

**Table S1.** Proportion of various types of AS events.

|       | A3SS  | A5SS  | MXE  | RI    | SE   |
|-------|-------|-------|------|-------|------|
| AvsAE | 28.51 | 17.61 | 0.32 | 49.30 | 4.25 |
| EvsAE | 28.56 | 17.58 | 0.36 | 49.68 | 3.81 |
| AvsE  | 28.40 | 17.93 | 0.33 | 49.21 | 4.12 |
| AvsAF | 28.45 | 17.62 | 0.35 | 49.11 | 4.47 |
| FvsAF | 28.48 | 17.95 | 0.34 | 48.72 | 4.51 |
| AvsF  | 28.42 | 17.93 | 0.32 | 48.94 | 4.39 |
| AvsAG | 28.48 | 17.75 | 0.35 | 49.36 | 4.07 |
| GvsAG | 28.70 | 17.79 | 0.35 | 49.17 | 3.99 |
| AvsG  | 28.53 | 17.57 | 0.32 | 49.33 | 4.25 |
| AvsAH | 28.24 | 18.23 | 0.35 | 49.11 | 4.08 |
| HvsAH | 28.46 | 18.44 | 0.34 | 49.05 | 3.71 |
| AvsH  | 28.54 | 17.78 | 0.32 | 49.24 | 4.13 |
| BvsBE | 28.44 | 17.28 | 0.32 | 49.84 | 4.12 |
| EvsBE | 28.52 | 17.78 | 0.33 | 49.49 | 3.88 |
| BvsE  | 28.31 | 16.99 | 0.33 | 50.33 | 4.03 |
| BvsBF | 28.51 | 16.89 | 0.35 | 50.10 | 4.15 |
| FvsBF | 28.53 | 17.76 | 0.32 | 48.89 | 4.50 |
| BvsF  | 28.48 | 17.39 | 0.32 | 49.42 | 4.39 |
| BvsBG | 28.36 | 16.96 | 0.32 | 50.29 | 4.08 |
| GvsBG | 28.69 | 17.60 | 0.32 | 49.42 | 3.96 |
| BvsG  | 28.34 | 17.11 | 0.36 | 50.02 | 4.17 |
| BvsBH | 28.22 | 17.04 | 0.33 | 50.10 | 4.32 |
| HvsBH | 28.70 | 17.76 | 0.32 | 49.39 | 3.83 |
| BvsH  | 28.41 | 17.21 | 0.32 | 49.92 | 4.14 |
| CvsCE | 28.38 | 17.91 | 0.33 | 49.45 | 3.95 |
| EvsCE | 28.39 | 17.65 | 0.37 | 49.57 | 4.04 |
| CvsE  | 28.39 | 17.68 | 0.34 | 49.77 | 3.83 |
| CvsCF | 29.01 | 17.77 | 0.29 | 48.94 | 3.99 |
| FvsCF | 28.84 | 17.54 | 0.32 | 48.86 | 4.44 |
| CvsF  | 28.54 | 18.15 | 0.33 | 48.81 | 4.17 |
| CvsCG | 28.42 | 18.00 | 0.30 | 49.24 | 4.04 |
| GvsCG | 28.49 | 17.89 | 0.32 | 49.24 | 4.06 |
| CvsG  | 28.59 | 17.94 | 0.33 | 49.08 | 4.05 |
| CvsCH | 28.43 | 18.04 | 0.33 | 49.08 | 4.12 |
| HvsCH | 28.54 | 17.76 | 0.32 | 49.45 | 3.93 |
| CvsH  | 28.60 | 17.70 | 0.29 | 49.45 | 3.96 |
| DvsDE | 28.67 | 17.43 | 0.39 | 49.61 | 3.90 |
| EvsDE | 28.55 | 17.09 | 0.40 | 50.00 | 3.96 |
| DvsE  | 28.43 | 17.69 | 0.36 | 49.82 | 3.70 |
| DvsDF | 28.41 | 17.86 | 0.32 | 49.30 | 4.11 |
| FvsDF | 28.46 | 17.96 | 0.28 | 48.77 | 4.52 |

