Supplemental Material

for *Plant Physiology* article

Analyses of advanced rice anther transcriptomes reveal global tapetum secretory functions and potential proteins for lipid exine formation

by Ming-Der Huang et al.

List of Contents:

Supplemental Table S1. *Top 50 transcripts in anther-minus-other-organs transcriptomes of various developmental stages.*

Table S1-Meiosis

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os09g35700	Lipid-transfer protein	16,153	49,751	13,603	81	1	4	1	0	0	0	0	0	0	708	0	0		
Os01g12020	Lipid-transfer protein	9,549	9,683	105	29	19	8	0	0	0	0	0	0	0	120	0	0		TRIM
Os04g44600	Unknown protein	5,688	41	23	0	0	0	0	0	0	0	0	0	0	82	0	0		TRIM
Os04g58120	Unknown protein	4,960	243	28	0	0	0	0	0	0	0	0	0	0	165	0	0	PFG, RMD	
Os08g10500	Unknown protein	2,912	1,526	570	338	55	214	1	0	102	15	5	75	61	0	107	30	Genoplante, PFG	TRIM
Os08g43240	Unknown protein	2,752	182	2	0	0	0	0	0	0	0	0	0	0	154	0	0		
Os01g49650	Lipid-transfer protein	2,632	1,850	39	9	0	0	0	0	0	0	0	0	0	1,591	0	0	Genoplante, PFG	
Os05g35266	β-1,3-galactosyltransferase	2,099	41	158	11	0	1	5	4	3	0	0	10	0	36	3	135		TRIM
Os06g37680	Unknown protein	1,874	6	30	4	0	0	0	0	0	0	0	0	0	68	0	0		TRIM
Os08g03520	Glycine-rich protein 2b	1,782	2,108	1,598	3,136	206	66	2	47	15	0	0	72	87	69	167	0		
Os05g44120	Unknown protein	1,750	1,003	164	8	1	5	0	0	0	0	0	0	0	448	0	0		
Os05g09580	Unknown protein	1,742	64	441	26	1	4	0	164	0	0	0	77	16	131	3	0		TRIM
Os08g41950	SRF-type transcription factor	1,720	119	1,621	67	26	28	13	0	0	0	0	0	0	17	297	10	PFG, TRIM, UCD	TRIM
Os05g30400	Unknown protein	1,555	1	59	1	0	0	0	0	0	0	0	0	0	43	0	0	Genoplante, RTIM	
Os03g14140	Proline-rich protein	1,472	1,447	4	0	0	0	0	0	0	0	0	0	0	211	0	0		TRIM
Os01g39710	Unknown protein	1,394	81	0	0	0	0	0	0	0	0	0	0	0	129	0	0		
Os01g41710	Chlorophyll a-b binding protein	1,373	11,472	17,209	17,289	2,617	45	0	29	20	0	0	0	0	369	55	0	PFG, TRIM	
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os01g14850	MFS18 protein	1,237	2,407	426	88	10	1	0	0	0	0	0	0	0	0	0	0		TRIM
Os03g51470	Unknown protein	1,055	197	2	8	4	2	0	0	0	0	0	0	0	1	0	0		TRIM
Os01g48770	60S ribosomal protein L37a	1,053	1,031	184	2,216	567	110	2	72	30	27	0	0	0	3	103	0	PFG	
Os03g49600	β-glucosidase	1,010	635	171	73	24	39	5	0	0	0	0	0	0	34	25	0	Genoplante, PFG, RTIM	
Os11g09280	Protein disulfide isomerase	921	182	707	215	13	8	0	0	0	0	5	0	7	12	55	0	PFG	
Os03g24300	Unknown protein	918	77	16	0	0	0	0	0	0	0	0	0	0	263	0	0		
Os01g09320	NADP-dependent malic enzyme	909	876	1,960	527	85	44	43	0	24	42	0	54	38	25	105	0		
Os04g37680	Gibberellin receptor	839	384	137	1	0	0	0	4	0	0	0	4	0	81	0	0	TRIM	TRIM
Os08g40150	AT-hook DNA-binding protein	838	1,060	455	458	121	50	1	0	77	7	0	12	0	8	35	0	PFG	
Os03g47910	Unknown protein	807	2,357	923	3	0	0	0	0	0	0	0	0	0	489	0	0		
Os11g41610	40S ribosomal protein S29	791	916	704	2,387	641	87	4	0	14	0	0	2	0	0	19	0	RMD, ZJU	
Os01g18870	DNA binding protein	759	26	25	1	0	0	0	0	0	0	0	0	0	0	0	0	PFG, TRIM	
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os01g66700	β-hexosaminidase	730	96	43	4	8	10	2	0	0	0	0	0	0	98	0	12	Genoplante, RTIM, TRIM	TRIM
Os03g46110	Unknown protein	659	3	0	0	0	0	2	0	0	0	0	0	0	102	0	0	SHIP, UCD	TRIM
Os08g38300	Histone H2B	628	1	84	1	0	1	16	0	0	0	0	0	39	1	0	0	PFG, TRIM	TRIM
Os02g08090	Small nuclear ribonucleoprotein F	576	394	455	466	152	66	32	0	29	0	0	0	0	0	0	20		TRIM
Os03g39610	Chlorophyll a-b binding protein	569	1,070	1,205	716	248	4	0	0	0	0	0	0	0	346	97	0	PFG	
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os08g43290	Lipid-transfer protein	554	6,768	1,261	28	0	0	0	0	0	0	0	0	0	3,537	0	0		TRIM
Os06g02144	6-phosphogluconate dehydrogenase	544	1,174	660	617	189	62	0	0	0	0	1	0	14	0	25	0		
Os01g65590	β-1,3-galactosyltransferase	525	4	255	10	0	0	4	0	0	0	0	0	0	0	0	0	PFG	
Os05g41870	Unknown protein	508	5	1	0	0	0	0	0	0	0	0	0	0	68	0	0		
Os10g21910	Acetyl-coenzyme A carboxylase	495	1,300	332	254	37	42	0	5	0	0	0	8	0	0	0	0	PFG	
Os12g38900	Chorismate mutase	479	101	1	0	0	0	0	0	0	0	0	0	0	79	0	0	PFG, RTIM	TRIM
Os03g45120	Ribosome inactivating protein	465	8	80	0	0	0	0	0	0	0	0	0	0	12	0	0	PFG	
Os09g08430	60S ribosomal protein L17	464	2	581	4	0	0	1	0	0	0	0	0	23	0	0	0	PFG	
Os10g25230	ZIM motif family protein	453	425	743	2,315	146	42	13	0	0	0	0	0	8	0	14	0		TRIM
Os05g01820	Cytochrome b5	442	585	661	349	187	82	1	18	57	75	26	39	33	94	30	6	Genoplante, TRIM	TRIM
Os01g15830	Peroxidase	408	1	175	0	0	0	0	0	0	0	0	1	0	0	0	0		
Os08g01410	Organic anion transporter	406	74	24	10	18	2	0	0	0	0	0	0	0	0	0	1	PFG, RTIM	
Os01g37950	Unknown protein	392	789	1,700	4,045	214	797	4	19	0	0	0	2	36	22	0	0		

Available DNA (T-DNA or *Tos17* transposon) insertion mutants were searched for from SIGnAL (http://signal.salk.edu/) and TRIM (http://trim.sinica.edu.tw/). Sources include
GENO (representing Genoplate, http://urgi.versailles.inra.fr/OryzaTagLine/);
PFG (http://an6.postech.ac.kr/pfg/index.php); RMD (http://rmd.ncpgr.cn/); RTIM, (http://tos.nias.affrc.go.jp/);
UCD, (http://www-plb.ucdavis.edu/Labs/sundar/Rice_Genomics.htm); and
ZJU, (http://www.genomics.zju.edu.cn/ricetdna.html).
Activation mutants are available only from TRIM as T-DNA insertion mutants.

