

SUPPLEMENTAL TABLES

**Supplemental Table S1.** Alignment of a whole set of reads (14,326,619 from a replicate of dormant red rice seeds incubated at 30 °C for 8 d), with publicly available genome sequences of *Oryza* species.

Species	Overall read mapping rate	Number of multiple alignments
<i>Oryza sativa ssp japonica</i>	97.5%	1,670,920 (12.0%) have multiple alignments (3202 have >20)
<i>Oryza rufipogon</i>	95.1%	873,313 ( 6.4%) have multiple alignments (0 have >20)
<i>Oryza sativa ssp indica</i>	94.6%	2,097,638 (15.5%) have multiple alignments (204 have >20)
<i>Oryza nivara</i>	93.6%	954,611 ( 7.1%) have multiple alignments (0 have >20)
<i>Oryza barthii</i>	89.8%	1,081,042 ( 8.4%) have multiple alignments (0 have >20)
<i>Oryza glumaepatula</i>	89.0%	657,466 ( 5.2%) have multiple alignments (0 have >20)
<i>Oryza glaberrima</i>	82.1%	1,299,343 (11.0%) have multiple alignments (4 have >20)
<i>Oryza longistaminata</i>	75.9%	833,692 ( 7.7%) have multiple alignments (0 have >20)
<i>Oryza meridionalis</i>	73.3%	961,661 ( 9.2%) have multiple alignments (0 have >20)
<i>Oryza punctata</i>	54.7%	1,129,289 (14.4%) have multiple alignments (9 have >20)
<i>Oryza brachyantha</i>	22.2%	312,783 ( 9.8%) have multiple alignments (0 have >20)

**Supplemental Table S2.** Most abundant mRNAs detected in imbibed caryopses across all six tested conditions. The most relevant GO (gene ontology) terms are shown.

