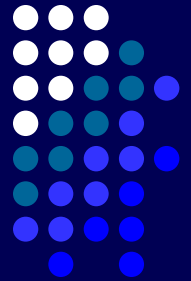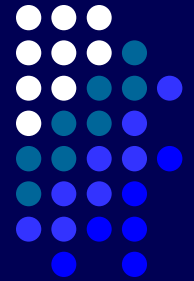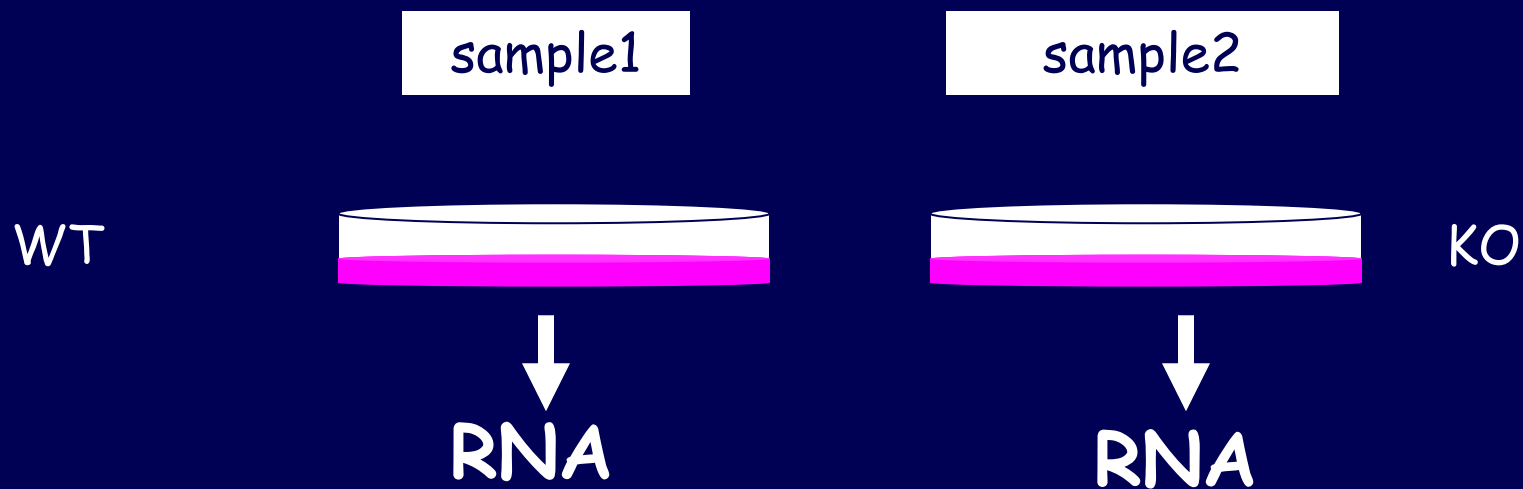# Data Analysis of DNA Microarrays

Can we detect knockdown of gene expression using DNA microarrays?

Starting with two biological samples

sample1

sample2

WT

KO

RNA

RNA

A. RNA Isolation

WT KO
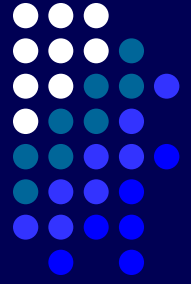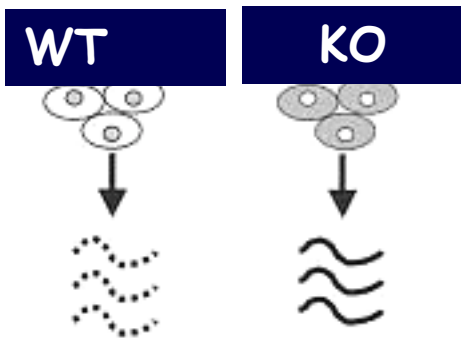
B. cDNA Generation

C. Labeling of Probe

Reverse Transcriptase

Fluorescent Tags

+
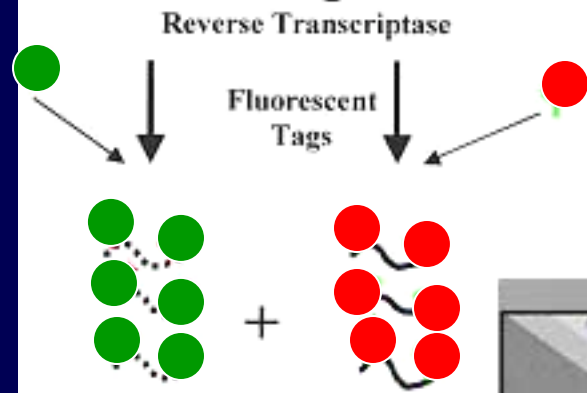
D. Hybridization to Array

E. Imaging

Sample A > B

Sample B > A

Sample A = B
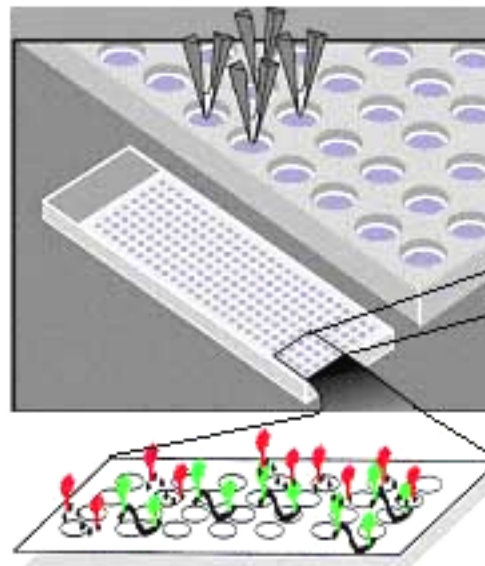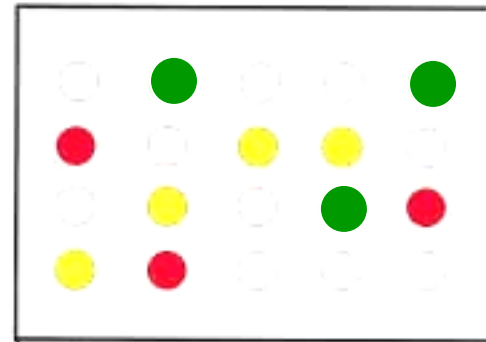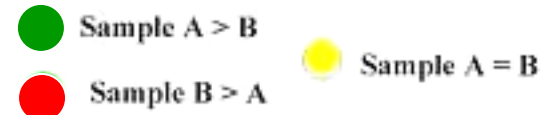
Green=cy3
Red=cy5
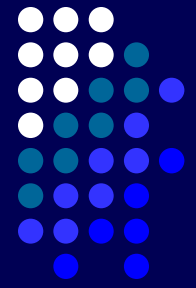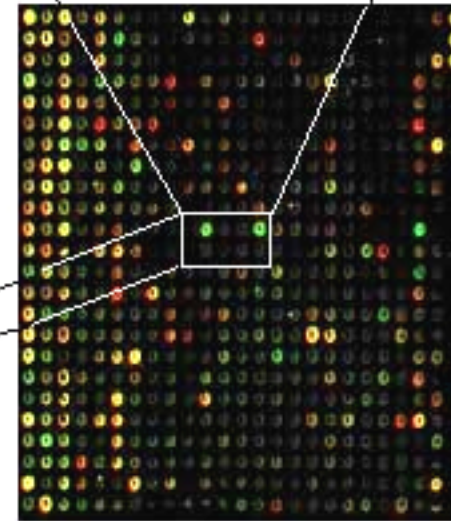
Microarray Measurements

Signal: Spotted arrays

Spotted microarrays

www.molgen.mpg.de

cy5

cy3
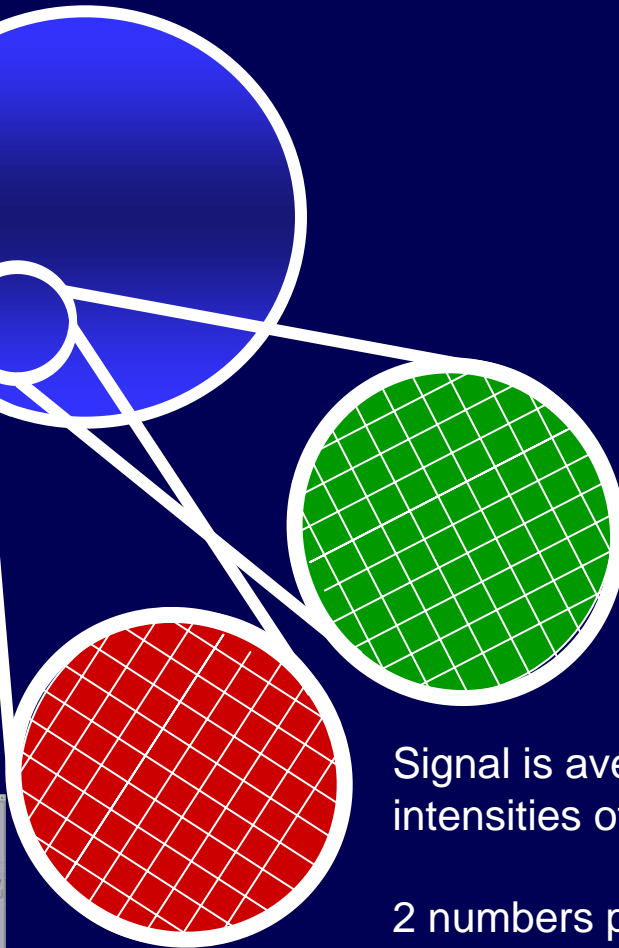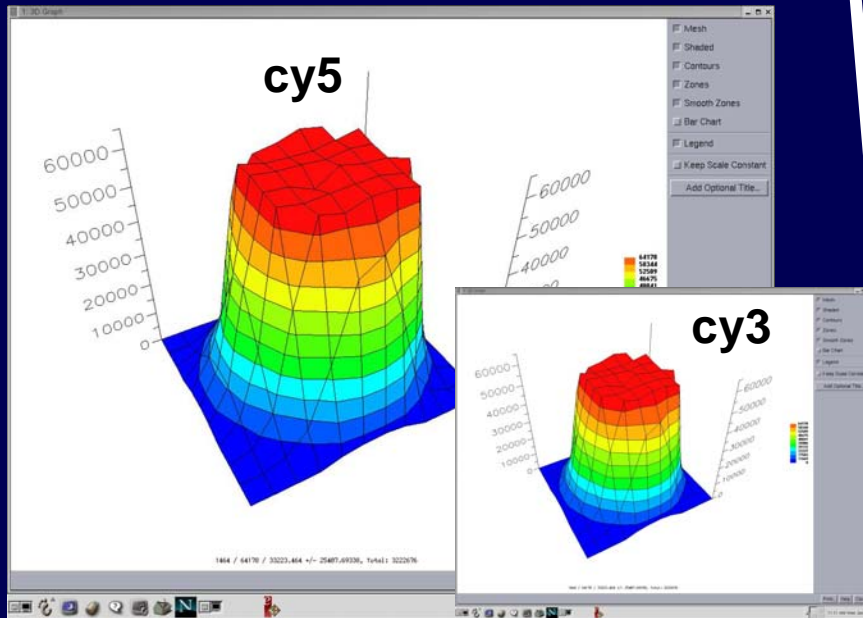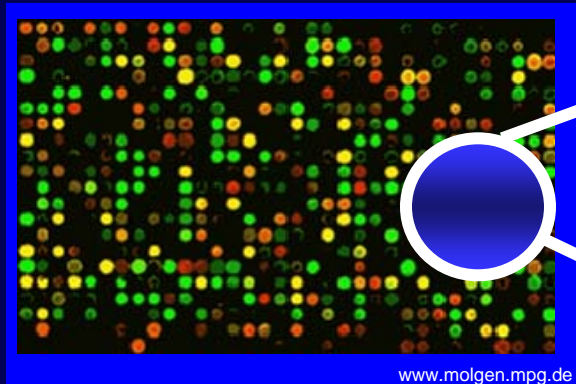
Signal is average of pixel intensities of spot

2 numbers per spot

Red=500
Green=100
Red/Green=5 (5 Fold Greater)
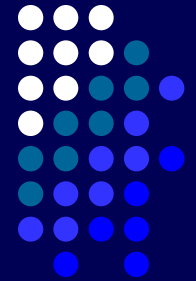
Processing microarrays:
Scanning and Image analysis

microarray → Agilent scanner → image → Feature extractor → Txt file
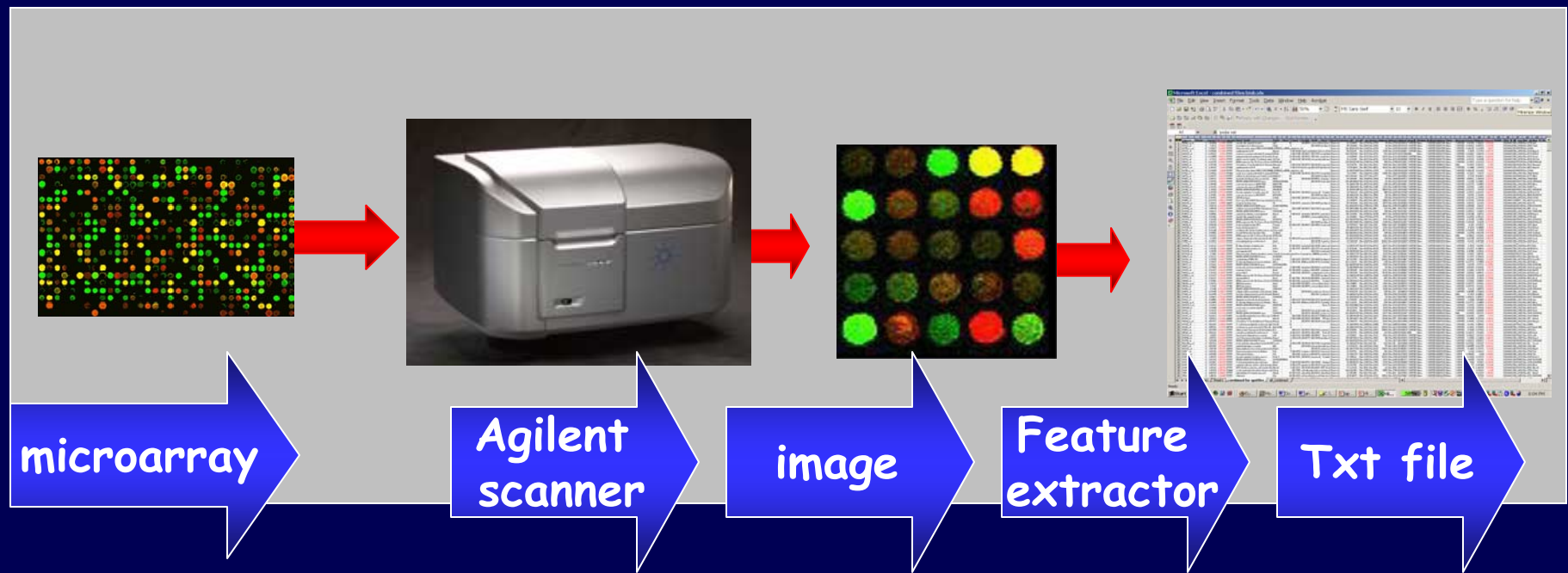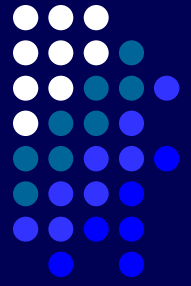
File is large
Need to truncate

Spot Intensity: Mean or Median?
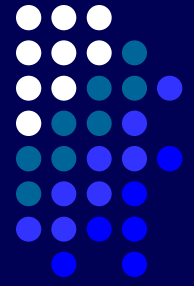
- Which is more affected by extremes?
- Which is better estimate of spot intensity?

