



Starting with two biological samples



using DNA microarrays?









B) Die Ky ywei jeunt Trans Das Das Werden under Strassen and Stra		******				· <u></u>										_
Image: State Bit in the Bi	8)	Eile Edi	View ((nsert Fg	rmat Ioo	ls <u>D</u> ata	Window	Help								Type
	ED			49 84	X Do DR	• at 1 m	0.14	L I dia	Arial		v 10	T B	л п ≡	= = 3	S %	
Nome Nome <th< th=""><th></th><th></th><th></th><th>× 104</th><th>n - 1 - 4</th><th>• • •</th><th>· (- ·) Z</th><th></th><th>1 101100</th><th></th><th>- 10</th><th>1</th><th></th><th></th><th>5 * 70</th><th>/ .00</th></th<>				× 104	n - 1 - 4	• • •	· (- ·) Z		1 101100		- 10	1			5 * 70	/ .00
Strate IV Vintory I Image: Strate IV	1		1 🗢 🖄	50	8 49 69 1				view							
A. B. TYPE UYPE bat text <t< td=""><td>5</td><td>Snaglt 🖻</td><td>Window</td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td></td></t<>	5	Snaglt 🖻	Window													
A B C D E F O H J K L M H C 2 FEXAMUATANCE J Protect distant, Dari Scan, Mari Mari Mari Mari Mari Mari Mari Mari	-	A1	-	& TYPE												
United test <		A	В	C	D	F	F	G	н	1	J	K	1	M	N	C
2 FERRATAL Constraint	1	TYPE	text	text	text	text	integer	foat	float	text	text	text	integer	integer	integer	integ
3 DATA 0.25.4.5 reserver seasone seasones Agains To 2 5 5.5.515115_514488_D, Dismissione 1 1 2.5.22 0 DVPC data faster	2	FEPARAN	Protocol N	Protocol d	Scan Date	Scan Sca	Scan Nun	Scan Mici	Scan Mic	Scan Orig	Grid Nam	Grid Date	Grid Num	Grid Num	Grid Num	Grid
Image: Constraint of the sector of	3	DATA	GE2-v4 91	*******	*******	Agilent Te	2	5	5	c1516f15-c	014868 D		1	1	532	
S IVTE foat integer in	4	•														
6 STATS gback/berg/gback/berg/gback/berg/sbackack/berg/sbackackackack/berg/sback/berg/sback/berg/	5	TYPE	float	float	float	integer	integer	float	float	float	integer	integer	float	float	float	float
7 DATA 31 455 35 7.0412 1000 66316 12.247 <th12.247< th=""> 12.247 12.24</th12.247<>	6	STATS	gDarkOffse	gDarkOffse	gDarkOffs	egDarkOffs	gSaturatio	rDarkOffse	rDarkOffse	rDarkOffse	rDarkOffse	rSaturation	gAvgSig28	FrAvgSig2E	gAvgSig2E	IrAvgS
Texture Integer Integer <t< td=""><td>7</td><td>DATA</td><td>38.455</td><td>39</td><td>7.04102</td><td>1000</td><td>65261</td><td>38.817</td><td>39</td><td>24.6422</td><td>1000</td><td>65196</td><td>1.2247</td><td>1.23544</td><td>1.01242</td><td>0.99</td></t<>	7	DATA	38.455	39	7.04102	1000	65261	38.817	39	24.6422	1000	65196	1.2247	1.23544	1.01242	0.99
9 TYPE: refere note refere note refere note not not <	8	•														
Bit PEALINE Feature Notice Cold Sold registration <	9	TYPE	integer	integer	integer	integer	text	integer	text	integer	integer	text	text	text	text	float
IDAA IDAA <th< td=""><td>10</td><td>FEATURE</td><td>FeatureNu</td><td>Row</td><td>Col</td><td>SubTypeN</td><td>SubTypeN</td><td>Start</td><td>Sequence</td><td>ProbeUID</td><td>ControlTyp</td><td>ProbeNam</td><td>GeneNam</td><td>Systemati</td><td>Descriptio</td><td>Posit</td></th<>	10	FEATURE	FeatureNu	Row	Col	SubTypeN	SubTypeN	Start	Sequence	ProbeUID	ControlTyp	ProbeNam	GeneNam	Systemati	Descriptio	Posit
