2.79e-07	4.59e-05	8.84
6345			106220156	-2.4	-5.69	2.83e-07	4.6e-05	8.83
41	LOC645550	XM_928570.1	5690403	-2.4	-5.69	2.94e-07	4.7e-05	8.8
6347			6900167	-3	-5.68	2.97e-07	4.7e-05	8.79
6348			103190068	2.1	5.68	3.04e-07	4.74e-05	8.77
42	LOC391670	XR_019025.1	7550703	-1.9	-5.67	3.12e-07	4.79e-05	8.74
6350			106770014	-1.9	-5.67	3.15e-07	4.79e-05	8.74
6351			102450601	-3	-5.65	3.39e-07	5.1e-05	8.67
43	ATXN1	NM_000332.2	5080154	-1.8	-5.6	4.1e-07	6.08e-05	8.5
6353			102480162	-2.8	-5.59	4.23e-07	6.21e-05	8.47
6354			6220494	-2	-5.56	4.88e-07	7.08e-05	8.34
44	LOC152118	XM_098163.3	4920341	5.1	5.55	5.03e-07	7.14e-05	8.32
6356			103840575	2	5.55	5.05e-07	7.14e-05	8.31
45	GIPC1	NM_005716.2	4850088	-2	-5.5	6.06e-07	8.46e-05	8.15
6358			1090170	-2	-5.5	6.14e-07	8.46e-05	8.14
46	SLC38A4	NM_018018.2	2260181	-2.2	-5.5	6.19e-07	8.46e-05	8.13
6360			101770270	-1.9	-5.47	6.89e-07	9.31e-05	8.04
47	MYOM2	NM_003970.1	4050717	1.6	5.46	7.27e-07	9.7e-05	7.99
6362			100540373	-2.4	-5.45	7.33e-07	9.7e-05	7.98
6363			102060735	-2.5	-5.45	7.46e-07	9.77e-05	7.97
6364			2760204	-2.6	-5.42	8.4e-07	0.000108	7.86
6365			106450088	-2.8	-5.42	8.45e-07	0.000108	7.86
48	PPOX	NM_000309.2	3120609	1.9	5.4	9.16e-07	0.000115	7.78
49	LOC100131722	XM_001725235.1	6290647	-2.4	-5.4	9.18e-07	0.000115	7.78
6368			3840348	-1.9	-5.38	9.91e-07	0.000123	7.71
50	SYT14L	NM_001014372.3	4850292	-2.2	-5.36	1.04e-06	0.000128	7.67

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			2230497	-2.1	-5.36	1.08e-06	0.000131	7.64
6371			4280731	-2	-5.35	1.09e-06	0.000131	7.63
51	ZXDC	NM_001040653.1	5080121	-2.1	-5.34	1.13e-06	0.000134	7.6
52	C19ORF56	NM_016145.1	3800079	-3.4	-5.34	1.16e-06	0.000137	7.57
6374			100050079	-1.8	-5.3	1.33e-06	0.000155	7.45
6375			102940348	2	5.29	1.37e-06	0.000158	7.43
6376			104730441	-1.9	-5.26	1.53e-06	0.000176	7.32
53	DENND5A	NM_015213.2	2640408	-2	-5.26	1.55e-06	0.000176	7.32
6378			101050161	-2.1	-5.22	1.83e-06	0.000206	7.17
54	RPL13	NM_033251.1	840242	-2.2	-5.21	1.88e-06	0.000209	7.14
6380			106940324	-3.1	-5.2	2e-06	0.00022	7.09
55	CCK	NM_000729.3	2030524	-2	-5.2	2e-06	0.00022	7.09
6382			2650687	-2	-5.19	2.07e-06	0.000225	7.06
56	LOC643220	XR_038958.1	4590162	-1.9	-5.17	2.17e-06	0.000232	7.01
6384			101050075	-2.4	-5.17	2.17e-06	0.000232	7.01
6385			104590402	-2.1	-5.17	2.2e-06	0.000233	7
57	HS.439870	Hs.439870	6370497	-2.5	-5.15	2.36e-06	0.000247	6.94
6387			3360039	-1.9	-5.15	2.38e-06	0.000247	6.93
6388			103120048	-2.1	-5.15	2.4e-06	0.000247	6.92
58	LOC731641	Hs.570007	3520592	-2.6	-5.11	2.78e-06	0.000284	6.79
59	IL26	NM_018402.1	6550008	5.4	5.09	2.98e-06	0.000302	6.73

Table 16: Top 120 genes (all arrays)