Image

Median=60,000
Mean=60,000

Median=60,000
Mean=70,000

All pixels of a spot are used to calculate a Mean or Median Intensity

Subtracting Background

Microsoft Excel - US22502724_SLOT01_S01_GE2-v4_91_1_11

File Edit View Insert Format Tools Data Window S-PLUS Help Adobe PDF

Type a question for help

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A21   TYPE

Reduce number of rows
Remove rows 1-21

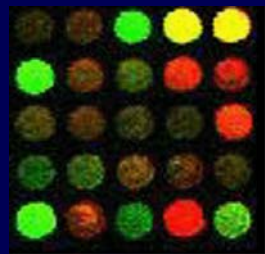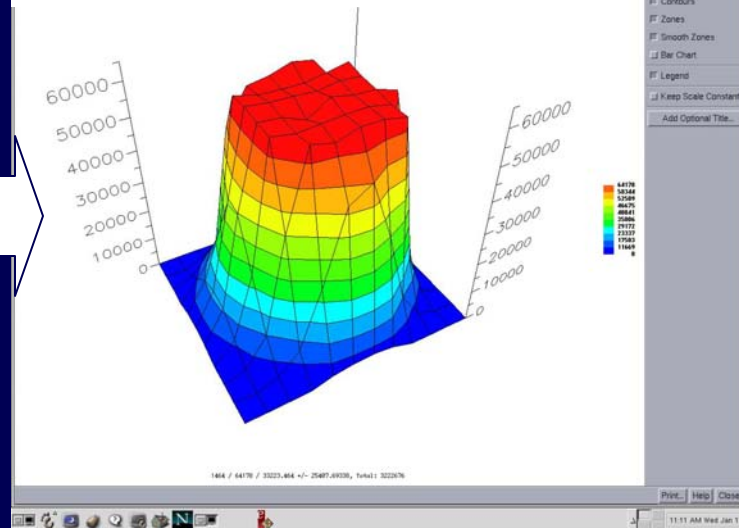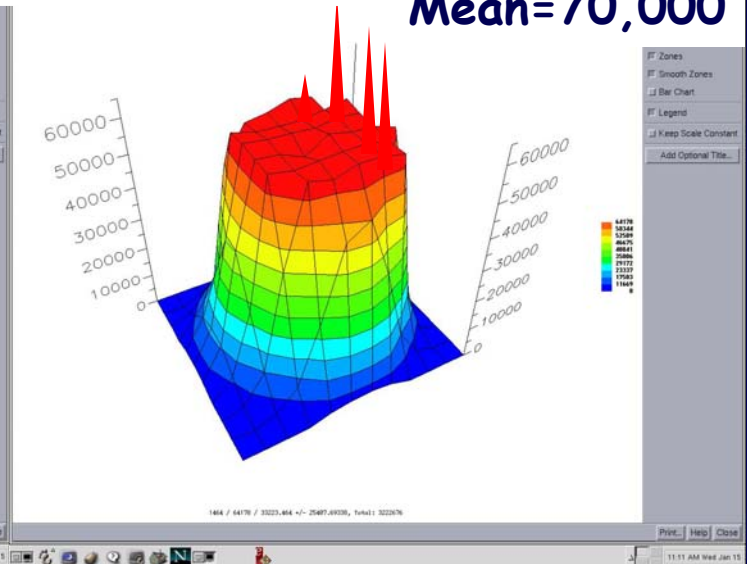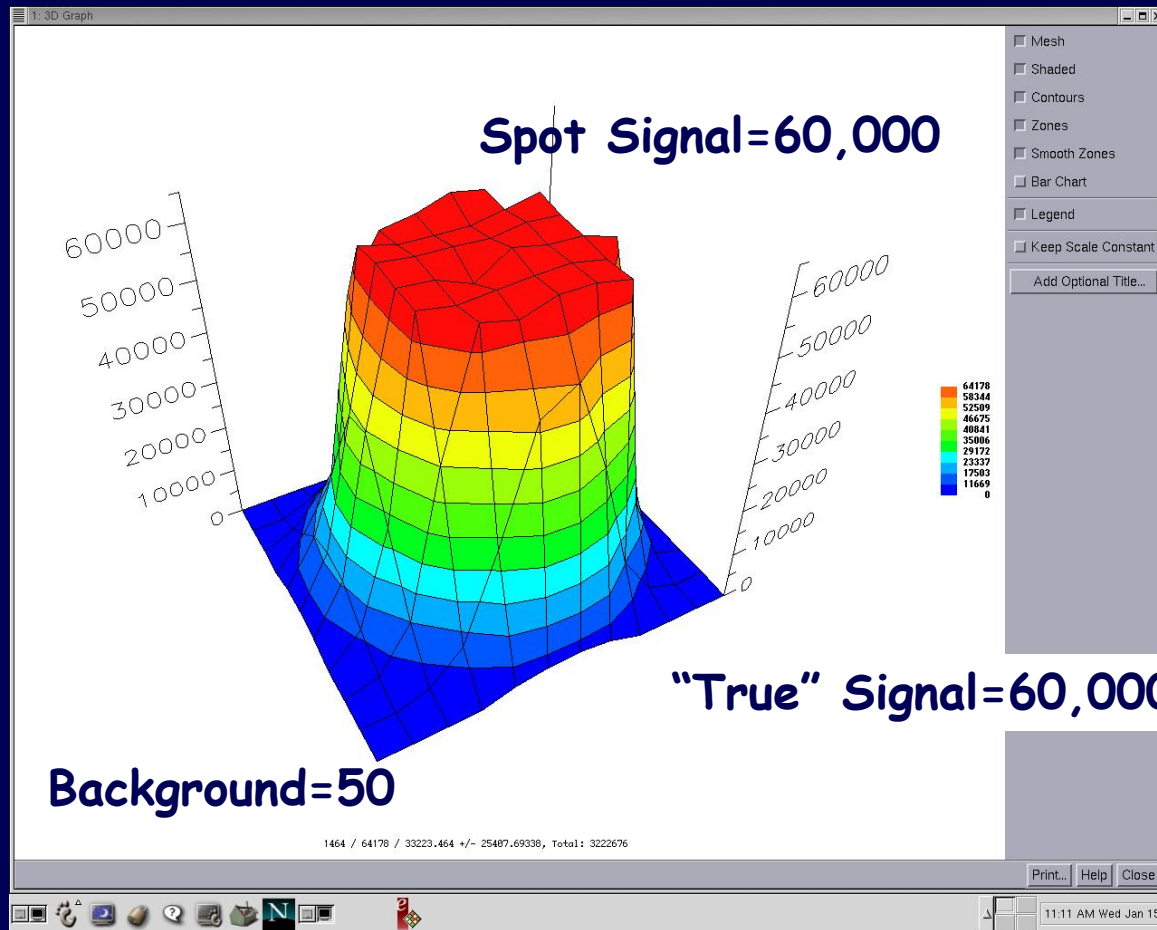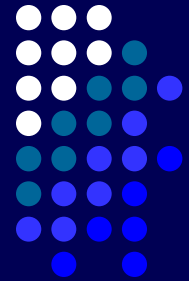|	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	TYPE	text	text	text	text	integer	float	float	text	text	text	integer	integer	integer	integer	float	float	flo
2	FEPARAM	Protocol_N	Protocol_d	Scan_Date	Scan_Sca	Scan_Num	Scan_Micr	Scan_Micr	Scan_Orig	Grid_Name	Grid_Date	Grid_Num	Grid_Num	Grid_Numf	Grid_Num	Grid_Row	Grid_ColS	Gr
3	en_reject_	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	SpotAnaly	OutlierFlag	OutlierFlag	Ou
4	tionOn	BGSubtrac	BGSubtractor_Spa!															
5	tialDetr																	
6	endOn	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	BGSubtrac	Dy
7	ingleTextF	FeatureEx	FeatureEx	FeatureEx	FeatureExtractor_OutputQCReportGraphText												
8	DATA	GE2-v4_91	########	########	Agilent Tec	2	10	10	f9acf157-2	013384_D	########	1	1	101	107	188.148	211.667	
9	*																	
10	TYPE	float	float	float	integer											float	float	int
11	float	float	float	integer	integer													
12	STATS	gDarkOffs	gDarkOffs	gDarkOffs	gDarkOffs									g2B	gRatioSig2	rRatioSig2	gN
13	rcntBGPo	TotalPrcntl	gNumNegE	gNonCtrlN	gLinearDy									alDe	gSpatialDe	gSpatialDe	rS
14	w2	gNegCtrlN	gNegCtrlA	gNegCtrlSI	gNe!													
15	gCtrlAve																	
16	BGSubSig	gNegCtrlSI	rNegCtrlNu	rNegCtrlAv	rNegCtrlSD										ligh	NonCtrlAb	NonCtrlSD	Nc
17	rOutlierFla	OutlierFlag	OutlierFlag	GriddingSt	NumGeneN													
18	DATA	38.799	39	5.61421	1000	65251	38.885	38	24.25	1000	65199	2.16982	1.37143	1.96661	1.24578	1.10333	1.10086	
19	-2.60514	4.6578	3294.4	3484.8	32.2301	60.4006	196.637	247.73	17.3607	45.3759	2.04715	1.35981	0	1443	9593	34.0256	24.3342	
20	*																	
21	TYPE	integer	integer	integer	integer	text	integer	integer	text	text	text	text	float	float	float	float	float	flo
22	FEATURE	FeatureNu	Row	Col	SubTypeM	SubTypeN	ProbeUID	ControlTyp	ProbeNam	GeneNam	Systemati	Descriptio	PositionX	PositionY	LogRatio	LogRatioE	PValueLog	gS
23		rBGUsed	gBGSDUs	rBGSDUs	IsNormaliz	gDyeNorm	rDyeNorm	gDyeNorm	rDyeNorm	DyeNormC	ErrorMode	xDev	gSpatialDe	rSpatialDe	gSpatialDe	rSpatialDe	SpotExten	Sp
24	DATA	1	1	1	260	BrightCorn	0	1	BrightCorn	BrightCorn	BrightCorner		345.769	143	0.00E+00	1.34E+00	1.00E+00	
25	DATA	2	1	2	66	Structural	1	-1	(-)3xSLv1	NegativeC	NegativeControl		366.145	142.908	0.00E+00	1.25E+00	1.00E+00	
26	DATA	3	1	3	0		2	0	A_06_P24	NHX1	YDR456W	BioProces	388.37	142.356	2.82E-01	6.91E-02	4.61E-05	
27	DATA	4	1	4	0		3	0	A_06_P72	SKI3	YPR189W	BioProces	408.277	141.213	6.22E-01	3.37E-01	6.47E-02	
28	DATA	5	1	5	0		4	0	A_06_P25	POL5	YEL055C	BioProces	430.844	142.797	0.00E+00	1.31E+00	1.00E+00	
29	DATA	6	1	6	0		5	0	A_06_P65	ORF:YOR	YOR200W	BioProces	452.726	141.608	0.00E+00	1.26E+00	1.00E+00	
30	DATA	7	1	7	0		6	0	A_06_P49	GIS3	YLR094C	BioProces	471.939	142.596	-5.82E-01	8.93E-02	7.23E-11	
31	DATA	8	1	8	1028	E1A	7	1	(+)E1A_r6	E1A_r60_r	E1A_r60_n11		494.81	142.282	0.00E+00	1.36E+00	1.00E+00	
32	DATA	9	1	9	0		8	0	A_06_P69	ALG5	YPL227C	BioProces	516	142.176	0.00E+00	1.26E+00	1.00E+00	
33	DATA	10	1	10	0		9	0	A_06_P51	SEC61	YLR378C	BioProces	536.754	141.593	-1.53E-01	7.46E-02	4.00E-02	
34	DATA	11	1	11	0		10	0	A_06_P25	TTR1	YDR513W	BioProces	556.899	141.861	3.51E-01	6.94E-02	4.25E-07	
35	DATA	12	1	12	0		11	0	A_06_P42	ORF:YJR0	YJR014W	BioProces	579.596	142.096	6.26E-02	6.33E-02	3.23E-01	
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37	DATA	14	1	14	0		13	0	A_06_P18	CDC48	YDL126C	BioProces	621.394	142.019	5.43E-02	6.16E-02	3.78E-01	

