

Table S1. Correlation coefficient (Pearson) of log₂-ratios for five replicates of shoot vs. root experiment

Replicate	7921(S-cy5 Vs. R-cy3)	7940(S-cy5 Vs. R-cy3)	7926(S-cy3 Vs. R-cy5)	7941(S-cy3 Vs. R-cy5)	7936(S-cy3 Vs. R-cy5)
7921(S-cy5 Vs. R-cy3)	-----	0.94	0.93	0.94	0.93
7940(S-cy5 Vs. R-cy3)	0.94	-----	0.95	0.96	0.94
7926(S-cy3 Vs. R-cy5)	0.93	0.95	-----	0.97	0.98
7941(S-cy3 Vs. R-cy5)	0.94	0.96	0.97	-----	0.98
7936(S-cy3 Vs. R-cy5)	0.93	0.94	0.98	0.98	-----

* The reference (shoot) mRNA comes from the same mRNA preparation.

The root mRNA used in 7936, 7940 and 7941 came from the same mRNA preparation, and 7921 and 7926 were derived from two separate mRNA preparations of the roots harvested at the same time. Vs: versus; 7921,7940,7926,7941 and 7936 represented barcode number of the slide.

Table S2. Number of cDNA clones showing preferential expression ratios

Ratio	R/S	A/S	UP/S	5hrP/S	5hrP/UP	5DAP/UP	10EN/5DAP	10EM/5DAP
2	318	334	543	1334	200	381	171	334
1/2	1098	1073	845	1185	170	353	390	331
4	48	84	114	152	32	61	8	67
1/4	661	543	486	400	13	33	20	67
8	10	29	25	24	7	25	4	29
1/8	408	263	204	148	2	4	5	21

*S: Green shoot; R: Root; A: Anther; UP: Un-pollination; 5hrP: 0-5hr after pollination;

5DAP: Five days after pollination (pistil); 10EN: Endosperm (ten days after pollination); 10EM: Embryo (ten days after pollination)

Table S3. Examples of the top ten genes with putative function that are highly expressed in root, shoot, anther, 5DAP, 10d endosperm and 10d embryo, respectively

Classification	Clone ID	Closest hit to nr	Description	E-value	Log2-Ratios (Q-RT*)	Putative function assignment
R/S						
	y613c04	AB021746	Nicotianamine synthase 1	1E-115	4.909	Stress/Fe metabolism and homeostasis
	y721g07	Q40633	Metallothionein-like protein type 1.	5E-18	4.717	Stress
	y831f06	BAB17823	Nicotianamine synthase 2	1E-10	4.653	Stress/Fe metabolism and homeostasis
	y829c09	AAC31615	Impedance induced protein	1E-33	3.605	Stress
	y807e10	T50838	Peptidylprolyl isomerase ROC7	4E-79	3.414	
	y625d11	L36883	Thionin (BTH7)	7E-26	3.01(9.93*)	Stress
	y691d09	P14654	Glutamine synthetase root isozyme	1E-107	3.062	Assimilation of external ammonia
	y826h11	T09998	12-oxophytodienoate reductase	5E-36	2.896	Jasmonate signal pathway
	p707a12	NP_199918	Mitochondrial carrier protein family	2E-42	2.868	Transport
	y807f10	AAM28296	Peroxidase	2E-53	2.825	Stress /defense
R/S						
	y736b07	P18567	Rubisco small chain c precursor	7E-88	-7.624	Energy/metabolism
	y733f10	L22155	Mitochondrial rbcS mRNA	1E-49	-7.583	Energy/metabolism
	y683a03	AAK76469	Putative vesicle transport protein	7E-13	-7.551	Transport
	p627a01	T50783	Protein phosphatase 2C-like protein	5E-36	-6.513	Signal transduction
	y698f10	AB034698	RuBisCO activase large isoform precursor	8E-33	-6.299	Energy/metabolism
	y703h08	P12089	Rubisco large subunit	0	-6.215	Energy/metabolism
	y611a06	AF148666	Maturase (matK)	4E-24	-5.799	Energy/metabolism
	y745d10	AF154423	Putative beta-galactosidase (TBG5)	3E-31	-5.746	Energy/metabolism
	p663f06	X02595	ATP synthase CF-O subunit I & III	1E-73	-4.741	Energy/metabolism

