**Table S1.** Genotypes of $T_0$ transformants.

| $T_0$ plant No. | MADS26 | Bsrd1 | ELF3 | ERF922 | $T_0$ plant No. | MADS26 | Bsrd1 | ELF3 | ERF922 |
|---|---|---|---|---|---|---|---|---|---|
| 1 | -14/+1 | 0 | -4/-2 | -1 | 36 | -2/+1 | -3/+3 | -4/-1 | -1/+1 |
| 2 | -1 | +1 | -3/-1 | 0 | 37 | 0 | -1 | 0 | +1/-4 |
| 3 | -18/+1 | -1/+3 | -4 | +1 | 38 | 0 | +1 | 0 | 0 |
| 4 | +1 | +1 | +1 | -22/+1 | 39 | -2 | 0 | -2/0 | 0 |
| 5 | -3/+1 | +2/+3 | -3 | -24/-12 | 40 | -15/-5 | +2 | -2 | -24/-23 |
| 6 | -18/-2 | 0 | -2/+1 | +1 | 41 | -2/+1 | +3 | -2 | -3/+1 |
| 7 | -3/-2 | +2 | -2 | 0 | 42 | -12/+1 | -1/+1 | -4/-3 | -23/+1 |
| 8 | -2/-1 | +2 | -5/+1 | +1 | 43 | -3/+1 | 0 | -1 | +1 |
| 9 | -2 | +1/+2 | -1 | -25/-2 | 44 | 0 | 0 | -1 | -1 |
| 10 | 0 | 0 | -1 | -6/+1 | 45 | 0 | 0 | 0 | +1/-5 |
| 11 | -5/+1 | 0 | -4/-2 | 0 | 46 | -1/+1 | +2 | -2 | 0 |
| 12 | -22/-5 | +1/+3 | -1 | +1 | 47 | -5/+1 | 0/+2 | -4/-1 | +1 |
| 13 | -14/-1 | +1/+3 | -3 | -1/+1 | 48 | 0 | 0 | 0 | -1 |
| 14 | -10/-2 | +3 | -1 | -6/0 | 49 | -2/+1 | +2 | -4/0 | 0 |
| 15 | -2 | +3 | -3 | -28/-8 | 50 | -3/+1 | +3 | -6/-2 | -1 |
| 16 | -8/+1 | +3 | -4/+1 | +1 | 51 | -1 | 0/+2 | 0 | 0 |
| 17 | -5/-1 | +1 | 0 | 0 | 52 | -4/+1 | 0 | -3/0 | -16/0 |
| 18 | +1 | +3 | -2 | +1 | 53 | +1 | +3 | -3/-1 | 0 |
| 19 | -3/+1 | -7/+2 | -2 | -50/0 | 54 | -5/+1 | -13/+2 | -4/-1 | -15/0 |
| 20 | -5/-1 | +1/+3 | 0 | 0 | 55 | -27/-4 | +2 | -2/-1 | -6/0 |
| 21 | -6/-4 | 0 | -1 | -8/0 | 56 | -1 | 0 | -18/-3 | 0 |
| 22 | -3/-2 | +2 | -4 | 0 | 57 | -2/-1 | -6/+3 | -3 | -62 |
| 23 | +1 | +3 | -4 | -7 | 58 | -2 | 0/+2 | -4/-3 | -25/0 |
| 24 | -27/-5 | +3 | 0 | 0 | 59 | -14/-10 | +2 | -3/-1 | -9/0 |
| 25 | -2/-1 | +1/+3 | -1 | -23/+1 | 60 | -13/-3 | -1/+2 | -6/-2 | -1 |
| 26 | -14/-2 | +3 | -2/0 | 0 | 61 | -12/-2 | 0/+2 | -8/-1 | 0 |
| 27 | -5/-2 | +3 | -2 | 0/+1 | 62 | -11/-1 | 0/+2 | -4/0 | -25/0 |
| 28 | +1 | +3 | 0 | -11/+1 | 63 | 0 | -13/+2 | 0 | 0 |
| 29 | -15/-8 | +3 | -2 | -37/-25 | 64 | 0 | 0 | -2 | -1 |
| 30 | -2/+1 | +1 | -51/ | -24/-9 | 65 | -5/+1 | +2 | -4/0 | 0 |
| 31 | -2 | +3 | -1/+1 | 0 | 66 | -18/-8 | +2 | -38/+1 | -3/+1 |
| 32 | -4 | +3 | -3/-1 | -8 | 67 | -3/+1 | -13/+2 | -4/-3 | -22/-1 |
| 33 | -4/-1 | +2 | -4/-2 | -29/0 | 68 | -5/-2 | +3 | -3/-1 | -16/0 |
| 34 | 0 | 0/+2 | -4/-1 | -23/+1 | 69 | +1 | 0/+3 | -1 | 0 |
| 35 | 0 | 0 | 0 | -13/+1 | 70 | -7/-4 | +2/+3 | -4/-3 | -1/0 |
| 71 | -1 | -20 | -3 | -6/0 | 107 | -13/-11 | +2 | -2 | -25 |
| 72 | -7/+2 | -26/+3 | -5/+1 | +1/0 | 108 | -5/-2 | +2/+3 | -3/-1 | 0 |
| 73 | -23/-6 | +2 | -1 | 0/+1 | 109 | -3/-2 | -2/+3 | +1 | -1/+1 |
| 74 | -25/+1 | +1/+2 | -2/0 | -1 | 110 | -4 | 0 | 0 | -3/+1 |
| 75 | 0 | 0 | -1 | 0 | 111 | -40/-2 | +1/+3 | -4/-1 | 0 |
| 76 | -4/-3 | 0/+3 | -3/-1 | 0 | 112 | -2/+1 | 3 | -13/-3 | +1/0 |
| 77 | -4/-2 | +1/+3 | -5 | -6/0 | 113 | -18/-2 | 0 | 0 | -17/+2 |
| 78 | -7/-4 | 0/+3 | -9/-3 | -64/-1 | 114 | -2 | 0/+2 | 0 | 0 |
| 79 | -3/-2 | +3 | -3 | -5/0 | 115 | -21/-1 | +1 | -3/-4 | -8/0 |
| 80 | -2/+1 | +2/+3 | -3 | -35/0 | 116 | -2 | -5/+2 | -6/-2 | 0 |
| 81 | -1/+1 | 0/+2 | -3/+1 | -4/-1 | 117 | -2/0 | +2/+4 | -4 | -1/0 |

| | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|
| 82 | -3/-2 | 0/+3 | -3/0 | 0 | 118 | -2/+1 | +3 | -3/-1 | 0/+1 |
| 83 | -7/+1 | -9/0 | -3 | -1 | 119 | -14/-3 | -18/-15 | -5/-2 | 0 |
| 84 | -5/-1 | 0 | -4/+1 | +2 | 120 | -5/-3 | 0 | -1 | 0 |
| 85 | -2/-1 | -1/+3 | -4/-3 | -2/+1 | 121 | -1 | -6/0 | -115/-3 | -21/0 |
| 86 | -4/-2 | -2/+2 | -5/-4 | 0 | 122 | -1 | +2 | -3 | -4/0 |
| 87 | -10/-1 | 0 | -1 | 0 | 123 | -5/-1 | 0/+2 | -3/-1 | 0 |
| 88 | -4/-2 | +3 | -3 | -1/0 | 124 | 0/+2 | 0 | -3/-1 | -1 |
| 89 | -23/0 | +1/+2 | 0 | 0 | 125 | -9/-5 | +3/+5 | -7/-1 | 0 |
| 90 | -3/-2 | +3 | -5 | 0/+51 | 126 | -9/-5 | +3/+5 | -3/0 | 0 |
| 91 | -2/+1 | 0/+2 | 0 | +1/-1 | 127 | -3/-1 | -4/+2 | +1 | +1 |
| 92 | -2/0 | 0 | 0 | -1 | 128 | -5/-3 | +2/+3 | -2 | 0 |
| 93 | -2/+1 | +2 | -4/-2 | -1/0 | 129 | -1 | +3 | -3/0 | -12/0 |
| 94 | -2/-1 | +2/+3 | -3 | 0 | 130 | -1 | 0 | -1 | -1 |
| 95 | 0 | 0 | 0 | -3/+1 | 131 | -1 | 0 | -1 | -2 |
| 96 | -4/-1 | -1 | -2 | 0 | 132 | -5 | +2 | -5/-3 | -1 |
| 97 | -11/-10 | 0/+3 | -2 | +2/0 | 133 | -3 | +3 | -3 | 0/+1 |
| 98 | -2/-1 | +3 | -3/-1 | +1 | 134 | -1 | +3/+5 | -3/-1 | +1 |
| 99 | -5/-1 | -6/+3 | -5/-4 | -6/0 | 135 | -3/-1 | -7/+3 | -3/-1 | +1 |
| 100 | -10/-3 | 0/+3 | -3/0 | 0 | 136 | -3/+2 | +3 | -2 | +1 |
| 101 | -1/+1 | -3/+2 | -3/-1 | +2/-1 | 137 | -1/+2 | 0/+5 | -1/0 | -9/+1 |
| 102 | +1 | -18/0 | -3/0 | 0 | 138 | 0 | 0 | +1 | +1 |
| 103 | -5/+1 | 0/+3 | -3/-1 | -3/+1 | 139 | 0 | +2 | +1 | +2 |
| 104 | -2/+1 | +3 | -17/-2 | -25/0 | 140 | -1 | +3 | -3/0 | 0 |
| 105 | -1/+1 | 0/+2 | -1 | 0 | 141 | -26/-23 | 0/+2 | -1/+1 | -9 |
| 106 | 0 | -1 | -2 | +5/-1 | 142 | 0/+2 | -4/0 | -4/-3 | -5/+1 |