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AS1   rBGMedianSignal

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	FEATURE	FeatureNu	Row	Col	SubTypeM	SubTypeN	ProbeUID	ControlTyp	ProbeNam	GeneNam	Systemati	Descriptio	PositionX	PositionY	LogRatio	LogRatioE	PValueLog	gS
2		rBGUsed	gBGSDUs	rBGSDUse	IsNormaliz	gDyeNorm	rDyeNorm	gDyeNorm	rDyeNorm	DyeNormC	ErrorMode	xDev	gSpatialDe	rSpatialDe	gSpatialDe	rSpatialDe	SpotExten	Sp
3	DATA	1	1	1	260	BrightCorn	0	1	BrightCorn	BrightCorn	BrightCorner		345.769	143	0.00E+00	1.34E+00	1.00E+00	
4	DATA	2	1	2	66	Structural	1	-1	(-)3xSLv1	NegativeC	NegativeControl		366.145	142.908	0.00E+00	1.25E+00	1.00E+00	
5	DATA	3	1	3	0		2	0	A_06_P24	NHX1	YDR456W	BioProces	388.37	142.356	2.82E-01	6.91E-02	4.61E-05	
6	DATA	4	1	4	0		3	0	A_06_P72	SKI3	YPR189W	BioProces	408.277	141.213	6.22E-02	3.37E-01	6.47E-02	
7	DATA	5	1	5	0		4	0	A_06_P25	POL5	YEL055C	BioProces	430.844	142.797	0.00E+00	1.31E+00	1.00E+00	
8	DATA	6	1	6	0		5	0	A_06_P65	ORF:YOR:	YOR200W	BioProces	452.726	141.608	0.00E+00	1.26E+00	1.00E+00	
9	DATA	7	1	7	0		6	0	A_06_P49	GIS3	YLR094C	BioProces	471.939	142.596	-5.82E-01	8.93E-02	7.23E-11	
10	DATA	8	1	8	1028	E1A	7	1	(+)E1A_r6	E1A_r60_r	E1A_r60_n11		494.81	142.282	0.00E+00	1.36E+00	1.00E+00	
11	DATA	9	1	9	0		8	0	A_06_P69	ALG5	YPL227C	BioProces	516	142.176	0.00E+00	1.26E+00	1.00E+00	
12	DATA	10	1	10	0		9	0	A_06_P51	SEC61	YLR378C	BioProces	536.754	141.593	-1.53E-01	7.46E-02	4.00E-02	
13	DATA	11	1	11	0		10	0	A_06_P25	TTR1	YDR513W	BioProces	556.899	141.861	3.51E-01	6.94E-02	4.25E-07	
14	DATA	12	1	12	0		11	0	A_06_P42	ORF:YJR0	YJR014W	BioProces	579.596	142.096	6.26E-02	6.33E-02	3.23E-01	
15	DATA																	
16	DATA																	
17	DATA																	
18	DATA																	
19	DATA																	
20	DATA																	
21	DATA																	
22	DATA																	
23	DATA	21	1	21	0		20	0	A_06_P14	ISW1	YBR245C	BioProces	768.852	143.492	3.05E-01	6.24E-02	2.13E-04	
24	DATA	22	1	22	1028	E1A	21	1	(+)E1A_r6	E1A_r60_a	E1A_r60_a97		789.352	141.926	0.00E+00	1.31E+00	1.00E+00	
25	DATA	23	1	23	0		22	0	A_06_P64	PIN2	YOR104W	BioProces	811.786	142.3	5.85E-02	9.91E-02	5.55E-01	
26	DATA	24	1	24	0		23	0	A_06_P66	HSD1	YOR311C	BioProces	832.746	141.701	-7.91E-02	6.68E-02	2.36E-01	
27	DATA	25	1	25	0		24	0	A_06_P14	CDC47	YBR202W	BioProces	854.538	142.077	2.68E-01	1.68E-01	1.11E-01	
28	DATA	26	1	26	0		25	0	A_06_P48	MEF1	YLR069C	BioProces	875.175	141.786	2.37E-01	8.27E-02	4.20E-03	
29	DATA	27	1	27	0		26	0	A_06_P12	ILS1	YBL076C	BioProces	893.364	141.955	1.08E+01	3.84E-01	5.04E-03	
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32	DATA	30	1	30	0		28	0	A_06_P19	PTP1	YDL230W	BioProces	960.925	141.403	-1.48E-02	7.92E-02	8.52E-01	
33	DATA	31	1	31	0		29	0	A_06_P17	ARP2	YDL029W	BioProces	981.333	142.527	3.54E-01	6.97E-02	3.81E-07	
34	DATA	32	1	32	0		30	0	A_06_P26	PRE1	YER012W	BioProces	1001.41	141.744	2.77E-01	6.68E-02	3.39E-05	
35	DATA	33	1	33	0		31	0	A_06_P52	FPR4	YLR449W	BioProces	1022.7	143	3.43E-01	7.88E-02	1.36E-05	
36	DATA	34	1	34	0		32	0	A_06_P52	ORF:YLR4	YLR455W	BioProces	1044.45	141.078	-2.36E-01	6.89E-02	6.31E-04	
37	DATA	35	1	35	0		33	0	A_06_P47	UBI4	YLL039C	BioProces	1066.4	142.455	-1.94E-01	6.39E-02	2.45E-03	

Copy columns A, G, I, J, K, L, AI, AR, AS into new sheet**

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Type a question for help

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A1   fx   FEATURES

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	FEATURE	ProbeUID	ProbeNam	GeneName	Systematic	gMedianSi	rMedianSig	gBGMedia	rBGMedia	Signal							
2		rDyeNorms	rDyeNorml	DyeNormC	ErrorModel												
3	DATA	0	BrightCorn	BrightCorn	BrightCorn	85	86.5	65	83								
4	DATA	1	(-)3xSLv1	NegativeC	NegativeC	83	84	65	83								
5	DATA	2	A_06_P24	NHX1	YDR456W	336	609	65	83								
6	DATA	3	A_06_P72	SKI3	YPR189W	92	119.5	66	83								
7	DATA	4	A_06_P25	POL5	YEL055C	80.5	85.5	66	81								
8	DATA	5	A_06_P65	ORF:YOR	YOR200W	81	82	65	82								
9	DATA	6	A_06_P49	GIS3	YLR094C	504	214	65	83								
10	DATA	7	(+)E1A_r6	E1A_r60_r	E1A_r60_r	77	82.5	64	83								
11	DATA	8	A_06_P69	ALG5	YPL227C	80	85	65	82								
12	DATA	9	A_06_P51	SEC61	YLR378C	317	207	65	82								
13	DATA	10	A_06_P25	TTR1	YDR513W	1269	3859	66	84								
14	DATA	11	A_06_P42	ORF:YJR0	YJR014W	475	660	66	83								
15	DATA	12	A_06_P48	SSK1	YLR006C	334	185	66	82								
16	DATA	13	A_06_P18	CDC48	YDL126C	5405	11816	66	83								
17	DATA	14	(+)E1A_r6	E1A_r60_a	E1A_r60_a	77	80	67	82								
18	DATA	15	A_06_P18	QRI1	YDL103C	93	266	68	84								
19	DATA	16	A_06_P10	ORF:Q018	Q0182	75	91	66	82								
20	DATA	17	A_06_P13	SUP45	YBR143C	639	602	66	81								
21	DATA	18	A_06_P16	RPS14A	YCR031C	5088	19468	66	81								
22	DATA	19	A_06_P56	ORF:YMR	YMR172C-	85	90	69	82								
23	DATA	20	A_06_P14	ISW1	YBR245C	180	299	70	83								
24	DATA	21	(+)E1A_r6	E1A_r60_a	E1A_r60_a	77	82	67	83								
25	DATA	22	A_06_P64	PIN2	YOR104W	166	180	65	83								
26	DATA	23	A_06_P66	HSD1	YOR311C	394.5	322.5	65	83								
27	DATA	24	A_06_P14	CDC47	YBR202W	105	144	64	82								
28	DATA	25	A_06_P48	MEF1	YLR069C	179.5	258	65	83								
29	DATA	26	A_06_P12	ILS1	YBL076C	86	108	65	82								
30	DATA	27	A_06_P17	PRP11	YDL043C	74	81	64	82								
31	DATA	21	(+)E1A_r6	E1A_r60_a	E1A_r60_a	73	81	63	80								
32	DATA	28	A_06_P19	PTP1	YDL230W	188	209	65	81								
33	DATA	29	A_06_P17	ARP2	YDL029W	849	2005	64	83								
34	DATA	30	A_06_P26	PRE1	YER012W	770	1640	65	82								
35	DATA	31	A_06_P52	FPR4	YLR449W	197	378	64	83								
36	DATA	32	A_06_P52	ORF:YLR4	YLR455W	479	324	64	83								
37	DATA	33	A_06_P47	UBI4	YLL039C	25207	38522	65	84								

Sheet1 / Sheet2 / Sheet3 /

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Microsoft Excel - Book1

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Type a question for help

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SUM   =F3-H3

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	FEATURE	ProbeUID	ProbeNam	GeneName	Systemati	gMedianSi	rMedianSig	gBGMedia	rBGMedianSignal								
2		rDyeNorm	rDyeNorm	DyeNormC	ErrorModel												
3	DATA	0	BrightCorn	BrightCorn	BrightCorn	85	86.5	65	83	=F3-H3							
4	DATA	1	(-)3xSLv1	NegativeC	NegativeC	83	84	65	83								
5	DATA	2	A_06_P24	NHX1	YDR456W	336	609	65	83								
6	DATA	3	A_06_P72	SKI3	YPR189W	92	119.5	66	83								
7	DATA	4	A_06_P25	POL5	YEL055C	80.5	85.5	66	81								
8	DATA	5	A_06_P65	ORF:YOR	YOR200W	81	82	65	82								
9	DATA	6	A_06_P49	GIS3	YLR094C	504	214	65	83								
10	DATA	7	(+)E1A_r6	E1A_r60_r	E1A_r60_r	77	82.5	64	83								
11	DATA	8	A_06_P69	ALG5	YPL227C	80	85	65	82								
12	DATA	9	A_06_P51	SEC61	YLR378C	317	207	65	82								
13	DATA	10	A_06_P25	TTR1	YDR513W	1269	3859	66	84								
14	DATA	11	A_06_P42	ORF:YJR0	YJR014W	475	660	66	83								
15	DATA	12	A_06_P48	SSK1	YLR006C	334	185	66	82								
16	DATA	13	A_06_P18	CDC48	YDL126C	5405	11816	66	83								
17	DATA	14	(+)E1A_r6	E1A_r60_a	E1A_r60_a	77	80	67	82								
18	DATA	15															
19	DATA	16															
20	DATA	17															
21	DATA	18															
22	DATA	19															
23	DATA	20															
24	DATA	21															
25	DATA	22															
26	DATA	23															
27	DATA	24	A_06_P14	CDC47	YBR202W	105	144	64	82								
28	DATA	25	A_06_P48	MEF1	YLR069C	179.5	258	65	83								
29	DATA	26	A_06_P12	ILS1	YBL076C	86	108	65	82								
30	DATA	27	A_06_P17	PRP11	YDL043C	74	81	64	82								
31	DATA	21	(+)E1A_r6	E1A_r60_a	E1A_r60_a	73	81	63	80								
32	DATA	28	A_06_P19	PTP1	YDL230W	188	209	65	81								
33	DATA	29	A_06_P17	ARP2	YDL029W	849	2005	64	83								
34	DATA	30	A_06_P26	PRE1	YER012W	770	1640	65	82								
35	DATA	31	A_06_P52	FPR4	YLR449W	197	378	64	83								
36	DATA	32	A_06_P52	ORF:YLR4	YLR455W	479	324	64	83								
37	DATA	33	A_06_P47	UBI4	YLL039C	25207	38522	65	84								

Create background subtracted column for red and green signals

Sheet1 / Sheet2 / Sheet3

Point   NUM

SUM   =G3-I3

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q
1	FEATURE	ProbeUID	ProbeNam	GeneName	Systemati	gMedianSi	rMedianSig	gBGMedia	rBGMedianSignal								
2		rDyeNorm	rDyeNorm	DyeNormC	ErrorModel												
3	DATA	0	BrightCorn	BrightCorn	BrightCorn	85	86.5	65	83	20	=G3-I3						
4	DATA	1	(-)3xSLv1	NegativeCo	NegativeCo	83	84	65	83								
5	DATA	2	A_06_P24	NHX1	YDR456W	336	609	65	83								
6	DATA	3	A_06_P72	SKI3	YPR189W	92	119.5	66	83								
7	DATA	4	A_06_P25	POL5	YEL055C	80.5	85.5	66	81								
8	DATA	5	A_06_P65	ORF:YOR:	YOR200W	81	82	65	82								
9	DATA	6	A_06_P49	GIS3	YLR094C	504	214	65	83								
10	DATA	7	(+)E1A_r6	E1A_r60_r	E1A_r60_r	77	82.5	64	83								
11	DATA	8	A_06_P69	ALG5	YPL227C	80	85	65	82								
12	DATA	9	A_06_P51	SEC61	YLR378C	317	207	65	82								
13	DATA	10	A_06_P25	TTR1	YDR513W	1269	3859	66	84								
14	DATA	11	A_06_P42	ORF:YJR0	YJR014W	475	660	66	83								
15	DATA	12	A_06_P48	SSK1	YLR006C	334	185	66	82								
16	DATA	13	A_06_P18	CDC48	YDL126C	5405	11816	66	83								
17	DATA	14	(+)E1A_r6	E1A_r60_a	E1A_r60_a	77	80	67	82								
18	DATA	15	A_06_P18	QRI1	YDL103C	93	266	68	84								
19	DATA	16	A_06_P10	ORF:Q018	Q0182	75	91	66	82								
20	DATA	17	A_06_P13	SUP45	YBR143C	639	602	66	81								
21	DATA	18	A_06_P16	RPS14A	YCR031C	5088	19468	66	81								
22	DATA	19	A_06_P56	ORF:YMR	YMR172C-	85	90	69	82								
23	DATA	20	A_06_P14	ISW1	YBR245C	180	299	70	83								
24	DATA	21	(+)E1A_r6	E1A_r60_a	E1A_r60_a	77	82	67	83								
25	DATA	22	A_06_P64	PIN2	YOR104W	166	180	65	83								
26	DATA	23	A_06_P66	HSD1	YOR311C	394.5	322.5	65	83								
27	DATA	24	A_06_P14	CDC47	YBR202W	105	144	64	82								
28	DATA	25	A_06_P48	MEF1	YLR069C	179.5	258	65	83								
29	DATA	26	A_06_P12	ILS1	YBL076C	86	108	65	82								
30	DATA	27	A_06_P17	PRP11	YDL043C	74	81	64	82								
31	DATA	21	(+)E1A_r6	E1A_r60_a	E1A_r60_a	73	81	63	80								
32	DATA	28	A_06_P19	PTP1	YDL230W	188	209	65	81								
33	DATA	29	A_06_P17	ARP2	YDL029W	849	2005	64	83								
34	DATA	30	A_06_P26	PRE1	YER012W	770	1640	65	82								
35	DATA	31	A_06_P52	FPR4	YLR449W	197	378	64	83								
36	DATA	32	A_06_P52	ORF:YLR4	YLR455W	479	324	64	83								
37	DATA	33	A_06_P47	UBI4	YLL039C	25207	38522	65	84								