A/S	y802a09	P06528	ATP synthase b chain	3E-83	-4.603	Energy/metabolism
	p402f12	S31710	Pollen-specific protein	1E-31	5.355	Organ specific protein
	y641g03	NP_177487	Protein kinase,putative	5E-22	5.231	Signal transduction
	y641g12	P06353	Histone h3	1E-102	5.118	Cellular organization
	y770g12	BAB90152	Calcyclin binding protein-like	3E-30	4.645	Cell fate
	y682a07	AF326977	Alpha 14-glucan phosphorylase H isozyme	4E-11	4.605(4.811*)	Energy /metabolism
	p768b08	NP_181728	Putative protein kinase	2E-9	4.27	Signal transduction
	y730b11	T51181	Actin 1	1E-180	3.936	Cellular organization
	p645c11	T04335	MADS box protein	1E-141	3.567(12.74*)	Transcription
	p623c04	AF360190	Putative kinase	3E-46	3.554	Signal transduction
	p541b06	T01213	Beta-amylase	1E-24	3.489(6.28*)	Energy/metabolism
5DAP/UP	y790g04	T02979	Pyruvate orthophosphate dikinase	1E-115	6.492	Carbohydrate Metabolism
	p780a10	T02666	Germin-like protein 16	2E-14	5.03	Defense /stress
	p530c10	S19139	Sucrose synthase 2	1E-92	4.818	Carbohydrate Metabolism
	p523d11	JX0243	1, 4-alpha-glucan branching enzyme	2E-52	4.693	Carbohydrate Metabolism
	p524d05	AF141954	Granule-bound starch synthase	5E-75	4.626	Carbohydrate Metabolism
	y730e07	BAA77260	Alanine aminotransferase	2E-54	4.067	Amino Acid Metabolism
	y760g09	P15280	Glucose-1-phosphate adenylyltransferase small subunit	5E-29	3.889	Carbohydrate Metabolism
	p472e10	AAM00285	Putative EREBP-type transcription factor	7E-33	3.642	Transcription
	y678g10	AJ011921	Putative amino acid selective channel protein	2E-53	3.549	Transport
	p756a09	AB015615	Isoamylase	1E-53	3.352	Carbohydrate Metabolism
EM/5DAP						

y716g06	L36883	Thionin (BTH7)	3E-29	7.364	Defense/stress
y844h11	AJ277468	Putative Bowman Birk trypsin inhibitor.	5E-26	4.937	Defense/stress
y756d06	AF085717	Putative callose synthase catalytic subunit	5E-16	4.656	Defense/stress
p684b11	T03779	Protein LEA type 1	6E-15	4.623	Defense/stress
y778d02	AAD46405	Ethylene-responsive small GTP-binding protein	1E-39	4.538	Signal transduction
y681d09	U57639	Hydrophobic LEA-like protein	6E-76	4.467	Defense/stress
y814d03	BAA78762	Similar to PRP gene	7E-23	4.46	Defense/stress
y875h11	U57638	Metallothionein-like protein mRNA	1E-134	3.828	Defense/stress
y794d08	AAD31338	Putative proteinase	1E-34	3.749	Protein destination
y717f08	AF017360	Lipid transfer protein LPT III mRNA	3E-91	3.684	Defense/stress

EN/5DAP

y609b11	AF323610	Glucanase (GLU)	2E-47	3.672	Defense/stress
p659a09	U83669	Low molecular mass heat shock protein Oshsp17.3	3E-30	3.565	Protein destination
y681d09	U57639	Hydrophobic LEA-like protein	6E-76	3.152	Defense/stress
p622c02	AAM75346	DNA-binding protein phosphatase 2C	2E-34	2.647	Signal transduction
p753d06	T02667	Proteinase inhibitor	3E-31	2.638	Defense/stress
y700f01	BAC45198	Putative RAB24 protein	3E-29	2.442	Protein destination
p684b11	T03779	Protein LEA type 1	6E-15	2.376	Defense/stress
p899d05	T08122	Cysteine endopeptidase precursor	2E-37	2.139	Protein destination
p771d08	AF077337	Heat shock protein 101 (HSP101)	3E-20	2.13	Protein destination
y856f09	P33278	Protein translation factor sui1 homolog	2E-52	2.01	Protein synthesis