Table S1-Tetrad

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os09g35700	Lipid-transfer protein	16,153	49,751	13,603	81	1	4	1	0	0	0	0	0	0	708	0	0		
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os01g03670	Dihydroflavonol-4-reductase	47	11,738	1,649	16	5	3	1	0	0	0	0	0	0	117	0	0		
Os01g41710	Chlorophyll a-b binding protein	1,373	11,472	17,209	17,289	2,617	45	0	29	20	0	0	0	0	369	55	0	PFG, TRIM	
Os01g12020	Lipid-transfer protein	9,549	9,683	105	29	19	8	0	0	0	0	0	0	0	120	0	0		TRIM
Os02g45530	Glucose-methanol-choline	131	7,496	3,672	4	0	0	0	0	0	0	0	0	0	0	0	0	TRIM	TRIM
Os08g43290	Lipid-transfer protein	554	6,768	1,261	28	0	0	0	0	0	0	0	0	0	3,537	0	0		TRIM
Os07g46210	Unknown protein	2	5,127	2,210	26	0	0	0	0	0	0	0	0	0	25	0	0		TRIM
Os10g42620	Dihydroflavonol-4-reductase	9	4,613	2,445	345	7	1	1	22	0	0	0	0	8	26	3	0	PFG, RMD, TRIM	TRIM
Os04g08280	Unknown protein	2	3,728	342	7	0	0	1	0	0	0	0	0	0	119	0	0		
Os04g27950	Unknown protein	16	3,015	273	128	33	9	0	0	0	0	0	4	0	15	0	0	PFG, RMD	TRIM
Os01g14850	MFS18 protein	1,237	2,407	426	88	10	1	0	0	0	0	0	0	0	0	0	0		TRIM
Os02g44630	Aquaporin	477	2,391	1,496	883	421	685	0	149	112	29	0	51	346	245	51	70	PFG, RTIM	
Os03g47910	Unknown protein	807	2,357	923	3	0	0	0	0	0	0	0	0	0	489	0	0		
Os08g03520	Glycine-rich protein 2b	1,782	2,108	1,598	3,136	206	66	2	47	15	0	0	72	87	69	167	0		
Os01g41170	Unknown protein	0	1,914	8,675	22,039	1,105	7	0	0	0	0	0	0	0	318	0	242	PFG	
Os01g49650	Lipid-transfer protein	2,632	1,850	39	9	0	0	0	0	0	0	0	0	0	1,591	0	0	Genoplante, PFG	
Os08g03682	Cytochrome P450	43	1,705	812	5	1	0	2	0	0	0	0	0	3	469	0	0		
Os02g38260	Hydrolase	0	1,628	96	5	0	0	0	0	0	0	0	0	0	46	0	0		
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os08g10500	Unknown protein	2,912	1,526	570	338	55	214	1	0	102	15	5	75	61	0	107	30	Genoplante, PFG	TRIM
Os03g14140	Proline-rich protein	1,472	1,447	4	0	0	0	0	0	0	0	0	0	0	211	0	0		TRIM
Os08g45150	Proline-rich protein	6	1,413	5,527	2,515	1	1	3	0	0	0	0	0	0	256	0	0	RMD, UCD	
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os10g21910	Acetyl-coenzyme A carboxylase	495	1,300	332	254	37	42	0	5	0	0	0	8	0	0	0	0	PFG	
Os01g05670	3-oxo-5-alpha-steroid 4-dehydrogenase	275	1,217	772	398	72	23	1	0	0	0	0	1	0	29	21	0	PFG, RMD, RTIM	TRIM
Os06g02144	6-phosphogluconate dehydrogenase	544	1,174	660	617	189	62	0	0	0	0	1	0	14	0	25	0		
Os03g39610	Chlorophyll a-b binding protein	569	1,070	1,205	716	248	4	0	0	0	0	0	0	0	346	97	0	PFG	
Os08g40150	AT-hook DNA-binding protein	838	1,060	455	458	121	50	1	0	77	7	0	12	0	8	35	0	PFG	
Os04g44510	GRAM domain containing protein	330	1,044	296	332	75	45	0	0	0	0	0	28	0	0	0	0	PFG, RMD, RTIM	TRIM
Os01g48770	60S ribosomal protein L37a	1,053	1,031	184	2,216	567	110	2	72	30	27	0	0	0	3	103	0	PFG	
Os09g32020	Ubiquitin fusion degradation protein	4	1,020	73	4	2	0	1	0	0	0	0	1	25	341	18	2	PFG	
Os05g44120	Unknown protein	1,750	1,003	164	8	1	5	0	0	0	0	0	0	0	448	0	0		
Os03g15710	Strictosidine synthase	33	942	830	43	5	1	0	0	0	0	0	0	0	22	0	0		
Os11g41610	40S ribosomal protein S29	791	916	704	2,387	641	87	4	0	14	0	0	2	0	0	19	0	RMD, ZJU	
Os01g09320	NADP-dependent malic enzyme	909	876	1,960	527	85	44	43	0	24	42	0	54	38	25	105	0		
Os01g56530	LOB domain protein	0	849	808	62	1	1	0	0	0	0	0	0	0	0	0	0	TRIM	
Os01g14880	Hypothetical protein	0	813	361	2	0	0	0	0	0	0	0	0	0	125	0	0		TRIM
Os01g37950	Unknown protein	392	789	1,700	4,045	214	797	4	19	0	0	0	2	36	22	0	0		
Os11g30560	Glucose/ribitol dehydrogenase	22	740	403	3	0	0	0	0	0	2	0	0	0	0	0	0	PFG	
Os08g34210	NADP-GAPDH	93	726	206	130	43	18	0	0	60	0	5	1	0	0	0	0	Genoplante, PFG, RMD, TRIM	TRIM
Os05g47980	ATP synthase	281	721	349	1,131	3,937	1,125	19	86	29	11	6	9	0	14	33	139	PFG, SHIP, TRIM	TRIM
Os03g11350	Cytokinin-O-glucosyltransferase	0	693	142	17	0	0	0	0	0	0	0	0	0	183	0	0	PFG	
Os04g48210	Cytochrome P450	0	674	448	10	29	8	0	0	0	0	0	0	0	139	0	4		
Os05g41110	60S ribosomal protein L30	357	664	632	1,729	422	58	2	0	0	0	0	0	10	0	0	0	PFG	TRIM
Os09g13930	Unknown protein	14	655	6	1	1	2	0	0	0	0	0	0	0	396	0	0	PFG	
Os10g37420	Cytochrome b5	246	648	951	587	70	70	0	0	6	0	0	0	0	0	0	0	GSNU	TRIM
Os04g42060	Cytochrome c oxidase	246	646	360	1,013	2,497	1,458	127	0	0	0	0	0	0	0	0	17	PFG, RTIM	TRIM
Os07g31300	ATP synthase delta chain	193	646	665	728	1,084	235	8	4	0	0	0	0	0	0	0	0		
Os08g44840	Acyltransferase	88	642	651	165	10	4	0	0	0	0	0	0	0	0	8	0	PFG, TRIM	TRIM

Table S1-Early-Vacuolated

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os01g41710	Chlorophyll a-b binding protein	1,373	11,472	17,209	17,289	2,617	45	0	29	20	0	0	0	0	369	55	0	PFG, TRIM	
Os09g35700	Lipid-transfer protein	16,153	49,751	13,603	81	1	4	1	0	0	0	0	0	0	708	0	0		
Os01g41170	Unknown protein	0	1,914	8,675	22,039	1,105	7	0	0	0	0	0	0	0	318	0	242	PFG	
Os07g37850	Unknown protein	143	23	7,997	31	0	0	0	0	0	0	0	0	23	1,410	10	0		TRIM
Os08g45150	Proline-rich protein	6	1,413	5,527	2,515	1	1	3	0	0	0	0	0	0	256	0	0	RMD, UCD	
Os02g45530	Glucose-methanol-choline oxidoreductase	131	7,496	3,672	4	0	0	0	0	0	0	0	0	0	0	0	0	TRIM	TRIM
Os05g40010	Lipid-transfer protein	5	381	3,165	2,495	15	90	0	0	0	0	0	5	0	0	18	17	CSIRO	
Os02g01980	Proline-rich protein	1	131	2,831	0	0	0	4	0	0	0	0	0	0	96	0	0		
Os10g42620	Dihydroflavonol-4-reductase	9	4,613	2,445	345	7	1	1	22	0	0	0	0	8	26	3	0	PFG, RMD, TRIM	TRIM
Os07g46210	Unknown protein	2	5,127	2,210	26	0	0	0	0	0	0	0	0	0	25	0	0		TRIM
Os04g33930	Lipid binding protein	0	0	2,114	38	1	0	0	0	0	0	0	0	0	0	0	0	PFG	TRIM
Os02g09420	Cyclase	116	5	2,015	2	0	0	0	0	0	0	0	0	0	0	15	0		
Os01g09320	NADP-dependent malic enzyme	909	876	1,960	527	85	44	43	0	24	42	0	54	38	25	105	0		
Os02g01190	Unknown protein	80	146	1,747	0	0	0	0	0	0	0	0	0	0	508	0	0	RMD, TRIM	
Os01g37950	Unknown protein	392	789	1,700	4,045	214	797	4	19	0	0	0	2	36	22	0	0		
Os07g37100	Nucleoside transporter	28	275	1,650	316	24	30	44	96	110	0	10	21	0	0	4	3	PFG, RTIM, TRIM	TRIM
Os01g03670	Dihydroflavonol-4-reductase	47	11,738	1,649	16	5	3	1	0	0	0	0	0	0	117	0	0		
Os08g41950	SRF-type transcription factor	1,720	119	1,621	67	26	28	13	0	0	0	0	0	0	17	297	10	PFG, TRIM, UCD	TRIM
Os08g03520	Glycine-rich protein 2b	1,782	2,108	1,598	3,136	206	66	2	47	15	0	0	72	87	69	167	0		
Os12g18960	Nodulin-like protein	240	426	1,584	2,987	763	439	2	0	0	0	0	0	0	0	0	22	PFG	
Os03g10320	Unknown protein	6	0	1,332	2	0	0	0	0	4	0	0	0	0	0	0	6	PFG	TRIM
Os05g35740	Subtilisin propeptide domain containing protein	73	35	1,318	87	27	16	1	58	54	0	0	0	0	2	0	0	PFG	
Os08g43290	Lipid-transfer protein	554	6,768	1,261	28	0	0	0	0	0	0	0	0	0	3,537	0	0		TRIM
Os02g30200	PE-PGRS family protein	5	296	1,241	1,775	49	8	2	0	0	0	0	0	0	0	0	0	PFG, UCD	TRIM
Os03g39610	Chlorophyll a-b binding protein	569	1,070	1,205	716	248	4	0	0	0	0	0	0	0	346	97	0	PFG	
Os03g08790	Aspartic proteinase	61	158	1,128	1	0	0	0	33	0	0	0	4	137	123	12	0	Genoplante	TRIM
Os02g49870	Unknown protein	194	2	1,127	4	0	0	0	0	9	0	0	0	117	0	9	0		TRIM
Os10g37420	Cytochrome b5	246	648	951	587	70	70	0	0	6	0	0	0	0	0	0	0	GSNU	TRIM
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os03g47910	Unknown protein	807	2,357	923	3	0	0	0	0	0	0	0	0	0	489	0	0		
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os09g35800	UDP-glucose 4-epimerase	28	103	895	1,229	10	6	4	0	19	0	0	0	0	0	0	0	TRIM	TRIM
Os08g29770	Endoglucanase	0	402	876	1,017	164	63	0	0	16	0	0	0	0	0	0	0	PFG	
Os06g12320	Amino acid/polyamine transporter	1	140	873	543	11	0	0	0	20	0	0	0	0	0	0	0	PFG	
Os06g12350	Amino acid transporter	0	4	870	84	3	1	0	0	0	0	0	0	0	0	0	0	PFG	
Os02g07820	Unknown protein	12	270	831	2,719	245	71	0	0	0	0	0	0	0	0	0	6		
Os03g15710	Strictosidine synthase	33	942	830	43	5	1	0	0	0	0	0	0	0	22	0	0		
Os08g03682	Cytochrome P450	43	1,705	812	5	1	0	2	0	0	0	0	0	3	469	0	0		
Os01g56530	LOB domain protein	0	849	808	62	1	1	0	0	0	0	0	0	0	0	0	0	TRIM	
Os03g18420	NADH-ubiquinone oxidoreductase	386	98	786	48	114	38	35	38	0	0	0	0	17	92	30	56	PFG	
Os01g05670	3-oxo-5-alpha-steroid 4-dehydrogenase	275	1,217	772	398	72	23	1	0	0	0	0	1	0	29	21	0	PFG, RMD, RTIM	TRIM
Os05g30580	Subtilisin-like protease	0	2	748	1	0	0	0	0	0	0	0	0	0	0	0	0	PFG	TRIM
Os10g25230	ZIM motif family protein	453	425	743	2,315	146	42	13	0	0	0	0	0	8	0	14	0		TRIM
Os06g40150	Ethylene responsive element	11	67	733	72	1	0	0	0	0	0	0	0	0	6	0	0	PFG, TRIM	TRIM
Os01g53240	RD22-like protein	108	10	732	108	0	0	1	16	0	0	0	0	21	366	0	0		
Os06g42310	β-galactosidase	0	1	732	5	0	0	40	0	0	0	0	0	0	0	0	0		
Os12g37870	ATP-citrate synthase	380	259	726	601	106	43	27	0	0	10	0	0	0	0	0	0	PFG, TRIM	TRIM
Os11g09280	Protein disulfide isomerase	921	182	707	215	13	8	0	0	0	0	5	0	7	12	55	0	PFG	
Os11g41610	40S ribosomal protein S29	791	916	704	2,387	641	87	4	0	14	0	0	2	0	0	19	0	RMD, ZJU	