Deck Deck <thdeck< th=""> Deck Deck <thd< td=""><td>11</td><td>DATA</td><td>1</td><td>1</td><td>1</td><td>0</td><td></td><td>0</td><td></td><td>0</td><td>1</td><td>GE_Bright</td><td>GE_Bright</td><td>GE_Bright</td><td>Corner</td><td>368</td></thd<></thdeck<>	11	DATA	1	1	1	0		0		0	1	GE_Bright	GE_Bright	GE_Bright	Corner	368
Bit DATA Come Standard Libracione Li	12	DATA	2	1	2	66	Structural	0		1	1	DarkCorne	DarkCorne	DarkCome	H	3/
Image: Data Come Second Come Second	13	DATA	3	1	3	66	Structural	0		1	1	DarkCorne	DarkCorne	DarkCome	M	3/4
Big Data Frequence Reduce number of rows Come Store	14	DATA	4	_						-				kCome	NT	3/0
Dip Data Preduce the full local Off Total Come Social Data Bata Remove rows 1-21but save Come Social Soc	10	DATA	5		Dec	1100	D	ımh	on	ot .	204	10		ACOING INCOME	n	3/3
IDAA Image: Constraint of the second se	17	DATA	7		NEU	IUCE			61			0		kCome	я ч	- 34
Image: Space sector Image: Space sector <thimage: sector<="" space="" th=""> Image: Space sector Image: Space sector</thimage:>	18	ΠΑΤΑ	8							04				kCome	n w	205
20 DATA 10 Comer 39 21 DATA 10 Comer 39 22 DATA 11 Row 10011 Comer 39 22 DATA 11 14 0 Ottorian 0001100 0001100 30 22 DATA 15 14 0 0101000 7 0.4.32 P140Agr MU001414 30	19	DATA	9		Ron	10V6	r n	2WC	1 -	21	b	11 9	ave	kCome	M .	381
Zi DATA 11 Comer 31 Zi DATA 11 Row 10!! 10! 10! 10!!	20	DATA	10		1011				-					kCome	M.	391
ZE DATA 12 COM LOPE Common 2 is a com	21	DATA	11			. 41								kCome	ar M	39
22 DATA 13 COURTING mum c2 29 22 DATA 13 4 0 0 TCGTGTCC 7 0.4.52 P40 Aap 14 0 0 TCGTGTCC 7 0.4.52 P40 Aap 14 0 0 TCGTGTCC 7 0.4.52 P40 Aap 14 0 0 TCGTGTCC 7 0.4.52 P40 Aap 140 0 0 TCGTGTCC 7 0.4.52 P40 Aap 140 0 120 TCGTGTCC 7 0.4.52 P40 Aap 140 140 140 140	22	DATA	12		KOW	/ 10	<u>, </u>							0099	Mus muse	397
28 (DATA 14 14 0 01CTGTGCI 7 0.A.S2 P49.Agr. PMI.0072/Mag.muscl 4/2 26 (DATA 15 1 15 0 0ACTAMA 9 0.A.S2 P49.Agr. PMI.0072/Mag.muscl 4/2 26 (DATA 16 1 16 0 TCACATGC 11 0.A.S1 P33 Ment MM.001MM muscl 4/2 26 (DATA 16 1 16 0 TCACATGC 11 0.A.S1 P33 Ment MM.001MM muscl 4/2 27 (DATA 16 1 0 0.CTCACTH 10 0.A.S2 P40.2GV38/McM081Hz2Me muscl 4/2 28 (DATA 19 19 0 0.CTCACTH 16 0.A.S2 P40.2GV38/McM38/ME muscl 4/2 29 (DATA 20 0 0.CAGGGCA 10 0.A.S2 P40.2GV38/McM38/M muscl 4/2 20 (DATA 21 21 0 0.TMA4AG 20 0.A.S1 P55.4SV18/F44/397H Min muscl 4/2 30 (DATA 22 2 0 0.A.S2 P69.P68.Hz18 (MA1011Hz19Hm muscl 4/2 <td>23</td> <td>DATA</td> <td>13</td> <td></td> <td>0087;</td> <td>Mus muso</td> <td>399</td>	23	DATA	13											0087;	Mus muso	399
ŽE (DATA 15 15 0 0/ACTAAA 9 0.A.52_PE1 AX06412 AX65412 AX	24	DATA	14	1	14	0		0	TCTGTGC	7	0	A_52_P40	Aqp7	NM_0074	Mus muso	402
ZB (DATA 16 1 6 0 0TCACATOC 11 0.A 51 P33 Hunt MM 001MMAs muck 400 ZD (DATA 16 1 0 0TCACATOC 11 0.A 51 P33 Hunt MM 001MMAs muck 400 ZB (DATA 19 1 0 0TCACATOC 16 0.A 52 P50 (2008)KM 0005 Hunt muck 40 ZB (DATA 19 1 0 0 CTCACTAT 16 0.A 52 P50 (2008)KM 0005 Hunt muck 42 ZB (DATA 20 0 0CATGGCAT 18 0.A 52 P50 (2008)KM 0005 Hunt muck 42 ZB (DATA 21 21 0 0TGAAAG 29 0.A 51 P55 HUNT HUNT MUKK 42 ZB (DATA 22 2 0 0 TGAAAG 20 0.A 51 P55 HUNT HUNT HUNT HUNT HUNT HUNT HUNT HUNT	25	DATA	15	1	15	0		0	AACTAAA	9	0	A 52 P81	AK046412	AK046412	Mus musc	