Rank	Gene id.	Description of encoded product	Gene ontology
1	OS07G0206500 <sup>1</sup>	13 kDa prolamin	GO:0045735 nutrient reservoir activity
2	OS01G0762500 <sup>1</sup>	Glutelin type-A 1 (GluA-1)	GO:0045735 nutrient reservoir activity
3	OS07G0206400 <sup>1</sup>	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
4	OS10G0400200 <sup>1</sup>	Glutelin type-A (GluA-2)	GO:0045735 nutrient reservoir activity
5	OS03G0766100 <sup>1</sup>	10 kDa prolamin	GO:0045735 nutrient reservoir activity
6	OS06G0507200 <sup>1</sup>	Prolamin	GO:0045735 nutrient reservoir activity
7	OS08G0104400 <sup>1</sup>	Putative uncharacterized protein	GO:0008150 biological_process GO:0003674 molecular_function
8	OS07G0214300 <sup>1</sup>	Seed allergenic protein RAG2 (albumin)	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
9	OS07G0529800	Protein translation factor SUI1 homolog (eIF-1)	GO:0006413 translational initiation GO:0003743 translation initiation factor activity GO:0006417 regulation of translation
10	OS11G0582400 <sup>1</sup>	Antimicrobial peptide MBP-1 family	GO:0050832 defence response to fungus
11	OS02G0249600 <sup>1</sup>	Glutelin type B-2 (GluB-2)	GO:0045735 nutrient reservoir activity
12	OS05G0499100 <sup>1</sup>	19 kDa globulin (Glb1)	GO:0045735 nutrient reservoir activity
13	OS11G0703900	DnaK-type molecular chaperone hsp70	GO:0006950 response to stress GO:0005524 ATP binding
14	OS02G0453600 <sup>1</sup>	Glutelin (GluC)	GO:0045735 nutrient reservoir activity
15	OS02G0161900	Polyubiquitin 6	GO:0016874 ligase activity
16	OS12G0269200 <sup>1</sup>	Prolamin PPROL 17D	GO:0045735 nutrient reservoir activity
17	OS05G0349800	Embryonic abundant protein 1 (Late Embryogenesis Abundant protein OsEm)	GO:0048700 acquisition of desiccation tolerance in seed GO:0048316 seed development GO:0009737 response to abscisic acid
18	OS03G0793700	Cupin family protein; globulin-like (acts as zinc metalloprotease)	GO:0045735 nutrient reservoir activity
19	OS10G0542100 <sup>1</sup>	Class II metallothionein-like protein 1A	GO:0008270 zinc ion binding
20	OS07G0638300	1-Cys peroxiredoxin A (1Cys-Prx)	GO:0051920 peroxiredoxin activity GO:0016491 oxidoreductase activity
21	OS03G0663750	Not annotated	
22	OS03G0670700	Retrotransposon protein, putative, Ty1-copia subclass	GO:0003676 nucleic acid binding RNA secondary structure unwinding GO:0003690 double-stranded DNA binding GO:0032508 DNA duplex unwinding GO:0003697 single-stranded DNA binding GO:0006406 mRNA export from nucleus GO:0009737 response to abscisic acid GO:0016310 phosphorylation GO:0016301 kinase activity GO:0009507 chloroplast
23	OS04G0589800	OSJNBa0086O06.12 protein	GO:0009790 embryo development
24	OS07G0213800	Allergenic protein	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
25	OS11G0660500	Translationally-controlled tumor protein homolog (TCTP)	GO:0040014 regulation of multicellular organism growth GO:0001558 regulation of cell growth GO:0048768 root hair cell tip growth GO:0009791 post-embryonic development GO:0007346 regulation of mitotic cell cycle GO:0008283 cell proliferation GO:0010252 auxin homeostasis GO:0009579 thylakoid GO:0009507 chloroplast
26	OS05G0542500	Late embryogenesis abundant protein, group 3 (putative dehydrin OsLEA3-1)	
27	OS07G0214600 <sup>1</sup>	Allergen RA16	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
28	OS01G0256500	Zinc inducible protein-like	GO:0006950 response to stress
29	OS11G0454300	Water stress-inducible protein Rab21 (OsRab16A)	GO:0009415 response to water GO:0006950 response to stress
30	OS07G0215500 <sup>1</sup>	Seed allergenic protein RA5	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
31	OS05G0140800	Glucose and ribitol dehydrogenase homolog	GO:0016491 oxidoreductase activity
32	OS04G0510900 <sup>1</sup>	Plant seed peroxygenase	GO:0071614 linoleic acid epoxygenase activity GO:0034389 lipid particle organization GO:0031407 oxylipin metabolic process GO:0004392 heme oxygenase (decyclizing) activity GO:0031969 chloroplast membrane GO:0009737 response to abscisic acid GO:0016165 linoleate 13S-lipoxygenase activity GO:0031408 oxylipin biosynthetic process
33	OS01G0705200	WSI18 protein induced by water stress	
34	OS01G0905800	Fructose-bisphosphate aldolase	GO:0004332 fructose-bisphosphate aldolase activity
35	OS01G0124401 <sup>1</sup>	Bowman-Birk type bran trypsin inhibitor	GO:0004867 serine-type endopeptidase inhibitor activity
36	OS03G0427300 <sup>1</sup>	Glutelin type-A 3 (GluA-3)	GO:0045735 nutrient reservoir activity
37	OS11G0211800 <sup>1</sup>		GO:0008200 ion channel inhibitor activity
38	OS02G0586900	Putative uncharacterized protein	
39	OS02G0249000 <sup>1</sup>	Glutelin C / B-2-type (GluD-1)	GO:0045735 nutrient reservoir activity
40	OS05G0569500	Putative embryo-specific protein Ose731	GO:0009737 response to abscisic acid
41	OS06G0612800	Zinc finger A20 and AN1 domain-containing stress-associated protein 8	GO:0003677 DNA binding
42	OS05G0489600	ADP-ribosylation factor 2	GO:0007264 small GTPase mediated signal transduction GO:0005525 GTP binding GO:0006471 protein ADP-ribosylation
43	OS12G0464400	Oxidoreductase, short chain dehydrogenase/reductase family protein	GO:0016491 oxidoreductase activity

<sup>1</sup> Genes that contain the AAATAA motif in their 3' UTR sequence.

**Supplemental Table S3.** Most intensely expressed genes detected in imbibed caryopses (first 12 genes for each condition).

