



Research Core Unit Transcriptomics

Microarray Study Designs using Agilent Expression Arrays

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Introduction

The right choice of the experimental design is an important prerequisite for a successful microarray study. Unlike Affymetrix, the Agilent microarray platform allows to choose between two different modes of hybridization, i.e. Single-Color or Dual-Color.

Both "color modes" have particular characteristics that should be considered before taking a final decision.

In this manual, advantages and disadvantages of both color modes are briefly discussed and examples of appropriate study designs are presented.^{*}**

^{*} Please note that all exemplarily depicted designs refer to just one loaded microarray slide, containing 4 microarrays. Thus, most of these designs are primarily suited for an initial pilot experiment rather than supporting a comprehensive study and meeting stringent statistical demands.

^{**} For further information beyond the scope of this manual we recommend: Patterson et al. (2006), "Performance comparison of one-color and two-color platforms within the MicroArray Quality Control (MAQC) project".

Characteristics of the Dual-Color mode

The underlying methodical concept is a co-hybridization of two differently labeled RNA samples to one microarray. One of the samples to be compared is labeled with Cy3 or Alexa555 (green channel) while the other is labeled with Cy5 or Alexa647 (red channel). Differential mRNA expression is deduced from differences in fluorescence intensities between both channels, measured at the identical position (feature / spot) of one and the same microarray.

Advantages of the Dual-Color mode

- Dual-Color results provided in our standard excel file formats are a bit more clearly arranged as compared to Single-Color results.
- Informative p-values, calculated by Agilent's Feature Extraction software, indicate the probability that the measured difference in intensities reflects a true difference in abundance of the two competing labeled RNA species. By default, these p-values are only available in the Dual-Color mode.
- Dual-Color derived ratios are more robust against moderate hybridization artifacts and thus less prone to false-positive results. This is, because the most frequently occurring hybridization artifacts tend to affect both color channels similarly. Therefore, the resulting detraction is often minimized/equalized after calculating ratios of intensities of the two channels.
- In the case of a common-reference design (Figure 3), locally restricted impairments in the hybridization performance can be recognized by an "abnormal behavior" of the intensities of the common-reference sample.
- In some cases, the dual-color approach is more reliable in detecting small intensity differences; however, there are also exceptions to this rule.

• Depending on the underlying biological study design and the experimenter's objective, the dual-color approach might be advantageous regarding the overall costs, especially if the study should primarily serve as a pilot or screening approach.

Disadvantages of the Dual-Color mode

- The ratio values are compressed, i.e. a 10-fold change in real ends in a fold change of about 6.5, indicated by the microarray results. However, this effect is largely balanced regarding both labeling directions, i.e. green/red and red/green ratios, and throughout the whole intensity (and ratio) range.
- Cy dyes slightly influence each other. Dyes have, for example, particular similarities, i.e. "red-labeled" samples are slightly more similar among each other as compared to "green-labeled" samples (and vice versa). This leads to a slight bias due to these individual dye properties. Anyhow, most of the resulting systematic impairments can be estimated by a "self-self hybridization" (see Figure 4) or can be partly equalized by a dye-swap design (see Figure 2).
- The Dual-Color design is less flexible to future extensions of the study (e.g. depending on the permanent availability of the generated batch of a fluorescently-labeled common reference sample; see Figure 3).

Conclusion

The dual-color mode is recommended for cost-efficient screening approaches and preliminary experiments.