+, insertion -, deletion, the letter or number followed by represents the bases inserted/deleted or the number of bases inserted/deleted, 0, no base change. Highlighted with yellow-colored background is the $T_0$ transformants selected for screening quadruple mutants.

**Table S2.** Target sequence and PAM sequence (underlined) of target genes.

| Gene | Target sequence and PAM |
|---|---|
| ***OsERF922*** | ACAGAGACACGTCCACGCG **TGG** |
| ***OsBsr-d1*** | GTGGCTGTGCCCAGCGCCCG **CGG** |
| ***OsELF3-2*** | GTGCCGTCCCACCGCTTCAG **CGG** |
| ***OsMads26*** | GGAGCTCTCCATCCTCTGCG **AGG** |

**Table S3.** Primers used in this work.

| Primer name | Primer Sequence |
|---|---|
| Mads26 F | GGAGCTATCGATCATCAAGC |
| Mads26 R | GGCTAGCTAACAACTGAAATGG |
| Bsr-d1 F | CAACGGGGACAGATATGACG |
| Bsr-d1 R | TTCGAGTCACCAGCGGATG |
| ELF3-2 F | ACCTGCGGCCTACGAATCGATCG |
| ELF3-2 R | TTGAATACGCACGCAACGGAAGG |
| ERF922 F | CACCTCTCTCGATCGTCTCAT |
| ERF922 R | CGCTCCCCTGCCTCC |
| Cas9-F | CAAGCAGTCCGGCAAGAC |
| CS9-R | GGACACCTGGGCCTTCTG |

| | |
|---|---|
| CaMV35S-F | CGACAGTGGTCCCAAAGA |
| CaMV35S-R | AAGACGTGGTTGGAACGTCTTC |
| HPT-F | GACATTGGGGAGTTTAGCGAGAG |
| HPT-R | ACGAGGTACCGGACTTCGC |