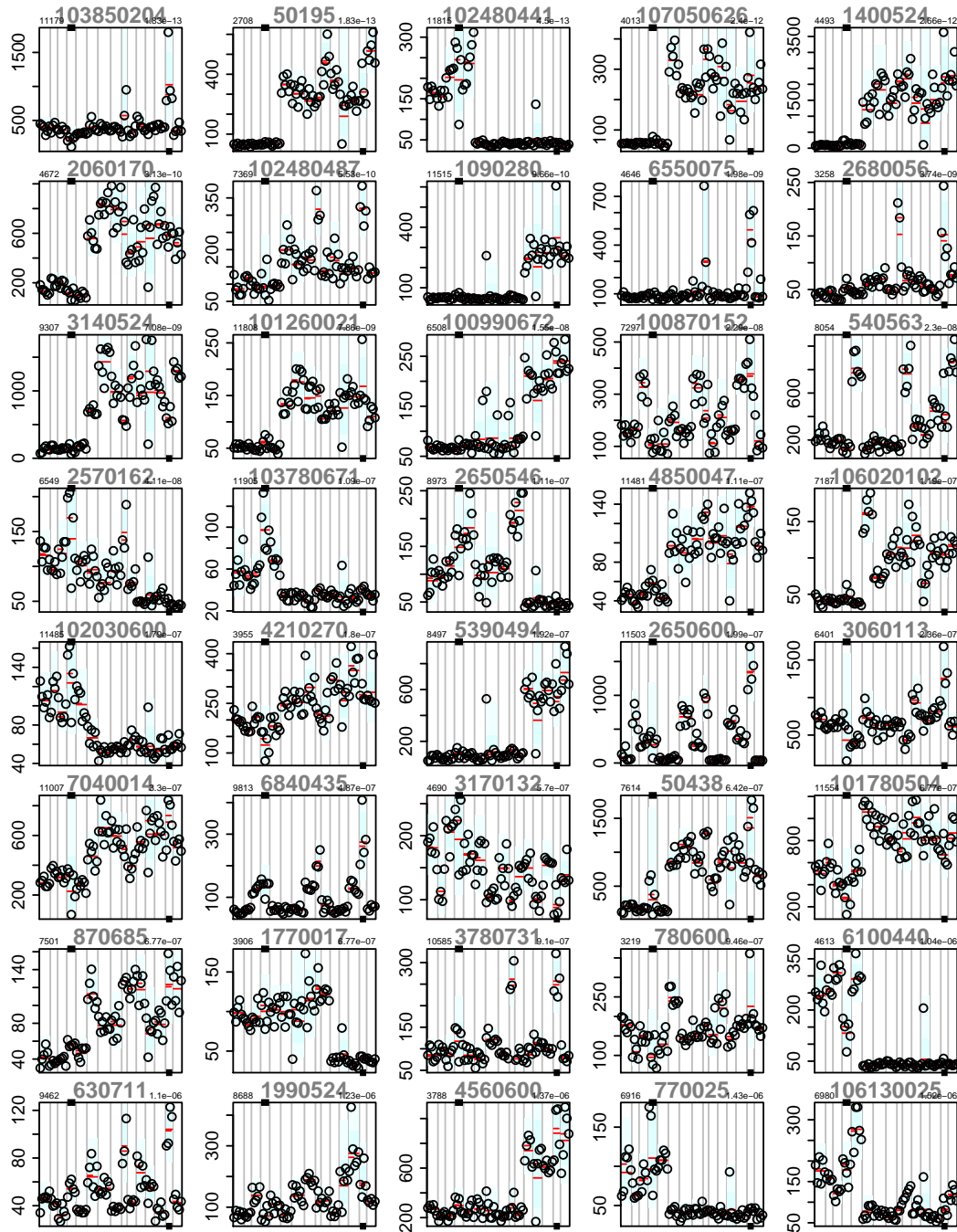


Figure 18a: Top 40 genes for contrast HLd (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

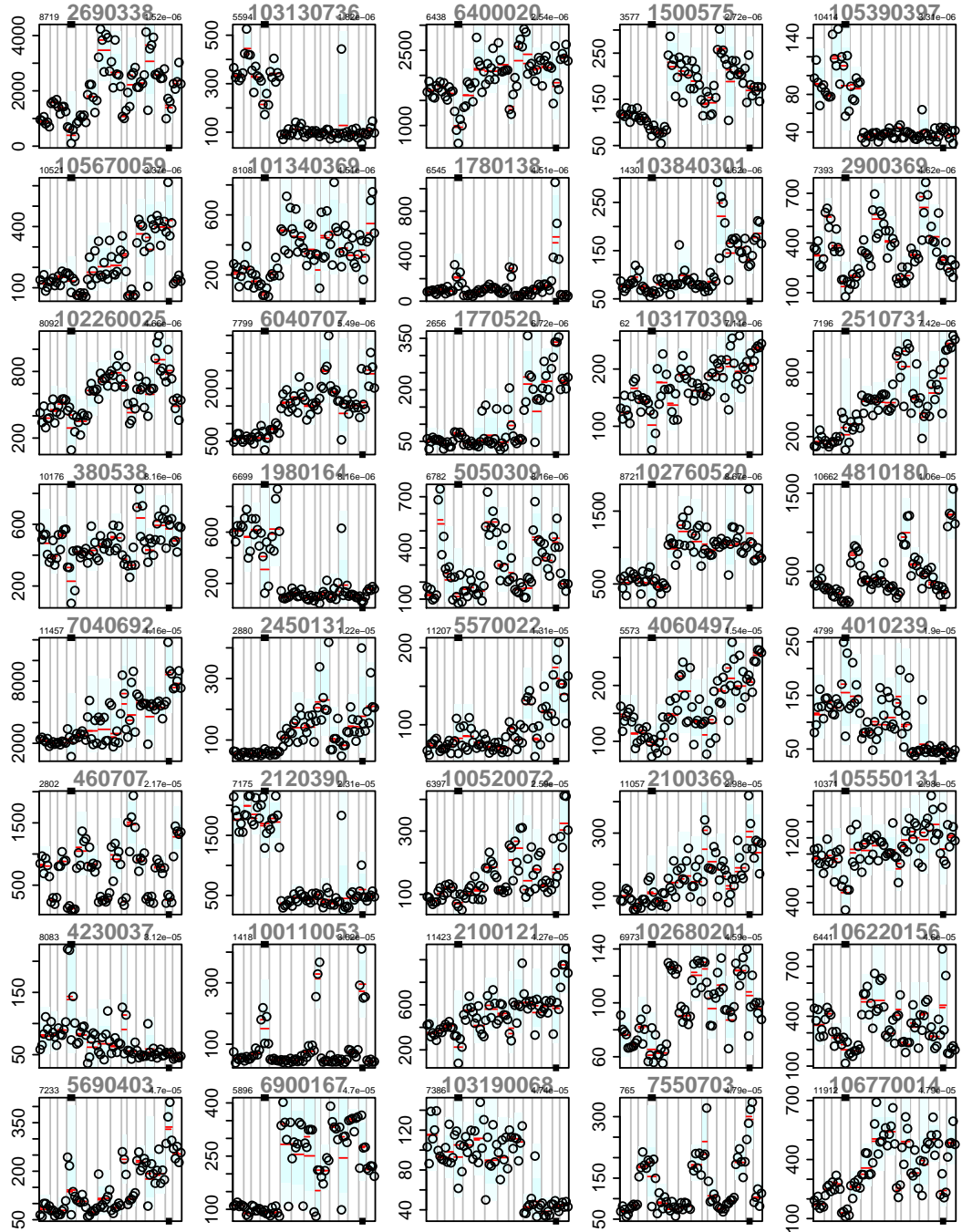


Figure 18b: Significant probes (41–80) for contrast HLd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