ZE DATA 11 0 0 CTCACTA 14 0 A.21 PAS (GRO) MAX 00051Mb mmc PAS ZD DATA 10 1 0 0 CTCACTA 14 0 A.21 PAS (GRO) MAX 00051Mb mmc 41 ZD DATA 10 1 0 0 CATACTACTA 16 0 A.22 PAS 20 0 CATACTACTACTA 10 A.31 PAS (ASS) MBM mmc 42 32 DATA 21 1 21 0 0 TGTGAAAG 20 A.31 PAS (ASS) MBM mmc 42 32 DATA 22 1 21 0 0 TGTGAAAG 20 A.31 PAS (ASS) MBM mmc 42 32 DATA 22 1 22 0 0 ACCATCTA 20 A.25 PAS (ASS) MBM mmc 42 32 DATA 32 DATA 32 DATA 32 DATA 32 DATA 32 DATA <td< td=""><td>26</td><td>DATA</td><td>16</td><td>1</td><td>16</td><td>0</td><td></td><td>0</td><td>TCAGTGC</td><td>11</td><td>0</td><td>A_51_P33</td><td>Hvcn1</td><td>NM_00104</td><td>Mus musc</td><td>407</td></td<>	26	DATA	16	1	16	0		0	TCAGTGC	11	0	A_51_P33	Hvcn1	NM_00104	Mus musc	407
28 DATA 19 1 19 0 0.7CCACTAI 16 0.A.S.2.Fb012208061.4A00H122.bits music 42 28 DATA 20 1 20 0.CATGGCAT 18 0.A.S.2.Fb012208061.4A00H122.bits music 42 28 DATA 20 1 20.A 27.Pb102CH38E0F03381Ms music 42 30 DATA 21 1 21 0 0.TGAAA62 20 A.S.1.P55.53106F14X039774.bits music 42 30 DATA 22 1 2.0 0.ACCATTO 20 A.S.2.P56.P5882.bits ML MUSTINB music 42 30 DATA 22 1 2.0 A.CCATTO 2.0 A.S.2.P56.P5882.bits ML MUSTINB music 42 30 DATA 22 1 2.0 A.S.2.P56.P5882.bits ML MUSTINB music 42	27	DATA	18	1	18	0		0	CTCACTA	14	0	A_51_P43	Gpr33	NM_00815	Mus muse	
28 [0ATA 20 1 20 0 0.4TGGCA 18 0.4, 52 729.LCX43466733388 Max musc. 42 30 [0ATA 21 1 21 0 0.TGGAAG 20 0.A, 52 754.S33106F144039774 Max musc. 42 31 [0ATA 22 1 22 0 4.52 768.Pfada M0.173 Max musc. 42 31 [0ATA 22 1 22 0 4.52 P58.Pfada M0.173 Max musc. 42 31 [0ATA 22 1 22 0 4.52 P58.Pfada M0.173 Max musc. 42 31 [0ATA 22 1 22 0 4.52 P58.Pfada M0.173 Max musc. 42 31 [0ATA 21 1 20 0 4.52 P58.Pfada M0.173 Max musc. 42 31 [0ATA 21 1 20 0 7.57 0 0.455 154.155024474.460.460.460.460.460.460.460.460.460.46	28	DATA	19	1	19	0		0	CTCACTA	16	0	A_52_P50	C230086J	(AK084122	Mus muse	- 41
30 DATA 21 1 21 0 0 TTGAAAG 20 0 A_51 P35/A330106F1AK039774 Mus musc 420 31 DATA 22 1 22 0 0 ACCATTG 22 0 A52 P68 <prdsss< td=""> NM 01378 Mus musc 422 32 DATA 23 0 0 CTCTCQC 21 0.4 51 P45140041/UMs musc 422 32 DATA 23 0 0 CTCTCQC 21 0.4 51 P45140041/UMs musc 422</prdsss<>	29	DATA	20	1	20	0		0	CATGGCA	18	0	A_52_P29	LOC43436	BC053388	Mus muso	417
31 DATA 22 1 22 0 0/ACCATTG 22 0/A 52 P68 Pdss2 NM 01378/Nus musc 422 0/A 52 P68 Pdss2 NM 01378/Nus musc 422 0/A 52 P68 Pdss2 NM 01378/Nus musc 423 0/A 52 P68 Pdss2 NM 01378/Nus Pds 428 0/A 52 P68 Pds 428	30	DATA	21	1	21	0		0	TTGAAAG	20	0	A_51_P35	A330106F	AK039774	Mus muse	420
22UDATA 22 1 22 0 0 0TCTTC/CC 24 0 A 51 D41 1110014///MA 02052Mup mupp	31	DATA	22	1	22	0		0	ACCATTG	22	0	A_52_P68	Ptdss2	NM_0137	Mus muso	422
32 DRTA 23 1 23 0 0101033 24 07 51 41110014K1111 0200211051050	32	DATA	23	1	23	0		0	TCTTCGG	24	0	A_51_P41	1110014K	(NM_0286)	Mus muse	1