|       | A3SS  | A5SS  | MXE  | RI    | SE   |
|-------|-------|-------|------|-------|------|
| DvsF  | 28.47 | 18.04 | 0.29 | 49.01 | 4.19 |
| DvsDG | 28.39 | 17.74 | 0.32 | 49.55 | 4.00 |
| GvsDG | 28.29 | 17.46 | 0.32 | 49.68 | 4.25 |
| DvsG  | 28.75 | 17.73 | 0.32 | 49.42 | 3.78 |
| DvsDH | 28.41 | 18.06 | 0.31 | 49.23 | 3.99 |
| HvsDH | 28.42 | 18.06 | 0.31 | 49.23 | 3.97 |
| DvsH  | 28.75 | 17.73 | 0.32 | 49.42 | 3.78 |

**Table S2.**Go term classification table of DASGs in different cross combinations.

| GO Term<br>(level1)   | GO Term (level2)                    | GO ID<br>(level1) | Number of Genes |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------|-------------------------------------|-------------------|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                       |                                     |                   | AE              | AF  | AG  | AH  | BE  | BF  | BG  | BH  | CE  | CF  | CG  | CH  | DE  | DF  | DG  | DH  |
| Biological<br>Process | metabolic process                   | GO:0008150        | 154             | 136 | 137 | 159 | 129 | 142 | 92  | 121 | 139 | 147 | 126 | 127 | 110 | 133 | 119 | 114 |
| Biological<br>Process | locomotion                          | GO:0008150        | /               | 1   | 1   | 1   | 2   | 1   | 2   | 1   | 1   | 1   | 2   | /   | /   | 1   | 1   | /   |
| Biological<br>Process | rhythmic process                    | GO:0008150        | 6               | 2   | 5   | 6   | 4   | 4   | 2   | 2   | 5   | 6   | 4   | 2   | 6   | 4   | 4   | 3   |
| Biological<br>Process | cellular process                    | GO:0008150        | 171             | 140 | 142 | 164 | 142 | 152 | 109 | 133 | 149 | 153 | 126 | 128 | 115 | 133 | 124 | 115 |
| Biological<br>Process | multi-organism<br>process           | GO:0008150        | 25              | 23  | 20  | 26  | 22  | 20  | 14  | 22  | 25  | 21  | 19  | 19  | 16  | 24  | 14  | 15  |
| Biological<br>Process | response to<br>stimulus             | GO:0008150        | 97              | 81  | 80  | 98  | 89  | 82  | 58  | 76  | 83  | 85  | 69  | 68  | 62  | 76  | 65  | 64  |
| Biological<br>Process | reproductive<br>process             | GO:0008150        | 19              | 16  | 16  | 24  | 20  | 23  | 13  | 18  | 22  | 20  | 18  | 21  | 20  | 17  | 16  | 20  |
| Biological<br>Process | immune system<br>process            | GO:0008150        | 10              | 8   | 6   | 11  | 9   | 12  | 7   | 10  | 9   | 12  | 7   | 8   | 6   | 10  | 9   | 7   |
| Biological<br>Process | reproduction                        | GO:0008150        | 19              | 16  | 16  | 24  | 20  | 23  | 13  | 18  | 22  | 20  | 18  | 21  | 20  | 17  | 16  | 20  |
| Biological<br>Process | multicellular<br>organismal process | GO:0008150        | 35              | 24  | 27  | 35  | 33  | 32  | 16  | 32  | 38  | 32  | 27  | 28  | 28  | 33  | 24  | 24  |
| Biological            | growth                              | GO:0008150        | 11              | 12  | 10  | 14  | 11  | 11  | 8   | 12  | 11  | 12  | 6   | 12  | 10  | 7   | 7   | 9   |