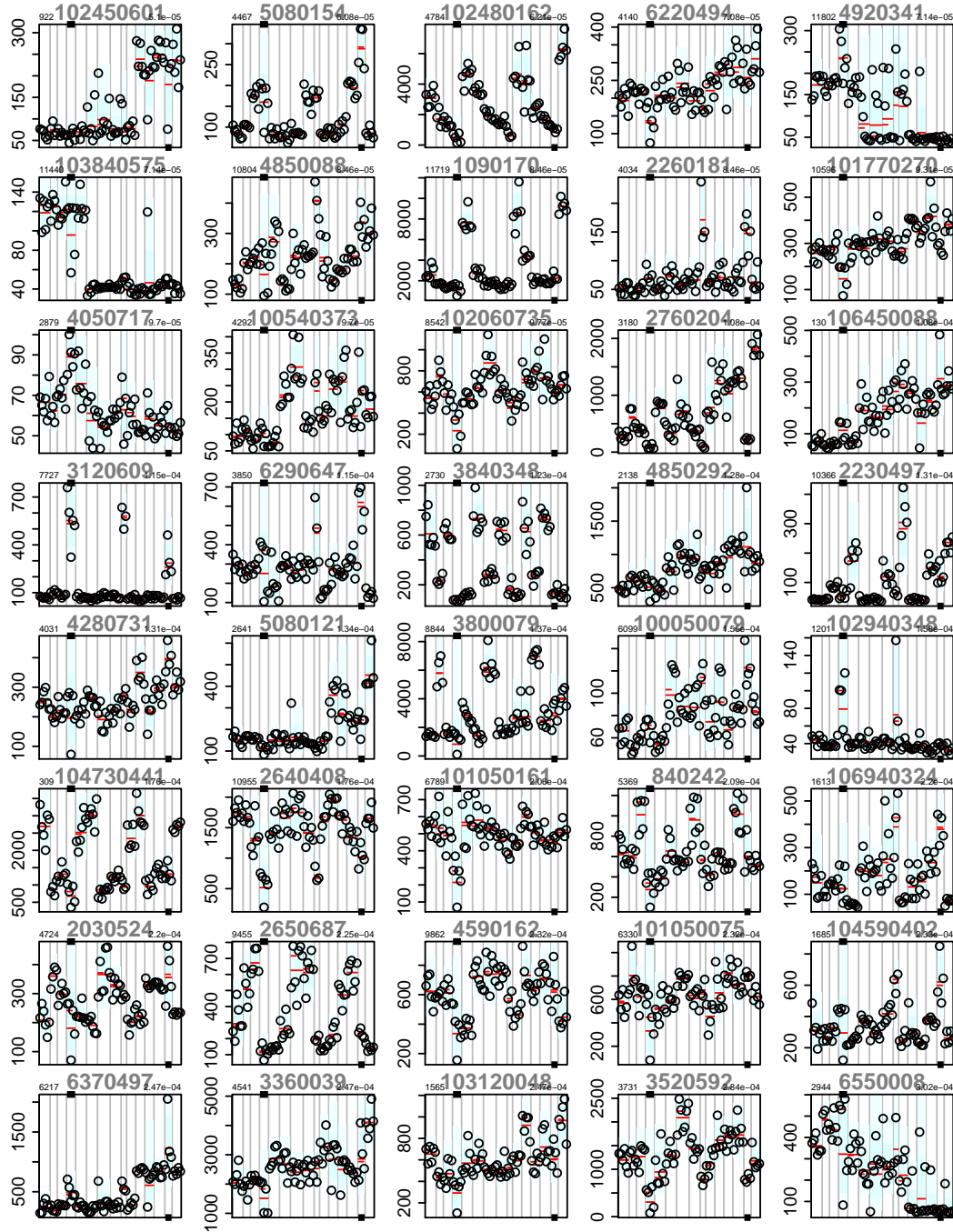


Figure 18c: Significant probes (81–120) for contrast HLd (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

3.2.15 Contrast HLp

Using the matrix representing the contrast defined by HAB_PVNu - LAB_PVNu

HLp	
HAB_PVNu	1
LAB_PVNu	-1

The statistics for the top 120 genes across the contrast (out of 297 genes having adjusted p -values below 0.05) are shown in table 17, the corresponding expression plots are shown in Figs. 19a-c on pages 137 through 139.