Dual-Color designs

	Block of array	Block of data array 2			Block of data array 3				Block of data array 4 I						
Sorting keys at present, the table is sorted according to sorting key #1 (column A) Gene probe information	Condition 1 Condition 2		Condition 3	Condition 4			Condition 5	Condition 6			Condition 7	Condition 8	•	Flags: "1" suboptin features at least o out of a microarra hybridize	' for nal (in)ne श्री बys ३d)
ABCDEFGHIJKLMNOPQ R S	TU	V W X	Y	Z	AA	AB AC	AD	AE	AF	AG AH	AI	AJ	AK	AL AMAN	
1 SSSSSSSFFSrrpcgnu GeneName	gProces (Proces	RATIO PValueL gli	gProces	Proces F	RATIO F	∾alueL gls	Coces	Proces	RATIO	PValueL gls	gProces	Proces	RATIO	PValueL gls All	
2 ####1### ANM e1 2 Gen#1 H	25 21	0.83 0.6477 0	586	642	1.09	0.5238 0	264	10	0.04	0.0000 0	22	92	4.26	0.0000 0 0	
3 ####2 #9 # ANrre1.1 Gen#2 H	75 349	4.67 0.0000 0	932	1373	1.47	0.0079 0	210	- 4	0.02	0.0000 0	12	669	54.94	0.0000 0 0	
4 ####3 ### AAL1 e1 / 2 Gen#3 H	30 52	1.72 0.0592 0	4720	5451	1.15	0.3106 0	425	13	0.03	0.0000 0	9	138	15.94	0.0000 0 0	
5 ##### 4 ### FAKE e1 / 2 Gen#4 H	26 26	0.99 0.9795 0	120	158	1.31	0.0656 0	158	118	0.75	0.0467 0	2761	40253	14.58	0.0000 0 0	
6 ####5 ### ANTI e1 / 2 Gen#6 H	88 386	4.39 0.0000 0	10	8	0.75	0.4643 0	1094	1076	0.98	0.9030 0	457	8168	17.86	0.0000 0 0	
7 ####6### ANITEL 1 Gen#6 H	426 1307	3.06 0.0000 0	95920	110242	1.15 T	OP2%/ 0	140	45	0.32	0.0000 0	10	52	4.95	0.0000 0 0	
8 ####7 ### ANrre1 1 Gen#7 H	14 37	2.70 0.0191 0	7015	8524	1.22	0.1715 0	158	15	0.09	0.0000 0	12	144	11.90	0.0000 0 0	
9 ####8 ### ANM e1 / 3 Gen#8 H	40 47	1.17 0.5230 0	6357	7737	1.22	0.1682 0	755	1358	1.80	0.0001 0	6	108	18.35	0.0000 0 0	
10 ##### 9 ### # ANM e1 10 Gen#9 H	21 50	2.36 0.0110 0	61965	66687	1.08 T	OP2%I 0	90	101	1.12	0.4807 0	13	87	6.61	0.0000 0 0	
11 ######## ANrre1 1 Gen#10 H	181 705	3.89 0.0000 0	16902	18643	1.10	0.4890 0	81	83	1.02	0.8845 0	12	19	1.64	0.6180 0 0	

Figure 1: Dual-Color design#1:

8 different samples on a single slide.

	Block of data array 1	Block of data array 2	Block of data array 3	Block of data array 4			
	Ļ	Ļ	Ļ	\downarrow			
Sorting keys at present, the table is sorted according to sorting key #1 (column A) Gene probe information	Condition 1 replicate#f	Condition 1 replicate#2 Condition 2 replicate#2	Condition 3 replicate#f	Condition Condit			
	T U V W	X Y Z AA AB A	AC AD AE AF AG A	H AI AJ AK AL AMAN			
1 SSSSSSSFFSrrpdgnu GeneName Dg	Proces (Proces RATIO PValue)	FisrProces gProces RATIO PValueL1	File gProces rProces RATIO PValueL F	Is rProces gProces RATIO PValueL Fig Fig			
2 4 # 5 # # # # # # ANrre1 10 Gen#1 H	59 14221 242.14 0.0000	0 61 17062 280.35 0.0000	0 586 642 1.09 0.5238 0	J 454 651 1.43 0.0131 0 0			
3 6 # # # # # # # # ANrre1 1 Gen#2 H	252 59917 237.99 0.0000	0 342 67459 197.08 0.0000	0 932 1373 1.47 0.0079 0	572 1228 2.15 0.0000 0 0			
4 ######### ANrire1 i 1 Gen#3 H	22 4666 207.71 0.0000	0 25 3806 154.03 0.0000	0 4720 5451 1.15 0.3106 0	3712 5212 1.40 0.0191 0 0			
5 ########## ANrire1 /10 Gen#4 H	148 21196 143.40 0.0000	0 172 18434 107.08 0.0000	0 120 158 1.31 0.0656 0	116 101 0.86 0.3123 0 0			
6 ########### ANrre1 / 2 Gen#6 H	3 273 102.66 0.0000	0 5 331 72.44 0.0000	0 10 8 0.75 0.4643 0	1 8 9 1.07 0.8762 0 0			
	2534 1//986 /0.23 0.0000	0 3072 302685 98.52 0.0000		1 83432 99297 1.19 0.2610 0 0			
S WWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWWW	14 936 07.18 0.0000	0 10 596 39.01 0.0000	0 2013 8324 1.22 0.1/15 0	4431 6587 1.49 0.0066 0 0 7432 6330 0.99 0.4100 0 0			
10 mm mm mm mm Abradt 1 Gente	12 004 00.13 0.000	0 2459 139352 56 29 0.0000	0 61965 6697 1.09 0.2610 0	1 56421 72242 1 29 0 0827 0 0			
11 ############ ANrre1.11 Gen#10 H	106 5534 52.26 0.0000	0 170 4293 25.26 0.0000	0 16902 18643 1.10 0.4890 0	19055 17540 0.92 0.5585 0 0			

Figure 2: Dual-Color design#2:

4 different samples on a slide including two replicates per sample and a dye-swap.