| GO Term<br>(level1) | GO Term (level2)                              | GO ID<br>(level1) | Number of Genes |     |     |     |     |     |    |     |     |     |    |     |    |     |    |     |
|---------------------|---|-------------------|-----------------|-----|-----|-----|-----|-----|----|-----|-----|-----|----|-----|----|-----|----|-----|
|                     |   |                   | AE              | AF  | AG  | AH  | BE  | BF  | BG | BH  | CE  | CF  | CG | CH  | DE | DF  | DG | DH  |
| Process             |   |                   |                 |     |     |     |     |     |    |     |     |     |    |     |    |     |    |     |
| Biological Process  | localization                                  | GO:0008150        | 60              | 42  | 44  | 54  | 44  | 39  | 34 | 39  | 50  | 45  | 36 | 51  | 31 | 41  | 36 | 40  |
| Biological Process  | negative regulation of biological process     | GO:0008150        | 7               | 6   | 5   | 7   | 8   | 8   | 4  | 5   | 7   | 6   | 4  | 3   | 4  | 7   | 2  | 2   |
| Biological Process  | positive regulation of biological process     | GO:0008150        | 5               | 10  | 7   | 5   | 10  | 9   | 5  | 6   | 8   | 10  | 4  | 7   | 12 | 12  | 10 | 8   |
| Biological Process  | cellular component organization or biogenesis | GO:0008150        | 46              | 43  | 36  | 50  | 38  | 46  | 40 | 37  | 44  | 50  | 35 | 40  | 34 | 39  | 40 | 36  |
| Biological Process  | biological regulation                         | GO:0008150        | 76              | 76  | 68  | 76  | 72  | 74  | 51 | 61  | 71  | 68  | 53 | 54  | 53 | 71  | 58 | 53  |
| Biological Process  | single-organism process                       | GO:0008150        | 132             | 110 | 107 | 130 | 118 | 124 | 84 | 107 | 126 | 128 | 99 | 107 | 94 | 108 | 93 | 103 |
| Biological Process  | regulation of biological process              | GO:0008150        | 63              | 61  | 57  | 64  | 60  | 61  | 43 | 51  | 61  | 57  | 47 | 44  | 45 | 61  | 52 | 44  |
| Biological Process  | signaling                                     | GO:0008150        | 21              | 16  | 17  | 22  | 19  | 17  | 12 | 20  | 24  | 17  | 14 | 13  | 14 | 21  | 16 | 15  |
| Biological Process  | developmental process                         | GO:0008150        | 41              | 36  | 38  | 51  | 39  | 44  | 29 | 40  | 46  | 45  | 33 | 37  | 37 | 36  | 31 | 32  |
| Molecular Function  | catalytic activity                            | GO:0003674        | 102             | 91  | 86  | 109 | 89  | 89  | 69 | 86  | 98  | 97  | 87 | 88  | 76 | 75  | 92 | 79  |