	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
1	ST7	NM_018412.3	4570575	-9.8	-19.9	3.75e-30	4.56e-26	44.8
2	KIR2DL5B	NM_001018081.1	5550017	-6.6	-18.5	2.28e-28	1.38e-24	42.6
3	RAB25	NM_020387.1	50195	-10	-16.5	1.54e-25	6.26e-22	38.9
6274			102480441	6.3	14.6	1.06e-22	3.22e-19	34.8
4	OR8B2	NM_001005468.1	6100440	7.2	14.1	5.88e-22	1.43e-18	33.7
5	SDHAP3	NR_003263.2	1400524	-20	-13.3	1.4e-20	2.83e-17	31.6
6277			107050626	-4.7	-12	1.53e-18	2.66e-15	28.3
6278			105570368	3.2	11.8	4.31e-18	5.89e-15	27.6
6279			106020102	-3.1	-11.8	4.36e-18	5.89e-15	27.6
6280			106400035	6.8	11.2	4.1e-17	4.99e-14	25.9
6281			106550070	-3.1	-11.1	5.31e-17	5.88e-14	25.8
6282			2650546	4.1	11	8.05e-17	8.16e-14	25.5
6	NARG1	NM_057175.3	3140524	-7.1	-10.9	1.2e-16	1.13e-13	25.2
6284			380692	3.4	10.6	3.68e-16	3.2e-13	24.3
7	EIF4B	NM_001417.2	5390494	-8.2	-10.4	1e-15	8.13e-13	23.6
6286			106760170	4.4	10.4	1.22e-15	9.28e-13	23.5
6287			102360148	-2.8	-10	4.89e-15	3.5e-12	22.4
6288			103840575	3.1	9.96	6e-15	4.06e-12	22.3
8	ZNF680	NM_178558.2	1090280	-5.7	-9.68	1.91e-14	1.22e-11	21.4
9	GLMN	NM_053274.1	2850609	2.5	9.52	3.75e-14	2.28e-11	20.9
10	LOC730990	XM_001722060.1	2060170	-5.1	-9.38	6.53e-14	3.78e-11	20.5
6292			870685	-2.6	-9.29	9.49e-14	5.19e-11	20.2
11	ZXDC	NM_001040653.1	5080121	-3.1	-9.28	9.81e-14	5.19e-11	20.1
6294			106110139	4.2	9.21	1.32e-13	6.7e-11	19.9
12	OR10S1	NM_001004474.1	6110292	3.8	8.82	6.82e-13	3.32e-10	18.6
6296			105390397	2.4	8.7	1.15e-12	5.24e-10	18.2
6297			1770017	2.7	8.69	1.16e-12	5.24e-10	18.2
6298			100990672	-3.4	-8.63	1.53e-12	6.65e-10	18
6299			106450088	-4.2	-8.52	2.39e-12	1e-09	17.7
6300			103800239	2.7	8.46	3.01e-12	1.22e-09	17.5
13	SPDYE1	NM_001031618.1	770025	2.8	8.45	3.16e-12	1.24e-09	17.5
6302			100520072	-3.1	-8.36	4.73e-12	1.8e-09	17.1
14	LOC100133443	XM_001716638.1	2640717	-2.7	-8.3	5.9e-12	2.18e-09	17
6304			103130736	3.1	8.24	7.74e-12	2.77e-09	16.7
15	C3ORF57	NM_145035.2	4560600	-3.3	-8.23	8.15e-12	2.84e-09	16.7
6306			106130025	2.3	8.19	9.33e-12	3.15e-09	16.6
16	ZNF175	NM_007147.2	6940458	-3.2	-8.09	1.47e-11	4.84e-09	16.2
17	LOC100132934	XM_001723077.1	2120390	3.5	7.93	2.87e-11	9.2e-09	15.7
18	ZMIZ1	NM_020338.2	2450131	-3.7	-7.92	2.98e-11	9.31e-09	15.7
6310			103840301	-2.3	-7.91	3.1e-11	9.44e-09	15.7
19	HS.551438	Hs.551438	50438	-4.7	-7.88	3.48e-11	1.03e-08	15.6
20	OR5P2	NM_153444.1	770280	4.1	7.88	3.55e-11	1.03e-08	15.5

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	ILMN_Gene	Search_Key	A_A_Id	FC	t	P.Value	adj.P.Val	B
21	HS.538100	Hs.538100	1500575	-2.2	-7.73	6.46e-11	1.83e-08	15.1
22	LOC648704	XM.937786.1	4850047	-2.2	-7.69	7.71e-11	2.13e-08	14.9
23	UBE2K	NM.001111112.1	6220021	6.1	7.53	1.48e-10	4.02e-08	14.4
24	NKX2-1	NM.003317.3	4060497	-2.4	-7.47	1.92e-10	5.07e-08	14.2
6317			4010239	3.5	7.45	2.14e-10	5.51e-08	14.1
6318			104780484	3.7	7.44	2.17e-10	5.51e-08	14.1
25	CKAP2L	NM.152515.2	6380324	-2.4	-7.3	3.99e-10	9.91e-08	13.6
6320			101260021	-2.3	-7.28	4.31e-10	1.05e-07	13.6
26	HS.439870	Hs.439870	6370497	-3.2	-7.23	5.25e-10	1.25e-07	13.4
27	CYC1	NM.001916.2	1770520	-4.9	-7.16	7.11e-10	1.66e-07	13.2
6323			6040707	-2.8	-7.1	9.09e-10	2.06e-07	13
6324			2190438	2.3	7.1	9.15e-10	2.06e-07	13
6325			103190068	2.3	7.01	1.3e-09	2.88e-07	12.7
6326			101980400	-3.3	-6.99	1.42e-09	3.09e-07	12.6
28	DHX32	NM.018180.2	1980164	4	6.94	1.78e-09	3.8e-07	12.4
6328			102450601	-3.4	-6.91	1.97e-09	4.14e-07	12.3
6329			102340121	1.7	6.86	2.48e-09	5.12e-07	12.1
6330			5050039	3.8	6.84	2.73e-09	5.46e-07	12.1
29	ALPI	NM.001631.2	2570162	2.3	6.83	2.74e-09	5.46e-07	12.1
30	OGFOD1	NM.001031707.1	2510731	-3.4	-6.82	2.97e-09	5.84e-07	12
6333			104920288	3.5	6.79	3.34e-09	6.45e-07	11.9
31	WWC1	NM.015238.1	1090575	-2	-6.76	3.74e-09	7.11e-07	11.8
32	ALOX15	XM.937556.1	1230722	2.8	6.73	4.27e-09	7.99e-07	11.7
6336			102480324	2.6	6.71	4.66e-09	8.59e-07	11.6
6337			103780671	2	6.58	7.85e-09	1.43e-06	11.2
33	LOC390251	XR.040181.1	3140341	3.5	6.48	1.2e-08	2.15e-06	10.9
6339			2100369	-2.8	-6.38	1.8e-08	3.18e-06	10.5
6340			105390722	-1.9	-6.32	2.31e-08	4.01e-06	10.3
34	P2RY14	NM.014879.3	1340364	2.4	6.31	2.36e-08	4.04e-06	10.3
35	LOC645550	XM.928570.1	5690403	-2.4	-6.29	2.53e-08	4.28e-06	10.3
6343			2690017	-2.2	-6.27	2.85e-08	4.75e-06	10.2
6344			106510441	1.9	6.18	4.02e-08	6.62e-06	9.88
36	TRIM36	NM.018700.3	1690402	-2	-6.13	4.92e-08	7.93e-06	9.72
6346			102230086	20	6.13	4.95e-08	7.93e-06	9.71
6347			106770014	-1.9	-6.12	5.23e-08	8.27e-06	9.67
6348			610086	2.4	6.06	6.68e-08	1.04e-05	9.47
6349			6840088	-1.9	-6.04	7.23e-08	1.11e-05	9.4
37	LOC100131209	XM.001725125.1	6380253	1.8	5.94	1.08e-07	1.64e-05	9.08
38	LOC729815	XR.037436.1	2450450	-2.2	-5.93	1.1e-07	1.65e-05	9.06
6352			104560161	-7.5	-5.88	1.33e-07	1.97e-05	8.91
39	G3BP2	NM.012297.3	7100156	2.2	5.86	1.47e-07	2.16e-05	8.82
6354			100540373	-2.3	-5.76	2.17e-07	3.14e-05	8.51
6355			101340161	1.9	5.71	2.66e-07	3.81e-05	8.34
6356			101170242	3.1	5.69	2.85e-07	4.03e-05	8.28
6357			430670	3.3	5.69	2.89e-07	4.04e-05	8.27
6358			101780341	2.2	5.66	3.22e-07	4.45e-05	8.18
6359			104200717	-1.8	-5.66	3.27e-07	4.47e-05	8.17
40	GSTZ1	NM.001513.2	7040044	2	5.62	3.85e-07	5.21e-05	8.03
6361			5340195	-1.9	-5.61	3.91e-07	5.22e-05	8.02
6362			102680201	-1.5	-5.58	4.54e-07	6.01e-05	7.9
41	LOC653853	XM.936030.1	2470440	1.7	5.55	4.99e-07	6.53e-05	7.82
6364			2760204	-2.4	-5.55	5.04e-07	6.53e-05	7.81
6365			5890048	-3.3	-5.54	5.19e-07	6.65e-05	7.79
42	ACOT9	NM.001037171.1	5220497	-2.9	-5.53	5.41e-07	6.86e-05	7.75
6367			101850056	-1.9	-5.51	5.91e-07	7.41e-05	7.68
43	VPS13B	NM.181661.1	2120368	3.6	5.48	6.61e-07	8.21e-05	7.59
6369			103130204	-5.1	-5.46	7.25e-07	8.86e-05	7.51

