

Table S3. Significantly differentially expressed genes.

| Gene ID | | | | | description |
|--------------|---------------------|-------------------|------------------------|-------------------|---------------------------|
| a | FPKM _{mGA} | FPKM _m | FPKM _{wt} | FPKM _m | |
| OS01G0256500 | 111601.50 | 291251.10 | 207709.36 | 294198. | LEA-5 |
| OS03G0159600 | 1819.93 | 8177.40 | 10056.83 | 8247.76 | Seed maturation protein |
| OS03G0168100 | 2564.30 | 7673.76 | 9692.15 | 7749.36 | LEA-3 |
| OS03G0197300 | 14451.37 | 52231.60 | 50474.80 | 52702.8 | Cupin 1 |
| OS03G0663800 | 187.39 | 1862.15 | 747.42 | 1879.23 | Cupin 1 |
| OS03G0747400 | 308.49 | 2190.61 | 1208.32 | 2209.72 | Seed maturation protein |
| OS03G0747500 | 307.35 | 1510.17 | 809.24 | 1523.56 | Seed maturation protein |
| OS03G0793700 | 3811.01 | 38233.88 | 15852.14 | 38559.8 | Cupin 1 |
| OS04G0589800 | 5021.79 | 18148.51 | 15282.35 | 18317.9 | LEA-25 |
| OS08G0127900 | 3626.92 | 16969.55 | 7848.61 | 17121.9 | 11-S seed storage protein |
| OS12G0626500 | 103.30 | 1166.20 | 736.95 | 1175.43 | Seed maturation protein |
| OS03G0342900 | 770.47 | 2671.60 | 1902.64 | 2697.52 | Dormancy associated |
| OS03G0607200 | 480.89 | 2027.50 | 1041.83 | 2048.19 | GA regulated protein |
| OS11G0671000 | 485.25 | 2198.98 | 995.56 | 2221.54 | Dormancy associated |
| OS02G0186200 | 15.84 | 56.75 | 16.80 | 57.26 | Cytochrome P450 |
| OS03G0856700 | 1121.73 | 5239.61 | 2617.93 | 5298.03 | GA20ox |
| OS06G0562200 | 72.99 | 347.76 | 153.49 | 350.82 | PYR/PYL |
| OS10G0564500 | 179.77 | 740.14 | 455.90 | 746.66 | SnRK2 |
| OS06G0612800 | 8783.12 | 28685.08 | 17515.81 | 28950.2 | Zinc finger |
| OS01G0702500 | 181.92 | 2957.40 | 2253.26 | 2980.62 | Dehydrin |
| OS01G0762500 | 1391.53 | 2157.24 | 756.29 | 2182.47 | 11-S seed storage protein |
| OS02G0242600 | 31.30 | 91.69 | 6.86 | 92.48 | 11-S seed storage protein |
| OS02G0249000 | 141.35 | 192.49 | 62.89 | 194.64 | 11-S seed storage protein |
| OS02G0249600 | 1000.83 | 1676.17 | 347.41 | 1693.82 | 11-S seed storage protein |
| OS03G0427300 | 290.45 | 779.86 | 187.30 | 787.33 | 11-S seed storage protein |
| OS10G0400200 | 937.97 | 1408.66 | 548.97 | 1424.94 | 11-S seed storage protein |
| OS02G0453600 | 331.55 | 437.83 | 79.18 | 443.20 | Cupin 1 |
| b | FPKM _{wt} | FPKM _m | log ₂ Ratio | pval | |
| OS01G0762500 | 756.29 | 2182.47 | -1.52 | 5.67E-05 | 11-S seed storage protein |
| OS02G0242600 | 6.86 | 92.48 | -3.75 | 1.54E-05 | 11-S seed storage protein |
| OS02G0249000 | 62.89 | 194.64 | -1.62 | 7.82E-05 | 11-S seed storage protein |
| OS02G0249600 | 347.41 | 1693.82 | -2.28 | 2.14E-09 | 11-S seed storage protein |
| OS03G0427300 | 187.30 | 787.33 | -2.07 | 2.88E-07 | 11-S seed storage protein |
| OS10G0400200 | 548.97 | 1424.94 | -1.37 | 2.69E-04 | 11-S seed storage protein |
| OS02G0453600 | 79.18 | 443.20 | -2.48 | 1.30E-08 | Cupin 1 |
| OS05G0328800 | 12.69 | 53.75 | -2.08 | 1.36E-04 | alpha-amylase inhibitor |
| OS05G0331532 | 6.38 | 31.65 | -2.30 | 1.38E-04 | alpha-amylase inhibitor |
| OS07G0219400 | 80.96 | 237.74 | -1.55 | 1.58E-04 | Bifunctional inhibitor |
| OS06G0569900 | 0 | 12.16 | Infinite | 1.61E-05 | Cytochrome P450 |
| c | FPKM _{wt} | FPKM _m | log ₂ Ratio | pval | |