3,	Microsoft E	Excel - 20_1	109(F07)_T	RGreen						
	Elle Edit Vi	iew Insert For	mat <u>T</u> ools <u>D</u> a	sta <u>Window E</u>	(elp					Type a question for
D		a (A 1 49 (A 1)	K Do 1994 - 1997	0.00.141	1 COL C E Arial		× 10 × 10	Z 11 = =		• • • • • • • • • • • • • • • • • • •
-		- 14 V 14 I	N 14 44 1 V							
9		90000	Re 🔁 🖓 Re		End Review					
5	Snagit 🛃 🗰	indow	-							
-	A1 👻	6 Genelik	ame							
	A	В	с	D	E	F	G	н	1	J
1	GeneName	SystematicNam	Description	gMeanSignal	rMeanSignal	gMedianSignal	rMedianSignal	gBGMeanSignal	rBGMeanSignal	gBGMedianSign rBG
	Cer1	NM_009912	Mus musculus (c 5.91E+01	7.95E+01	59	80	5.86E+01	7.84E+01	58
	Nppa	NM_008725	Mus musculus r	n 7.66E+01	8.49E+01	65	78.5	5.78E+01	7.73E+01	58
	Aqp7	NM_007473	Mus musculus a	a 5.80E+01	7.45E+01	59	74	5.78E+01	7.88E+01	58
5	AK046412	AK046412	Mus musculus a	a 9.21E+01	8.33E+01	68	83	5.84E+01	7.78E+01	58
	Hvcn1	NM_001042489	Mus musculus I	h 5.68E+01	7.55E+01	56	74	5.84E+01	7.77E+01	58
	Gpr33	NM_008159	Mus musculus (6 5.72E+01	7.43E+01	57	74	5.89E+01	7.88E+01	59
1	C230086J09Rik	AK084122	Mus musculus '	1 5.66E+01	7.68E+01	57	74	5.86E+01	7.89E+01	58
	LOC434369	BC053388	Mus musculus t	s 8.36E+01	9.51E+01	79	82.5	5.88E+01	7.85E+01	59
	A330106F07R6	K AK039774	Mus musculus a	a 5.8/E+01	7.98E+01	59	82	5.90E+01	7.78E+01	59
	Ptossz	NM_013782	Mus musculus	p 1.06E+02	8.42E+01	30	83	5.86E+01	7.79E+01	58
	1110014K05Kik	C NM_028622	Mus musculus I	5.75E+01	7.85E+01	5/	79	5.96E+01	7.68E+01	60
-	Elmo 1	AK 14 1940	Mus musculus	5.33E+01	7.02E+01	60.5	70	5.00E+01	7.04E+01	59
÷	Crimon	NRA 446400	Mus musculus (0.34E+01	1.000-401	10	10011	0.54E+01	0.0000-001	0.9
ř	Pent1	_								
	Sex9	onv	COLU	mne		. NI				
8	Tmem144	-UUY	Colu	11/15), IN,	- A FI	, AL	, AJ	, AN
9	AK039768									
	Syne1		AC	AT						
1	Ank1	4R. /	43. /	ΑΙ.	AU					
	H2-M10.5									
	lsgf3g	NM_008394	Mus musculus i	5.82E+01	7.94E+01	58	78.5	6.13E+01	8.19E+01	60.5
4	BC056923	NM_173395	Mus musculus (c 6.17E+01	8.39E+01	61	85	6.13E+01	7.97E+01	60
	Pusl1	AK151452	Mus musculus I	5.75E+01	7.57E+01	58	75	5.99E+01	7.77E+01	60
6	5330410G16Rik	K NM_182991	Mus musculus I	F 5.86E+01	7.47E+01	57.5	74.5	5.96E+01	7.98E+01	59
7	Ldir	NM_010700	Mus musculus I	k 5.94E+01	8.13E+01	59	79	5.94E+01	7.98E+01	59
8	Hps5	NM_001005247	Mus musculus I	5.91E+01	7.26E+01	59	73	5.93E+01	7.85E+01	59
9	Thoc1	AK042548	Mus musculus	7 5.90E+01	7.59E+01	59.5	75.5	5.98E+01	7.90E+01	59
	VVnic1	NM_198703	Mus musculus 1	v 5.95E+01	r.73E+01	58	76	5.95E+01	7.94E+01	59
1	AKU32795	AK032795	Mus musculus	5.65E+01	r.78E+01	56	77	6.01E+01	7.90E+01	60
	5001	AV021492	Mus musculus s	5.9/E+01	7.88E+01	60	79 5	5.91E+01	7.81E+01	59
-	0.0010000	AK031462	Mus musculus	1 5.79E+01	7.86E+01	50	/6.5	5.92E+01	7.93E+01	59
-	DE056575	PE056575	III M RC2 MUS	6.04E+01	3.33E+01 7.94E+01	61	79.5	6.51E+01	0.39E+01	61
	DE906075	DE900070	01-M-DG2-001-N-	0.0/E+01	7.34E+01	50	70.5	5.30E+01	0.02E+01	60
70	00303200	0/03/03/200	043303205 0020	N 0.10E+U1	r.33E+01	63		0.946+01	r.0/E+01	23