Table S4. Transcript abundance and distribution of 370 cDNA clones differentially expressed in 5hrP vs.UP experiment

Description		Down-regulated gene (Relative abundance in UP)	Up-regulated gene (Relative abundance in 5hrP)
Signal intensity range	Relative abundance (%)	No. of genes (No. of genes tested by Q-RT)	No. of genes (No. of genes tested by Q-RT)
>4DR	>0.066	4(2)	0
4DR-5DR	0.066-0.02	37(7)	32(2)
5DR-6DR	0.02-0.0066	55(9)	57(9)
<6DR	<0.0066	74(6)	111(18)

Table S5. Validation of some up-regulated and down-regulated genes by Real-Time PCR in 5hrP vs. UP experiment

Clone ID	Closest hit to nr	Description	E-value	Log2-Ratios (M)*	Log2-Ratios (Q-RT)
p714f02	AAL11444	Pathogenesis-related protein (PR4)	4E-40	4.234	3.34
y625d11	L36883	Thionin (BTH7)	7E-26	2.216	2.5
p898a08	AF274850	Pathogenesis-related protein PR-10a	5E-58	3.321	4.3
p751f10	T06213	Probable aspartic proteinase	4E-7	2.699	3.34
y661f05	T50662	UVB-resistance protein UVR8	6E-9	2.626	2.9
p839d08	NP_565330	Subtilisin-like serine protease, putative	2E-18	3.252	3.677
p596c09	P19656	Nonspecific lipid-transfer protein precursor	7E-6	2.444	3.45
y659a07	L37289	Chitinase	4E-29	-4.05	-4.45
y674c04	AB027429	Beta 1,3-glucanase (PR-2)	1E-105	-1.172	-2.801
y845e05	T06802	Cold acclimation protein WCOR410b	1E-50	-2.164	-0.57
y695d11	AAC97511	Low temperature and salt responsive protein LTI6B	2E-11	-1.756	-1.21
p684b11	T03779	Protein LEA type 1	6E-15	-1.29	-1.1
p811e06	AJ224327	Aquaporin	1E-125	-1.088	-2.089
p638g09	NP_196564	Receptor protein kinase	9E-37	2.013	1.035
p751d05	NP_191470	Receptor-like protein kinase	7E-8	2.287	1.895
y758h05	AY035226	CBL-interacting protein kinase 23	6E-63	1.621	2.624
p732f09	AF093604	Apyrase (Atapy1)	7E-16	1.866	1.812
y687a02	AF181661	EF-hand Ca ²⁺ -binding protein CCD1 (ccd1)	3E-15	-1.438	-0.411
p808d10	AF042840	Calmodulin	1E-121	-1.456	-0.794
y718g04	AF276703	Vacuolar acid invertase (INV2) gene	8E-98	-2.658	-4.744
y836b05	AF093629	Inorganic pyrophosphatase	1E-120	-1.954	-1.082
y789e10	D50317	ADP glucose pyrophosphorylase large subunit	1E-173	1.125	1.45

p650g03	P27489	Chlorophyll a-b binding protein 13 precursor	3E-97	1.436	1.236
p552b04	BAB18280	Putative transcription factor X1	5E-30	-1.028	-0.802
y824d02	AF254558	NAC6 (NAC6) gene	0	-1.047	-2.785
y712d12	BAB12694	Putative zinc finger transcription factor	2E-14	-1.114	-1.871
p732c02	AF306349	MADS box protein AP2L	3E-23	-1.257	-2.255
p423c01	BAB63576	Putative photoreceptor-interacting protein-like protein	5E-5	1.071	0.819
y831f12	T02663	Abscisic acid- and stress-induced protein	3E-20	1.255	2.41
y775f07	AF261272	Beta-expansin	4E-86	-1.379	-1.932
y732b09	AAN11203	Putative jacalin homolog	2E-31	1.214	1.657
y746g03	P35135	Ubiquitin-conjugating enzyme e2-17 kda	2E-48	-1.12	-0.439
p408c03	AB033537	26S proteasome regulatory particle triple-A ATPase	3E-68	1.983	0.594
p773g11	AF263381	SKP1 interacting partner 5	4E-43	-2.898	-0.536
y689b08	AAK16647	F-box containing protein TIR1	5E-45	-1.022	-1.135
p607b04	AAL40895	Phosphoethanolamine methyltransferase	4E-89	2.979	3.397
p826g08	AAG46123	Hypothetical protein	4E-44	3.684	6.86
p807b11		No significant homology	4.6	-2.356	-2.888
p752c09		No significant homology	1.6	2.679	3.395