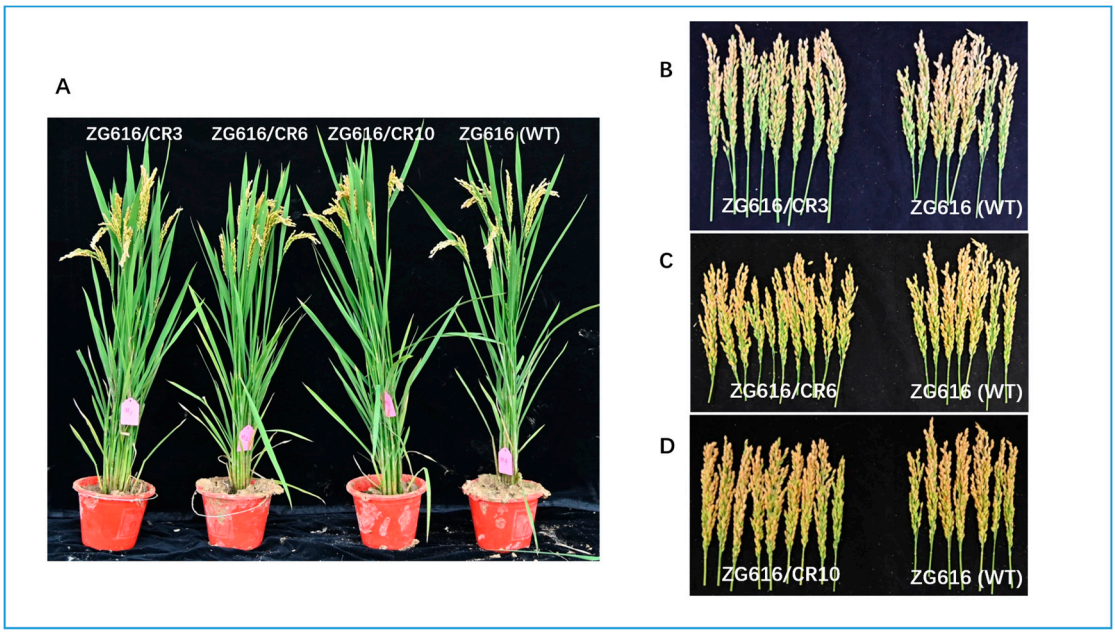
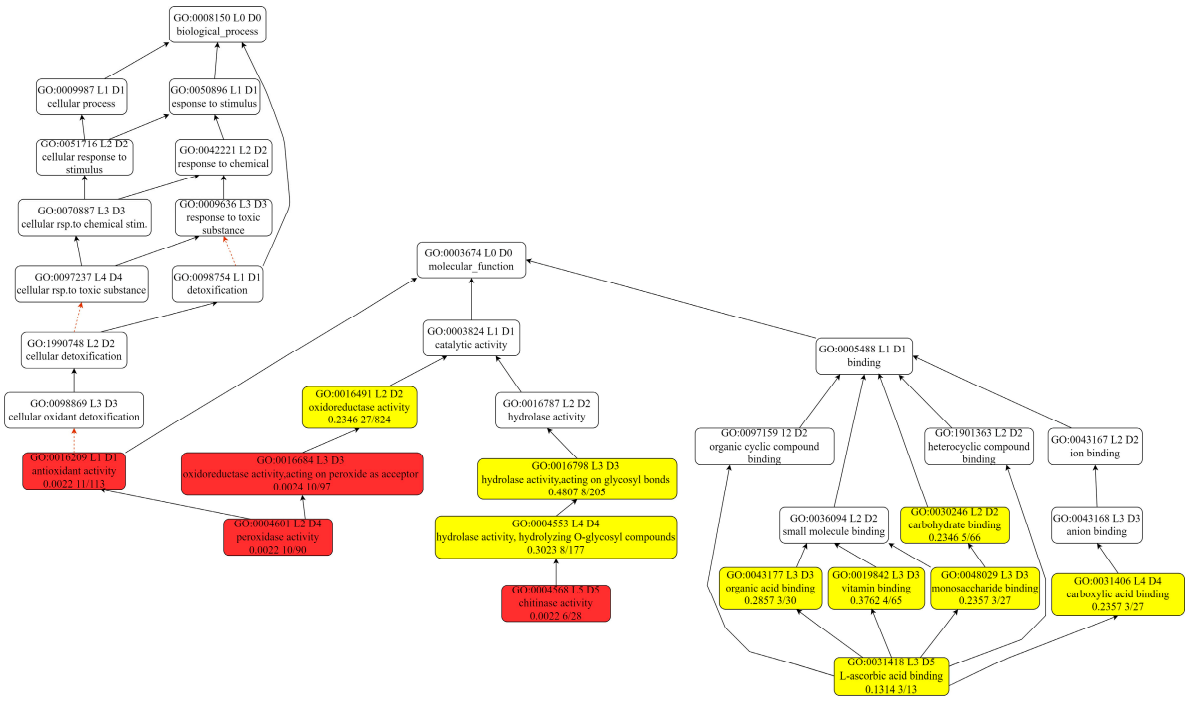