e Edit Vie	ew Insert For	mat Tools Da	ita Window H	ielo					Type a guestion f	or held
	L D. 149 (N. 1.)	(D. (0)	- Pr - 1 A I	1.000						
M (6)(3		6 MI 10 - VI	- / • (- • Z+	1 300 - 2 1000		• 10 • B	- x <u>0</u> /= =		7 30 43 J 37 J	
220	315013	1 (2) (P) Re								
alt 🖅 Wir	ndow	-			-					
• • :	× √ & =F2-J2									
В	C	D	E	F	G	н	1	J	К	L
tematicNam	Description	gMeanSignal	rMeanSignal	gMedianSignal	rMedianSignal	gBGMeanSignal	rBGMeanSignal	gBGMedianSign	rBGMedianSignal	
009912	Mus musculus c	5.91E+01	7.95E+01	59	80	5.86E+01	7.84E+01	58	78 =	2-J2
008725	Mus musculus n	7.66E+01	8.49E+01	65	78.5	5.78E+01	7.73E+01	58	77	
007473	Mus musculus a	5.80E+01	7.45E+01	59	74	5.78E+01	7.88E+01	58	78	
46412	Mus musculus a	9.21E+01	8.33E+01	68	83	5.84E+01	7.78E+01	58	77	
001042489	Mus musculus h	5.68E+01	7.55E+01	56	74	5.84E+01	7.77E+01	58	78	
008159	Mus musculus G	5.72E+01	7.43E+01	57	74	5.89E+01	7.88E+01	59	78	
84122	Mus musculus 1	5.66E+01	7.68E+01	57	74	5.86E+01	7.89E+01	58	78	
63388	Mus musculus s	8 36E+01	9.51E+01	79	82.5	5.88E+01	7.85E+01	59	78	
39774	Mus musculus a	5.87E+01	7.98E+01	59	82	5.90E+01	7.78E+01	59	17	
013782	Mus musculus p	1.05E+02	8.42E+01	95	83	5.86E+01	7.79E+01	58	77	
028622	Mus musculus F	5 75E+01	7.85E+01	57	79	5.96E+01	7.68E+01	60	77	
41948	Mus musculus 1	5.99E+01	7.82E+01	60.5	77	5.86E+01	7.84E+01	59	78	
198093	Mus musculus e	5.72E+01	7 80E+01	57	79	5.94E+01	7.87E+01	59	78	
145123	Mus									
027869	Mus									
011448	Mue									
027495	Mus Con		haal			· · hand · · · ·				
39768	Mus	гате	Daci	karol	na s	прть	асте		imn -	
163399	Mun			.9						
021169	Mug C									
177637	Mus TOI	r rec	and	are	en si	onals				
008394	Mus			9.0		giiaia				
172206	Mus mussion a	6 17E+01	9 20E+01	61	95	6.12E+01	7.975+01	60	79	
61462	Mue mueculue h	6 76E+01	7.57E+01	68	75	6.99E+01	7 77E+01	60	76	
102001	Mus musculus E	6 965+01	7.475+01	E7 6	74.6	E 96E+01	7.995+01	60	79	
010700	Mus musculus P	5.00E+01	9.125+01	57.5	79.0	5.30L+01	7.000+01	50	70	
001006247	Mus musculus II	5.04E+01	7.05E+01	60	73	5.04E+01	7.96E+01	03	7.0	
40540	Mus musculus 7	5.91E+01	7.695+01	50 G	76.6	5.53E+01	7.00E+01	50	70	
100702	Mus musculus /	5.90E+01	7.73E+01	09.0	10.0	0.30E+01	7.94E+01	50	79	
120/03	Mus musculus V	5.95E+01	7.73E+01	50	76	5.95E+01	7.940+01	53	79	
32130	MUS MUSCUIUS 1	5.65E+01	7.78E+01	56	11	6.01E+01	7.90E+01	60	79	
003127	Mus musculus s	5.9/E+01	7.88E+01	60	79	5.91E+01	7.81E+01	59	11	
31462	Mus musculus 1	5.79E+01	7.86E+01	58	78.5	5.92E+01	r.93E+01	59	78	
145418	Mus musculus c	6.04E+01	9.33E+01	61	81	6.51E+01	8.39E+01	61	80	
56575	UI-M-BG2-bbl-h-l	5.87E+01	7.94E+01	58	78.5	5.98E+01	8.02E+01	60	79	
	In the second se									