		Block of data array 1 ↓			Block of data array 2 ↓			Block of data array 3 ↓				Block of data array 4 ↓					
Sorting keys at present, the table is sorted according to sorting key #1 (column A) Gene probe information	Gene probe information ↓	Condition 1	Condition 2			Condition 1	Condition 3			Condition 1	Condition 4			Condition 1	Condition 5		Flags: "1" fo suboptimal features (in at least one out of all microarrays hybridized)
ABCDEFGHIJ		T	U	V	w x	Y	Z	AA	AB AC	AD	AE	AF	AG AH	Al	AJ	AK	AL AMAN
1 SSSSSSSFF	SrirpdgnuiGeneName	gProces	Proces	RATIO	PValueL FI:	gProces	rProces	RATIO	PValueL Fla	gProces	rProces	RATIO	PValueL Fla	gProces	rProces	RATIO	PValueLFI
2 ##### # # # # # #	Neret 1 Gent	230	1320	0.05	0.0000 0	201	725	3.61	0.0000 0	173	3	0.02	0.0000 0	204	10	0.04	0.0000 0 0
	Al 1 e1 / Gen#3	443	2932	6.62	0,0000 0	374	6	0.02	0.0000 0	346	B	0.02	0.0000 0	425	13	0.03	0.0000 0 0
5 # # # # 4 # # # #	AKE e1 1 Gen#4	164	618	3.78	0.0000 0	138	12	0.09	0.0000 0	124	3	0.03	0.0000 0	158	118	0.75	0.0467 0 0
6 ####5###	Nrre1 2 Gen#5	1027	879	0.86	0.2750 0	957	1831	1.91	0.0000 0	911	26	0.03	0.0000 0	1094	1076	0.98	0.9030 0 0
7 # # # # 6 # # # #	Nrre1 1 Gen#6	1 144	15	0.10	0.0000 0	126	373	2.95	0.0000 0	121	4	0.03	0.0000 0	140	45	0.32	0.0000 0 0
8 # # # # 7 # # # A	Nrre1 1 Gen#7	179	9	0.05	0.0000 0	171	613	3.58	0.0000 0	141	5	0.03	0.0000 0	158	15	0.09	0.0000 0 0
9 # # # # 8 # # # #	NM e1 3 Gen#8	H 765	2633	3.44	0.0000 0	657	335	0.51	0.0000 0	595	26	0.04	0.0000 0	755	1358	1.80	0.0001 0 0
10 # # # # 9 # # # #	NM e1 10 Gen#9	H 89	123	1.38	0.0632 0	84	129	1.53	0.0131 0	81	4	0.05	0.0000 0	90	101	1.12	0.4807 0 0
11 # # # # # # # # A	Nrre1 2 Gen#10	83	258	3.11	0.0000 0	68	55	0.81	0.2516 0	64	3	0.05	0.0000 0	81	83	1.02	0.8845 0 0

Figure 3: Dual-Color design#3:

5 (1+4) different samples on a slide including a common reference sample.



Figure 4: Dual-Color design#4:

4 (1+3) different samples on a slide including a common reference and a self-self-hybridization.



Figure 5: Dual-Color design#5:

2 (1+1) different samples on a slide with 4 replicates per sample and a balanced dye-swap design.

Characteristics of the Single-Color mode

The underlying methodical concept is a hybridization of one labeled RNA sample (labeled with Cy3 or Alexa555; green channel) to one microarray. Differential mRNA expression is deduced from differences in fluorescence intensity comparing a particular scanned region (feature/spot) of **one** microarray with the same region of **one** (or several) **other** microarray(s).

Advantages of the Single-Color mode

- The experimental design is quite simple: one sample one microarray one data set.
- A study can be easily extended by subsequently generated samples that shall be analyzed in the context of already existing data.
- There is no need to take dye biases into account while defining the study design.
- A big advantage of the single-color mode is the "equivalence" of all samples to be compared. Every single sample can be compared with every other sample under

exactly the same consistent accuracy. The deduced pairwise comparisons again can be compared with each other, i.e. "ratios of ratios".

- Some analyses perform optimal just with single-color data such as (intensity-based) clustering and principal component analysis.
- There is no compression of ratio values as evident as with dual-color data. Single-Color designs are more appropriate to quantify absolute differences in mRNA abundance.

Disadvantages of the Single-Color mode

- Based on our experience with the Agilent microarray platform, slight impairments in hybridization performance generally occur sporadically, rather than systematically (this means: different regions and spots are adversely affected on different microarrays). Unlike in the dual-color mode, these inaccuracies are not equalized when ratios are generated. Thus, misinterpretations can result (false positively regulated candidates), especially in cases when i) only one probe per mRNA is present on the array, or ii) the number of analyzed samples (arrays) per condition is restricted to n=1. However, in the majority of cases, technical impairments should be indicated by the flag entries provided.
- The provided standard result file format might be a bit less clearly arranged than in case of a dual-color design.
- A p-value is not provided in our standard result table.

Conclusion

The single-color platform is recommended for large microarray studies and/or in cases in which comprehensive data analyses are planned.

Single-Color designs



Figure 6: Single-Color design#1:

4 different samples on a slide.



Figure 7: Single-Color design#2:

2 different samples on a slide including 2 replicates.

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