Table S1-Late-Vacuolated

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os01g41170	Unknown protein	0	1,914	8,675	22,039	1,105	7	0	0	0	0	0	0	0	318	0	242	PFG	
Os01g41710	Chlorophyll a-b binding protein	1,373	11,472	17,209	17,289	2,617	45	0	29	20	0	0	0	0	369	55	0	PFG, TRIM	
Os03g22460	Unknown protein	944	3,218	2,087	5,104	1,523	175	6	726	542	8	0	94	0	0	332	13		TRIM
Os01g37950	Unknown protein	392	789	1,700	4,045	214	797	4	19	0	0	0	2	36	22	0	0		
Os08g03520	Glycine-rich protein 2b	1,782	2,108	1,598	3,136	206	66	2	47	15	0	0	72	87	69	167	0		
Os02g07260	Phosphoglycerate kinase	1,264	1,450	1,823	3,025	2,245	959	103	420	91	72	0	118	9	47	171	103		
Os12g18960	Nodulin-like protein	240	426	1,584	2,987	763	439	2	0	0	0	0	0	0	0	0	22	PFG	
Os02g07820	Unknown protein	12	270	831	2,719	245	71	0	0	0	0	0	0	0	0	0	6		
Os08g45150	Proline-rich protein	6	1,413	5,527	2,515	1	1	3	0	0	0	0	0	0	256	0	0	RMD, UCD	
Os05g40010	Lipid-transfer protein	5	381	3,165	2,495	15	90	0	0	0	0	0	5	0	0	18	17	CSIRO	
Os11g41610	40S ribosomal protein S29	791	916	704	2,387	641	87	4	0	14	0	0	2	0	0	19	0	RMD, ZJU	
Os10g25230	ZIM motif family protein	453	425	743	2,315	146	42	13	0	0	0	0	0	8	0	14	0		TRIM
Os01g48770	60S ribosomal protein L37a	1,053	1,031	184	2,216	567	110	2	72	30	27	0	0	0	3	103	0	PFG	
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os02g30200	PE-PGRS family protein	5	296	1,241	1,775	49	8	2	0	0	0	0	0	0	0	0	0	PFG, UCD	TRIM
Os05g41110	60S ribosomal protein L30	357	664	632	1,729	422	58	2	0	0	0	0	0	10	0	0	0	PFG	TRIM
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os02g32080	Unknown protein	0	34	470	1,459	237	3	0	0	0	0	0	0	0	0	0	0		TRIM
Os10g37400	Unknown protein	6	290	438	1,396	67	0	0	0	0	0	0	0	0	0	0	0		
Os10g05720	Lipid binding protein	0	79	131	1,325	0	0	0	0	0	0	0	0	0	71	0	0	PFG, TRIM	TRIM
Os09g35800	UDP-glucose 4-epimerase	28	103	895	1,229	10	6	4	0	19	0	0	0	0	0	0	0	TRIM	TRIM
Os05g47980	ATP synthase	281	721	349	1,131	3,937	1,125	19	86	29	11	6	9	0	14	33	139	PFG, SHIP, TRIM	TRIM
Os08g29770	Endoglucanase	0	402	876	1,017	164	63	0	0	16	0	0	0	0	0	0	0	PFG	
Os04g42060	Cytochrome c oxidase	246	646	360	1,013	2,497	1,458	127	0	0	0	0	0	0	0	0	17	PFG, RTIM	TRIM
Os10g39130	MADS-box transcription factor	262	794	501	1,001	361	266	1	0	170	7	6	29	11	68	5	5	PFG, UCD	
Os08g36860	ent-kaurenoic acid oxidase	10	55	303	972	92	11	2	0	10	0	0	0	0	0	76	0	No hit	
Os06g16290	h/ACA ribonucleoprotein complex subunit 2	197	235	250	948	49	3	0	14	1	0	0	0	0	0	0	0	PFG	
Os07g40740	Heparanase-like protein	0	5	102	947	42	0	1	0	0	0	0	0	0	0	0	0		
Os04g55660	GDSL-motif lipase	0	26	337	919	25	1	3	0	0	0	0	0	0	0	0	10	PFG, RMD, UCD	TRIM
Os04g47250	Cytochrome P450	32	189	471	914	3	0	0	15	0	0	0	9	92	35	8	0		TRIM
Os02g55600	Unknown protein	23	222	602	870	291	96	1	0	0	0	0	0	0	0	0	5		TRIM
Os02g49350	Plastocyanin-like domain containing protein	0	0	140	785	907	5	2	0	0	0	0	0	0	0	0	128	PFG	
Os01g65880	MtN3 and saliva related trans membrane	334	351	287	730	281	14	0	0	44	2	0	27	29	18	0	7	PFG, TRIM	TRIM
Os07g31300	ATP synthase delta chain	193	646	665	728	1,084	235	8	4	0	0	0	0	0	0	0	0		
Os03g39610	Chlorophyll a-b binding protein	569	1,070	1,205	716	248	4	0	0	0	0	0	0	0	346	97	0	PFG	
Os06g46680	Cytochrome P450	206	225	688	676	10	2	0	0	0	0	0	0	0	0	0	0	PFG, TRIM	TRIM
Os01g04730	60S ribosomal protein L26-1	477	285	130	658	88	13	1	0	17	22	2	28	0	18	116	0		
Os06g36010	Cupredoxin domain containing protein	0	0	75	652	186	2	1	0	0	0	0	0	0	0	0	0		
Os03g56241	40S ribosomal protein S29	370	249	309	629	90	34	0	13	36	0	0	27	7	18	75	0	PFG, TRIM, UCD	
Os06g02144	6-phosphogluconate dehydrogenase	544	1,174	660	617	189	62	0	0	0	0	1	0	14	0	25	0		
Os10g33990	Unknown protein	108	533	526	602	63	74	0	3	4	0	0	11	1	0	0	0		
Os12g37870	ATP-citrate synthase	380	259	726	601	106	43	27	0	0	10	0	0	0	0	0	0	PFG, TRIM	TRIM
Os03g14450	Enolase	241	133	140	598	120	53	4	6	0	85	0	103	0	2	0	11	SHIP, RMD	TRIM
Os10g37420	Cytochrome b5	246	648	951	587	70	70	0	0	6	0	0	0	0	0	0	0	GSNU	TRIM
Os06g44660	Arabinogalactan protein	0	114	14	557	1,196	21	16	0	0	0	0	0	0	0	12	54		
Os01g53710	Protein phosphatase	143	418	314	544	16	6	0	0	0	2	0	18	42	0	0	0	PFG, RMD	
Os06g12320	Amino acid/polyamine transporter	1	140	873	543	11	0	0	0	20	0	0	0	0	0	0	0	PFG	
Os01g09320	NADP-dependent malic enzyme	909	876	1,960	527	85	44	43	0	24	42	0	54	38	25	105	0		
Os05g51530	ATP synthase	110	387	396	503	444	173	8	0	6	83	0	0	0	0	0	0	PFG	TRIM