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





Corrected corrected 8 0 0 E 0 0 H 3 K K M 2141.48 P27875 30 385 213 14 13 355 755 2141.48 P27875 128 31 11 13 14 2141.48 P27876 YVR2505 125 215 14 19 14 3497.45 P287274 YVR2505 125 215 14 1915 154 3497.45 P287274 YVR2505 158 72 84 1915 154 3497.45 P287211 YVR1900 158 158 114 2015 3589.47 P127211 YVR1900 158 68 150 124 2015 3589.47 P127211 YVR1900 159 68 150 124 2015 3689.47 P127211 YVR1900 159 159 68 150 124	9165	010	Rep (P) Rep	ly with Changes.	. End Revi	ew	Gree	n ba	ckground	red bad	kgro	und	
V € x=x=x=y=1/2/375 B) C D E B) C				,			cor	recte	d	correc	ted		
B C D E F G H J JK L M 511,48, P42,037 YH82052 503 285 565	VE	=average	j2:J10275										
\$\$11.48, \$P\$12617 YR4050 450 286.5 61 83 351 255.5 \$\$12.44, AP\$12600 YR4050 181 331 161 83 317 75.5 \$\$17.44, AP\$12600 YR4050 181 336.5 71 85 141 \$\$17.44, AP\$12600 YR4050 181 326.5 71 81 174.5 275.5 \$\$17.44, AP\$12600 YR11570 YR1050 181 326.5 71 81 174.5 275.5 154.5 \$\$18.44, AP\$12771 YR1050 271.8 71.8 81.7 174.5 277.5 154.5 \$\$18.44, AP\$1277.11 YR8040 277.5 181.6 80 1154 250.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 156.5 157.5	В	С	D	E	F	G	H	1	J	K	L	M	N
2744 A& P26266 9 YER030 106 5 210 74 89 310 138 2744 A& P26266 9 YER030 106 5 210 74 89 310 138 3469 A& P26277 YER030 1181 2862 5 71 80 11747 2775 5 3469 A& P26277 YER030 1181 2862 5 71 80 11747 2775 5 2841 A& P26277 YER030 1181 2862 5 71 80 1191 1191 1191 1191 1191 1191 1191	561	A_06_P61	ZRG17	YNR039C	430	288.5	65	83	365	205.5			
2112 A B 198 2017 VEX250 VEX 13 203 64 86 81 115 2-44 2012 A B 198 2017 VEX250 VEX 13 203 64 10 115 2-44 2844 A B 198 2017 VEX250 VEX 198 2085 71 60 116 116 2017 1177 2775 5 2844 A B 198 2017 VEX 199 2017 118 2018 71 66 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 11 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1 VEX 199 2017 1359 64 10 1134 1459 1 2864 A B 192 2017 VEX 199 2017 1 VEX	2744	A_06_P26	ZRG8	YER033C	105.5	213	74	83	31.5	130			
4156.4 B P22817 V 24253 V 77.5 225 24 1 85 07 215 254.4 B P22817 V 24253 V 225 225 2 6 1 105 77.5 254.4 B P2871 V 241.75V 725 1538 69 83 135 1455 254.4 B P2871 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.4 B P2870 V 241.75V 725 1538 69 83 135 1455 254.2 B P2870 V 241.75V 724 2555 254.2 B P2870 V 241.75V 724 2555 255.2 B P2870 V 241.75V 724 2552 255 255.2 B P2870 V 241.75V 724 2552 2552 255 255.2 B P2870 V 241.75V 724 2552 2552 255 255.2 B P2870 V 241.75V 724 2552 255 255.2 B P2870 V 241.75V 724 2552 2552 255 255.2 B P2870 V 241.75V 724 2552 255 255.2 B P2870 V 241.75V 724	2744	A_06_P26	ZRG8	YER033C	183	338.5	66	84	117	254.5			
3894,0,0,0,0,0,0 101 2005,0,0,0 101 2005,0,0,0 101 1	4872	A_06_P32	ZRT1	YGL255W	173.5	236	64	82	109.5	154			
2834.0.0p.942.0013 YK31707 2013 2713 2718	3450	A_06_P49	ZRT2	YLR130C	1818	2862.5	71	83	1747	2779.5			
State Create mean signal to estimate cycl State	2594	A_06_P45	ZRT3	YKL175W	252.5	291.5	72	84	180.5	207.5			
988 (A. 9, P22 (A1) 1988 (BC) 2075 2011 61 89 214 2025 988 (A. 9, P22 (A1) 1988 (BC) 2075 2016 61 89 214 2025 245 (A. 9, P22 (A1) 2016 2016 2016 2016 2016 2016 2016 2016	2594	A_06_P45	ZR13	YKL175W	1205	1538	69	83	1136	1455			
Step A. R. P12.22A1 V180405 270 2386.5 61 83 270 237.5 Step A. R. P12.22A1 V180405 270 2386.5 61 83 270 237.5 Step A. R. P12.2A1 V180405 217.6 135.4 61 83 2700 233.61 Step A. R. P12.2A1 V180405 217.7 135.4 61 83 2700 233.61 Step A. R. P12.2A1 V180405 217.7 135.44 61 83 2700 233.61 Step A. R. P12.2A1 V180405 217.7 135.44 61 83 2700 233.61 Create mean signal to estimate dye I 1	5968	A_06_P12	ZTA1	YBR046C	1375	2101	61	80	1314	2021			
484.4,96,P192,201 YUR280C 2115 716 81 714 203.5 282.2, 06,P192,201 YUR280C 5112 1354 66 81 13541 ************************************	5968	A_06_P12	ZTA1	YBR046C	2970	4380.5	68	83	2902	4297.5			
2452 A (6 PPC 2VF1 VIL241C 5174 1554 65 B) Texamp(2745/24) AVEX.c(mmbert, (number2)) Create mean signal to estimate dye i	4654	A_06_P35	ZUO1	YGR285C	2815	2136.5	71	83	2744	2053.5			
Create mean signal to estimate dye	2452	A_06_P60	ZWF1	YNL241C	5174	13544	65	83	5109	13461			
Create mean signal to estimate dye !													
Create mean signal to estimate dye									=average(j2:J1027	9			
Create mean signal to estimate dye l									AVERAGE(num	ber1, [number3	!],)		
Create mean signal to estimate dye l													
Create mean signal to estimate dye l													
Create mean signal to estimate dye													
Create mean signal to estimate dye													
Create mean signal to estimate dye l													
Create mean signal to estimate dye i													
							_ Cre	ate i	nean sign	ial to es	tima'	te dye	зЬ
								_				· · ·	