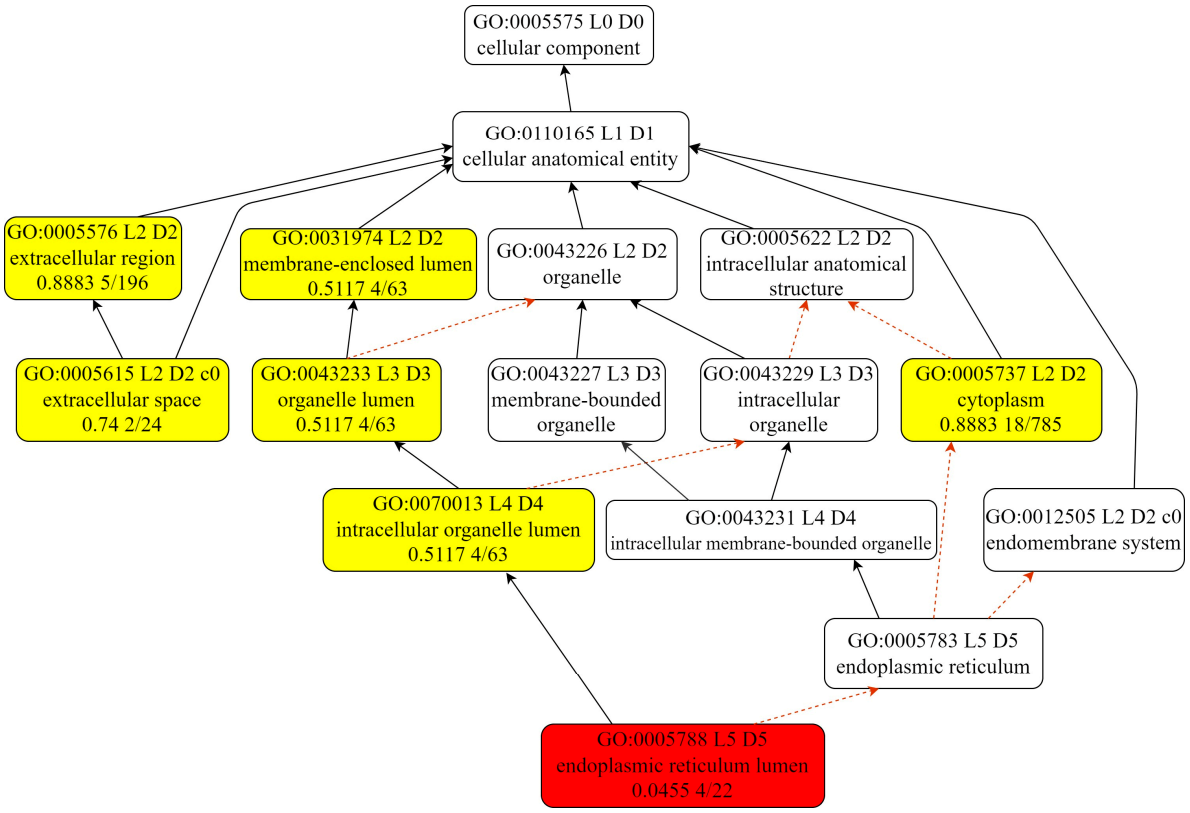