Table S1-Mitosis

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os02g03510	Fibroin heavy chain precursor	1	2	1	129	6,191	8,237	1,167	0	0	0	0	0	0	0	0	773		
Os01g14940	Pectinesterase inhibitor	0	0	0	8	4,562	2,223	183	0	0	0	0	0	0	0	33	894		TRIM
Os05g47980	ATP synthase	281	721	349	1,131	3,937	1,125	19	86	29	11	6	9	0	14	33	139	PFG, SHIP, TRIM	TRIM
Os01g15610	Unknown protein	25	40	27	146	3,619	250	9	0	0	0	0	1	0	0	0	0	PFG	
Os01g69020	Fibroin heavy chain precursor-like protein	0	0	18	644	3,398	2,075	602	0	0	0	0	0	0	0	0	124		
Os01g41710	Chlorophyll a-b binding protein	1,373	11,472	17,209	17,289	2,617	45	0	29	20	0	0	0	0	369	55	0	PFG, TRIM	
Os04g42060	Cytochrome c oxidase	246	646	360	1,013	2,497	1,458	127	0	0	0	0	0	0	0	0	17	PFG, RTIM	TRIM
Os02g07260	Phosphoglycerate kinase	1,264	1,450	1,823	3,025	2,245	959	103	420	91	72	0	118	9	47	171	103		
Os01g13440	Unknown protein	0	0	0	5	1,512	2,480	107	0	0	0	0	0	0	0	0	0		
Os06g44660	Arabinogalactan protein	0	114	14	557	1,196	21	16	0	0	0	0	0	0	0	12	54		
Os07g31300	ATP synthase delta chain	193	646	665	728	1,084	235	8	4	0	0	0	0	0	0	0	0		
Os02g50980	Unknown protein	0	0	1	15	1,072	807	65	0	0	0	0	0	0	0	2	75	No hit	
Os03g10640	Calcium-transporting ATPase	116	17	14	60	1,044	436	63	0	165	0	0	6	30	0	32	195	PFG, RMD, RTIM	TRIM
Os04g32330	Dihydrolipoyllysine-residue succinyltransferas	269	255	260	284	937	286	31	179	16	4	18	12	0	17	64	44	PFG, RMD	
Os02g49350	Plastocyanin-like domain containing protein	0	0	140	785	907	5	2	0	0	0	0	0	0	0	0	128	PFG	
Os12g18960	Nodulin-like protein	240	426	1,584	2,987	763	439	2	0	0	0	0	0	0	0	0	22	PFG	
Os11g19160	β-D-xylosidase	0	0	0	85	754	19	1	0	0	0	0	0	0	0	0	148	PFG, TRIM	
Os03g07480	Sucrose Transporter	7	9	0	0	660	76	1	0	0	62	0	0	0	0	0	1	PFG, RMD, RTIM, SHIP	TRIM
Os03g10334	Unknown protein	0	1	2	2	659	377	103	0	0	0	0	0	0	0	0	34		
Os11g41610	40S ribosomal protein S29	791	916	704	2,387	641	87	4	0	14	0	0	2	0	0	19	0	RMD, ZJU	
Os06g38980	Polyadenylate-binding protein	4	173	31	354	605	55	4	0	2	0	0	0	0	0	0	31	TRIM	
Os01g48770	60S ribosomal protein L37a	1,053	1,031	184	2,216	567	110	2	72	30	27	0	0	0	3	103	0	PFG	
Os04g57560	Lysine-specific histone demethylase	36	38	70	71	539	188	13	0	48	29	0	21	0	0	0	0	Genoplante, PFG, UCD	
Os01g71240	Calcium-transporting ATPase	0	7	4	42	537	155	27	0	0	0	0	0	0	0	0	32	PFG, RTIM, UCD	TRIM
Os05g44760	Hexokinase	20	55	56	137	524	236	26	0	9	0	0	1	9	0	0	32	Genoplante	
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os11g07280	Coatomer subunit beta	186	579	396	409	482	151	31	0	10	46	0	22	58	206	46	44	PFG	
Os01g74450	Aquaporin	0	1	6	175	461	121	61	0	1	0	0	2	0	0	0	0	PFG	TRIM
Os05g49170	COR413-like protein	36	33	13	128	449	21	5	0	0	0	0	1	0	0	0	0		TRIM
Os05g51530	ATP synthase	110	387	396	503	444	173	8	0	6	83	0	0	0	0	0	0	PFG	TRIM
Os05g41110	60S ribosomal protein L30	357	664	632	1,729	422	58	2	0	0	0	0	0	10	0	0	0	PFG	TRIM
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os02g10470	Calcium ion binding protein	44	161	123	97	358	100	12	0	0	0	0	0	0	0	18	6		TRIM
Os12g36630	Fiber protein	10	4	4	36	356	14	2	0	0	0	0	0	0	0	0	9		TRIM
Os06g48050	Unknown protein	0	4	0	4	352	204	8	0	0	0	0	0	0	0	0	0	CSIRO	
Os01g68030	Unknown protein	186	153	219	244	306	65	10	0	0	0	0	10	0	0	5	5		
Os02g55600	Unknown protein	23	222	602	870	291	96	1	0	0	0	0	0	0	0	0	5		TRIM
Os09g15770	Eukaryotic translation initiation factor 5	198	249	332	439	285	116	3	0	3	0	0	0	0	0	0	0		TRIM
Os04g39590	Arabinogalactan protein	0	0	2	26	284	44	5	0	0	0	0	0	0	0	0	21		TRIM
Os08g01090	B3 DNA binding domain containing protein	68	298	242	427	283	96	28	0	2	0	0	0	0	0	0	0	RMD	
Os03g56940	Unknown protein	0	0	3	325	282	1	0	0	0	0	0	0	0	0	0	25	No hit	
Os01g65880	MtN3 and saliva related trans membrane protein	334	351	287	730	281	14	0	0	44	2	0	27	29	18	0	7	PFG, TRIM	TRIM
Os02g41820	Unknown protein	145	352	362	312	265	180	11	0	6	0	0	5	0	0	5	25	PFG, SHIP	
Os07g11060	Unknown protein	50	123	156	193	250	121	11	0	0	0	0	2	0	0	0	0	Genoplante, PFG	
Os02g07820	Unknown protein	12	270	831	2,719	245	71	0	0	0	0	0	0	0	0	0	6		
Os05g38180	Yip1 domain containg protein	150	238	114	340	244	127	12	0	0	3	0	10	0	29	18	8	PFG, TRIM	
Os03g60390	PHD finger protein	66	307	260	327	243	82	2	0	0	0	0	0	0	0	0	0	PFG	TRIM
Os02g32080	Unknown protein	0	34	470	1,459	237	3	0	0	0	0	0	0	0	0	0	0		TRIM
Os01g40650	Unknown protein	81	59	70	182	234	121	29	0	0	0	0	0	0	0	0	0	PFG	