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	ILMN_Gene	Search_Key	A_A.Id	FC	t	P.Value	adj.P.Val	B
6370			102120270	-2.2	-5.46	7.28e-07	8.86e-05	7.51
44	DEFB114	NM_001037499.1	6620411	1.8	5.43	8.12e-07	9.78e-05	7.42
45	LOC654056	XM_938485.1	4120288	1.7	5.41	8.83e-07	0.000105	7.35
6373			102030600	1.7	5.41	8.86e-07	0.000105	7.35
46	LOC648289	XM_937347.1	6860021	-1.9	-5.36	1.07e-06	0.000125	7.19
6375			2030114	2.5	5.34	1.14e-06	0.000131	7.14
47	IL26	NM_018402.1	6550008	4.9	5.34	1.14e-06	0.000131	7.14
6377			102760520	-1.9	-5.27	1.52e-06	0.000173	6.9
48	LOC653428	XM_927368.1	580095	1.6	5.25	1.61e-06	0.000181	6.86
49	GZMH	NM_033423.2	2370010	-1.8	-5.25	1.65e-06	0.000184	6.84
50	LILRA3	NM_006865.2	6110037	-2.4	-5.24	1.69e-06	0.000187	6.82
6381			4540494	-2.6	-5.23	1.76e-06	0.000193	6.78
51	RPS21	NM_001024.3	2690338	-2.4	-5.22	1.79e-06	0.000194	6.77
6383			103440338	-1.7	-5.22	1.82e-06	0.000195	6.76
52	HS.555574	Hs.555574	1990082	-2.1	-5.22	1.83e-06	0.000195	6.75
6385			104280487	-2.9	-5.18	2.11e-06	0.00022	6.64
53	UPK3A	NM_006953.2	1990541	-2	-5.18	2.11e-06	0.00022	6.63
54	SNAR-I	NR_024343.1	2370164	-1.7	-5.18	2.11e-06	0.00022	6.63
6388			60204	4.2	5.17	2.18e-06	0.000225	6.61
6389			104120092	-1.5	-5.16	2.27e-06	0.000232	6.57
55	LOC100130828	XM_001726738.1	1580750	2.2	5.16	2.3e-06	0.000233	6.56

Table 17: Top 120 genes (all arrays)