Sheet1 / Sheet2 / Sheet3 /

Point   NUM

start

B	C	D	E	F	G	H	I	J	K	L	M	N
1	(-)3xSLv1	NegativeControl	NegativeCo	165	108.5	83	86	82	22.5			
1	(-)3xSLv1	NegativeControl	NegativeCo	102	94	63	82	39	12			
1	(-)3xSLv1	NegativeControl	NegativeCo	101	94	63	81	38	13			
1	(-)3xSLv1	NegativeControl	NegativeCo	98	89	61	82	37	7			
1	(-)3xSLv1	NegativeControl	NegativeCo	160.5	116	83	87	77.5	29			
	-)3xSLv1	NegativeControl	NegativeCo	167	127	84	87	83	40			
	-)3xSLv1	NegativeControl	NegativeCo	102	93.5	63	83	39	10.5			
	-)3xSLv1	NegativeControl	NegativeCo	175.5	118.5	83	87	92.5	31.5			
	-)3xSLv1	NegativeControl	NegativeCo	107	95.5	61	82	46	13.5			
	+)E1A_r6	E1A_r60_1	E1A_r60_	87	106.5	68	84	19	22.5			
	+)E1A_r6	E1A_r60_1	E1A_r60_	84	87	68	85	16	2			
	+)E1A_r6	E1A_r60_1	E1A_r60_	79	85	68	85	11	0			
	+)E1A_r6	E1A_r60_1	E1A_r60_	77	84.5	66	83	11	1.5			
	+)E1A_r6	E1A_r60_1	E1A_r60_	84	83	67	83	17	0			
	+)E1A_r6	E1A_r60_1	E1A_r60_	81	88	68	84	13	4			
	+)E1A_r6	E1A_r60_1	E1A_r60_	83	84	67	83	16	1			
	+)E1A_r6	E1A_r60_1	E1A_r60_	89.5	93	70	83	19.5	10			
	+)E1A_r6	E1A_r60_1	E1A_r60_	89	89.5	72	84	17	5.5			
	+)E1A_r6	E1A_r60_1	E1A_r60_	114	103	90	83	24	20			
	+)E1A_r6	E1A_r60_1	E1A_r60_	87	84.5	69	82	18	2.5			
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1										
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	123	114.5	75	84.5	56	50			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	80	90.5	63	82	17	8.5			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	110	97	65	82	45	15			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	112	102	72	84	40	18			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	89	102	65	81	24	21			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	96	98	62	83	34	15			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	156	120	82	85	74	35			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	90	85	68	82.5	22	2.5			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	103	110	70	84	33	26			
79	(+)E1A_r6	E1A_r60_1	E1A_r60_	88	92	67	82	21	10			

Delete unused negative and positive control: eQCs

B	C	D	E	F	G	H	I	J	K	L	M	N
510	(+)eQC-39	EQC	EQC	71	82	66	84	5	-2			
510	(+)eQC-39	EQC	EQC	67.5	80.5	65	82	2.5	-1.5			
510	(+)eQC-39	EQC	EQC	71	84	67	83	4	1			
510	(+)eQC-39	EQC	EQC	75	84	67	83	8	1			
510	(+)eQC-39	EQC	EQC	80	86	68	85	12	1			
510	(+)eQC-39	EQC	EQC	90	95	70	85	20	10			
510	(+)eQC-39	EQC	EQC	79	87	68	83	11	4			
510	(+)eQC-39	EQC	EQC	80	82	69	82	11	0			
510	(+)eQC-39	EQC	EQC	116	109	72	83	44	26			
510	(+)eQC-39	EQC	EQC	95.5	88.5	72	85	23.5	3.5			
510	(+)eQC-39	EQC	EQC	87	91	72	83	15	8			
510	(+)eQC-39	EQC	EQC	98.5	92.5	73	85	25.5	7.5			
510	(+)eQC-39	EQC	EQC	118	104	76	102	42	2			
510	(+)eQC-39	EQC	EQC	84	88.5	71	85	13	3.5			
510	(+)eQC-39	EQC	EQC	79	82	66	83	13	-1			
510	(+)eQC-39	EQC	EQC	77	84.5	65	81	12	3.5			
510	(+)eQC-39	EQC	EQC	139	104	81	86	58	18			
510	(+)eQC-39	EQC	EQC	95	89	74	84	21	5			
510	(+)eQC-39	EQC	EQC	86	90	68	82	18	8			
510	(+)eQC-39	EQC	EQC	80.5	83	66	82	14.5	1			
510	(+)eQC-39	EQC										
510	(+)eQC-39	EQC										
510	(+)eQC-39	EQC										
510	(+)eQC-39	EQC										
6304	A_06_P10	ORF:Q0010										
959	A_06_P10	ORF:Q0017										
959	A_06_P10	ORF:Q0017										
4760	A_06_P10	COX1	Q0045	117	97	62	82	55	15			
4760	A_06_P10	COX1	Q0045	178	116	73	82	105	34			
6303	A_06_P10	AI1	Q0050	238	101.5	75	84	163	17.5			
6303	A_06_P10	AI1	Q0050	327	115	67	83	260	32			
435	A_06_P10	AI2	Q0055	76	85	66	83	10	2			
435	A_06_P10	AI2	Q0055	107	94	75	83	32	11			
6302	A_06_P10	AI3	Q0060	532	374	76.5	84	455.5	290			
6302	A_06_P10	AI3	Q0060	250	196	64	82	186	114			
1066	A_06_P10	AI4	Q0065	6244.5	12696.5	67	83	6177.5	12613.5			
1066	A_06_P10	AI4	Q0065	8037	15373	77	84	7960	15289			

Delete unused negative and positive control: eQCs

B	C	D	E	F	G	H	I	J	K	L	M	N
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	94	148	68	86	26	62			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	87	146.5	65	84	22	62.5			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	111	188.5	72	85	39	103.5			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	123	233	69	85	54	148			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	139	244.5	67	84	72	160.5			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	157	122	82	86	75	36			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	104	141	67	83	37	58			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	151	138	80	87	71	51			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	143	140	79	84	64	56			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	117	116.5	75	85	42	31.5			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	118	224	65	84	53	140			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	84	109	65	82	19	27			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	82.5	117	64	82	18.5	35			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	112	171.5	65	81	47	90.5			
72	(+)E1A_r6	E1A_r60_n9	E1A_r60_r	83	107	61	81	22	26			
1319	A_06_P70	EAF3	YPR023C	3093	2800	67	83	3026	2717			
1319	A_06_P70	EAF3	YPR023C	3891	2618	80	85	3811	2533			
5343	A_06_P25	EAF5	YEL018W	795	537	76	85	719	452			
650	A_06_P43	EAF6	YJR082C	1511	617	68	84	1443	533			
650	A_06_P43	EAF6	YJR082C	2447.5	1022	72	84	2375.5	938			
3745	A_06_P46	EAP1										
3745	A_06_P46	EAP1										
3765	A_06_P45	EBP2										
5570	A_06_P21	EBS1										
5570	A_06_P21	EBS1										
3308	A_06_P50	ECI1										
6266	A_06_P10	ECM1										
5330	A_06_P25	ECM10	YEL030W	224	435	65	82	155	357			
5410	A_06_P24	ECM11	YDR446W	105	200	70	83	35	117			
4585	A_06_P35	ECM12	YHR021W	140	117	73	83	67	34			
4585	A_06_P35	ECM12	YHR021W	109	117	68.5	83	40.5	34			
4995	A_06_P11	ECM13	YBL043W	2569	297	79	85	2490	212			
4995	A_06_P11	ECM13	YBL043W	3379.5	921	65	83	3314.5	838			
4486	A_06_P37	ECM14	YHR132C	472	658	63	82	409	576			
4486	A_06_P37	ECM14	YHR132C	1000	1192.5	77	85	923	1107.5			
6240	A_06_P11	ECM15	YBL001C	3544.5	10097	67.5	84	3477	10013			
2888	A_06_P55	ECM16	YMR128W	152	151	71	83	81	68			

Delete unused negative and positive control: eQCs
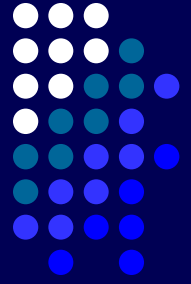
Within-Slide Normalization

- Normalization balances red and green intensities.
- Imbalances can be caused by
  - Different incorporation of dyes
  - Different degradation of dye
- In practice, we usually need to increase the red intensity a bit to balance the green
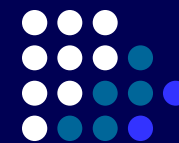
cy3 and cy5: Commonly used dyes

cy5

~700 emission

cy3

cy5

Fig 1 – CyDye structures
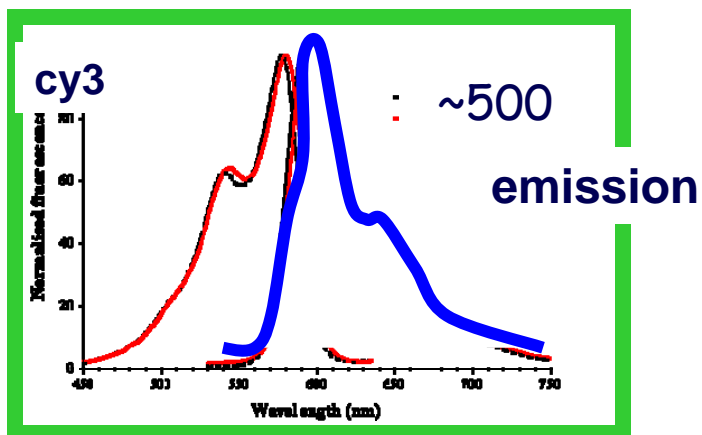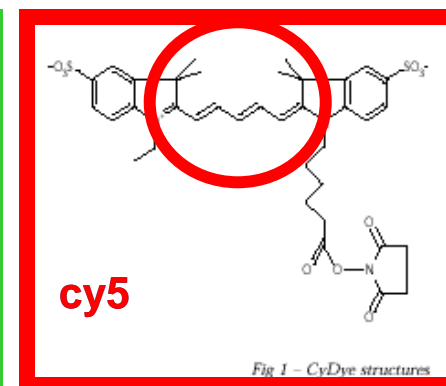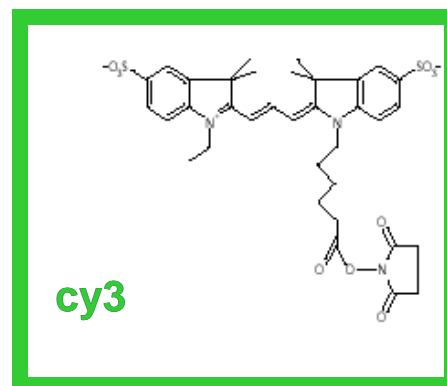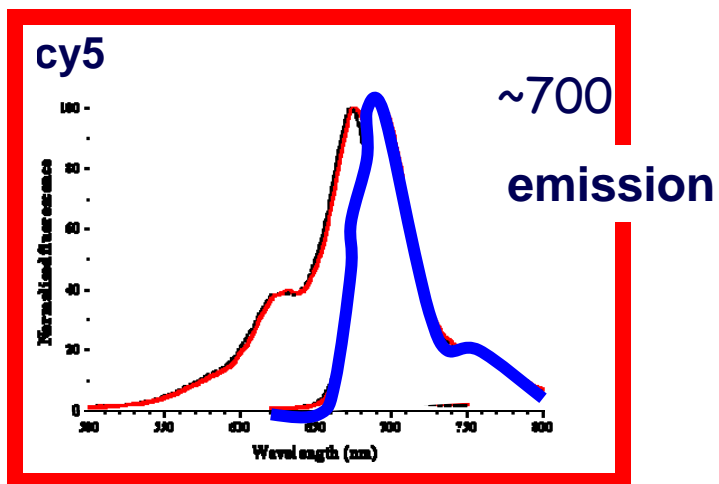
Light sensitivity: cy5 more easily degraded

cy3

~500 emission

Let's begin the normalization process:

Green background red background
corrected corrected

`=average(j2:J10275`

B	C	D	E	F	G	H	I	J	K	L	M	N
561	A_06_P61	ZRG17	YNR039C	430	288.5	65	83	365	205.5			
2744	A_06_P26	ZRG8	YER033C	105.5	213	74	83	31.5	130			
2744	A_06_P26	ZRG8	YER033C	183	338.5	66	84	117	254.5			
4872	A_06_P32	ZRT1	YGL255W	173.5	236	64	82	109.5	154			
3450	A_06_P49	ZRT2	YLR130C	1818	2862.5	71	83	1747	2779.5			
2594	A_06_P45	ZRT3	YKL175W	252.5	291.5	72	84	180.5	207.5			
2594	A_06_P45	ZRT3	YKL175W	1205	1538	69	83	1136	1455			
5968	A_06_P12	ZTA1	YBR046C	1375	2101	61	80	1314	2021			
5968	A_06_P12	ZTA1	YBR046C	2970	4380.5	68	83	2902	4297.5			
4654	A_06_P35	ZUO1	YGR285C	2815	2136.5	71	83	2744	2053.5			
2452	A_06_P60	ZWF1	YNL241C	5174	13544	65	83	5109	13461			

`=average(j2:J10275`

AVERAGE(**number1**, [number2], ...)