Table S1-Mature-Pollen

		SBS							MPSS										
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen											Insertion mutant	Activation mutant
									TPM										
Os02g03510	Fibroin heavy chain precursor	1	2	1	129	6,191	8,237	1,167	0	0	0	0	0	0	0	0	773		
Os01g13440	Unknown protein	0	0	0	5	1,512	2,480	107	0	0	0	0	0	0	0	0	0		
Os04g42060	Cytochrome c oxidase	246	646	360	1,013	2,497	1,458	127	0	0	0	0	0	0	0	0	17	PFG, RTIM	TRIM
Os05g47980	ATP synthase	281	721	349	1,131	3,937	1,125	19	86	29	11	6	9	0	14	33	139	PFG, SHIP, TRIM	TRIM
Os02g50980	Unknown protein	0	0	1	15	1,072	807	65	0	0	0	0	0	0	0	2	75		
Os01g37950	Unknown protein	392	789	1,700	4,045	214	797	4	19	0	0	0	2	36	22	0	0		
Os06g48320	Lipid binding protein	64	299	126	213	319	643	122	0	0	0	0	0	0	0	0	43	PFG	
Os01g58910	Hs1pro-1-like protein	3	160	220	103	184	442	0	0	0	7	0	87	0	28	31	35	Genoplante, GSNU, PFG, RMD	
Os12g18960	Nodulin-like protein	240	426	1,584	2,987	763	439	2	0	0	0	0	0	0	0	0	22	PFG	
Os06g50100	Protein kinase	98	40	32	30	134	258	11	15	0	0	0	0	0	0	37	0	PFG,	TRIM
Os01g15610	Unknown protein	25	40	27	146	3,619	250	9	0	0	0	0	1	0	0	0	0	PFG	
Os05g44760	Hexokinase	20	55	56	137	524	236	26	0	9	0	0	1	9	0	0	32	Genoplante	
Os07g31300	ATP synthase delta chain	193	646	665	728	1,084	235	8	4	0	0	0	0	0	0	0	0		
Os10g33640	Serine/threonine-protein kinase	1	5	3	1	157	225	42	0	3	0	0	0	0	0	7	21	Genoplante	
Os01g63690	Nematode-resistance protein	112	417	193	193	57	216	0	0	0	0	6	27	0	0	8	0	PFG	TRIM
Os02g50990	RING-H2 finger protein	4	16	18	24	83	210	7	0	0	0	0	0	0	0	0	0	Genoplante, RTIM, SHIP, TRIM	
Os06g48050	Unknown protein	0	4	0	4	352	204	8	0	0	0	0	0	0	0	0	0	CSIRO	
Os02g41820	Unknown protein	145	352	362	312	265	180	11	0	6	0	0	5	0	0	5	25	PFG, SHIP	
Os04g33200	Unknown protein	73	526	581	459	180	173	25	0	0	0	0	0	0	0	0	11	Genoplante, PFG, RTIM, TRIM	TRIM
Os03g59380	Lipid-transfer protein	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3		TRIM
Os01g33060	HEAT repeat family protein	60	104	88	88	118	147	24	0	0	0	0	0	0	0	12	9	PFG, SHIP	
Os04g32920	Potassium transporter	15	82	201	143	70	144	0	0	0	2	1	0	0	0	0	0	Genoplante, PFG, RTIM, OSTID	
Os06g39050	Syntaxin	0	0	0	1	74	130	5	0	0	0	0	0	0	0	0	18		
Os01g10040	Cytochrome P450	27	55	63	68	31	128	0	0	0	0	0	0	0	0	0	0	PFG, RMD, SHIP, TRIM	TRIM
Os05g38180	Yip1 domain containg protein	150	238	114	340	244	127	12	0	0	3	0	10	0	29	18	8	PFG, TRIM	
Os07g11060	Unknown protein	50	123	156	193	250	121	11	0	0	0	0	2	0	0	0	0	Genoplante, PFG	
Os05g07700	60S ribosomal protein L10-3	555	1,323	924	1,716	411	117	6	5	20	0	1	14	0	10	0	0	PFG, TRIM	TRIM
Os09g15770	Eukaryotic translation initiation factor 5	198	249	332	439	285	116	3	0	3	0	0	0	0	0	0	0		TRIM
Os12g07230	Calcium-dependent protein kinase	118	214	148	156	172	115	9	0	0	0	0	0	0	1	0	0	PFG	
Os09g30478	Unknown protein	43	102	78	140	105	113	19	0	0	0	0	0	0	0	0	0		TRIM
Os02g10470	Calcium ion binding protein	44	161	123	97	358	100	12	0	0	0	0	0	0	0	18	6		TRIM
Os03g28260	Retrotransposon protein	0	0	0	2	21	98	3	0	0	0	0	0	0	0	0	0	PFG	
Os03g51210	Unknown protein	1	0	2	17	126	97	9	0	0	0	0	0	0	0	0	12	GSNU	
Os02g55600	Unknown protein	23	222	602	870	291	96	1	0	0	0	0	0	0	0	0	5		TRIM
Os02g39950	Calcium binding protein	7	4	5	2	111	95	13	0	0	0	0	0	0	0	0	4	Genoplante, PFG, SHIP	
Os03g54980	Unknown protein	303	381	83	387	187	93	2	0	0	0	0	0	0	0	0	0	TRIM	TRIM
Os03g02740	Phospholipase D	18	16	2	15	173	92	10	0	0	0	0	0	0	4	14	0	PFG, RTIM	
Os05g40010	Lipid-transfer protein	5	381	3,165	2,495	15	90	0	0	0	0	0	5	0	0	18	17	CSIRO	
Os01g39399	Hypothetical protein	0	0	0	1	44	90	0	0	0	0	0	0	0	0	0	0		
Os07g13280	RNA-binding domain containing protein	32	23	14	26	57	84	9	0	0	0	0	0	0	0	14	1	PFG	
Os09g29380	Unknown protein	127	120	163	150	53	83	12	0	0	0	0	9	0	0	0	0		
Os03g60390	PHD finger protein	66	307	260	327	243	82	2	0	0	0	0	0	0	0	0	0	PFG	TRIM
Os07g38380	Unknown protein	28	112	44	58	43	79	2	0	0	0	1	0	0	0	0	0	PFG	
Os07g42660	Caltractin	101	115	62	97	84	75	13	0	0	0	0	0	6	29	4	0	PFG	TRIM
Os10g33990	Unknown protein	108	533	526	602	63	74	0	3	4	0	0	11	1	0	0	0		
Os09g32240	Lipid binding protein	58	131	311	319	103	74	8	0	0	0	0	0	0	0	0	0	PFG	
Os08g03450	60S ribosomal protein L37	751	1,562	912	1,887	411	72	7	10	9	0	0	2	0	0	11	0	RMD	
Os01g57110	ATP binding protein	76	262	232	190	98	72	6	0	3	0	0	0	0	0	0	0	PFG, RMD,TRIM	TRIM
Os02g07820	Unknown protein	12	270	831	2,719	245	71	0	0	0	0	0	0	0	0	0	6		
Os04g59120	Unknown protein	0	0	0	2	0	70	0	0	0	0	0	2	0	0	0	0	UCD	

Table S1-Pollen (Pollen-minus-other-organs)