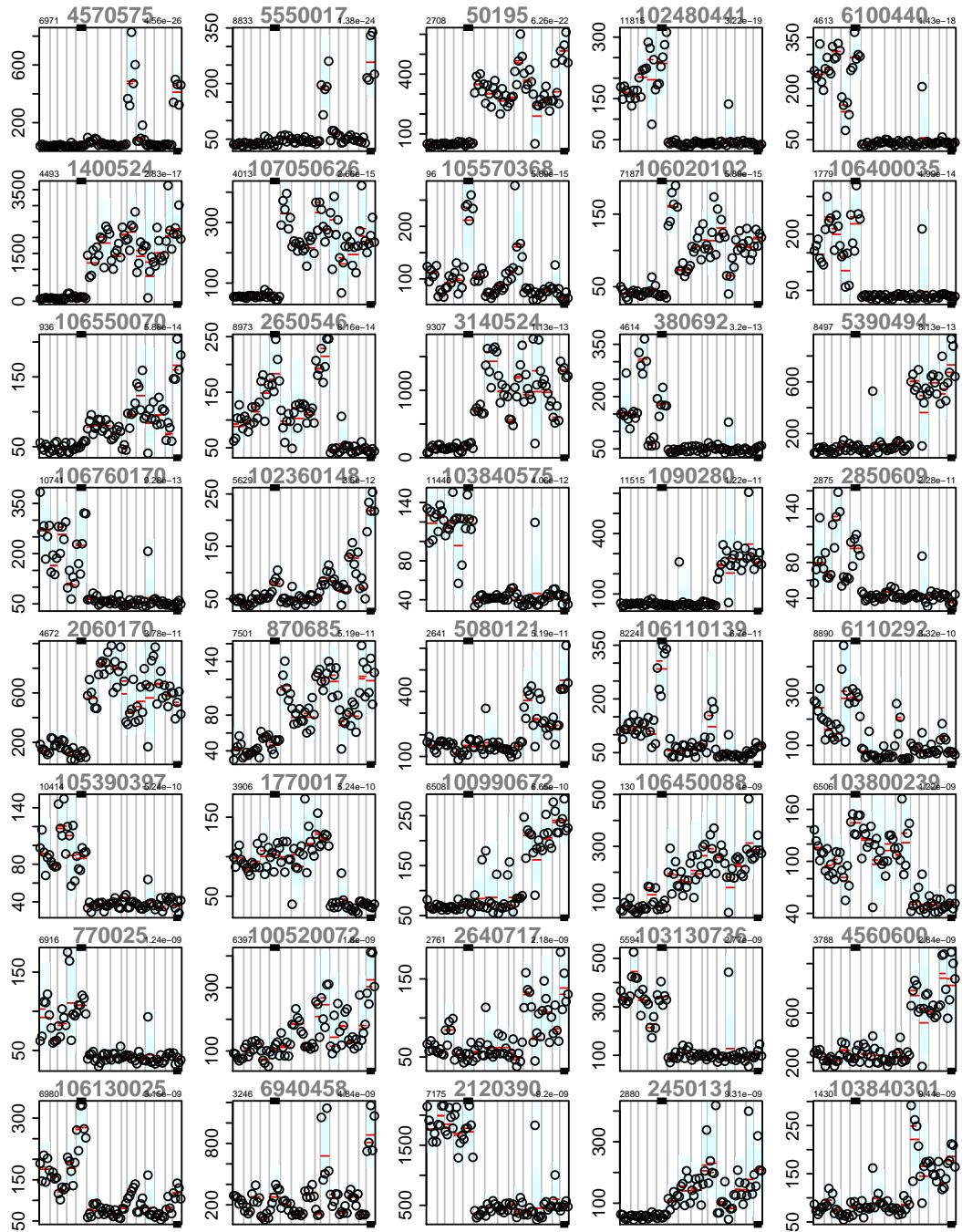


Figure 19a: Top 40 genes for contrast HLP (the groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