Create mean signal to estimate dye bias

green   red

B	C	D	E	F	G	H	I	J	K	L	M	N
4872	A_06_P32	ZRT1	YGL255W	173.5	236	64	82	109.5	154			
3450	A_06_P49	ZRT2	YLR130C	1818	2862.5	71	83	1747	2779.5			
2594	A_06_P45	ZRT3	YKL175W	252.5	291.5	72	84	180.5	207.5			
2594	A_06_P45	ZRT3	YKL175W	1205	1538	69	83	1136	1455			
5968	A_06_P12	ZTA1	YBR046C	1375	2101	61	80	1314	2021			
5968	A_06_P12	ZTA1	YBR046C	2970	4380.5	68	83	2902	4297.5			
4654	A_06_P35	ZUO1	YGR285C	2815	2136.5	71	83	2744	2053.5			
2452	A_06_P60	ZWF1	YNL241C	5174	13544	65	83	5109	13461			
								1350.949187	2315.146974			
									=K10277/J10277			

1.7 FC difference

Create mean signal to estimate dye bias

fx =K2/1.7

B	C	D	E	F	G	H	I	J	K	L	M	N
ProbeUID	ProbeNam	GeneName	Systematic	gMedianSi	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected			
3?05	A_06_P45	1-Oct	YKL1?4C	508.5	301	73	84	435.5	217	127.6471		
3?05	A_06_P45	1-Oct	YKL1?4C	325	263.5	60	80	265	183.5	107.9412		
2?55	A_06_P54	AAC1	YMR?56C	1919	2029	70	83	1849	1946	1144.706		
2955	A_06_P54	AAC1	YMR056C	1941	2177	64	82	1877	2095	1232.353		
6119	A_06_P13	AAC3	YBR085W	141	111.5	65	82	76	29.5	17.35294		
6119	A_06_P13	AAC3	YBR085W	95.5	102.5	64	81	31.5	21.5	12.64706		
1626	A_06_P43	AAD10	YJR155W	223	135	87.5	84	135.5	51	30		
1626	A_06_P43	AAD10	YJR155W	1700	604.5	72	83	1628	521.5	306.7647		
2361	A_06_P61	AAD14	YNL331C	235	117	68	83	167	34	20		
2093	A_06_P63	AAD15	YOL165C	103	102	65	83	38	19	11.17647		
5869	A_06_P17	AAD3	YCR107W	242	216	74	84	168	132	77.64706		
1459	A_06_P19	AAD4	YDL243C	113	94	69	84	44	10	5.882353		
1459	A_06_P19	AAD4	YDL243C	282	395	72	83	210	312	183.5294		
5116	A_06_P28	AAD6	YFL056C	215.5	163	62	81	153.5	82	48.23529		
5116	A_06_P28	AAD6	YFL056C	314	270	67	81	247	189	111.1765		
2545	A_06_P59	AAH1	YNL141W	233.5	164	91	85	142.5	79	46.47059		
2545	A_06_P59	AAH1	YNL141W	138	110	64	81	74	29	17.05882		
6299	A_06_P10	AAP1	Q0080	587	253	77	85	510	168	98.82353		
6299	A_06_P10	AAP1	Q0080	529	250	65	82	464	168	98.82353		
4558	A_06_P36	AAP1'	YHR047C	626	2123							
6191	A_06_P12	AAR2	YBL074C	275	139							
3821	A_06_P45	AAT1	YKL106W	636	629							
3821	A_06_P45	AAT1	YKL106W	280.5	430							
3537	A_06_P48	AAT2	YLR027C	6453	6925							
4971	A_06_P30	ABC1	YGL119W	400.5	459.5	70	86	330.5	373.5	219.7059		
4971	A_06_P30	ABC1	YGL119W	220	184.5	63	81	157	103.5	60.88235		
6019	A_06_P14	ABD1	YBR236C	362.5	575	75	83	287.5	492	289.4118		
6019	A_06_P14	ABD1	YBR236C	473	930	68	82	405	848	498.8235		
787	A_06_P45	ABF1	YKL112W	1307.5	176	71	83	1236.5	93	54.70588		
787	A_06_P45	ABF1	YKL112W	4147	409	76	87	4071	322	189.4118		
2946	A_06_P54	ABF2	YMR072W	7888.5	12876	71	85	7817.5	12791	7524.118		
2946	A_06_P54	ABF2	YMR072W	5054	7319.5	67	83	4987	7236.5	4256.765		
1881	A_06_P43	ABM1	YJR108W	198	331	86	83	112	248	145.8824		
1881	A_06_P43	ABM1	YJR108W	225.5	521.5	68	84	157.5	437.5	257.3529		
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290		
1816	A_06_P66	ABP140	YOR239W	178	407	68	83	110	324	190.5882		

Normalize your lower abundant channel (increase) by factor to have mean Expression across the array equal

Calculating Differences in Gene Expression

Spotted microarrays

www.molgen.mpg.de
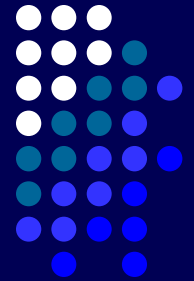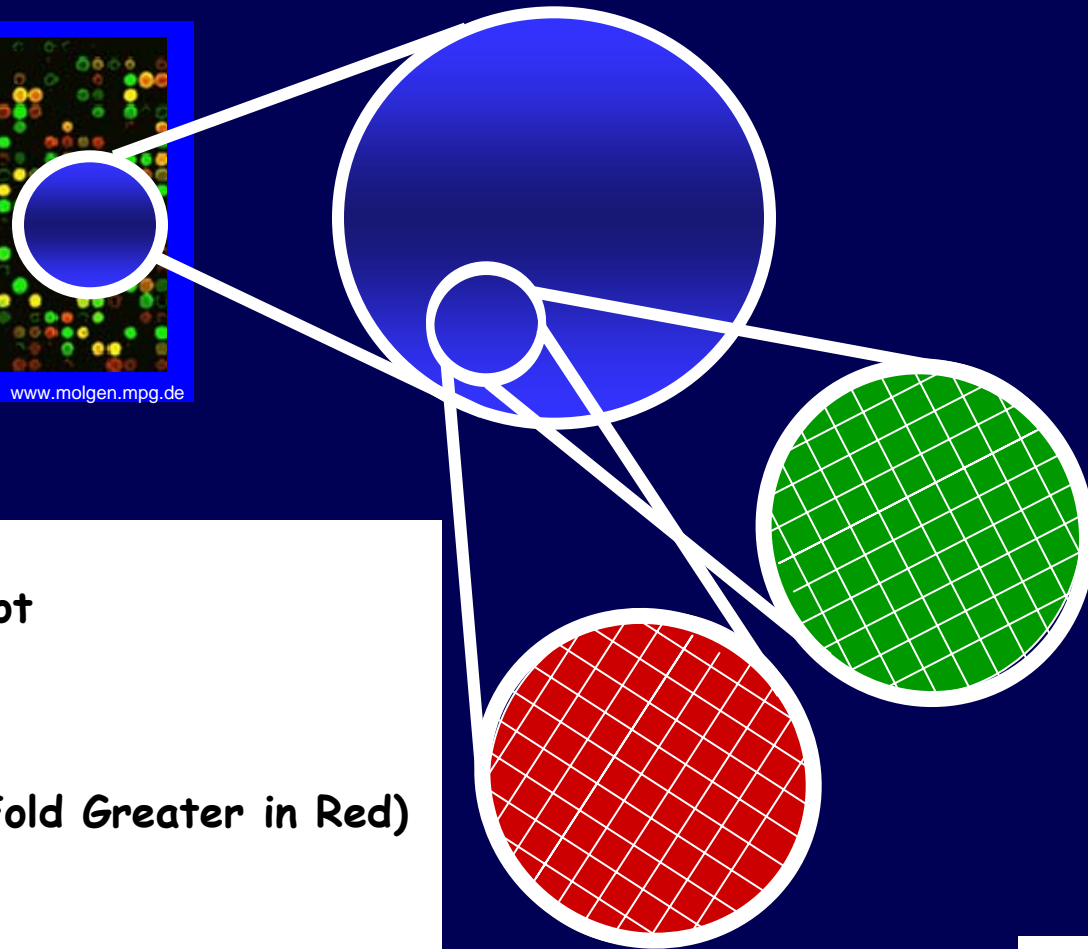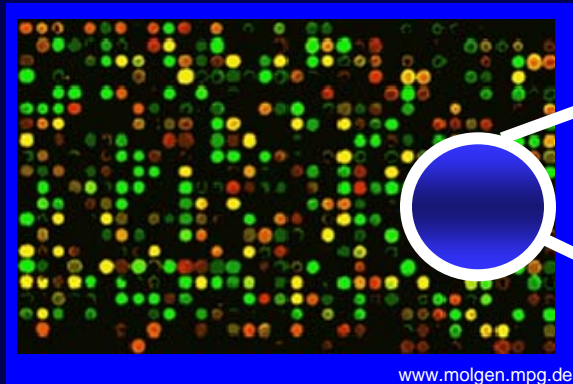
2 numbers per spot

Red=500
Green=100
Red/Green=5 (5 Fold Greater in Red)

Red=100
Green=500
Red/Green=0.2 (5 Fold Less in Red)

$$Log2(5)=\sim+2$$
$$Log2(0.2)=\sim-2$$

ProbeID	ProbeNam	GeneName	Systematic	gMedianSi	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected	red normalized		
3 05	A_06_P45		1-Oct YKL1 4C	508.5	301	73	84	435.5	217	127.6471	0.293105	
3 05	A_06_P45		1-Oct YKL1 4C	325	263.5	60	80	265	183.5	107.9412		
2 55	A_06_P54 AAC1		YMR 56C	1919	2029	70	83	1849	1946	1144.706		
2955	A_06_P54	AAC1	YMR056C	1941	2177	64	82	1877	2095	1232.353		
6119	A_06_P13	AAC3	YBR085W	141	111.5	65	82	76	29.5	17.35294		
6119	A_06_P13	AAC3	YBR085W	95.5	102.5	64	81	31.5	21.5	12.64706		
1626	A_06_P43	AAD10	YJR155W	223	135	87.5	84	135.5	51	30		
1626	A_06_P43	AAD10	YJR155W	1700	604.5	72	83	1628	521.5	306.7647		
2361	A_06_P61	AAD14	YNL331C	235	117	68	83	167	34	20		
2093	A_06_P63	AAD15	YOL165C	103	102	65	83	38	19	11.17647		
5869	A_06_P17	AAD3	YCR107W	242	216	74	84	168	132	77.64706		
1459	A_06_P19	AAD4	YDL243C	113	94	69	84	44	10	5.882353		
1459	A_06_P19	AAD4	YDL243C	282	395	72	83	210	312	183.5294		
5116	A_06_P28	AAD6	YFL056C	215.5	163	62	81	153.5	82	48.23529		
5116	A_06_P28	AAD6	YFL056C	314	270	67	81	247	189	111.1765		
2545	A_06_P59	AAH1	YNL141W	233.5	164	91	85	142.5	79	46.47059		
2545	A_06_P59	AAH1	YNL141W	138	110	64	81	74	29	17.05882		
6299	A_06_P10	AAP1	Q0080	587	253	77	85	510	168	98.82353		
6299	A_06_P10	AAP1	Q0080	529	250							
4558	A_06_P36	AAP1'	YHR047C	626	2123							
6191	A_06_P12	AAR2	YBL074C	275	139							
3821	A_06_P45	AAT1	YKL106W	636	629							
3821	A_06_P45	AAT1	YKL106W	280.5	430							
3537	A_06_P48	AAT2	YLR027C	6453	6925							
4971	A_06_P30	ABC1	YGL119W	400.5	459.5	70	86	330.5	373.5	219.7059		
4971	A_06_P30	ABC1	YGL119W	220	184.5	63	81	157	103.5	60.88235		
6019	A_06_P14	ABD1	YBR236C	362.5	575	75	83	287.5	492	289.4118		
6019	A_06_P14	ABD1	YBR236C	473	930	68	82	405	848	498.8235		
787	A_06_P45	ABF1	YKL112W	1307.5	176	71	83	1236.5	93	54.70588		
787	A_06_P45	ABF1	YKL112W	4147	409	76	87	4071	322	189.4118		
2946	A_06_P54	ABF2	YMR072W	7888.5	12876	71	85	7817.5	12791	7524.118		
2946	A_06_P54	ABF2	YMR072W	5054	7319.5	67	83	4987	7236.5	4256.765		
1881	A_06_P43	ABM1	YJR108W	198	331	86	83	112	248	145.8824		
1881	A_06_P43	ABM1	YJR108W	225.5	521.5	68	84	157.5	437.5	257.3529		
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290		
1816	A_06_P66	ABP140	YOR239W	178	407	68	83	110	324	190.5882		

Compare expression of each Channel (using normalized channel In one condition)

ProbeID	ProbeName	GeneName	Systematic	gMedianSig	rMedianSig	gBGMedian	rBGMedian	green corrected	red corrected	red normal	red vs green	
3505	A_06_P45		1-Oct YKL184C	508.5	301	73	84	435.5	217	127.6471	0.293105	=log(M2,2)
3505	A_06_P45		1-Oct YKL184C	325	263.5	60	80	265	183.5	107.9412	0.407325	
2955	A_06_P54		YMR056C	1919	2029	70	83	1849	1946	1144.706	0.619095	
2955	A_06_P54	AAC1	YMR056C	1941	2177	64	82	1877	2095	1232.353	0.656555	
6119	A_06_P13	AAC3	YBR085W	141	111.5	65	82	76	29.5	17.35294	0.228328	
6119	A_06_P13	AAC3	YBR085W	95.5	102.5	64	81	31.5	21.5	12.64706	0.401494	
1626	A_06_P43	AAD10	YJR155W	223	135	87.5	84	135.5	51	30	0.221402	
1626	A_06_P43	AAD10	YJR155W	1700	604.5	72	83	1628	521.5	306.7647	0.18843	
2361	A_06_P61	AAD14	YNL331C	235	117	68	83	167	34	20	0.11976	
2093	A_06_P63	AAD15	YOL165C	103	102	65	83	38	19	11.17647	0.294118	
5869	A_06_P17	AAD3	YCR107W	242	216	74	84	168	132	77.64706	0.462185	
1459	A_06_P19	AAD4	YDL243C	113	94	69	84	44	10	5.882353	0.13369	
1459	A_06_P19	AAD4	YDL243C	282	395	72	83	210	312	183.5294	0.87395	
5116	A_06_P28	AAD6	YFL056C	215.5	163	62	81	153.5	82	48.23529	0.314236	
5116	A_06_P28	AAD6	YFL056C	314	270	67	81	247	189	111.1765	0.450107	
2545	A_06_P59	AAH1	YNL141W	233.5	164	91	85	142.5	79	46.47059	0.326109	
2545	A_06_P59	AAH1	YNL141W	138	110	64	81	74	29	17.05882	0.230525	
6299	A_06_P10	AAP1	Q0080	587	253	77	85	510	168	98.82353	0.193772	
6299	A_06_P10	AAP1	Q0080	529	250	65	82	464	168	98.82353	0.212982	
4558	A_06_P36	AAP1'	YHR047C	626	2123	63	83	563	2040	1200	2.131439	
6191	A_06_P12	AAR2	YBL074C	275	139	67	82	208	57	33.52941	0.161189	
3821	A_06_P45	AAT1	YKL106W	636	629	73	85					
3821	A_06_P45	AAT1	YKL106W	280.5	430	62	81					
3537	A_06_P48	AAT2	YLR027C	6453	6925	67	84	6386	6841	4024.118	0.630147	
4971	A_06_P30	ABC1	YGL119W	400.5	459.5	70	86	330.5	373.5	219.7059	0.664768	
4971	A_06_P30	ABC1	YGL119W	220	184.5	63	81	157	103.5	60.88235	0.387786	
6019	A_06_P14	ABD1	YBR236C	362.5	575	75	83	287.5	492	289.4118	1.00665	
6019	A_06_P14	ABD1	YBR236C	473	930	68	82	405	848	498.8235	1.231663	
787	A_06_P45	ABF1	YKL112W	1307.5	176	71	83	1236.5	93	54.70588	0.044243	
787	A_06_P45	ABF1	YKL112W	4147	409	76	87	4071	322	189.4118	0.046527	
2946	A_06_P54	ABF2	YMR072W	7888.5	12876	71	85	7817.5	12791	7524.118	0.962471	
2946	A_06_P54	ABF2	YMR072W	5054	7319.5	67	83	4987	7236.5	4256.765	0.853572	
1881	A_06_P43	ABM1	YJR108W	198	331	86	83	112	248	145.8824	1.302521	
1881	A_06_P43	ABM1	YJR108W	225.5	521.5	68	84	157.5	437.5	257.3529	1.633987	
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290	4.900417	
1816	A_06_P66	ABP140	YOR239W	178	407	68	83	110	324	190.5882	1.73262	