Condition	Incubation temperature (°C)	Time of incubation	Most expressed transcripts		
			Gene id.	Description (short)	Gene ontology (short)
Dormant	30	8 hours	OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS10G0400200	Glutelin type-A 2	GO:0045735 nutrient reservoir activity
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS03G0766100	10 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS06G0507200	Prolamin	GO:0045735 nutrient reservoir activity
			OS07G0214300	Seed allergenic protein RAG2	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
			OS02G0249600	Glutelin type-B 2	GO:0045735 nutrient reservoir activity
			OS11G0582400	Embryo-specific protein	GO:0050832 defense response to fungus
			OS02G0453600	Glutelin	GO:0045735 nutrient reservoir activity
			OS05G0499100	19 kDa globulin	GO:0045735 nutrient reservoir activity
			OS03G0197300	protein	GO:0045735 nutrient reservoir activity
		8 days	OS02G0161900	Polyubiquitin 6	GO:0016874 ligase activity GO:0005737 cytoplasm
			OS11G0703900	DnaK-type molecular chaperone hsp70-rice; Heat shock cognate 70 kDa protein	GO:0006950 response to stress GO:0000166 nucleotide binding GO:0005524 ATP binding
			OS02G0586900	Putative uncharacterized protein	
			OS08G0104400	Putative uncharacterized protein	GO:0008150 biological_process GO:0003674 molecular_function
			OS07G0529800	Protein translation factor SUI1 homolog	GO:0006413 translational initiation GO:0003743 translation initiation factor activity GO:0006417 regulation of translation
			OS11G0660500	Translationally-controlled tumor protein homolog	GO:0040014 regulation of multicellular organism growth GO:0001558 regulation of cell growth GO:0009791 post-embryonic development GO:0007346 regulation of mitotic cell cycle GO:0008283 cell proliferation GO:0009790 embryo development GO:0048364 root development GO:0010252 auxin homeostasis GO:0009579 thylakoid GO:0048046 apoplast GO:0009507 chloroplast GO:0005886 plasma membrane GO:0005634 nucleus GO:0005737 cytoplasm
			OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS03G0670700	Retrotransposon protein, putative, Ty1-copia subclass	GO:0003676 nucleic acid binding GO:0000166 nucleotide binding GO:0010501 RNA secondary structure unwinding GO:0003690 double-stranded DNA binding GO:0032508 DNA duplex unwinding GO:0003697 single-stranded DNA binding GO:0006406 mRNA export from nucleus GO:0009737 response to abscisic acid GO:0005730 nucleolus GO:0005618 cell wall GO:0005777 peroxisome GO:0016310 phosphorylation GO:0016301 kinase activity GO:0007623 circadian rhythm GO:0009507 chloroplast GO:0005886 plasma membrane GO:0005737 cytoplasm GO:0005634 nucleus
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS02G0465900	protein; Putative OsCTTP	GO:0010288 response to lead ion
			OS01G0256500	Zinc inducible protein	GO:0006950 response to stress
	10	8 hours	OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS10G0400200	Glutelin type-A 2	GO:0045735 nutrient reservoir activity
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS03G0766100	10 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS06G0507200	prolamin	GO:0045735 nutrient reservoir activity
			OS11G0582400	Embryo-specific protein	GO:0050832 defense response to fungus
			OS07G0214300	Seed allergenic protein RAG2	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