TIGR_gene	Annotation	SBS							MPSS									Insertion mutant	Activation mutant
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen		
		Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature pollen												
									TPM										
Os07g01770	GTPase activating protein	19	0	17	2	204	1,149	19,760	0	0	0	0	38	0	80	231	3,608	RMD	
Os05g46530	Pectinesterase inhibitor	0	0	2	17	413	1,127	12,650	0	0	0	0	0	0	0	902	26,161	Genoplante, PFG	TRIM
Os04g32680	Pollen Ole e 1 allergen and extensin family protein	0	0	12	15	208	616	12,600	0	0	0	0	0	0	0	88	299		
Os05g51090	MtN3 and saliva related trans membrane protein	0	2	3	2	32	302	12,429	0	0	0	0	0	0	0	93	1,188	Genoplante	
Os05g30940	Vacuolar calcium binding protein	0	1	0	21	1,200	8,116	11,040	0	0	40	0	0	0	0	0	213	TRIM	TRIM
Os06g03390	Unknown protein	0	1	0	50	2,518	8,301	10,094	0	0	0	0	0	0	0	0	314		TRIM
Os12g42650	Unknown protein	1	4	1	52	2,229	7,792	9,201	0	0	0	0	0	0	0	0	130	PFG	TRIM
Os04g33710	Unknown protein	0	0	3	9	276	823	8,969	0	0	0	0	0	0	0	129	2,845		
Os02g10530	Unknown protein	0	0	2	1	3	25	8,316	0	0	0	0	0	0	0	0	250		
Os12g07700	NFU-like protein	2	1	0	8	579	4,494	8,252	0	0	0	0	0	0	0	85	1,320	RTIM	
Os07g26480	Desiccation-associated protein	0	0	0	1	87	400	7,586	0	0	0	0	0	0	0	41	791	Genoplante, PFG	
Os01g20970	c/VIF2	0	0	0	0	2	13	7,450	0	0	0	0	0	0	0	0	532		
Os01g21970	PTI1-like kinase	11	0	2	0	2	7	7,203	0	0	0	0	0	0	0	224	2,295	RMD, RTIM	
Os04g50216	Unknown protein	422	2	382	1	1	26	7,070	0	109	0	0	123	0	0	48	108	TRIM	TRIM
Os07g49100	Pectinesterase	1	2	0	19	208	4,963	6,522	0	0	0	0	0	0	0	0	41	RTIM	
Os10g35930	LIM domain-containing protein	3	1	1	0	28	155	6,487	49	10	0	21	2	7	0	575	24,900	PFG, RTIM	
Os10g32810	b-amylase	1	0	19	7	41	290	6,057	0	0	0	0	0	0	0	111	390	TRIM	
Os06g40890	Exopolygalacturonase	0	0	0	39	973	4,665	5,895	0	0	0	0	0	0	0	0	1,060	PFG	
Os05g20150	ATP binding protein	0	0	0	0	11	90	5,874	0	0	0	0	0	0	0	0	72	PFG	
Os02g39380	Calmodulin	1	0	1	0	33	112	5,473	0	0	0	0	0	0	0	0	685	SHIP	
Os02g17240	Pollen-specific kinase partner protein	0	0	0	0	0	1	5,459	0	0	0	0	0	0	0	0	4	UCD	
Os01g59360	Calcium-dependent protein kinase	0	0	0	4	237	731	5,261	0	0	0	0	0	0	0	34	1,673	Genoplante	
Os04g57350	EH-domain-containing protein	3	0	0	26	833	3,016	5,007	0	0	0	0	0	38	0	220	2,375	PFG, RMD, RTIM, TRIM	TRIM
Os05g33580	Unknown protein	1	0	0	5	171	938	4,629	0	0	0	0	0	0	0	0	54		TRIM
Os02g32740	SNAP25-like protein	0	0	3	0	5	83	4,569	0	0	0	0	0	0	0	0	129		
Os01g27190	CaLB domain containing protein	0	0	0	2	177	805	4,261	0	0	0	0	0	0	0	41	1,749	PFG	
Os01g23880	Unknown protein	0	0	0	0	39	169	3,990	0	0	0	0	0	0	0	9	605		
Os01g48410	Unknown protein	0	3	0	8	468	2,433	3,850	0	0	0	0	0	0	0	0	530	PFG	
Os04g38560	Pectinesterase	0	0	0	0	12	75	3,420	0	0	0	0	0	0	0	84	792	PFG, RTIM, UCD	
Os01g17390	Cyclin-like F-box	18	2	21	1	22	143	3,347	14	92	12	0	56	5	16	10	272	PFG, TRIM, RTIM	TRIM
Os03g27110	Catalytic/ hydrolase	0	0	1	8	377	2,536	3,317	0	0	0	0	0	0	0	42	1,361		TRIM
Os06g10210	Unknown protein	85	2	39	0	2	29	3,261	0	0	0	14	5	4	4	7	60	RTIM	
Os03g21880	Unknown protein	0	0	0	0	1	22	3,254	0	0	0	0	0	0	0	0	5	PFG	
Os02g24430	Phosphatidylinositol transporter	0	1	0	1	26	1,068	3,229	0	0	0	0	0	0	0	2	101		TRIM
Os02g07900	ANTH domain containing protein	0	1	0	8	329	2,243	3,176	0	0	0	0	0	0	0	59	1,004	PFG, RTIM	
Os12g35710	Extensin-like protein	0	0	0	1	4	13	3,162	0	0	0	0	0	0	0	34	104		TRIM
Os05g38770	Protein kinase	2	0	0	1	204	991	3,038	0	0	0	0	0	0	0	0	15		TRIM
Os10g32590	Unknown protein	0	0	0	4	178	819	3,026	0	0	0	0	0	0	0	0	195		
Os03g12570	DNA cytosine methyltransferase	16	6	1	8	4	21	2,883	0	0	0	0	0	0	0	8	137	PFG, GSNU, RTIM, TRIM, UCD	TRIM
Os06g05260	Pectate lyase	0	0	0	8	163	2,470	2,841	0	0	0	0	0	0	0	0	0	Genoplante	TRIM
Os12g12860	Calcium-dependent protein kinase	0	0	1	1	8	112	2,736	0	0	0	0	0	0	0	69	2,133	TRIM, UCD	TRIM
Os08g38250	Unknown protein	0	0	1	0	3	13	2,557	0	0	0	0	0	0	0	0	1,570		
Os04g21340	Unknown protein	0	0	2	1	71	521	2,548	0	0	0	0	0	0	0	73	1,600	PFG	
Os01g10890	CBL-interacting serine/threonine-protein kinase	5	6	1	1	206	1,478	2,536	0	0	0	0	0	0	0	3	76	Genoplante, GSNU, PFG	
Os03g50280	Unknown protein	237	7	37	1	13	135	2,513	0	0	0	0	0	16	0	92	230	Genoplante, RMD	
Os01g10470	Rapid alkalinization factor	0	0	0	1	18	577	2,433	0	0	0	0	0	0	0	77	348		
Os11g23220	Unknown protein	0	1	0	8	361	1,476	2,398	0	0	0	0	0	0	0	19	255	UCD	
Os01g16470	Phosphatidylinositol 3- and 4-kinase	0	0	0	2	46	870	2,185	0	0	0	0	0	0	0	0	613		
Os02g35300	Protein kinase domain containing protein	0	0	0	9	146	1,045	2,181	0	0	0	0	0	0	0	4	0		
Os06g46560	Unknown protein	0	1	0	3	29	326	2,180	0	0	0	0	0	0	0	15	1,258	TRIM	TRIM

Table S2. *Anther-minus-pollen transcripts whose ortholog transcripts/proteins are known to be present in or restricted to the tapeta in anthers of different species.* Anther-minus-pollen transcripts are those that possess TPM >5X those in pollen. Their presence in various anther, pollen (current SBS results) and other organs (reported MPSS results) transcriptomes are shown. Rice ortholog transcripts with TPM lower than 20 are excluded to avoid background noises.

Transcripts of rice genes	Transcripts/proteins of rice orthologs known to be restricted to the tapetum in anthers	SBS							MPSS									
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen
		Meio	Tetrad	Early vacu	Late Vacu	Mitosis	Mature pollen										
									TPM								
Os01g49650	TomA5B (Tomato) [1]	2,632	1,850	39	9	0	0	0	0	0	0	0	0	0	1,591	0	0
Os03g18850	LLA-15 (Lily) [2]	24	2	1	2	0	0	1	0	0	13	0	3	0	25	0	0
Os03g59380	bvLTP-1 (Sugar beet) [3]	1,358	17,792	20,728	35,555	512	169	1	0	0	0	0	0	0	399	29	3
Os03g07140	MS2 (Arabidopsis)[4]	2	40	624	1	2	0	1	0	0	0	0	0	0	274	0	0
Os04g39470	AtMYB103 (Arabidopsis)[5]	5	59	1	0	0	0	0	0	2	0	0	0	0	2	0	0
Os07g22850	PrChS1 (*Pinus radiata*) [6]	92	12	68	0	0	0	0	0	0	0	0	0	0	99	0	0
Os07g37090	RA39 (Rice)[7]	0	143	293	0	0	0	0	0	0	0	0	0	0	174	0	0
Os08g03682	CYP703 (Arabidopsis)[8]	43	1,705	812	5	1	0	2	0	0	0	0	0	3	469	0	0
Os08g38810	RAFTIN (Rice)[9]	35	25	136	47	0	0	0	0	0	0	0	0	0	609	0	0
Os08g43290	Osc4 (Rice) [10]	554	6,768	1,261	28	0	0	0	0	0	0	0	0	0	3,537	0	0
Os09g27620	MS1 (Arabidopsis) [11]	1	356	53	0	0	0	1	0	0	0	0	0	0	0	0	0
Os09g35700	YY1 (Rice) [12]	16,153	49,751	13,603	81	1	4	1	0	0	0	0	0	0	708	0	0
	Toma108z (Tomato) [13]																
	Mzm3-3 (Maiza) [14]																
Os10g34360	YY2 (Rice) [12]	5	134	78	0	0	0	0	0	0	0	0	0	0	1,333	0	0
	PrChS1 (*Pinus radiata*) [6]																
Os01g68870	MSP1 (Rice) [15]	25	32	12	9	3	1	0	0	0	0	0	0	24	3	40	0
	EMS/EXS (Arabidopsis) [16]																
Os02g02820	TDR (Rice) [17]	97	3	110	1	0	0	0	0	0	0	0	0	0	110	0	0
	DYT1 (Arabidopsis) [18]																
Os02g53200	Tag1 (Tobacco)[19]	30	1	1	0	0	0	0	227	24	22	4	78	253	386	224	1
Os04g38480	SERK1 (Arabidopsis)[20]	22	13	14	15	15	6	1	0	0	0	0	24	0	0	0	0
Os04g57490	OsCP1 (Rice)[21]	0	1	44	0	0	0	0	0	0	0	0	0	0	0	0	0
Os06g06980	AtTSM1 (Arabidopsis)[22]	70	1	9	1	0	1	0	519	305	210	269	295	1,323	1,367	259	0
Os09g32550	A6 (Arabidopsis)[23]	59	24	7	18	7	3	0	0	0	0	0	0	0	25	77	0
Os09g30320	RA8 (Rice)[24]	6	152	283	166	4	0	0	0	0	0	0	0	0	636	2	213
Os09g36730	AtMYB32 (Arabidopsis)[25]	11	148	139	19	0	0	0	190	29	471	2	204	68	361	0	0
Os12g02310	PrLTP1(*Pinus radiata*)[6]	23	0	8	0	0	4	0	704	316	0	0	0	605	206	0	0

References (according to the superscript numbers):

1. **Aguirre PJ, Smith AG** (1993) Molecular characterization of a gene encoding a cysteine-rich protein preferentially expressed in anthers of *Lycopersicon esculentum*. Plant Mol Biol **23:** 477-487
2. **Wang CS, Walling LL, Eckard KJ, Lord EM** (1992) Immunological characterization of a tapetal protein in developing anthers of *Lilium longiflorum*. Plant Physiol **99:** 822-829
3. **Matsuhira H, Shinada H, Yui-Kurino R, Hamato N, Umeda M, Mikami T, Kubo T** (2007) An anther-specific lipid transfer protein gene in sugar beet: its expression is strongly reduced in male-sterile plants with Owen cytoplasm. Physiol Plant **129:** 407-414
4. **Aarts MG, Hodge R, Kalantidis K, Florack D, Wilson ZA, Mulligan BJ, Stiekema WJ, Scott R,**