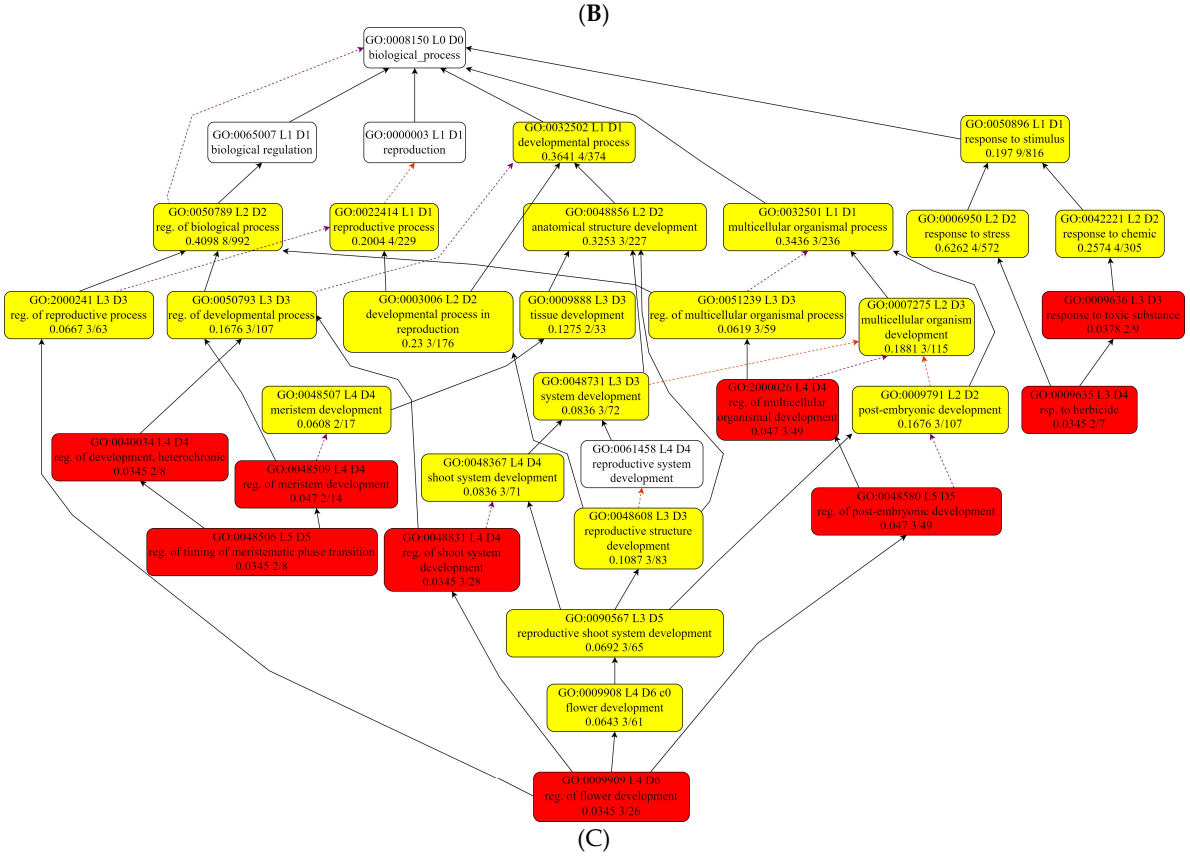

**Figure S1.** Photographs of representative plants of quadruple mutants and the wild type **(A)** at mature stage, and panicles from a single plants of quadruple mutants and the wild type **(B-D)**.