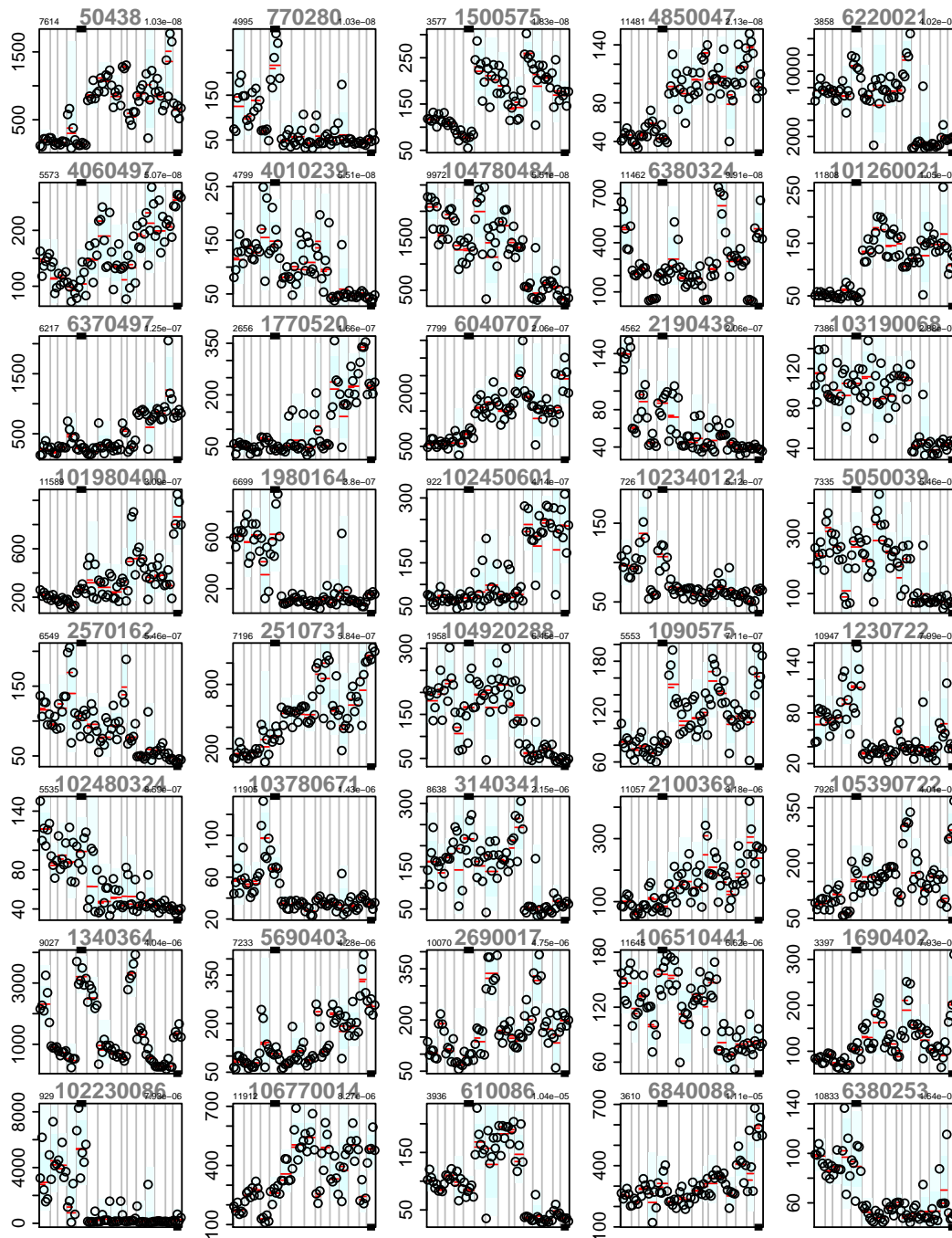


Figure 19b: Significant probes (41–80) for contrast HLP (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($\text{mean} \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB.Amyg—HAB.BAmy—HAB.Cing—HAB.DGyr—HAB.PVNu—NAB.Amyg—NAB.BAmy—NAB.Cing—NAB.DGyr—NAB.PVNu—LAB.Amyg—LAB.BAmy—LAB.Cing—LAB.DGyr—LAB.PVNu.

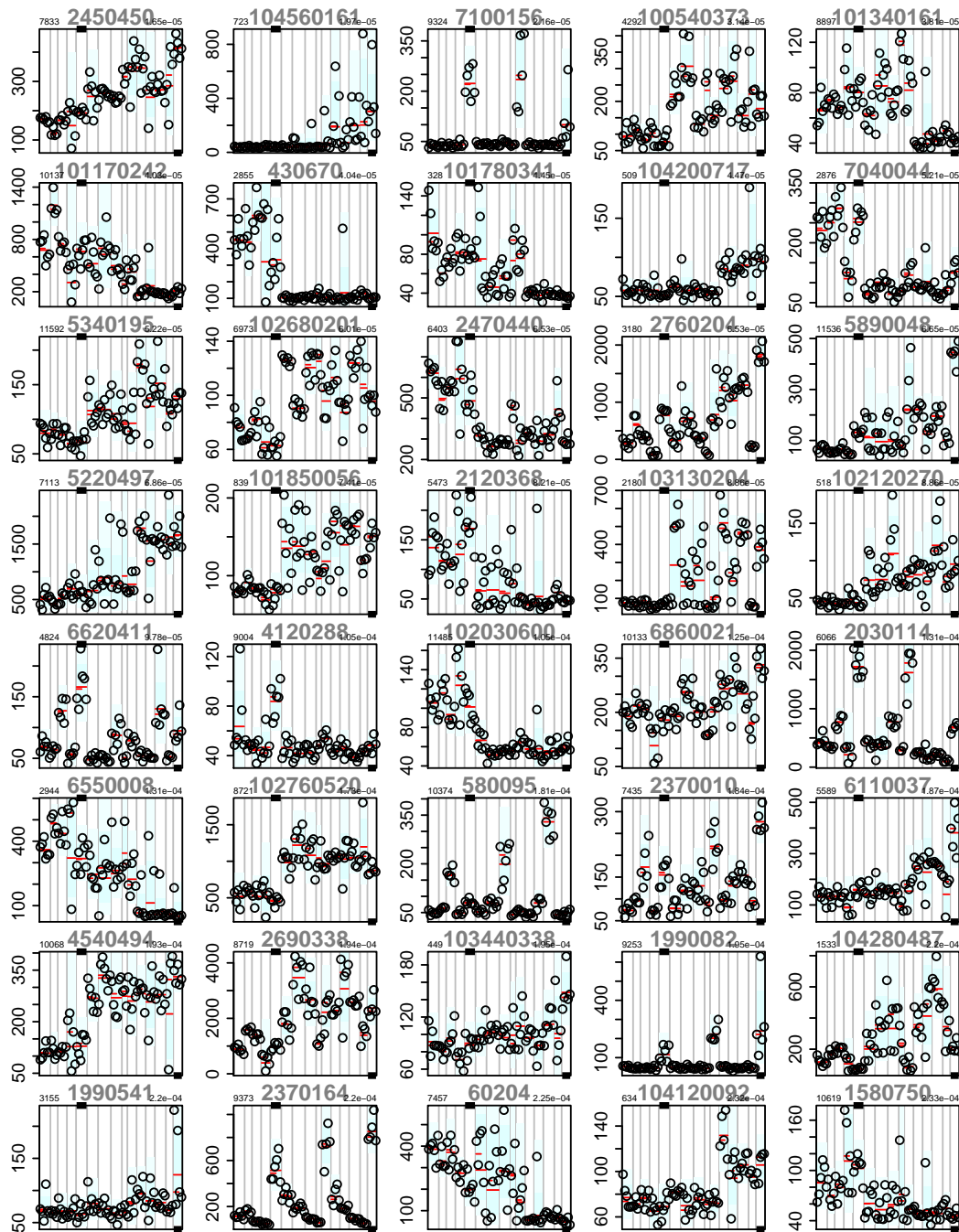


Figure 19c: Significant probes (81–120) for contrast HLP (the two groups defining the contrast are indicated by the bars across the top and bottom border of the plot). Normalised expression for the top genes across all arrays with their respective group mean (solid red line) and median (dashed red line) values. The range ($mean \pm \sigma$) is indicated by the light blue background shading, the adjusted p -values for each gene is shown above the plot. Groups are ordered HAB_Amyg—HAB_BAmy—HAB_Cing—HAB_DGyr—HAB_PVNu—NAB_Amyg—NAB_BAmy—NAB_Cing—NAB_DGyr—NAB_PVNu—LAB_Amyg—LAB_BAmy—LAB_Cing—LAB_DGyr—LAB_PVNu.