			OS05G0499100	19 kDa globulin	GO:0045735 nutrient reservoir activity
			OS02G0249600	Glutelin type-B 2	GO:0045735 nutrient reservoir activity
			OS03G0793700	Cupin family protein, expressed; Globulin protein	GO:0045735 nutrient reservoir activity
			OS02G0453600	Glutelin	GO:0045735 nutrient reservoir activity
		8 days	OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS10G0400200	Glutelin type-A 2	GO:0045735 nutrient reservoir activity
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS03G0766100	10 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS06G0507200	prolamin	GO:0045735 nutrient reservoir activity
			OS07G0214300	Seed allergenic protein RAG2	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
			OS05G0349800	Embryonic abundant protein 1	GO:0048700 acquisition of desiccation tolerance in seed GO:0048316 seed development GO:0009737 response to abscisic acid
			OS05G0499100	19 kDa globulin	GO:0045735 nutrient reservoir activity
			OS02G0249600	Glutelin type-B 2	GO:0045735 nutrient reservoir activity
			OS03G0663750		
			OS02G0453600	Glutelin	GO:0045735 nutrient reservoir activity
Nondormant	30	8 hours	OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS10G0400200	Glutelin type-A 2	GO:0045735 nutrient reservoir activity
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS03G0766100	10 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS07G0214300	Seed allergenic protein RAG2	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
			OS06G0507200	prolamin	GO:0045735 nutrient reservoir activity
			OS07G0529800	Protein translation factor SUI1 homolog	GO:0006413 translational initiation GO:0003743 translation initiation factor activity GO:0006417 regulation of translation
			OS06G0681400	Polyubiquitin	GO:0016874 ligase activity GO:0005737 cytoplasm
			OS05G0499100	19 kDa globulin	GO:0045735 nutrient reservoir activity
			OS02G0161900	Polyubiquitin 6	GO:0016874 ligase activity GO:0005737 cytoplasm
			OS08G0104400	uncharacterized protein	GO:0008150 biological_process GO:0003674 molecular_function
	10	8 days	OS07G0206500	13 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS01G0762500	Glutelin type-A 1	GO:0045735 nutrient reservoir activity
			OS08G0104400	protein	GO:0008150 biological_process GO:0003674 molecular_function
			OS07G0206400	13 kDa prolamin C	GO:0045735 nutrient reservoir activity
			OS10G0400200	Glutelin type-A 2	GO:0045735 nutrient reservoir activity
			OS07G0214300	Seed allergenic protein RAG2	GO:0016068 type I hypersensitivity GO:0005615 extracellular space GO:0004867 serine-type endopeptidase inhibitor activity
			OS11G0582400	Embryo-specific protein	GO:0050832 defense response to fungus
			OS03G0766100	10 kDa prolamin	GO:0045735 nutrient reservoir activity
			OS06G0507200	prolamin	GO:0045735 nutrient reservoir activity
			OS07G0529800	Protein translation factor SUI1 homolog	GO:0006413 translational initiation GO:0003743 translation initiation factor activity GO:0006417 regulation of translation
			OS03G0793700	Cupin family protein; Globulin	GO:0045735 nutrient reservoir activity
			OS05G0349800	Embryonic abundant protein 1	GO:0048700 acquisition of desiccation tolerance in seed GO:0048316 seed development GO:0009737 response to abscisic acid