| | | | | | |
|--------------|---------------------|-------------------|------------------------|----------|---------------------------|
| OS08G0338000 | 491.89 | 136.87 | 1.84 | 4.20E-06 | Myb/SANT-like domain |
| OS11G0492800 | 9.28 | 0 | Infinite | 2.79E-04 | Alpha/Beta hydrolase fold |
| OS11G0620300 | 314.16 | 23.71 | 3.72 | 2.34E-16 | Bifunctional inhibitor |
| OS06G0204100 | 164.95 | 4.76 | 5.11 | 4.38E-20 | Cytochrome P450 |
| OS07G0217600 | 13.53 | 0.43 | 4.96 | 5.30E-05 | Cytochrome P450 |
| OS09G0325700 | 953.36 | 302.30 | 1.65 | 1.87E-05 | PP2C |
| d | FPKM _{mGA} | FPKM _m | log ₂ Ratio | pval | |
| OS01G0256500 | 111601.50 | 291251.10 | -1.38 | 4.03E-04 | LEA-5 |
| OS03G0159600 | 1819.93 | 8177.40 | -2.16 | 6.31E-04 | Seed maturation protein |
| OS03G0168100 | 2564.30 | 7673.76 | -1.58 | 1.90E-04 | LEA-3 |
| OS03G0197300 | 14451.37 | 52231.60 | -1.85 | 4.15E-04 | Cupin 1 |
| OS03G0663800 | 187.39 | 1862.15 | -3.31 | 1.78E-08 | Cupin 1 |
| OS03G0747400 | 308.49 | 2190.61 | -2.82 | 3.31E-05 | Seed maturation protein |
| OS03G0747500 | 307.35 | 1510.17 | -2.29 | 4.85E-04 | Seed maturation protein |
| OS03G0793700 | 3811.01 | 38233.88 | -3.32 | 1.13E-05 | Cupin 1 |
| OS04G0589800 | 5021.79 | 18148.51 | -1.85 | 1.44E-04 | LEA-25 |
| OS08G0127900 | 3626.92 | 16969.55 | -2.22 | 4.29E-05 | 11-S seed storage protein |
| OS12G0626500 | 103.30 | 1166.20 | -3.49 | 2.38E-04 | Seed maturation protein |
| OS03G0342900 | 770.47 | 2671.60 | -1.79 | 1.28E-05 | Dormancy associated |
| OS03G0607200 | 480.89 | 2027.50 | -2.07 | 7.32E-07 | GA regulated protein |
| OS11G0671000 | 485.25 | 2198.98 | -2.18 | 8.20E-08 | Dormancy associated |
| OS02G0186200 | 15.84 | 56.75 | -1.84 | 3.62E-04 | Cytochrome P450 |
| OS03G0856700 | 1121.73 | 5239.61 | -2.22 | 3.26E-07 | GA20ox |
| OS06G0562200 | 72.99 | 347.76 | -2.25 | 2.39E-04 | PYR/PYL |
| OS10G0564500 | 179.77 | 740.14 | -2.04 | 3.05E-04 | SnRK2 |
| OS01G0702500 | 181.92 | 2957.40 | -4.02 | 1.20E-04 | Dehydrin |
| OS06G0612800 | 8783.12 | 28685.08 | -1.70 | 1.59E-04 | Zinc finger |
| e | FPKM _{mGA} | FPKM _m | log ₂ Ratio | pval | |
| OS01G0285300 | 63.76 | 18.57 | 1.77 | 4.69E-04 | SANT/Myb domain |
| OS12G0564100 | 97.47 | 25.19 | 1.95 | 2.67E-05 | SANT/Myb domain |
| OS11G0128500 | 24.32 | 2.12 | 3.51 | 3.24E-06 | SANT/Myb domain |
| OS03G0103100 | 383.49 | 79.17 | 2.27 | 9.22E-05 | lipid transfer protein |
| OS10G0191100 | 41.79 | 7.73 | 2.43 | 1.27E-05 | lipid transfer protein |
| OS10G0349300 | 1005.69 | 258.07 | 1.96 | 1.43E-06 | lipid transfer protein |
| OS10G0349400 | 465.67 | 87.29 | 2.41 | 2.90E-05 | lipid transfer protein |
| OS10G0552200 | 682.63 | 243.06 | 1.48 | 1.55E-04 | lipid transfer protein |
| OS07G0106200 | 961.10 | 330.04 | 1.54 | 8.10E-05 | Sugar transporter |
| OS11G0643800 | 345.80 | 99.82 | 1.79 | 1.95E-05 | Sugar transporter |
| OS08G0475400 | 650.73 | 216.41 | 1.58 | 1.22E-04 | Alpha hydrolase fold-3 |
| OS11G0138900 | 23.04 | 4.23 | 2.44 | 3.58E-04 | Alpha hydrolase fold |
| OS02G0596300 | 150.68 | 43.77 | 1.78 | 5.50E-04 | Cytochrome P450 |
| OS03G0225900 | 90.74 | 19.69 | 2.20 | 4.66E-04 | Cytochrome P450 |
| OS03G0367101 | 57.28 | 7.48 | 2.93 | 2.42E-07 | Cytochrome P450 |
| OS03G0760500 | 45.27 | 9.85 | 2.19 | 4.82E-05 | Cytochrome P450 |

| | | | | | |
|--------------|---------|--------|------|----------|-----------------|
| OS06G0110000 | 271.82 | 84.89 | 1.67 | 1.28E-04 | Cytochrome P450 |
| OS07G0603700 | 77.32 | 23.54 | 1.71 | 2.58E-04 | Cytochrome P450 |
| OS11G0289700 | 1334.61 | 295.90 | 2.17 | 3.74E-07 | Cytochrome P450 |
| OS12G0582700 | 67.86 | 19.84 | 1.77 | 4.91E-04 | Cytochrome P450 |
| OS01G0209700 | 32.74 | 7.49 | 2.12 | 5.58E-04 | GA2ox |

a: Genes have higher expression in mutant compared with both wild-type and mutant treated with GA treatment. b: Genes have higher expression in mutant only than wild-type. c: Genes have higher expression in wild-type compared to mutant. d: Genes have higher expression in mutant only than mutant with GA treatment. e: Genes have higher expression in mutant with GA compared to mutant. Gene IDs with red font were those also detected in proteomic study.