4 Synopsis

In summary, the contrasts yield the following results (corrected p -values):

	comparison	min. p-value	1e-06%	1e-04%	0.01%	1%
Combined 1	see page 44	6.5179×10^{-35}	246	314	454	734
HNa	HAB_Amyg – NAB_Amyg	1.7861×10^{-19}	44	69	110	195
HNb	HAB_BAmy – NAB_BAmy	2.7600×10^{-16}	19	41	72	137
HNc	HAB_Cing – NAB_Cing	4.6884×10^{-20}	41	60	92	173
HNd	HAB_DGyr – NAB_DGyr	4.3799×10^{-17}	16	31	71	205
HNp	HAB_PVNu – NAB_PVNu	6.8456×10^{-28}	42	61	94	174
LNa	LAB_Amyg – NAB_Amyg	4.8467×10^{-14}	27	47	86	165
LNb	LAB_BAmy – NAB_BAmy	1.7243×10^{-13}	8	22	45	89
LNc	LAB_Cing – NAB_Cing	1.2695×10^{-18}	31	55	79	188
LNd	LAB_DGyr – NAB_DGyr	1.5911×10^{-15}	14	23	42	85
LNp	LAB_PVNu – NAB_PVNu	8.4970×10^{-16}	22	38	65	146
HLa	HAB_Amyg – LAB_Amyg	1.0003×10^{-18}	33	55	120	224
HLb	HAB_BAmy – LAB_BAmy	6.6944×10^{-11}	6	13	28	79
HLc	HAB_Cing – LAB_Cing	1.4562×10^{-21}	30	58	111	202
HLd	HAB_DGyr – LAB_DGyr	1.8261×10^{-13}	12	34	93	715
HLp	HAB_PVNu – LAB_PVNu	4.5585×10^{-26}	40	66	101	213

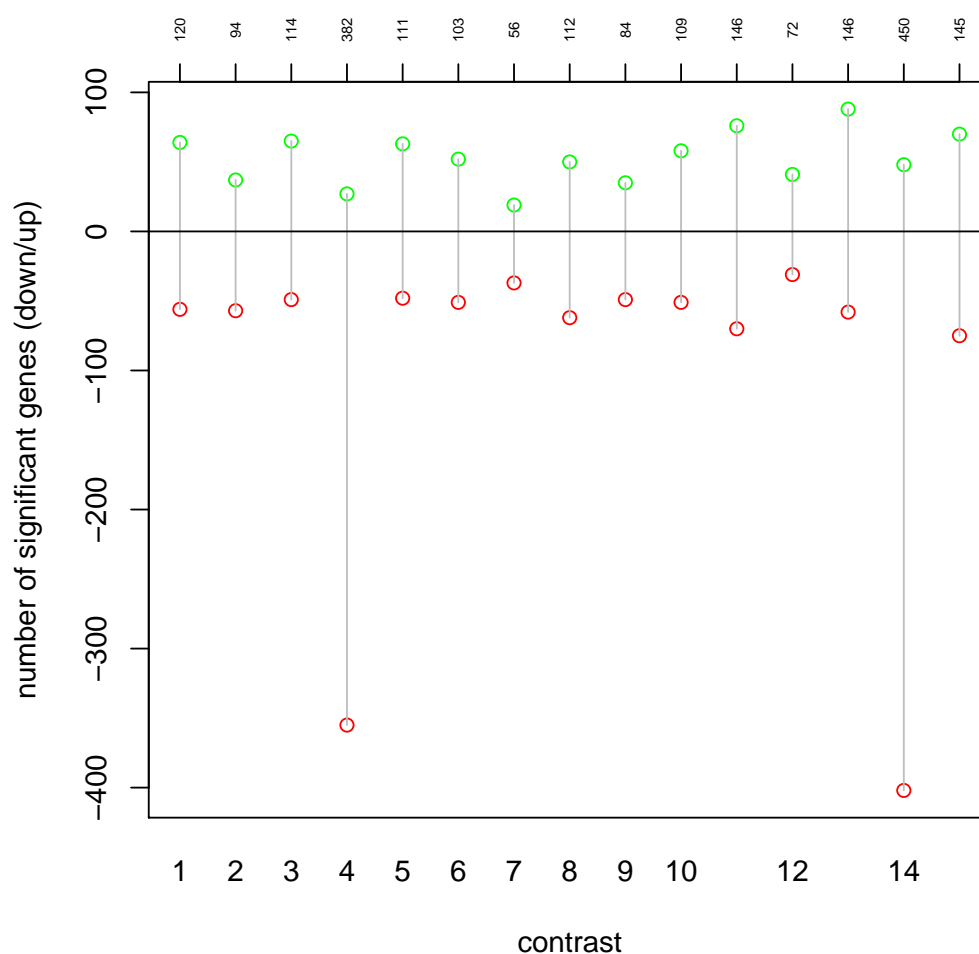
The columns headed by percent values show FDR-thresholds (sometimes referred to as q -values), which are interpreted as follows:

A value of n in the $p\%$ column of contrast C indicates, that of the top n probes $p\%$ are expected to be falsely detected and, therefore, about $n(1 - p\%)$ probes can be considered significant. This does not imply any judgment about which of the probes these are.

Looking over all contrasts for probes that make the FDR-cutoff at least once, we find

	1e-06 %	1e-04 %	0.01 %	1 %
passed	106	162	305	1153

Combining this with a fold-change cutoff of 1.00 we find what is depicted in the following plot. For each contrast the number of significant probes is shown, split in up- and down-regulated, the latter numbers being shown negative. Therefore, the vertical connecting lines represent the total number of “regulated” genes per contrast, which is also shown on the top of the plot.



5 Acknowledgements

This analysis was performed in R⁴ [?], making use of several packages available either via

CRAN (<http://cran.r-project.org/>)

xtable for table output

BioConductor (<http://www.bioconductor.org/>)

beadarray providing routines to handle ILLUMINA[®] BeadStudio data [3]

limma for statistical routines [6]

vsn for normalisation [4]

⁴R version 2.14.0 (2011-10-31)

running Sweave on LCHNLallnew.Rnw version 1.3+, as of 2012-03-23 17:05:16 (last check-out: 2012/01/26 13:47:17).

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File versions:

file	version	saved	last check-in
LCHNLallnew.Rnw	1.3+	as of 2012-03-23 17:05:16	2012/01/26 13:47:17
main_mod.Rnw	1.8+		2011/06/01 20:40:01
myQCP.R	1.5+		2011/06/04 10:34:29