Calculate log2 ratio of each channel

fx =LOG(M2,2)

ProbeID	ProbeName	GeneName	Systematic	gMedianSi	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected	red normal	red vs gree	log2 red vs gre
134	A_06_P72	ARR3	YPR201W	72	82.5	65	83	7	-0.5	-0.29412	-0.0 02	#NUM!
35	A_06_P51	CDA2	YLR308W	117	84	72	85	45	-1	-0.58824	-0.01307	#NUM!
	A_06_P79	PRP8	YPR 75W	82.5	81.5	66	83	16.5	-1.5	-0.88235	-0.05348	#NUM!
5325	A_06_P25	CYC7	YEL039C	698	46785	66	84	632	46701	27471.18	43.46705	5.44185
5325	A_06_P25	CYC7	YEL039C	885	33057	80	88	805	32969	19393.53	24.09134	4.590443
3030	A_06_P54	COQ5	YML110C	311	5003	70	83	241	4920	2894.118	12.00879	3.586019
3030	A_06_P54	COQ5	YML110C	785.5	11925	68	87	717.5	11838	6963.529	9.705267	3.278768
3696	A_06_P46	DAL80	YKR034W	98	556	68	85	30	471	277.0588	9.235294	3.207158
4756	A_06_P33	BTN2	YGR142W	1860	27389.5	63	84	1797	27305.5	16062.06	8.938263	3.159995
5133	A_06_P28	ACT1	YFL039C	310	3522	74	84	236	3438	2022.353	8.569292	3.099176
1373	A_06_P68	CAR1	YPL111W	350	3847.5	82	84	268	3763.5	2213.824	8.260536	3.046235
1322	A_06_P70	ATP20	YPR020W	333.5	3349.5	88	82	245.5	3267.5	1922.059	7.82916	2.968858
2344	A_06_P61	COS1	YNL336W	355	3665	77	83	278	3582	2107.059	7.579348	2.922074
443	A_06_P15	ARO4	YBR249C	244	2242	67	83	177	2159	1270	7.175141	2.843007
2686	A_06_P57	ASI3	YNL008C	96.5	422.5	68	84	28.5	338.5	199.1176	6.986584	2.804587
2344	A_06_P61	COS1	YNL336W	405	4089	62	82	343	4007	2357.059	6.871892	2.780707
4476	A_06_P37	DSE2	YHR143W	521	5193	61	80	460	5113	3007.647	6.538363	2.70893
426	A_06_P39	COX5B	YIL111W	2928.5	30483.5	71	85	2857.5	30398.5	17881.47	6.257732	2.64564
443	A_06_P15	ARO4	YBR249C	373	3333	65	84	308	3249	1911.176	6.205118	2.633459
4756	A_06_P33	BTN2	YGR142W	784	7470	81	88	703	7382	4342.353	6.176889	2.62688
717	A_06_P27	DSE1	YER124C	113	580	64	81	49	499	293.5294	5.990396	2.582651
426	A_06_P39	COX5B	YIL111W	1292.5	12492.5	64	82			.294	5.942445	2.571057
1204	A_06_P28	COS4	YFL062W	921	8540	63	82			.294	5.798711	2.535732
6254	A_06_P11	ADE1	YAR015W	536.5	4337	65	83	471.5	4254	2502.353	5.307217	2.407956
1204	A_06_P28	COS4	YFL062W	1152	9555	73	83	1079	9472	5571.765	5.163823	2.368439
1322	A_06_P70	ATP20	YPR020W	663	5310	67	84	596	5226	3074.118	5.157916	2.366788
4560	A_06_P36	DOG2	YHR043C	330.5	2412	64	84	266.5	2328	1369.412	5.138506	2.361349
4919	A_06_P31	COX4	YGL187C	1204	9828.5	63	82	1141	9746.5	5733.235	5.024746	2.329051
717	A_06_P27	DSE1	YER124C	1534	12402.5	69	84	1465	12318.5	7246.176	4.946196	2.306319
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290	4.900417	2.292904
3789	A_06_P44	COS5	YJR161C	634.5	4762.5	72	85	562.5	4677.5	2751.471	4.891503	2.290278
4476	A_06_P37	DSE2	YHR143W	1127	8722	68	84	1059	8638	5081.176	4.798089	2.26246
4009	A_06_P42	CYC1	YJR048W	1537	11628	73	89	1464	11539	6787.647	4.636371	2.212996
6254	A_06_P11	ADE1	YAR015W	607	4250.5	65	82	542	4168.5	2452.059	4.524094	2.177629
47	A_06_P14	CST13	YBR158W	486	3296	63	81	423	3215	1891.176	4.470866	2.160554
553	A_06_P22	ATP5	YDR298C	303	1866	68	84	235	1782	1048.235	4.460576	2.15723

What happened??

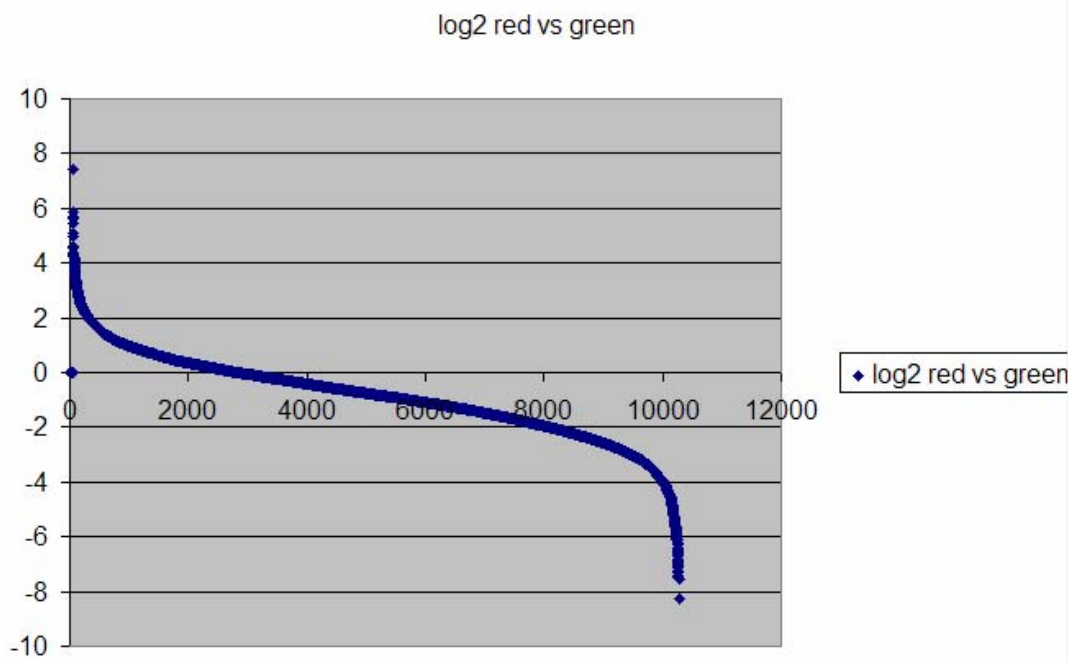| ProbeUID	ProbeName	GeneName	Systematic	gMedianSig	rMedianSig	gBGMedian	rBGMedian	green corrected	red corrected	red normal	red vs green	log2 red vs green
1134	A_06_P72	ARR3	YPR201W	72	82.5	65	83	7	0.5	0.294118	0.042017	-4.57289
2435	A_06_P51	CDA2	YLR308W	117	84	72	85	45	0.5	0.294118	0.006536	-7.25739
1157	A_06_P72	DPB2	YPR175W	82.5	81.5	66	83	16.5	0.5	0.294118	0.017825	-5.80993
5325	A_06_P25	CYC7	YEL039C	698	46785	66	84	632	46701	27471.18	43.46705	5.44185
5325	A_06_P25	CYC7	YEL039C	885	33057	80	88	805	32969	19393.53	24.09134	4.590443
3030	A_06_P54	COQ5	YML110C	311	5003	70	83	241	4920	2894.118	12.00879	3.586019
3030	A_06_P54	COQ5	YML110C	785.5	11925	68	87	717.5	11838	6963.529	9.705267	3.278768
3696	A_06_P46	DAL80	YKR034W	98	556	68	85	30	471	277.0588	9.235294	3.207158
4756	A_06_P33	BTN2	YGR142W	1860	27389.5	63	84	1797	27305.5	16062.06	8.938263	3.159995
5133	A_06_P28	ACT1	YFL039C	310	3522	74	84	236	3438	2022.353	8.569292	3.099176
1373	A_06_P68	CAR1	YPL111W	350	3847.5	82	84	268	3763.5	2213.824	8.260536	3.046235
1322	A_06_P70	ATP20	YPR020W	333.5	3349.5	88	82	245.5	3267.5	1922.059	7.82916	2.968858
2344	A_06_P61	COS1	YNL336W	355	3665	77	83	278	3582	2107.059	7.579348	2.922074
443	A_06_P15	ARO4	YBR249C	244	2242	67	83	177	2159	1270	7.175141	2.843007
2686	A_06_P57	ASI3	YNL008C	96.5	422.5	68	84	28.5	338.5	199.1176	6.986584	2.804587
2344	A_06_P61	COS1	YNL336W	405	4089	62	82	343	4007	2357.059	6.871892	2.780707
4476	A_06_P37	DSE2	YHR143W	521	5193	61	80	460	5113	3007.647	6.538363	2.70893
426	A_06_P39	COX5B	YIL111W	2928.5	30483.5	71	85	2857.5	30398.5	17881.47	6.257732	2.64564
443	A_06_P15	ARO4	YBR249C	373	3333	65	84	308	3249	1911.176	6.205118	2.633459
4756	A_06_P33	BTN2	YGR142W	784	7470	81	88	703	7382	4342.353	6.176889	2.62688
717	A_06_P27	DSE1	YER124C	113	580	64	81	49	499	293.5294	5.990396	2.582651
426	A_06_P39	COX5B	YIL111W	1292.5	12492.5	64	82					
1204	A_06_P28	COS4	YFL062W	921	8540	63	82					
6254	A_06_P11	ADE1	YAR015W	536.5	4337	65	83	471.5	4254	2502.353	5.307217	2.407956
1204	A_06_P28	COS4	YFL062W	1152	9555	73	83	1079	9472	5571.765	5.163823	2.368439
1322	A_06_P70	ATP20	YPR020W	663	5310	67	84	596	5226	3074.118	5.157916	2.366788
4560	A_06_P36	DOG2	YHR043C	330.5	2412	64	84	266.5	2328	1369.412	5.138506	2.361349
4919	A_06_P31	COX4	YGL187C	1204	9828.5	63	82	1141	9746.5	5733.235	5.024746	2.329051
717	A_06_P27	DSE1	YER124C	1534	12402.5	69	84	1465	12318.5	7246.176	4.946196	2.306319
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290	4.900417	2.292904
3789	A_06_P44	COS5	YJR161C	634.5	4762.5	72	85	562.5	4677.5	2751.471	4.891503	2.290278
4476	A_06_P37	DSE2	YHR143W	1127	8722	68	84	1059	8638	5081.176	4.798089	2.26246
4009	A_06_P42	CYC1	YJR048W	1537	11628	73	89	1464	11539	6787.647	4.636371	2.212996
6254	A_06_P11	ADE1	YAR015W	607	4250.5	65	82	542	4168.5	2452.059	4.524094	2.177629
47	A_06_P14	CST13	YBR158W	486	3296	63	81	423	3215	1891.176	4.470866	2.160554
553	A_06_P22	ATP5	YDR298C	303	1866	68	84	235	1782	1048.235	4.460576	2.15723

And NOW to the fun...

- How many genes were differentially expressed between your 2 samples?