*Data are presented as log₂ transformed ratios (5hrP/UP), and only 39 genes are shown. The primers used for Real-Time PCR are listed Table S7.

Table S6 Data from microarray experiments and Real-Time PCR analysis for four genes

Clone	Root/shoot		Anther/shoot		UP/shoot		5hrP/shoot		5hrP/UP		5DAP/UP		10EM/5DAP		10EN/5DAP	
	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR	Array	QRT-PCR
p596c09	-4.16	-10.19	1.03	-0.13	-3.02	-4.36	-0.69	-0.91	2.44	3.45	1.39	-2.02	-0.97	-2.27	-1.13	-2.98
p811e06	0.65	3.10	0.07	0.46	0.79	1.99	-0.03	-0.10	-1.09	-2.09	-0.59	-4.16	0.48	1.89	-0.09	-0.68
y695d11	1.88	1.46	-0.97	-0.94	3.08	2.99	0.76	1.78	-1.76	-1.21	-1.93	-6.43	-0.22	-0.45	-1.03	-3.68
y831f12	-0.22	0.33	-3.54	-7.11	-2.33	-4.60	-1.01	-2.18	1.26	2.41	2.03	1.85	-2.62	-9.85	-1.51	-2.74

*Data are presented as log₂ transformed ratios.

Table S7. Primers used for Real-Time PCR

Clone ID	Forward primer	Reverse primer
p714f02	TGGTCAACAATCCTCGCAATT	CTCGTGTGGCAAGTGTATCCA
y625d11	GACGGCATCATTGGCTTCTT	GACTTCTGCAAGCTGGGATGT
p898a08	CCGCCATGCCCAAAGTT	CATCCCCCTCGACCTCAAT
p751f10	CCATCCGAGCAGCGATCT	TGGAACAACTTAATTGGAGGAATT
y661f05	GATGCCTTTTCCAGCCTTCTC	TTTGGGTCTCGCCATCAGA
p839d08	ATTCATCAGTTAGTTCACATGAACAC	GGGATTTTCGGGCACATCTC
p596c09	AGGGAGCGTGCAACATAAAGTATA	ACAGCTGCGGCAGACATG
y659a07	CAGGAGTGAGTGGCAAAGCA	CGGCGGTGCAGTGAACA
y674c04	CATTTCTGCAGCGGTACT	TCGAATCGATCCCCTTGGA
y845e05	CCGTGGAAGAGCCAAAGAAG	CCCCGTTGTCATCGATCAC
y695d11	TGGGAACAAGCAGAAGAATGG	GCGGCGGCAGGATGA
p684b11	CTAGACGCCGTGAATGATTTCC	CGATACAGACTCAAAAACGACACAAA
p811e06	ACTAGAGATAGAGGGAATCGACAGATG	TGCAACGCAATCGTGATGT
p638g09	CGACACCGAAGGCGTACAC	CGTGCCCCAGAGCTAGCA
p751d05	GCTTCGCATATGTTCTTGTCTGT	TGACTTCCCATACCGAGAAGATC
y758h05	CAGACTTCAGTTGCCCGTCTT	TGGTGCTAGGATTAGGATCTAGTATTTTC
p732f09	TCCACGTAGCAATCCCCATAC	GCTTCGGTTTGAAGCCAAC
y687a02	TTCTCGTTGTTTCATAGCATCAGGAT	TGAGAGTACAAAATGCGATTGGAAT
p808d10	ACCAGTGTTTGCATCCCCTTA	CACTTCCCCTGCCGATGAT
y718g04	GAAAGATTTTGGCCGACTCGTA	AAGGAGGGAGGACATGCATTAC
y836b05	GATGCCATCAACGCAATCAA	GATCACTTCTCAAGCTCTCAATG