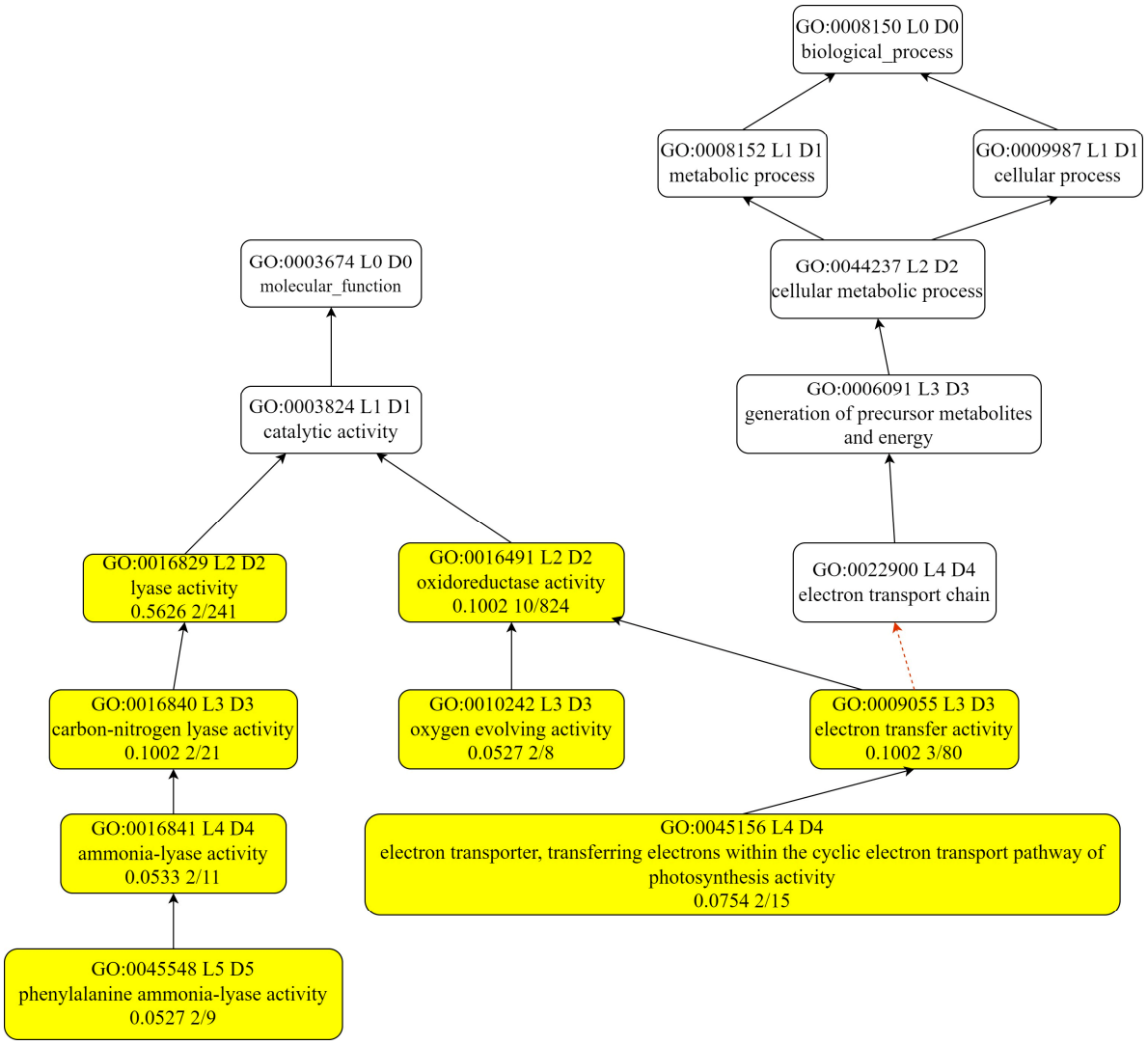

(**A**)


GO:0005575 L0 D0
cellular component
GO:0110165 L1 D1
cellular anatomical entity
GO:0005576 L2 D2
extracellular region
0.8883 5/196
GO:0031974 L2 D2
membrane-enclosed lumen
0.5117 4/63
GO:0043226 L2 D2
organelle
GO:0005622 L2 D2
intracellular anatomical structure
GO:0005615 L2 D2 c0
extracellular space
0.74 2/24
GO:0043233 L3 D3
organelle lumen
0.5117 4/63
GO:0043227 L3 D3
membrane-bounded organelle
GO:0043229 L3 D3
intracellular organelle
GO:0005737 L2 D2
cytoplasm
0.8883 18/785
GO:0070013 L4 D4
intracellular organelle lumen
0.5117 4/63
GO:0043231 L4 D4
intracellular membrane-bounded organelle
GO:0012505 L2 D2 c0
endomembrane system
GO:0005783 L5 D5
endoplasmic reticulum
GO:0005788 L5 D5
endoplasmic reticulum lumen
0.0455 4/22