| GO Term<br>(level1)   | GO Term (level2)   | GO ID<br>(level1) | Number of Genes |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----------------------|--|-------------------|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
|                       |  |                   | AE              | AF  | AG  | AH  | BE  | BF  | BG  | BH  | CE  | CF  | CG  | CH  | DE  | DF  | DG  | DH  |
| Molecular<br>Function | transcription factor<br>activity, protein<br>binding     | GO:0003674        | /               | 1   | 1   | /   | /   | 1   | /   | /   | /   | 1   | 2   | /   | /   | /   | /   | /   |
| Molecular<br>Function | binding  | GO:0003674        | 117             | 117 | 108 | 127 | 111 | 112 | 82  | 97  | 123 | 124 | 97  | 104 | 91  | 106 | 87  | 87  |
| Molecular<br>Function | structural molecule<br>activity                          | GO:0003674        | 3               | 4   | 5   | 5   | 2   | 5   | 4   | 1   | 1   | 3   | 5   | 3   | 3   | 6   | 4   | 3   |
| Molecular<br>Function | molecular function<br>regulator                          | GO:0003674        | 4               | 3   | 4   | 2   | 1   | 1   | 1   | 1   | 3   | 3   | 3   | 2   | 3   | 3   | 3   | 3   |
| Molecular<br>Function | signal transducer<br>activity                            | GO:0003674        | 1               | 1   | 1   | 1   | 2   | /   | 1   | /   | 1   | 1   | 1   | 2   | 2   | 2   | 1   | /   |
| Molecular<br>Function | molecular<br>transducer activity                         | GO:0003674        | 1               | 2   | /   | 2   | 1   | /   | 2   | 1   | 1   | 1   | 1   | 2   | 2   | 2   | 1   | /   |
| Molecular<br>Function | transporter activity                                     | GO:0003674        | 9               | 7   | 7   | 7   | 5   | 7   | 3   | 6   | 10  | 10  | 8   | 7   | 4   | 6   | 8   | 9   |
| Molecular<br>Function | nucleic acid binding<br>transcription factor<br>activity | GO:0003674        | 10              | 14  | 15  | 15  | 9   | 17  | 6   | 11  | 12  | 17  | 12  | 9   | 7   | 15  | 12  | 10  |
| Cellular<br>Component | organelle  | GO:0005575        | 185             | 156 | 160 | 191 | 165 | 171 | 125 | 148 | 166 | 172 | 151 | 160 | 129 | 143 | 140 | 142 |
| Cellular<br>Component | organelle part   | GO:0005575        | 55              | 44  | 46  | 60  | 47  | 55  | 42  | 49  | 49  | 51  | 44  | 53  | 40  | 40  | 42  | 53  |
| Cellular<br>Component | cell part  | GO:0005575        | 211             | 175 | 183 | 215 | 185 | 188 | 138 | 169 | 200 | 193 | 163 | 181 | 146 | 157 | 153 | 159 |

[illegible]

| GO Term<br>(level1)   | GO Term (level2)             | GO ID<br>(level1) | Number of Genes |    |    |    |    |    |    |    |    |    |    |    |    |    |    |    |
|-----------------------|------------------------------|-------------------|-----------------|----|----|----|----|----|----|----|----|----|----|----|----|----|----|----|
|                       |                              |                   | AE              | AF | AG | AH | BE | BF | BG | BH | CE | CF | CG | CH | DE | DF | DG | DH |
| Cellular<br>Component | virion part                  | GO:0005575        | 1               | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  | /  |
| Cellular<br>Component | extracellular region<br>part | GO:0005575        | /               | 1  | 1  | /  | /  | 1  | 1  | 1  | /  | 1  | /  | /  | /  | /  | /  | /  |

**Table S3.** KEGG enrichment analysis of DASGs in different cross combinations.

| Pathway                              | Pathway ID | Q value |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
|--------------------------------------|------------|---------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|
|                                      |            | AE      | AF   | AG   | AH   | BE   | BF   | BG   | BH   | CE   | CF   | CG   | CH   | DE   | DF   | DG   | DH   |
| Ubiquitin mediated proteolysis       | ko04120    | 0.00    | 0.00 | /    | 0.00 | 0.00 | 0.02 | 0.01 | 0.05 | 0.00 | /    | /    | 0.02 | 0.00 | /    | /    | /    |
| Circadian rhythm - plant             | ko04712    | 0.00    | /    | 0.02 | 0.01 | 0.01 | /    | /    | /    | 0.01 | 0.01 | 0.02 | /    | 0.05 | /    | /    | /    |
| Spliceosome                          | ko03040    | 0.00    | 0.01 | 0.02 | 0.00 | 0.00 | /    | 0.05 | 0.02 | 0.00 | 0.00 | 0.00 | /    | /    | 0.05 | /    | 0.00 |
| Glycosaminoglycan degradation        | ko00531    | 0.02    | /    | /    | /    | /    | /    | /    | /    | 0.02 | /    | /    | 0.01 | /    | /    | /    | /    |
| Porphyrin and chlorophyll metabolism | ko00860    | 0.05    | /    | /    | /    | /    | /    | /    | /    | /    | /    | /    | /    | /    | 0.02 | /    | /    |
| Basal transcription factors          | ko03022    | 0.05    | /    | 0.03 | /    | /    | /    | /    | /    | /    | /    | /    | /    | /    | /    | 0.02 | 0.02 |
| Peroxisome                           | ko04146    | /       | /    | /    | /    | /    | /    | /    | /    | 0.01 | /    | /    | 0.03 | /    | /    | /    | /    |
| beta-Alanine metabolism              | ko00410    | /       | /    | /    | /    | 0.00 | /    | /    | /    | 0.04 | /    | /    | /    | /    | /    | /    | /    |
| RNA transport                        | ko03013    | /       | /    | /    | /    | /    | /    | /    | 0.01 | /    | /    | /    | /    | /    | /    | /    | /    |
| Monoterpenoid biosynthesis           | ko00902    | /       | 0.01 | /    | /    | /    | /    | /    | 0.01 | /    | /    | /    | /    | /    | /    | /    | /    |
| Microbial metabolism in diverse      | ko01120    | /       | 0.01 | /    | /    | 0.02 | 0.01 | 0.03 | 0.01 | 0.03 | /    | /    | 0.04 | 0.00 | /    | /    | /    |