y789e10	TACACACATTTTAACGAGCGAAGAA	CGAGGGAAGATCCCAG
p650g03	GACGATGGCCTGGACGAA	CAAGGTCAAGGAGATCAAGAATGG
p552b04	TAAGTACTGAGCACTACGAAGCATGAAC	CGGAGGCCGAAGGAGATGA
y824d02	CGAGGCAGCAGCAGAAAAGAT	CGAATCAATCACCATGTACTATGTACA
y712d12	GGTGTGACCTCGACGTTGA	GCTTCCAATAGCGACTTGGAA
p732c02	AGACACTTCTCTGAATAACATAAGATCAAGA	TCTCCATCAGCAACTTTTCCTTCT
p423c01	CCCTCTTCGGCTCAGTGACA	GAGGCCTGAAACCTGAAAGATTT
y831f12	CATGCGTGGTGTGCTGTTT	CCCACCTGTCAGCCTCTC
y775f07	CCCGGTTTCTGCAAATCG	AATACTACTACTGCTATGATGTAATTGTGTTACC
y732b09	CGGATGTGTCCACTTCTCAA	CATAGCCAACCTCACGTTCTGT
y746g03	TGATAACGTCGTTGGGTTTCG	CAGAAGTACGCCATGGGCTAA
p408c03	TGTTCTTTTCCGTGTCTTTCTTCA	CGTGAGAGAAGGGTGCATGTAA
p773g11	GGCCGTCAGGACTAATGGAA	GAAAACAGAACTGCGAGAATAGATAGC
y689b08	TGTGCTGCGATGGGTTC	CGTCAATATAGTCTTCAATCAGATCCA
p607b04	CAACAGAAGACAGAGGATTCCAAAG	ACACGCTCATAGCGTAAGATTCC
p826g08	CACTGGTAGCCAGGCTGGAA	AAGGTGTGGTGCATGGAGAAG
p807b11	AGTACAAATTGTAACCAAGGTAGAATGC	CGGCTCCCTCGTTTCGTA
p752c09	GACCAACAAATTAAGCTAAAATATCACAGA	GCACCATGGGAAAAAAAAATCA
18S RNA	CGGCTACCACATCCAAGGAA	TGTCACTACCTCCCCGTGTCA

Figure S1. A representative section of rice cDNA microarray. Four fields are shown here, and one field consists of 16 rows and 38 columns. In total, there are 12 fields in a microarray slide. DR: dynamic range; RC: ratio control; 1NC: negative control (PolydA oligonucleotide). The dashed line shows the DR, RC and 1NC.

Figure S2. Correlation between the data from the different microarrays. Scatter plots of \log_2 (ratio) from different slides in the Root vs. Shoot experiment; 7921,7940,7926,7941 and 7936 represented as barcode number of the slide, more information is provided in Table 4.

Figure S3. Dynamic range and sensitivity of the detection in the 5hrP vs. UP experiment. The average hybridization signal intensity (normalized) of 6DR, 5DR, 4DR, 3DR and 370 differentially expressed genes were shown; Error bar represents 1SD

Figure S4. Correlation between the direct and indirect results. Direct: \log_2 (5hrP/UP); Indirect: \log_2 (5hrP/UP)= \log_2 (5hrP/S)- \log_2 (UP/S); r: Correlation coefficient. The differential expression genes were selected from the 5hrP vs. UP experiment and compared with the indirect results. If there is a missing value in 5hrP vs. S or UP vs. S experiments, the data of this cDNA clone was not to be used for the calculation.

Figure S5. Numbers of the differentially expressed genes grouped by their putative functions. The bars reflect comparisons 5hrP vs. UP (blue) and 5DAP vs. UP (red).