- Was the expression of your gene of interest significantly changed between the two samples?...can we assess this directly

ProbeUID	ProbeNam	GeneName	Systematic	gMedianSi	rMedianSig	gBGMedia	rBGMedia	green corr	red correct	red normal	red vs gre	log2 red vs green		
5884	A_06_P17	ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290	4.900417	2.292904		
5133	A_06_P28	ACT1	YFL039C	310	3522	74	84	236	3438	2022.353	8.569292	3.099176		
5133	A_06_P28	ACT1	YFL039C	6989.5	47331	63	83	6926.5	47248	27792.94	4.012552	2.00452		
6254	A_06_P11	ADE1	YAR015W	536.5	4337	65	83	471.5	4254	2502.353	5.307217	2.407956		
6254	A_06_P11	ADE1	YAR015W	607	4250.5	65	82	542	4168.5	2452.059	4.524094	2.177629		
2467	A_06_P59	ADE12	YNL220W	197	942.5	78	84	119	858.5	505	4.243697	2.085322		
4010	A_06_P42	ANB1	YJR047C	207	1051	73	89	134	962	565.8824	4.223003	2.078269		
443	A_06_P15	ARO4	YBR249C	244	2242	67	83	177	2159	1270	7.175141	2.843007		
443	A_06_P15	ARO4	YBR249C	373	3333	65	84	308	3249	1911.176	6.205118	2.633459		
2686	A_06_P57	ASI3	YNL008C	96.5	422.5	68	84	28.5	338.5	199.1176	6.986584	2.804587		
1322	A_06_P70	ATP20	YPR020W	333.5	3349.5	88	82	245.5	3267.5	1922.059	7.82916	2.968858		
1322	A_06_P70	ATP20	YPR020W	663	5310	67	84	596	5226	3074.118	5.157916	2.366788		
553	A_06_P22	ATP5	YDR298C	303	1866	68	84	235	1782	1048.235	4.460576	2.15723		
4756	A_06_P33	BTN2	YGR142W	1860	27389.5	63	84	1797	27305.5	16062.06	8.938263	3.159995		
4756	A_06_P33	BTN2	YGR142W	784	7470	81	88	703	7382	4342.353	6.176889	2.62688		
1373	A_06_P68	CAR1	YPL111W	350	3847.5	82	84	268	3763.5	2213.824	8.260536	3.046235		
1805	A_06_P52	CDC73	YLR418C	221	1173	72	83	149	1090	641.1765	4.303198	2.105409		
3030	A_06_P54	COQ5	YML110C	311	5003	70	83	241	4920	2894.118	12.00879	3.586019		
3030	A_06_P54	COQ5	YML110C	785.5	11925	68	87	717.5	11838	6963.529	9.705267	3.278768		
2344	A_06_P61	COS1	YNL336W	355	3665	77	83	278	3582	2107.059	7.579348	2.922074		
2344	A_06_P61	COS1	YNL336W	405	4089	62	82	343	4007	2357.059	6.871892	2.780707		
1204	A_06_P28	COS4	YFL062W	921	8540	63	82	858	8458	4975.294	5.798711	2.535732		
1204	A_06_P28	COS4	YFL062W	1152	9555	73	83	1079	9472	5571.765	5.163823	2.368439		
3789	A_06_P44	COS5	YJR161C	634.5	4762.5	72	85	562.5	4677.5	2751.471	4.891503	2.290278		
2431	A_06_P27	COX15	YER141W	209	897	95	83	114	814	478.8235	4.200206	2.07046		
4919	A_06_P31	COX4	YGL187C	1204	9828.5	63	82	1141	9746.5	5733.235	5.024746	2.329051		
426	A_06_P39	COX5B	YIL111W	2928.5	30483.5	71	85	2857.5	30398.5	17881.47	6.257732	2.64564		
426	A_06_P39	COX5B	YIL111W	1292.5	12492.5	64	82	1228.5	12410.5	7300.294	5.942445	2.571057		
47	A_06_P14	CST13	YBR158W	486	3296	63	81	423	3215	1891.176	4.470866	2.160554		
4009	A_06_P42	CYC1	YJR048W	1537	11628	73	89	1464	11539	6787.647	4.636371	2.212996		
5325	A_06_P25	CYC7	YEL039C	698	46785	66	84	632	46701	27471.18	43.46705	5.44185		
5325	A_06_P25	CYC7	YEL039C	885	33057	80	88	805	32969	19393.53	24.09134	4.590443		
3696	A_06_P46	DAL80	YKR034W	98	556	68	85	30	471	277.0588	9.235294	3.207158		
4560	A_06_P36	DOG2	YHR043C	330.5	2412	64	84	266.5	2328	1369.412	5.138506	2.361349		
717	A_06_P27	DSE1	YER124C	113	580	64	81	49	499	293.5294	5.990396	2.582651		
717	A_06_P27	DSE1	YER124C	1534	12402.5	69	84	1465	12318.5	7246.176	4.946196	2.306319		

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Chart 1

	C	D	E	F	G	H	I	J	K	L	M	N
1	ProbeNam	GeneName	Systemati	gMedianSi	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected	red normal	red vs gree	log2 red vs gre
2	A_06_P63	HXT11	YOL156W									
3	A_06_P72	MLC2	YPR188C									
4	A_06_P72	MMS1	YPR164C									
5	A_06_P25	MMS21	YEL019C									
6	A_06_P62	NDJ1	YOL104C									
7	A_06_P72	OPT2	YPR194C									
8	A_06_P14	ORF:YBR219C	YBR219C									
9	A_06_P14	ORF:YBR226C	YBR226C									
10	A_06_P16	ORF:YCL069W	YCL069W									
11	A_06_P17	ORF:YDL016C	YDL016C									
12	A_06_P20	ORF:YDR029W	YDR029W									
13	A_06_P20	ORF:YDR066C	YDR066C									
14	A_06_P20	ORF:YDR095C	YDR095C									
15	A_06_P28	ORF:YFL012W-A	YFL012W									
16	A_06_P34	ORF:YGR242W	YGR242W									
17	A_06_P38	ORF:YIL092W	YIL092W									
18	A_06_P39	ORF:YIL141W	YIL141W									
19	A_06_P39	ORF:YIL163C	YIL163C									
20	A_06_P40	ORF:YIR040C	YIR040C									
21	A_06_P42	ORF:YJR023C	YJR023C									
22	A_06_P44	ORF:YKL030W	YKL030W									
23	A_06_P45	ORF:YKL165C-A	YKL165C									
24	A_06_P47	ORF:YKR105C	YKR105C									
25	A_06_P51	ORF:YLR334C	YLR334C									
26	A_06_P51	ORF:YLR349W	YLR349W									
27	A_06_P51	ORF:YLR379W	YLR379W	55	64	73	65	22	-1	-0.58824	-0.02674	#NUM!
28	A_06_P52	ORF:YLR458W	YLR458W	81	84	72	84	9	0	0	0	#NUM!
29	A_06_P53	ORF:YML047W-A	YML047W	85	84.5	71	85	14	-0.5	-0.29412	-0.02101	#NUM!
30	A_06_P54	ORF:YMR013W-A	YMR013W	74	85	71	85	3	0	0	0	#NUM!
31	A_06_P55	ORF:YMR158W-A	YMR158W	85.5	83.5	68	84	17.5	-0.5	-0.29412	-0.01681	#NUM!
32	A_06_P57	ORF:YMR316C-A	YMR316C	79	82	68	84	11	-2	-1.17647	-0.10695	#NUM!
33	A_06_P58	ORF:YNL109W	YNL109W	99	83	65	84	34	-1	-0.58824	-0.0173	#NUM!
34	A_06_P59	ORF:YNL162W-A	YNL162W-	69	81	64	83	5	-2	-1.17647	-0.23529	#NUM!
35	A_06_P59	ORF:YNL226W	YNL226W	81	83	69	84	12	-1	-0.58824	-0.04902	#NUM!
36	A_06_P62	ORF:YOL035C	YOL035C	68.5	82	64	83	4.5	-1	-0.58824	-0.13072	#NUM!
37	A_06_P62	ORF:YOL046C	YOL046C	85.5	84	66	84	19.5	0	0	0	#NUM!

Sheet1 / Sheet2 / Sheet3

Ready

Chart title: log2 red vs green

♦ log2 red vs green

(Y-axis: 10, 8, 6, 4, 2, 0, -2, -4, -6, -8, -10; X-axis: 2000, 4000, 6000, 8000, 10000, 12000)

start   1:06 PM
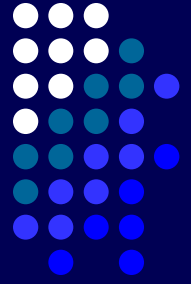
Create scatter plot of log2 ratios (green versus red)

log2 red vs green

tter Plot

2 fold increase

♦ log2 red vs green

2 fold decrease
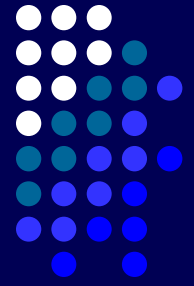
Distribution of log2 ratios

- What are we expecting????
- What color would all of these spots be??

Agilent Human 1A Oligo Microarray Kit (V2)
with SurePrint Technology

Catalog 60-mer Oligo

How many genes on the array?

Coverage you can count on

Designed to truly represent well-known genes in the human genome, Agilent's Human 1A Oligo microarray (V2) is comprised of 20,173 (60-mer) oligonucleotide probes, which span conserved exons across the transcripts of the targeted full-length genes. These probes represent 18,716 well-characterized, full-length, human genes from RefSeq and Incyte's Foundation Database. Much of the sequence and annotation information used in this microarray product is available only through Agilent and Incyte. Virtually all of the genes and corresponding probes have been mapped to the human genome DNA backbone. These probes have been experimentally validated in a laboratory which provides the researcher with maximal confidence in the probes and prevents redundancy in gene coverage.

Trends in Data
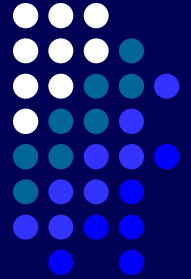
- How many changes do you see?
- What could these changes mean?
- How can we find out more about these genes and their functions?
- Which biological processes are up-regulated, down-regulated, no change?

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Sort...

Text to Columns...

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P1

	G	H	I	J	K	L	M	N	O	P
1	rMedianSi	gBGMedia	rBGMedia	green corrected	red corrected	red normal	red vs gree	log2 red vs green		
2	2693	70	88	9	2605	1532.353	170.2614	7.411608		BioProcess=vacuolar acidification*|MolFuncti
3	57476	82	86	567	57390	33758.82	59.53937	5.895772		BioProcess=mRNA catabolism|MolFunction=
4	26970.5	74	84.5	303	26886	15815.29	52.19569	5.705859		BioProcess=DNA dependent DNA replication
5	14111	71	84	170	14027	8251.176	48.53633	5.600993		BioProcess=biological_process unknown|Mol
6	1508	77.5	107	17	1401	824.1176	48.47751	5.599244		BioProcess=biological_process unknown|Mol
7	46785	66	84	632	46701	27471.18	43.46705	5.44185		
8	65214	67	85	1135	65129	38311.18	33.75434	5.077001		BioProcess=not yet annotated|MolFunction=
9	58869	66	82.5	1091	58786.5	34580.29	31.69596	4.986227		BioProcess=SRP-dependent, co-translational
10	33057	80	88	805	32969	19393.53	24.09134	4.590443		BioProcess=response to oxidative stress*|Mc
11	4282	63	81	106	4201	2471.176	23.31299	4.543062		BioProcess=biological_process unknown|Mol
12	1029.5	67	82	24	947.5	557.3529	23.22304	4.537485		BioProcess=osmosensory signaling pathway
13	65214	64	84	1815.5	65130	38311.76	21.1026	4.399349		BioProcess=ubiquitin-dependent protein catal
14	799	67	83	20	716	421.1765	21.05882	4.396353		
15	1923	67	82	53	1841	1082.941	20.43285	4.352819		BioProcess=UDP-N-acetylglucosamine biosy
16	18928.5	71	86	565.5	18842.5	11083.82	19.60004	4.292785		BioProcess=biological_process unknown|Mol
17	4190.5	70	84	128	4106.5	2415.588	18.87178	4.238159		BioProcess=translational termination|MolFun
18	507	67	83	13.5	424	249.4118	18.47495	4.207498		BioProcess=protein biosynthesis*|MolFunctic
19	4669	80	87	147	4582	2695.294	18.33533	4.196555		BioProcess=biological_process unknown|Mol
20	1586	63	82	51	1504	884.7059	17.34717	4.116629		BioProcess=biological_process unknown|Mol
21	14785	68	83	520	14702	8648.235	16.63122	4.055822		
22	12911.5	63	82	455.5	12829.5	7546.765	16.56809	4.050335		BioProcess=biological_process unknown|Mol
23	65214	64	83	2359	65131	38312.35	16.24093	4.021562		BioProcess=biological_process unknown|Mol
24	54761	70	84	2020	54677	32162.94	15.92225	3.992972		BioProcess=DNA replication initiation*|MolFu
25	551.5	66	82	17.5	469.5	276.1765	15.78151	3.980164		BioProcess=translational elongation|MolFunc
26	3129	69	86	115	3043	1790	15.56522	3.960254		BioProcess=not yet annotated|MolFunction=i
27	2898	68	83	107	2815	1655.882	15.47554	3.951917		BioProcess=mRNA splicing|MolFunction=not
28	6688	70	84	257	6604	3884.706	15.11559	3.917965		
29	65214	71	81	2601	65133	38313.53	14.73031	3.880716		BioProcess=not yet annotated|MolFunction=r
30	47623	65	83	1944	47540	27964.71	14.38514	3.846507		BioProcess=actin filament organization|MolFu
31	2186	76	86	87.5	2100	1235.294	14.11765	3.819428		BioProcess=ubiquitin-dependent protein catal
32	23997	68	82	1040.5	23915	14067.65	13.52008	3.757032		BioProcess=biological_process unknown|Mol
33	61899	68	84	2744.5	61815	36361.76	13.24896	3.727807		BioProcess=biological_process unknown|Mol
34	14821	68	83	670	14738	8669.412	12.93942	3.693701		BioProcess=stress response*|MolFunction=p
35	5164	74	87	231.5	5077	2986.471	12.90052	3.689357		
36	3316.5	78	86	149	3230.5	1900.294	12.75365	3.672838		BioProcess=biological_process unknown|Mol
37	2750.5	65	83	128	2667.5	1569.118	12.25873	3.615738		BioProcess=biological_process unknown|Mol

Sheet1 / Sheet2 / Sheet3

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	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	rMedianSig	gBGMedia	rBGMedia	green corrected	red corrected	red normal	red vs gree	log2 red vs green					
2	2693	70	88	9	2605	1532.353	170.2614	7.411608		BioProcess=vacuolar acidification*|MolFuncti			
3	57476	82	86	567	57390	33758.82	59.53937	5.895772		BioProcess=mRNA catabolism|MolFunction=			
4	26970.5	74	84.5	303	26886	15815.29	52.19569	5.705859		BioProcess=DNA dependent DNA replication			
5	14111	71	84	170	14027	8251.176	48.53633	5.600993		BioProcess=biological_process unknown|Mol			
6	1508	77.5	107	17	1401	824.1176	48.47751	5.599244		BioProcess=biological_process unknown|Mol			
7	46785	66	84	632	46701	27471.18	43.46705	5.44185					
8	65214	67	85	1135	65129	38311.18	33.75434	5.077001		BioProcess=not yet annotated|MolFunction=c			
9	58869	66	82.5	1091	58786.5	34580.29	31.69596	4.986227		BioProcess=SRP-dependent, co-translational			
10	33057	80	88							response to oxidative stress*|Mo			
11	4282	63	81							biological_process unknown|Mol			
12	1029.5	67	82							osmosensory signaling pathway			
13	65214	64	84							ubiquitin-dependent protein catal			
14	799	67	83										
15	1923	67	82							UDP-N-acetylglucosamine biosy			
16	18928.5	71	86							biological_process unknown|Mol			
17	4190.5	70	84							translational termination|MolFund			
18	507	67	83							protein biosynthesis*|MolFunctic			
19	4669	80	87							biological_process unknown|Mol			
20	1586	63	82							biological_process unknown|Mol			
21	14785	68	83										
22	12911.5	63	82							biological_process unknown|Mol			
23	65214	64	83							biological_process unknown|Mol			
24	54761	70	84							DNA replication initiation*|MolFu			
25	551.5	66	82							translational elongation|MolFunc			
26	3129	69	86							not yet annotated|MolFunction=i			
27	2898	68	83							mRNA splicing|MolFunction=not			
28	6688	70	84										
29	65214	71	81							not yet annotated|MolFunction=|			
30	47623	65	83							actin filament organization|MolFi			
31	2186	76	86							ubiquitin-dependent protein catal			
32	23997	68	82	1040.5	23915	14067.65	13.52008	3.757032		BioProcess=biological_process unknown|Mol			
33	61899	68	84	2744.5	61815	36361.76	13.24896	3.727807		BioProcess=biological_process unknown|Mol			
34	14821	68	83	670	14738	8669.412	12.93942	3.693701		BioProcess=stress response*|MolFunction=p			
35	5164	74	87	231.5	5077	2986.471	12.90052	3.689357					
36	3316.5	78	86	149	3230.5	1900.294	12.75365	3.672838		BioProcess=biological_process unknown|Mol			

Convert Text to Columns Wizard - Step 1 of 3

The Text Wizard has determined that your data is Delimited.