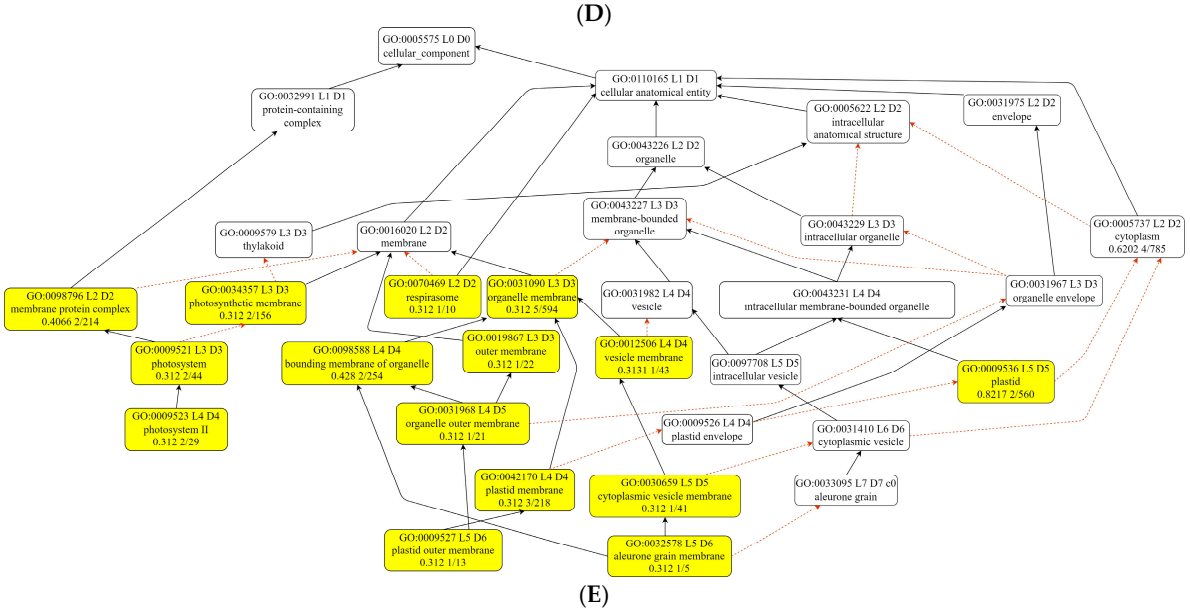
(**B**)


GO:0008150 L0 D0
biological_process
GO:0065007 L1 D1
biological regulation
GO:0000003 L1 D1
reproduction
GO:0032502 L1 D1
developmental process
0.3641 4/374
GO:0050896 L1 D1
response to stimulus
0.197 9/816
GO:0050789 L2 D2
reg. of biological process
0.4098 8/992
GO:0022414 L1 D1
reproductive process
0.2004 4/229
GO:0048856 L2 D2
anatomical structure development
0.3253 3/227
GO:0032501 L1 D1
multicellular organismal process
0.3436 3/236
GO:0006950 L2 D2
response to stress
0.6262 4/572
GO:0042221 L2 D2
response to chemic
0.2574 4/305
GO:2000241 L3 D3
reg. of reproductive process
0.0667 3/63
GO:0050793 L3 D3
reg. of developmental process
0.1676 3/107
GO:0003006 L2 D2
developmental process in reproduction
0.23 3/176
GO:0009888 L3 D3
tissue development
0.1275 2/33
GO:0051239 L3 D3
reg. of multicellular organismal process
0.0619 3/59
GO:0007275 L2 D3
multicellular organism development
0.1881 3/115
GO:0009636 L3 D3
response to toxic substance
0.0378 2/9
GO:0048731 L3 D3
system development
0.0836 3/72
GO:2000026 L4 D4
reg. of multicellular organismal development
0.047 3/49
GO:0009791 L2 D2
post-embryonic development
0.1676 3/107
GO:0009635 L3 D4
rsp. to herbicide
0.0345 2/7
GO:0048507 L4 D4
meristem development
0.0608 2/17
GO:0040034 L4 D4
reg. of development, heterochronic
0.0345 2/8
GO:0048509 L4 D4
reg. of meristem development
0.047 2/14
GO:0048367 L4 D4
shoot system development
0.0836 3/71
GO:0061458 L4 D4
reproductive system development
GO:0048580 L5 D5
reg. of post-embryonic development
0.047 3/49
GO:0048506 L5 D5
reg. of timing of meristematic phase transition
0.0345 2/8
GO:0048831 L4 D4
reg. of shoot system development
0.0345 3/28
GO:0048608 L3 D3
reproductive structure development
0.1087 3/83
GO:0090567 L3 D5
reproductive shoot system development
0.0692 3/65
GO:0009908 L4 D6 c0
flower development
0.0643 3/61
GO:0009909 L4 D6
reg. of flower development
0.0345 3/26

(**C**)




(**D**)




(**E**)

**Figure S2.** Analyses of the differentially expressed genes (DEGs) between quadruple mutant ZG616/CR3 and the wild type ZG616 by RNA-seq. DAG (Directed Acyclic Graph) of Go enrichment analysis of up-regulated DEGs in molecular function **(A)** and cellular component **(B)**. DAG (Directed Acyclic Graph) of Go enrichment analysis of down-regulated DEGs in biological process **(C)**, molecular function **(D)** and

cellular component **(E)**. The darkness level of color represents the enrichment level with red color as the most significant enrichment.