Pereira A (1997) The *Arabidopsis* MALE STERILITY 2 protein shares similarity with reductases in elongation/condensation complexes. Plant J **12:** 615-623

5. **Li SF, Higginson T, Parish RW** (1999) A novel MYB-related gene from *Arabidopsis thaliana* expressed in developing anthers. Plant Cell Physiol **40:** 343-347
6. **Walden AR, Walter C, Gardner RC** (1999) Genes expressed in Pinus radiata male cones include homologs to anther-specific and pathogenesis response genes. Plant Physiol **121:** 1103-1116
7. **Ding ZJ, Wu XH, Tai W** (2002) The rice tapetum-specific gene RA39 encodes a type I ribosome-inactivating protein. Sex Plant Reprod **15:** 205-212
8. **Morant M, Jorgensen K, Schaller H, Pinot F, Moller BL, Werck-Reichhart D, Bak S** (2007) CYP703 is an ancient cytochrome P450 in land plants catalyzing in-chain hydroxylation of lauric acid to provide building blocks for sporopollenin synthesis in pollen. Plant Cell **19:** 1473-1487
9. **Wang A, Xia Q, Xie W, Datla R, Selvaraj G** (2003) The classical Ubisch bodies carry a sporophytically produced structural protein (RAFTIN) that is essential for pollen development. Proc Natl Acad Sci U S A **100:** 14487-14492
10. **Tsuchiya T, Toriyama K, Ejiri S, Hinata K** (1994) Molecular characterization of rice genes specifically expressed in the anther tapetum. Plant Mol Biol **26:** 1737-1746
11. **Ito T, Shinozaki K** (2002) The MALE STERILITY1 gene of *Arabidopsis*, encoding a nuclear protein with a PHD-finger motif, is expressed in tapetal cells and is required for pollen maturation. Plant Cell Physiol **43:** 1285-1292
12. **Hihara Y, Hara C, Uchimiya H** (1996) Isolation and characterization of two cDNA clones for mRNAs that are abundantly expressed in immature anthers of rice (*Oryza sativa* L.). Plant Mol Biol **30:** 1181-1193
13. **Chen R, Smith AG** (1993) Nucleotide sequence of a stamen- and tapetum-specific gene from *Lycopersicon esculentum*. Plant Physiol **101:** 1413
14. **Lauga B, Charbonnel-Campaa L, Combes D** (2000) Characterization of MZm3-3, a Zea mays tapetum-specific transcript. Plant Sci **157:** 65-75
15. **Nonomura K, Miyoshi K, Eiguchi M, Suzuki T, Miyao A, Hirochika H, Kurata N** (2003) The MSP1 gene is necessary to restrict the number of cells entering into male and female sporogenesis and to initiate

anther wall formation in rice. Plant Cell **15:** 1728-1739

16. **Zhao DZ, Wang GF, Speal B, Ma H** (2002) The excess microsporocytes1 gene encodes a putative leucine-rich repeat receptor protein kinase that controls somatic and reproductive cell fates in the *Arabidopsis* anther. Genes Dev **16:** 2021-2031
17. **Li N, Zhang DS, Liu HS, Yin CS, Li XX, Liang WQ, Yuan Z, Xu B, Chu HW, Wang J, Wen TQ, Huang H, Luo D, Ma H, Zhang DB** (2006) The rice tapetum degeneration retardation gene is required for tapetum degradation and anther development. Plant Cell **18:** 2999-3014
18. **Zhang W, Sun Y, Timofejeva L, Chen C, Grossniklaus U, Ma H** (2006) Regulation of *Arabidopsis* tapetum development and function by DYSFUNCTIONAL TAPETUM1 (DYT1) encoding a putative bHLH transcription factor. Development **133:** 3085-3095
19. **Bucciaglia PA, Smith AG** (1994) Cloning and characterization of Tag 1, a tobacco anther beta-1,3-glucanase expressed during tetrad dissolution. Plant Mol Biol **24:** 903-914
20. **Colcombet J, Boisson-Dernier A, Ros-Palau R, Vera CE, Schroeder JI** (2005) *Arabidopsis* SOMATIC EMBRYOGENESIS RECEPTOR KINASES1 and 2 are essential for tapetum development and microspore maturation. Plant Cell **17:** 3350-3361
21. **Lee S, Jung KH, An G, Chung YY** (2004) Isolation and characterization of a rice cysteine protease gene, OsCP1, using T-DNA gene-trap system. Plant Mol Biol **54:** 755-765
22. **Fellenberg C, Milkowski C, Hause B, Lange PR, Bottcher C, Schmidt J, Vogt T** (2008) Tapetum-specific location of a cation-dependent O-methyltransferase in *Arabidopsis thaliana*. Plant J **56:** 132-145
23. **Hird DL, Worrall D, Hodge R, Smartt S, Paul W, Scott R** (1993) The anther-specific protein encoded by the *Brassica napus* and *Arabidopsis thaliana* A6 gene displays similarity to beta-1,3-glucanases. Plant J **4:** 1023-1033
24. **Jeon JS, Chung YY, Lee S, Yi GH, Oh BG, An G** (1999) Isolation and characterization of an anther-specific gene, RA8, from rice (*Oryza sativa* L.). Plant Mol Biol **39:** 35-44
25. **Preston J, Wheeler J, Heazlewood J, Li SF, Parish RW** (2004) AtMYB32 is required for normal pollen development in *Arabidopsis thaliana*. Plant J **40:** 979-995

Table S3. *Anther-minus-other-organs transcripts with TPM ≥100 that encode secretory proteins.* Transcripts with TPM ≥1,000 are shaded.