If this is correct, choose Next, or choose the data type that best describes your data.

Original data type

Choose the file type that best describes your data:

◉ Delimited   - Characters such as commas or tabs separate each field.
○ Fixed width   - Fields are aligned in columns with spaces between each field.

Preview of selected data:

```
1
2 BioProcess=vacuolar acidification*|MolFunction=monovalent inorg
3 BioProcess=mRNA catabolism|MolFunction=molecular_function unkno
4 BioProcess=DNA dependent DNA replication|MolFunction=DNA-direct
5 BioProcess=biological_process unknown|MolFunction=molecular_fun
```

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24 of 24 - Clipb

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P1

	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected	red normal	red vs gree	log2 red vs green					
2	2693	70	88	9	2605	1532.353	170.2614	7.411608		BioProcess=vacuolar acidification*|MolFunctio			
3	57476	82	86	567	57390	33758.82	59.53937	5.895772		BioProcess=mRNA catabolism|MolFunction=			
4	26970.5	74	84.5	303	26886	15815.29	52.19569	5.705859		BioProcess=DNA dependent DNA replication			
5	14111	71	84	170	14027	8251.176	48.53633	5.600993		BioProcess=biological_process unknown|Mol			
6	1508	77.5	107	17	1401	824.1176	48.47751	5.599244		BioProcess=biological_process unknown|Mol			
7	46785	66	84	632	46701	27471.18	43.46705	5.44185					
8	65214	67	85	1135	65129	38311.18	33.75434	5.077001		BioProcess=not yet annotated|MolFunction=(			
9	58869	66	82.5	1091	58786.5	34580.29	31.69596	4.986227		BioProcess=SRP-dependent, co-translational			
10	33057	80	88							response to oxidative stress*|M(			
11	4282	63	81							biological_process unknown|Mol			
12	1029.5	67	82							osmosensory signaling pathway			
13	65214	64	84							ubiquitin-dependent protein catal			
14	799	67	83										
15	1923	67	82							UDP-N-acetylglucosamine biosy			
16	18928.5	71	86							biological_process unknown|Mol			
17	4190.5	70	84							translational termination|MolFun(			
18	507	67	83							protein biosynthesis*|MolFunctio			
19	4669	80	87							biological_process unknown|Mol			
20	1586	63	82							biological_process unknown|Mol			
21	14785	68	83										
22	12911.5	63	82							biological_process unknown|Mol			
23	65214	64	83							biological_process unknown|Mol			
24	54761	70	84							DNA replication initiation*|MolFu			
25	551.5	66	82							translational elongation|MolFunc			
26	3129	69	86							not yet annotated|MolFunction=i			
27	2898	68	83							mRNA splicing|MolFunction=not			
28	6688	70	84										
29	65214	71	81							not yet annotated|MolFunction=|			
30	47623	65	83							actin filament organization|MolFu			
31	2186	76	86							ubiquitin-dependent protein catal			
32	23997	68	82	1040.5	23915	14067.65	13.52008	3.757032		BioProcess=biological_process unknown|Mol			
33	61899	68	84	2744.5	61815	36361.76	13.24896	3.727807		BioProcess=biological_process unknown|Mol			
34	14821	68	83	670	14738	8669.412	12.93942	3.693701		BioProcess=stress response*|MolFunction=p			
35	5164	74	87	231.5	5077	2986.471	12.90052	3.689357					
36	3316.5	78	86	149	3230.5	1900.294	12.75365	3.672838		BioProcess=biological_process unknown|Mol			
37	2750.5	65	83	128	2667.5	1569.118	12.25873	3.615738		BioProcess=biological_process unknown|Mol			

Convert Text to Columns Wizard - Step 2 of 3

This screen lets you set the delimiters your data contains. You can see how your text is affected in the preview below.

Delimiters
☑ Tab   ☐ Semicolon   ☐ Comma
☐ Space   ☑ Other: =

☐ Treat consecutive delimiters as one

Text qualifier: "

Data preview

BioProcess	vacuolar acidification*|MolFunction	monovalent i
BioProcess	mRNA catabolism|MolFunction	molecular_fu
BioProcess	DNA dependent DNA replication|MolFunction	DNA-directed
BioProcess	biological_process unknown|MolFunction	molecular_fu

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24 of 24 - Clipboa

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press Ctrl+C twice.

Options ▼

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P1

	G	H	I	J	K	L	M	N	O	P	Q	R	S
1	rMedianSig	gBGMedia	rBGMedian	green corrected	red corrected	red normal	red vs gree	log2 red vs green					
2	2693	70	88	9	2605	1532.353	170.2614	7.411608		BioProcess=vacuolar acidification*|MolFunctic			
3	57476	82	86	567	57390	33758.82	59.53937	5.895772		BioProcess=mRNA catabolism|MolFunction=			
4	26970.5	74	84.5	303	26886	15815.29	52.19569	5.705859		BioProcess=DNA dependent DNA replication			
5	14111	71	84	170	14027	8251.176	48.53633	5.600993		BioProcess=biological_process unknown|Mol			
6	1508	77.5	107	17	1401	824.1176	48.47751	5.599244		BioProcess=biological_process unknown|Mol			
7	46785	66	84	632	46701	27471.18	43.46705	5.44185					
8	65214	67	85	1135	65129	38311.18	33.75434	5.077001		BioProcess=not yet annotated|MolFunction=(			
9	58869	66	82.5	1091	58786.5	34580.29	31.69596	4.986227		BioProcess=SRP-dependent, co-translational			
10	33057	80	88							response to oxidative stress*|Mc			
11	4282	63	81							biological_process unknown|Mol			
12	1029.5	67	82							osmosensory signaling pathway			
13	65214	64	84							ubiquitin-dependent protein catal			
14	799	67	83										
15	1923	67	82							UDP-N-acetylglucosamine biosy			
16	18928.5	71	86							biological_process unknown|Mol			
17	4190.5	70	84							translational termination|MolFun			
18	507	67	83							protein biosynthesis*|MolFunctic			
19	4669	80	87							biological_process unknown|Mol			
20	1586	63	82							biological_process unknown|Mol			
21	14785	68	83										
22	12911.5	63	82							biological_process unknown|Mol			
23	65214	64	83							biological_process unknown|Mol			
24	54761	70	84							DNA replication initiation*|MolFu			
25	551.5	66	82							translational elongation|MolFunc			
26	3129	69	86							not yet annotated|MolFunction=i			
27	2898	68	83							mRNA splicing|MolFunction=not			
28	6688	70	84										
29	65214	71	81							not yet annotated|MolFunction=|			
30	47623	65	83							actin filament organization|MolFu			
31	2186	76	86							ubiquitin-dependent protein catal			
32	23997	68	82	1040.5	23915	14067.65	13.52008	3.757032		BioProcess=biological_process unknown|Mol			
33	61899	68	84	2744.5	61815	36361.76	13.24896	3.727807		BioProcess=biological_process unknown|Mol			
34	14821	68	83	670	14738	8669.412	12.93942	3.693701		BioProcess=stress response*|MolFunction=p			
35	5164	74	87	231.5	5077	2986.471	12.90052	3.689357					
36	3316.5	78	86	149	3230.5	1900.294	12.75365	3.672838		BioProcess=biological_process unknown|Mol			
37	2750.5	65	83	128	2667.5	1569.118	12.25873	3.615738		BioProcess=biological_process unknown|Mol			

Convert Text to Columns Wizard - Step 3 of 3

This screen lets you select each column and set the Data Format.

'General' converts numeric values to numbers, date values to dates, and all remaining values to text.

Column data format
- ● General
- ○ Text
- ○ Date: MDY
- ○ Do not import column (skip)

Advanced...

Destination: P1

Data preview

General	General		General
BioProcess	vacuolar acidification*|MolFunction		monovalent i
BioProcess	mRNA catabolism|MolFunction		molecular_fur
BioProcess	DNA dependent DNA replication	MolFunction	DNA-directed
BioProcess	biological_process unknown|MolFunction		molecular_fur

Cancel < Back Next > Finish

24 of 24 - Clipboard

Paste All Clear All

Click an item to paste:

integer
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Options ▼

Sheet1 / Sheet2 / Sheet3

Ready

NUM

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Q24   ▼   fx   DNA replication initiation*|MolFunction

	G	H	I	J	K	L	M	N	O	P	Q	R
1	rMedianSig	gBGMedia	rBGMediar	green corrected	red corrected	red normal	red vs gree	log2 red vs green				
2	2693	70	88	9	2605	1532.353	170.2614	7.411608		BioProces	vacuolar acidification*|M	monovaler
3	57476	82	86	567	57390	33758.82	59.53937	5.895772		BioProces	mRNA catabolism|MolF	molecular
4	26970.5	74	84.5	303	26886	15815.29	52.19569	5.705859		BioProces	DNA dependent DNA re	DNA-direc
5	14111	71	84	170	14027	8251.176	48.53633	5.600993		BioProces	biological_process unkn	molecular
6	1508	77.5	107	17	1401	824.1176	48.47751	5.599244		BioProces	biological_process unkn	molecular
7	46785	66	84	632	46701	27471.18	43.46705	5.44185				
8	65214	67	85	1135	65129	38311.18	33.75434	5.077001		BioProces	not yet annotated|MolFu	dolichyl-p
9	58869	66	82.5	1091	58786.5	34580.29	31.69596	4.986227		BioProces	SRP-dependent, co-tran	transporte
10	33057	80	88	805	32969	19393.53	24.09134	4.590443		BioProces	response to oxidative st	thiol-disul
11	4282	63	81	106	4201	2471.176	23.31299	4.543062		BioProces	biological_process unkn	molecular
12	1029.5	67	82	24	947.5	557.3529	23.22304	4.537485		BioProces	osmosensory signaling	enzyme a
13	65214	64	84	1815.5	65130	38311.76	21.1026	4.399349		BioProces	ubiquitin-dependent prot	adenosine
14	799	67	83	20	716	421.1765	21.05882	4.396353				
15	1923	67	82	53	1841	1082.941	20.43285	4.352819		BioProces	UDP-N-acetylglucosami	UDP-N-ac
16	18928.5	71	86	565.5	18842.5	11083.82	19.60004	4.292785		BioProces	biological_process unkn	molecular
17	4190.5	70	84	128	4106.5	2415.588	18.87178	4.238159		BioProces	translational termination	translatior
18	507	67	83	13.5	424	249.4118	18.47495	4.207498		BioProces	protein biosynthesis*|Mc	structural
19	4669	80	87	147	4582	2695.294	18.33533	4.196555		BioProces	biological_process unkn	molecular
20	1586	63	82	51	1504	884.7059	17.34717	4.116629		BioProces	biological_process unkn	molecular
21	14785	68	83	520	14702	8648.235	16.63122	4.055822				
22	12911.5	63	82	455.5	12829.5	7546.765	16.56809	4.050335		BioProces	biological_process unkn	molecular
23	65214	64	83	2359	65131	38312.35	16.24093	4.021562		BioProces	biological_process unkn	molecular
24	54761	70	84	2020	54677	32162.94	15.92225	3.992972		BioProces	DNA replication initiatio	chromatin
25	551.5	66	82	17.5	469.5	276.1765	15.78151	3.980164		BioProces	translational elongation|	translatior
26	3129	69	86	115	3043	1790	15.56522	3.960254		BioProces	not yet annotated|MolFu	isoleucine
27	2898	68	83	107	2815	1655.882	15.47554	3.951917		BioProces	mRNA splicing|MolFunc	not yet an
28	6688	70	84	257	6604	3884.706	15.11559	3.917965				
29	65214	71	81	2601	65133	38313.53	14.73031	3.880716		BioProces	not yet annotated|MolFu	protein ty
30	47623	65	83	1944	47540	27964.71	14.38514	3.846507		BioProces	actin filament organizati	structural
31	2186	76	86	87.5	2100	1235.294	14.11765	3.819428		BioProces	ubiquitin-dependent prot	proteason
32	23997	68	82	1040.5	23915	14067.65	13.52008	3.757032		BioProces	biological_process unkn	peptidyl-p
33	61899	68	84	2744.5	61815	36361.76	13.24896	3.727807		BioProces	biological_process unkn	molecular
34	14821	68	83	670	14738	8669.412	12.93942	3.693701		BioProces	stress response*|MolFu	protein ta
35	5164	74	87	231.5	5077	2986.471	12.90052	3.689357				
36	3316.5	78	86	149	3230.5	1900.294	12.75365	3.672838		BioProces	biological_process unkn	molecular
37	2750.5	65	83	128	2667.5	1569.118	12.25873	3.615738		BioProces	biological_process unkn	molecular

Sheet1 / Sheet2 / Sheet3

24 of 24 - Clipboard

Paste All   Clear All

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Options ▼

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Good luck!!