-	-			*											-
00	16	5312	1 1 1 1 1		with Chang		eview								
	F		_	_											
	L														
•	Ŀ	Jx =L2/J2	-		_		-								
R		C	D		E .	F	G	н		J	K	L	M	N	
robel	P	ProbeNam	GeneName		Syste natio	gMedianSi	MedianSig	gBGMedia r	BGMedia	green correct	ed red corrected	red normal	zed		
3	15	A_06_P45		1-04	YKL14C	508.5	301	73	84	4.3	.5 21/	127.6471	0.293105		
3	25	A_06_P45		1-04	YKL14C	325	263.5	60	80	2	65 183.5	107.9412			
2		1.00.004	4404		Marpacco.	1919	2029	70	82	18	49 1946	1144.706			
- 4	900	A_06_P54	AACT		TMRUSSU	1941	2111	64	04	10	2095	1232.353			
6	119	A_06_P13	AAC3		TBRUSSW	141	111.5	65	84		76 29.5	17.35294			
6	119	A_00_P13	AAD40		T DRU85W	95.5	102.5	07.0	81	3	.5 21.5	12.04706			
	020	A_00_P43	AAD10		TJR 155W	223	135	87.5	84	13	.5 51	30			
1	020	A 00 P43	AAD10		TJR 155W	1/00	004.5	12	83	16	20 521.5	300.7647			
- 2	201	A_06_P61	AAD14		TIVESSIC	235	117	00	0.		07 34	20			
- 4	033	A_06_P63	AADIS		FUL 165C	103	102	00	0.		30 15	11.1/64/			
0	009	A_06_P17	AAD3		YCR10/W	242	216	/4	04	1	00 134	77.64706			
	159	A_06_P19	AAD4		YDL243C	113	205	59	84		44 10	5.882353			
	100	A_06_P19	AADA		TUL243C	202	395	62	0.	45	10 312	103.5294			
2	110	A_06_P26	AADO		TFL050C	210.0	103	02	0	15.	1.0 02	40.23529			
	110	A_06_P26	AADO		TPLUSOG	314	210	0/	0	44	47 103	111.1705			
2	040	A 06 P59	AAHI		VAL 14 IV	233.5	104	91	00	144	74 26	46.47059			
6	200	A 00 P39	AAD1		00090	E97	262	77	0		14 23	17.03002			
0	200	A 00 P10	AAD1		00000	507	203	11	0:	5	10 166	56.62353			
0	233	A_06_P10	AAD4		VUD0470	523	200	Com	nare	evhres	sion of e	ach			
4	101	A 06 P36	AAP1		VEL 074C	020	120	Com		enpi es					
2	224	A 06 P42	AAT1		VKI 1061A	626	620	- Char	nel (using n	ormalizec	l chani	nel		
2	221	A 06 P45	AAT1		VICI 1001V	290.6	420	Trees							
- 3	537	A 05 P49	AAT2		YI P027C	6463	30.64	TU 0	ne ci	marrior	,				
3	071	A 06 P30	ABC1		YGL 119M	400.6	459.5	70	90	22	6 373.6	219 7059			
4	074	A 06 P30	ABC1		YGL119W		403.0	67	00	33	67 103.6	60 99236			
6	019	A 05 P14	ABD1		YBR236C	362.5	575	75	81	28	103.5	289.4118			
6	119	A 06 P14	ABD1		YBR236C	473	930	68	83	20	05 848	498 8235			
	787	A 06 P/14	ARE1		YKI 112W	1307.6	176	71	81	123	6 93	64 70588			
	787	A 05 P45	ARE1		YKI 112W	4147	409	76	81	12.3	71 322	189 4118			
2	46	A 06 P54	ARE2		YMR072W	7888.5	12876	70	84	781	5 12791	7524 118			
2	40	A 06 P54	ABE2		YMR072W	5054	7319.5	67	81	49	87 7236 4	4256 765			
1	RR 1	A 05 P43	ABM1		Y.IR108W	198	331	86	81	1	12 248	145 8824			
1	RR 1	A 06 P43	ABM1		Y IR 108W	225.5	521.5	68	8/	15	5 437.6	257 3529			
6	RR4	A 06 P17	ARD1		YCR088W	1150.5	9076	71	81	107	5 8993	5290			
			100 III		TORCOUT	1100.0			0.	107.		02.00			-

B	C	D	E	F	G	н	1	J	K	L	M	N
el D	ProbeNam GeneN	ame	Systemati	gMedianSi	rMedianSid	gBGMedia	rBGMediar	areen corrected	red corrected	red normal	red vs gree	n
3 05	A 06 P45	1-Oct	YKL14C	508.5	301	73	84	435.5	217	127.6471	0.293105	=log(N
3 05	A 06 P45	1-Oct	YKL14C	325	263.5	60	80	265	183.5	107.9412	0.407325	
2 **	- AC DEL ANOL		56C	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	100						199	
3821	A_06_P45_AAT1		YKL106W	636		alcula	te loa	2 ratio	of each	chani	ne 1384	
3821	A_06_P45_AAT1		YKL106W	280.5							561	
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	
	The second se				0070	74	0.2	1000 0	0000	5000	4.000447	