**Supplemental Table S4.** MapMan “transcription” sub-BINs for D 8 h 30 °C vs ND 8 h 30 °C, Wilcoxon Rank Sum Test with Benjamini and Hochberg correction.

<b>BIN</b>	<b>Name</b>	<b>Elements</b>	<b>P-value</b>
27.3.24	RNA.regulation of transcription.MADS box transcription factor family	11	3.149 E-4
27.3.37	RNA.regulation of transcription.AS2,Lateral Organ Boundaries Gene Family	8	0.002
27.3.6	RNA.regulation of transcription.bHLH,Basic Helix-Loop-Helix family	26	0.016
27.3.3	RNA.regulation of transcription.AP2/EREBP, APETALA2/Ethylene-responsive element binding protein family	33	0.016
27.3.7	RNA.regulation of transcription.C2C2 (Zn) CO-like, Constans-like zinc finger family	13	0.084
27.3.32	RNA.regulation of transcription.WRKY domain transcription factor family	14	0.104
27.3.20	RNA.regulation of transcription.G2-like transcription factor family, GARP	6	0.110
27.3.44	RNA.regulation of transcription.Chromatin Remodeling Factors	6	0.165
27.3.8	RNA.regulation of transcription.C2C2 (Zn) DOF zinc finger family	7	0.173
27.3.22	RNA.regulation of transcription.HB,Homeobox transcription factor family	14	0.260
27.3.63	RNA.regulation of transcription.PHD finger transcription factor	3	0.366
27.3.64	RNA.regulation of transcription.PHOR1	2	0.438
27.3.40	RNA.regulation of transcription.Aux/IAA family	6	0.538
27.3.60	RNA.regulation of transcription.NIN-like bZIP-related family	2	0.538
27.3.4	RNA.regulation of transcription.ARF, Auxin Response Factor family	6	0.581
27.3.69	RNA.regulation of transcription.SET-domain transcriptional regulator family	4	0.584
27.3.17	RNA.regulation of transcription.CPP (Zn), CPP1-related transcription factor family	2	0.616
28.1.3	DNA.synthesis/chromatin structure.histone	25	0.632
27.3.11	RNA.regulation of transcription.C2H2 zinc finger family	13	0.649
27.3.65	RNA.regulation of transcription.Polycomb Group (PcG)	2	0.649
27.3.39	RNA.regulation of transcription.AtSR Transcription Factor family	3	0.649
27.3.67	RNA.regulation of transcription.putative transcription regulator	22	0.649
27.3.16	RNA.regulation of transcription.CCAAT box binding factor family, HAP5	3	0.764
27.3.14	RNA.regulation of transcription.CCAAT box binding factor family, HAP2	3	0.764
27.3.36	RNA.regulation of transcription.Argonaute	1	0.764
27.3.5	RNA.regulation of transcription.ARR	1	0.767
27.3.9	RNA.regulation of transcription.C2C2 (Zn) GATA transcription factor family	2	0.767
27.3.49	RNA.regulation of transcription.GeBP like	2	0.780
27.3.57	RNA.regulation of transcription.JUMONJI family	4	0.782
27.3.59	RNA.regulation of transcription.Methyl binding domain proteins	1	0.791
27.3.30	RNA.regulation of transcription.Trihelix, Triple-Helix transcription factor family	2	0.799
27.3.35	RNA.regulation of transcription.bZIP transcription factor family	11	0.803
27.1.20	RNA.processing.degradation dicer	1	0.837
27.3.25	RNA.regulation of transcription.MYB domain transcription factor family	24	0.864
27.3.48	RNA.regulation of transcription.FHA transcription factor	1	0.866
27.3.10	RNA.regulation of transcription.C2C2 (Zn) YABBY family	3	0.906
27.3.71	RNA.regulation of transcription.SNF7	2	0.906
27.3.47	RNA.regulation of transcription.ELF3	1	0.910
27.3.19	RNA.regulation of transcription.EIN3-like (EIL) transcription factor family	2	0.910
27.3.50	RNA.regulation of transcription.General Transcription	3	0.941
27.3.1	RNA.regulation of transcription.ABI3/VP1-related B3-domain-containing transcription factor family	2	0.941
27.3.99	RNA.regulation of transcription.unclassified	37	0.944
27.3.52	RNA.regulation of transcription.Global transcription factor group	1	0.944
27.3.55	RNA.regulation of transcription.HDA	3	0.944
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	6	0.944
27.3.70	RNA.regulation of transcription.Silencing Group	1	0.944
27.3.26	RNA.regulation of transcription.MYB-related transcription factor family	4	0.944
27.3.27	RNA.regulation of transcription.NAC domain transcription factor family	2	0.946
17.3.2.2	hormone metabolism.brassinosteroid.signal transduction.BZR	1	0.950
27.3.21	RNA.regulation of transcription.GRAS transcription factor family	3	0.971
27.3.51	RNA.regulation of transcription.General Transcription, TBP-binding protein	1	0.983
27.3.12	RNA.regulation of transcription.C3H zinc finger family	6	0.988

**Supplemental Table S5. Primers used in this study for qPCR.**

<b>Gene</b>	<b>RAP ID</b>	<b>Primers sequences 5' to 3'</b>
<i>EXPA4</i>	Os05g0477600	CACTGCCAAGCTCCGCTTCAA TGCTGGTGATGGTGTCTAAACG
<i>SAU31</i> (Jain et al., 2006)	Os08g0118500	CCACCACTAGCTCGCTGTTA CACAAAAATCCGAGCCGTCA
<i>OPR</i>	Os06g0216300	TTCGATCGAGAAGAACCAAAGC CCACTTTCGCCGGTGCGTG
<i>OsTOR</i>	Os05g0235300	ATATCAGACGCCGTGCCATT ATGAGTACCAACCTGCACCG
<i>OsSAP11</i>	Os08g0504700	TCCCAAAGCAAAGCGAACC CGCCATGATCGAATCCGAGA
<i>ABI4</i> (Wang et al., 2015)	Os05g0351200	ACCCCTGGTTCGATCTCTTC AGCTGGAACGCCAAGCTAAG
<i>Edf</i> (Wang et al., 2016)	Os08g0366100	TCCGAACCAGCAGATCATCG GCATGGTATCAAAAGACCCAGC