

**Supplemental Table 3** Gene Ontology classification of differentially expressed genes (DEGs) in *M. oryzae* total RNA populations (FDR  $\leq$  5% and fold change  $\geq$  2) were included. AgriGO categories were used for transcripts and a  $p \leq 0.05$  and are presented in bold. The first number in each column header represents the number of genes in the gene list, while the number below in parentheses represents the number of probe sets in this list. The number of genes with the corresponding annotation in this genome, GO\_acc is the Gene Ontology accession number.

GO_acc	Term	bgitem	Induced	
			Poly	Total
			1471 (1141)	1231 (985)
GO:0005737	cytoplasm	5538	<b>465</b>	<b>429</b>
GO:0044444	cytoplasmic part	4920	395	<b>366</b>
GO:0003824	catalytic activity	3024	<b>262</b>	219
GO:0044267	cellular protein metabolic process	599	53	<b>54</b>
GO:0005198	structural molecule activity	433	<b>61</b>	<b>43</b>
GO:0003735	structural constituent of ribosome	338	<b>50</b>	27
GO:0005840	ribosome	86	<b>14</b>	<b>15</b>
GO:0006412	translation	126	12	<b>16</b>
GO:0004872	receptor activity	59	6	<b>8</b>
GO:0005506	iron ion binding	200	<b>31</b>	<b>20</b>
GO:0020037	heme binding	92	<b>21</b>	<b>14</b>
GO:0016740	transferase activity	1239	<b>117</b>	<b>107</b>
GO:0000287	magnesium ion binding	32	0	0
GO:0016757	transferase activity, transferring glycosyl groups	136	13	10
GO:0016758	transferase activity, transferring hexosyl groups	100	10	7
GO:0016762	xyloglucan:xyloglucosyl transferase activity	21	0	0
GO:0016772	transferase activity, transferring phosphorus-containing groups	668	60	<b>60</b>
GO:0016301	kinase activity	552	<b>58</b>	<b>58</b>
GO:0004672	protein kinase activity	321	<b>38</b>	<b>39</b>
GO:0016773	phosphotransferase activity, alcohol group as acceptor	369	<b>40</b>	<b>41</b>
GO:0006468	protein amino acid phosphorylation	132	15	<b>14</b>
GO:0006952	defense response	60	<b>12</b>	<b>11</b>
GO:0006519	cellular amino acid and derivative metabolic process	251	<b>40</b>	<b>34</b>
GO:0042180	cellular ketone metabolic process	151	<b>21</b>	14
GO:0019748	secondary metabolic process	73	<b>13</b>	<b>12</b>
GO:0009308	amine metabolic process	63	<b>11</b>	<b>9</b>
GO:0034641	cellular nitrogen compound metabolic process	61	<b>12</b>	<b>11</b>
GO:0044271	cellular nitrogen compound biosynthetic process	53	5	4
GO:0006725	cellular aromatic compound metabolic process	30	<b>7</b>	<b>7</b>
GO:0008171	O-methyltransferase activity	21	<b>5</b>	3
GO:0016835	carbon-oxygen lyase activity	14	<b>5</b>	3

GO:0006810	transport	468	<b>48</b>	40
GO:0015031	protein transport	95	<b>18</b>	<b>12</b>
GO:0051641	cellular localization	69	<b>17</b>	<b>10</b>
GO:0046907	intracellular transport	52	<b>14</b>	<b>9</b>
GO:0022857	transmembrane transporter activity	99	10	<b>13</b>
GO:0015833	peptide transport	37	4	<b>6</b>
GO:0015291	secondary active transmembrane transporter activity	29	2	<b>5</b>
GO:0031982	vesicle	1727	<b>200</b>	<b>193</b>
GO:0044425	membrane part	318	31	<b>40</b>
GO:0031224	intrinsic to membrane	246	<b>27</b>	<b>35</b>
GO:0016192	vesicle-mediated transport	37	<b>7</b>	4
GO:0016020	membrane	1509	120	111
GO:0050896	response to stimulus	568	36	31
GO:0006950	response to stress	342	25	22
GO:0009628	response to abiotic stimulus	190	10	6
GO:0007275	multicellular organismal development	128	4	2
GO:0009719	response to endogenous stimulus	119	5	6
GO:0009733	response to auxin stimulus	32	0	0
GO:0009790	embryonic development	48	0	0
GO:0045735	nutrient reservoir activity	44	1	0
GO:0043226	organelle	5561	410	377
GO:0009536	plastid	1921	109	96
GO:0044422	organelle part	358	16	14
GO:0009507	chloroplast	164	2	0
GO:0031090	organelle membrane	128	5	5
GO:0009579	thylakoid	115	2	0
GO:0044435	plastid part	103	1	0
GO:0042651	thylakoid membrane	64	0	0
GO:0055035	plastid thylakoid membrane	59	0	0
GO:0015979	photosynthesis	31	0	0

*fla6* plants at 32 HAI. DEGs identified in the polysomal considered significant if represented by 5 or more  
resents the total number of probe sets meeting these criteria  
st with AgriGO annotation(s). Bgitem refers to total  
ccession, Poly is Polyribosomal RNA, and Total is Total

Repressed	
Poly	Total
1385 (927)	897 (582)
370	215
<b>347</b>	195
182	132
26	14
11	2
10	1
0	0
1	3
5	3
13	8
6	0
77	59
<b>5</b>	2
<b>18</b>	<b>18</b>
<b>14</b>	<b>15</b>
<b>6</b>	<b>8</b>
35	25
32	23
14	11
7	14
11	4
2	2
14	10
8	7
4	2
5	2
<b>8</b>	<b>6</b>
6	<b>6</b>
0	0
0	1
0	0

16	8
0	0
0	0
0	0
4	5
3	1
2	2
103	58
18	14
17	13
0	0
<b>127</b>	67
43	<b>39</b>
24	<b>21</b>
<b>19</b>	<b>14</b>
11	<b>10</b>
<b>14</b>	<b>15</b>
<b>5</b>	<b>6</b>
6	7
<b>6</b>	0
<b>387</b>	223
<b>177</b>	<b>99</b>
<b>34</b>	18
<b>27</b>	<b>12</b>
<b>21</b>	8
<b>30</b>	<b>11</b>
<b>19</b>	<b>8</b>
<b>18</b>	<b>6</b>
<b>16</b>	5
<b>10</b>	<b>6</b>