		SBS							MPSS								
		Developing anthers						Pollen	Germina seed	Young leaf	Young root	Mature leaf	Mature root	Stem	Immature panicle	Ovary & stigma	Pollen
TIGR_gene	Annotation	Meiosis	Tetrad	Early vacu	Late Vacu	Mitosis	Mature pollen										
									TPM								
Os01g11710	Esterase	67	146	62	31	5	7	0	0	0	0	0	0	0	0	0	0
Os01g12020	Lipid-transfer protein	9,549	9,683	105	29	19	8	0	0	0	0	0	0	0	120	0	0
Os01g13200	Unknown protein	204	5	210	2	1	0	15	0	5	0	0	14	0	0	23	11
Os01g14880	Hypothetical protein	0	813	361	2	0	0	0	0	0	0	0	0	0	125	0	0
Os01g14940	Pectinesterase inhibitor	0	0	0	8	4,562	2,223	183	0	0	0	0	0	0	0	33	894
Os01g15610	Unknown protein	25	40	27	146	3,619	250	9	0	0	0	0	1	0	0	0	0
Os01g15830	Peroxidase	408	1	175	0	0	0	0	0	0	0	0	1	0	0	0	0
Os01g15970	Unknown protein	82	179	4	4	0	0	0	8	8	5	0	0	0	2	0	0
Os01g22380	Unknown protein	376	3	7	0	0	0	0	0	0	0	0	0	0	0	39	0
Os01g33670	Unknown protein	0	15	93	233	0	52	0	0	0	0	0	0	0	0	7	0
Os01g34920	β-galactosidase	0	6	252	37	0	0	0	0	0	0	0	0	0	0	0	24
Os01g49650	Lipid-transfer protein	2,632	1,850	39	9	0	0	0	0	0	0	0	0	0	1,591	0	0
Os01g53240	RD22-like protein	108	10	732	108	0	0	1	16	0	0	0	0	21	366	0	0
Os01g66700	β-hexosaminidase	730	96	43	4	8	10	2	0	0	0	0	0	0	98	0	12
Os01g68589	Lipid-transfer protein	129	0	41	0	0	0	0	4	0	8	0	0	0	0	16	0
Os02g01190	Unknown protein	80	146	1,747	0	0	0	0	0	0	0	0	0	0	508	0	0
Os02g10520	Protease	2	90	626	19	0	0	0	0	0	0	0	0	0	7	0	0
Os02g12270	Hypothetical protein	0	0	20	261	16	1	0	0	0	0	0	0	0	0	0	0
Os02g22480	Glycosyltransferase	98	129	103	106	45	36	0	0	0	0	0	0	0	0	13	16
Os02g28970	Unknown protein	247	41	2	0	0	0	0	0	0	0	0	0	0	0	0	0
Os02g40440	Proline-rich protein	74	2	291	2	0	0	0	0	0	0	0	0	0	31	3	0
Os02g42310	Serine carboxypeptidase	11	0	285	6	0	0	0	0	15	0	0	0	3	16	6	0
Os02g45530	GMC oxidoreductase	131	7,496	3,672	4	0	0	0	0	0	0	0	0	0	0	0	0
Os02g48110	Heat shock protein	254	293	12	136	90	10	5	10	0	0	19	5	20	0	0	11
Os03g08790	Aspartic proteinase	61	158	1,128	1	0	0	0	33	0	0	0	4	137	123	12	0
Os03g24300	Hypothetical protein	918	77	16	0	0	0	0	0	0	0	0	0	0	263	0	0
Os03g24910	Unknown protein	181	125	2	20	1	0	0	14	0	0	0	1	0	0	4	0
Os03g26430	Aldose 1-epimerase	6	0	272	0	0	0	1	0	0	0	0	0	0	0	0	0
Os03g43790	Unknown protein	7	241	3	0	0	0	0	0	0	0	0	0	0	0	0	0
Os03g47910	Unknown protein	807	2,357	923	3	0	0	0	0	0	0	0	0	0	489	0	0
Os03g48200	Ribosome inactivating protein	106	28	0	0	0	0	0	0	0	0	0	0	0	110	0	0
Os03g48220	Unknown protein	125	179	177	4	0	0	0	0	0	0	0	0	0	173	20	0
Os03g49600	β-glucosidase	1,010	635	171	73	24	39	5	0	0	0	0	0	0	34	25	0
Os03g52160	Unknown protein	280	43	1	0	0	0	0	0	0	0	0	0	0	34	0	0
Os03g53310	Suppressor/enhancer of lin-12	161	271	96	203	201	95	51	0	3	0	0	0	0	0	33	1
Os03g60370	Acid phosphatase	114	6	97	9	2	2	4	0	0	0	0	2	0	0	2	3
Os03g63390	Chemocyanin	3	233	31	3	0	0	0	0	0	0	0	0	0	0	0	0
Os04g33930	Lipid binding protein	0	0	2,114	38	1	0	0	0	0	0	0	0	0	0	0	0
Os04g35140	Protease	1	72	172	2	1	6	0	0	0	0	0	0	0	65	0	0
Os04g39590	Arabinogalactan protein	0	0	2	26	284	44	5	0	0	0	0	0	0	0	0	21
Os04g48400	GMC oxidoreductase	135	603	141	2	0	0	0	0	0	0	0	0	0	551	0	0
Os04g55660	GDSL-lipase	0	26	337	919	25	1	3	0	0	0	0	0	0	0	0	10
Os04g58120	Unknown protein	4,960	243	28	0	0	0	0	0	0	0	0	0	0	165	0	0
Os05g05920	Unknown protein	0	300	48	1	0	0	0	0	0	0	0	0	0	165	0	0
Os05g10210	Glycoprotein	131	14	2	0	0	0	0	0	0	0	0	0	25	190	0	0
Os05g30400	Unknown protein	1,555	1	59	1	0	0	0	0	0	0	0	0	0	43	0	0
Os05g35740	Subtilisin propeptide domain	73	35	1,318	87	27	16	1	58	54	0	0	0	0	2	0	0
Os05g40010	Lipid-transfer protein	5	381	3,165	2,495	15	90	0	0	0	0	0	5	0	0	18	17
Os05g44120	Unknown protein	1,750	1,003	164	8	1	5	0	0	0	0	0	0	0	448	0	0
Os05g44760	Hexokinase	20	55	56	137	524	236	26	0	9	0	0	1	9	0	0	32
Os06g05740	Unknown protein	276	8	31	7	4	0	3	0	28	0	0	1	0	0	0	0
Os06g42310	β-galactosidase	0	1	732	5	0	0	40	0	0	0	0	0	0	0	0	0
Os06g44660	Arabinogalactan protein	0	114	14	557	1,196	21	16	0	0	0	0	0	0	0	12	54
Os06g48020	Peroxidase	8	36	64	224	72	44	0	11	0	0	0	0	0	0	0	11
Os07g23730	Thaumatin-like protein	11	8	27	154	37	1	1	0	0	0	0	0	0	0	0	2
Os07g37850	Unknown protein	143	23	7,997	31	0	0	0	0	0	0	0	0	23	1,410	10	0
Os07g40740	Heparanase-like protein	0	5	102	947	42	0	1	0	0	0	0	0	0	0	0	0
Os07g41650	Pectinesterase	3	196	90	213	10	4	0	0	0	0	0	0	0	111	34	4
Os07g46210	Aspartic acid-rich protein	2	5,127	2,210	26	0	0	0	0	0	0	0	0	0	25	0	0
Os08g02094	Proline-rich protein	332	129	56	83	39	1	0	0	0	0	0	0	0	0	0	0
Os08g10670	Aspartyl protease	223	1	3	0	0	0	0	18	0	0	0	23	0	149	0	0
Os08g27210	Unknown protein	0	118	13	0	0	0	0	0	0	0	0	0	0	0	0	0
Os08g29770	Endoglucanase	0	402	876	1,017	164	63	0	0	16	0	0	0	0	0	0	0
Os08g43290	Lipid-transfer protein	554	6,768	1,261	28	0	0	0	0	0	0	0	0	0	3,537	0	0
Os08g45150	Proline-rich protein	6	1,413	5,527	2,515	1	1	3	0	0	0	0	0	0	256	0	0
Os09g13930	Unknown protein	14	655	6	1	1	2	0	0	0	0	0	0	0	396	0	0
Os09g19930	GMC oxidoreductase	124	75	42	58	2	0	0	0	0	0	0	0	1	89	0	0
Os09g30478	Unknown protein	43	102	78	140	105	113	19	0	0	0	0	0	0	0	0	0
Os09g35700	Lipid-transfer protein	16,153	49,751	13,603	81	1	4	1	0	0	0	0	0	0	708	0	0
Os10g05720	Lipid binding protein	0	79	131	1,325	0	0	0	0	0	0	0	0	0	71	0	0
Os10g36760	Peptidase	12	56	46	103	23	5	1	0	10	0	2	0	0	0	0	0
Os11g33134	Unknown protein	0	1	1	23	182	9	1	0	0	0	0	0	0	0	0	16
Os12g15470	Peptidase	10	33	96	178	13	23	0	0	6	0	1	0	0	0	0	15

Table S4. *Characteristics of rice spikelets and anthers of progressive developmental stages used for the construction of SBS transcriptomes.*

Developing anthers (stages)

		Meiosis	Tetrad	Early vacu	Late vacu	Mitosis	Mature Pollen
spikelet	Length (mm)	2.7±0.3	3.5±0.3	4.9±0.3	5.9±0.2	6.0±0.4	6.1±1.4
	Width (mm)	1.5±0.1	1.7±0.1	2.0±0.1	3.0±0.1	3.3±0.2	3.1±0.3
	Bracket Color	White	Yellowish white	Yellowish white	Light green	Green	Green
anther	Length	0.6±0.1	0.9±0.1	1.1±0.1	1.4±0.1	1.8±0.2	2.1±0.1
	Ratio*	0.29	0.34	0.41	0.42	0.53	0.66
	Color	White	Yellowish white	Yellowish white	Light yellow	Yellow	Yellow

Duration between stages (d)** 1.2 0.84-1.23 1.59-1.85 2.67-3.25 ~2

*, ratio of the longitudinal lengths of anther and spikelet.

** Durations between stages are averaged values from several collections and depend on the weather and positions of the spikelets on the plants.

Table S5. *Primers used for RT-PCR analysis.*

Gene ID	Annotation	Direction	Primer
Os09g35700	Lipid transfer protein	F	GATGGAGATGGTGTGCCAAGG
		R	TGAACGATCAGCAGAGCAAGC
Os08g44840	Acyltransferase	F	TTCGACGGGATGGTCTACCTC
		R	TAGCAAGCAACAAGGAATCCATG
Os04g48210	Cytochrome P450	F	GCTCATCTCCTTCCCGCTGT
		R	TCGTTTCATGCTCCACCGTG
Os05g40010	Lipid transfer protein	F	GTTGCACACAGGAGTTTGAGGT
		R	TTGGTGATTGATCGGACAAGC
Os02g07820	Unknown protein	F	GATGAGCTTTCTTGAGCAGGC
		R	TGACGCAAGTGTAGCTCTCAGAG
Os11g11710	Unknown protein	F	CTCTGCAACACCTGCTGCC
		R	AGGTCTTATCGGCGGTTGATC
Os10g40090	β-expansin	F	ATGATCTCCTGCGGCAACG
		R	GAGCCCTTCTCGACGTGGA
Os05g46530	Pectinesterase inhibitor	F	TGAAGCTGTCGATGAGGAAGG
		R	CGAGATACGCCACCACTTCTG
Os07g26480	Desiccation-associated protein	F	AGCGGCAGCATGGACATCA
		R	TTGGACTTCTTGGGCACGG
Os08g03682	Cytochrome P450	F	CGATCATGGGCTACGACATCC
		R	AGTCGAAGCAGTGGAAGAGCC
Os01g26000	Acyltransferases	F	GCACAGCTTACTGTTGGAGTACGG
		R	GGTTGAGGAAGTCGAAGAAGTCG
Os01g12020	Lipid transfer protein	F	CTCCCCTCCTCCACTAGACCAC
		R	ACTCGATTCCTCACGCTCTCAG
Os01g46950	Lipid transfer protein	F	TCCAGCAAGAGATCCATCAAGC
		R	TCTGCCTCACTGAACAATGGTC
Os08g43290	Lipid transfer protein	F	CACACACTCCCATCACTCCA
		R	TGTTGAAATCCCTCCTTTGG
Os11g37280	Lipid transfer protein	F	GTGCCGCCTCTCTACTCTTGC
		R	CATAGCACGACAGTAGCACGAGC
Os03g50890	Actin1	F	CCTCTTCCAGCCTTCCTTCAT
		R	ACGGCGATAACAGCTCCTCTT