🏷 🖄 🗁 🏷 🖉 🖓 🚱 🕅 👘			Review							
			_							
E =LOC(M2.2)										
R C D		F	G	н			K	1	м	M
nhel D. ProheNam GeneName	Systematic	MedianSi	rMedian Sir	oBGMedia	RGMedia	oreen corrected	red corrected	red normal	red vs orea	log2 red vs
1 84 A 05 P72 APP3	YPR: 1W	72	82.5	guomedia 65	83	green conected	-0.5	.0 29412	-0 1202	#NUMI
2 85 A 05 P51 CDA2	YLD3 8W	117	84	72	85	45	-1	.0 58824	-0.01307	ANUM
1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	NOD ISW	82.6	81.5	66	83	16.5	-15	.0.88235	-0.05348	ANUM
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 COO5	YML110C	311	5003	70	83	241	4920	2894 118	12 00879	3 586019
3030 A 05 P54 COO5	YML110C	785.5	11925	68	87	717.5	11838	6963 529	9 705267	3 278768
3696 A 05 P46 DAL80	YKR034W	98	556	68	85	30	471	277 0588	9 235294	3 207158
4756 A 06 P33 BTN2	YGR14200	1860	27389.5	63	84	1797	27305.5	16062.06	8 938263	3 159995
5133 A 06 P28 ACT1	YEL039C	310	3522	74	84	236	3438	2022 353	8 569292	3 099176
1373 A 06 P68 CAP1	YPI 111W	360	3847.6	82	84	268	3763.6	2213 824	8 260536	3.046236
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	YNI 336W	355	3665	77	83	278	3582	2107 059	7 579348	2 922074
443 A 05 P15 AR04	YBR249C	244	2242	67	83	177	2159	1270	7 175141	2 843007
2686 A 05 P57 ASI3	VNI 008C	96.5	422.5	68	84	28.5	338.5	199 1176	6 986584	2 804587
2344 A 05 P61 COS1	YNL 336W	405	4089	62	82	343	4007	2357.059	6 871892	2 780707
4476 A 06 P37 DSE2	VHD143W	521	5193	61	80	460	5113	3007.647	6 638363	2 70893
426 A 06 P39 COY6P	VII 111W	2928.6	30483.6	71	86	2957.6	30308.6	17881.47	6 267732	2.64564
443 A 06 P15 AR04	YBR249C	373	3333	65	84	308	3249	1911 176	6 205118	2 633459
4756 A 05 P33 BTN2	YGR142W	784	7470	81	88	703	7382	4342 353	6 176889	2 62688
717 A 05 P27 DSE1	YER124C	113	580	64	81	100	1002	1012.0000	5 990396	2 582651
426 A 05 P39 COY5B	YII 111W	1292.5	12492.5	64	82	W/hat I	hannanar	122 204	5 942445	2 571057
1204 A 05 P28 COS4	YEL062W	921	8540	63	82	witter	nuppener	294	5 798711	2 535732
6254 A 05 P11 ADE1	YAD016W	636.6	4337	60	83	471.6	4254	2502 353	6 307217	2 407956
1204 A 06 P28 COS4	YEL062W	1152	9555	73	83	1079	9472	5571 765	5 163823	2 368439
1322 A 05 P70 ATP20	YPR020W	663	5310	67	84	596	5226	3074 118	5 157916	2 366788
4550 A 05 P36 D0G2	YHR043C	330.5	2412	64	84	266.5	2328	1369.412	5 138506	2 361349
4919 A 05 P31 COX4	YGI 187C	1204	9828.5	63	82	1141	9746.5	5733 235	5.024746	2 329051
717 A 05 P27 DSE1	YER124C	1534	12402.5	60	84	1465	12318.6	7246 176	4 946196	2 306319
5884 A 05 P17 ABP1	YCR088W	1150.5	9076	71	83	1079.5	8993	5290	4 900417	2 292904
3789 A 06 P44 COS5	Y.IR161C	634.5	4762.5	72	85	562.5	4677.5	2751 471	4 891503	2 290278
4476 A 06 P37 DSF2	YHR143W	1127	8722	68	84	1059	8638	5081 176	4 798089	2 26246
4009 A 05 P42 CYC1	Y IR048W	1537	11628	73	89	1464	11539	6787 647	4 636371	2 212996
5254 A 05 P11 ADE1	YAR015W	607	4250.5	65	82	542	4168.5	2452.059	4 524094	2 177629
47 A OF D14 CST12	VDD160M	496	2200.0	62	02	422	4100.0	1001 170	4 470966	2 160664

🗞 🖄	5010	1 🔁 😰 🕅 Re			Review							
		d vs green										
В	C	D	E	F	G	н	1	J	K	L	M	N
obeUID	ProbeNam	GeneName	Systematic	MedianSi	rMedianSig	gBGMedia	rBGMediar	green corrected	red corrected	red normal	red vs gree	log2 red vs
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					1.0.500051
426	A 06 P39	COX5B	YIL111W	1292.5	12492.5	64	82	Correc	t for ne	aative	inter	isity i
1204	A 06 P28	COS4	YFL062W	921	8540	63	82					2
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
4005	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
43	A 06 D14	COT12	VDD460M	490	2206	62	01	422	2215	1001 176	4 470966	0.400004

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



Create scatter plot of log2 ratios (green versus red)										
teg2 red is green										

Distribution of log2 ratios

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

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 upregulated, down-regulated, no change?