Figure S1

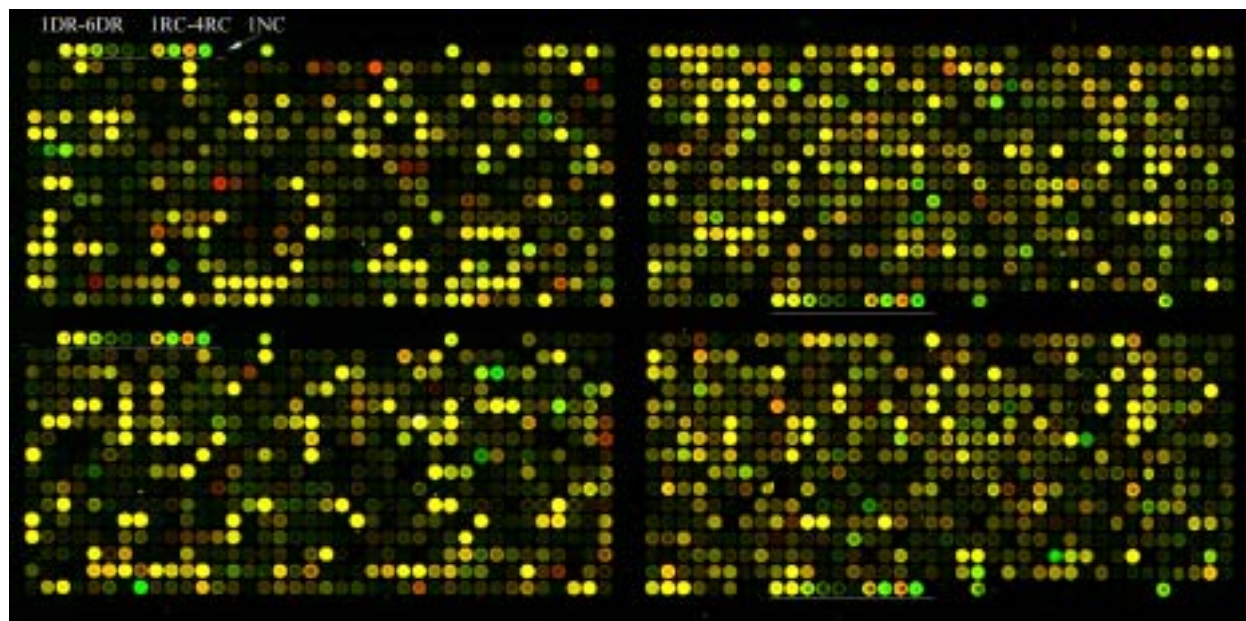


Figure S2

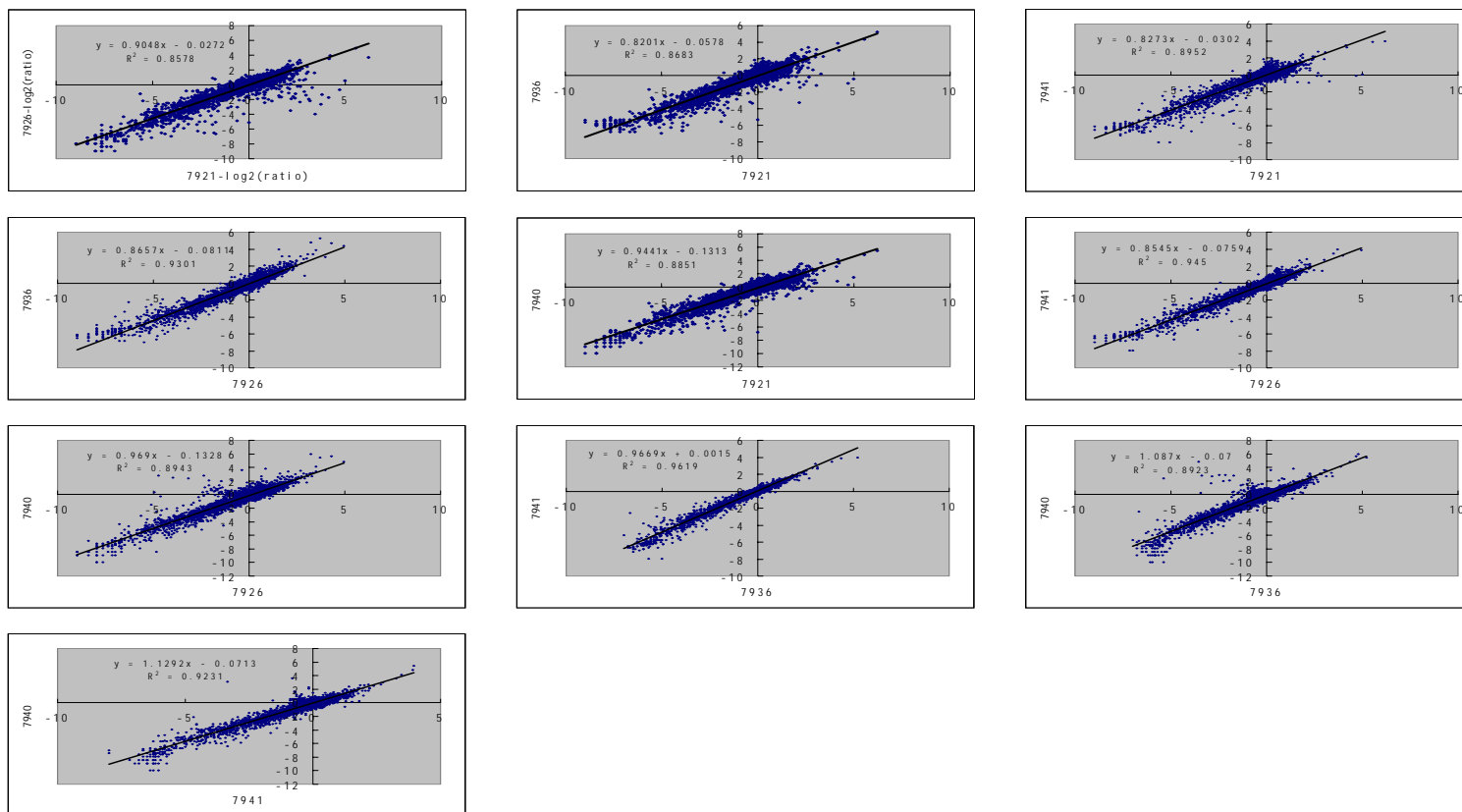


Figure S3

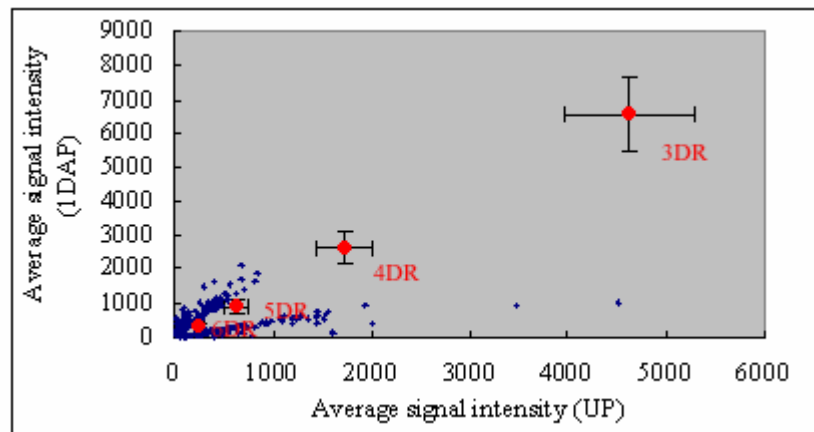


Figure S4

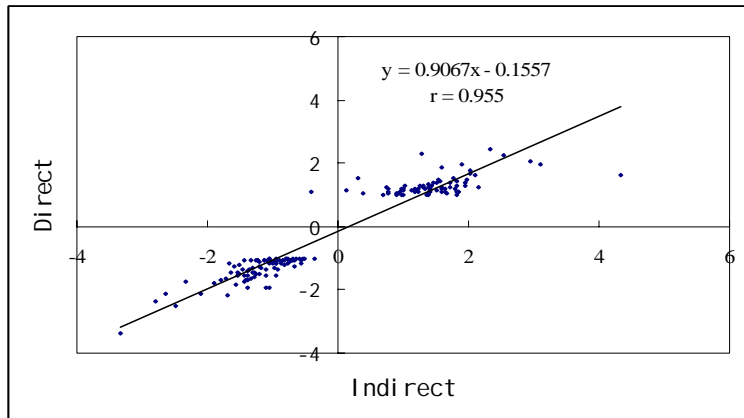


Figure S5