| Pathway                                     | Pathway ID | Q value |      |    |      |      |      |      |      |      |      |    |      |      |      |    |      |
|---|------------|---------|------|----|------|------|------|------|------|------|------|----|------|------|------|----|------|
|   |            | AE      | AF   | AG | AH   | BE   | BF   | BG   | BH   | CE   | CF   | CG | CH   | DE   | DF   | DG | DH   |
| environments                                |            |         |      |    |      |      |      |      |      |      |      |    |      |      |      |    |      |
| Carbon fixation in photosynthetic organisms | ko00710    | /       | 0.01 | /  | /    | 0.04 | 0.05 | 0.02 | /    | /    | /    | /  | /    | /    | /    | /  | /    |
| 2-Oxocarboxylic acid metabolism             | ko01210    | /       | 0.02 | /  | 0.01 | 0.00 | /    | 0.01 | 0.01 | 0.00 | 0.03 | /  | 0.02 | /    | /    | /  | 0.04 |
| Alanine, aspartate and glutamate metabolism | ko00250    | /       | /    | /  | /    | 0.04 | /    | /    | /    | /    | /    | /  | /    | /    | /    | /  | /    |
| Degradation of aromatic compounds           | ko01220    | /       | 0.02 | /  | /    | /    | 0.02 | /    | /    | 0.03 | /    | /  | /    | /    | /    | /  | /    |
| Endocytosis                                 | ko04144    | /       | /    | /  | /    | /    | /    | /    | /    | 0.03 | 0.03 | /  | /    | /    | 0.04 | /  | 0.05 |
| Arginine biosynthesis                       | ko00220    | /       | /    | /  | 0.04 | /    | /    | /    | 0.01 | /    | /    | /  | /    | /    | /    | /  | 0.01 |
| Glycine, serine and threonine metabolism    | ko00260    | /       | /    | /  | /    | 0.03 | 0.01 | /    | 0.01 | /    | /    | /  | /    | /    | /    | /  | /    |
| Fatty acid degradation                      | ko00071    | /       | /    | /  | /    | /    | /    | /    | /    | 0.05 | /    | /  | /    | /    | /    | /  | /    |
| Carbon metabolism                           | ko01200    | /       | 0.02 | /  | /    | 0.03 | 0.01 | 0.03 | /    | /    | /    | /  | /    | 0.00 | /    | /  | /    |
| Glyoxylate and dicarboxylate metabolism     | ko00630    | /       | /    | /  | /    | 0.04 | 0.02 | 0.03 | 0.01 | /    | /    | /  | /    | /    | /    | /  | /    |

| Pathway   | Pathway ID | Q value |      |      |      |      |      |      |      |    |      |      |      |      |      |      |      |
|---|------------|---------|------|------|------|------|------|------|------|----|------|------|------|------|------|------|------|
|   |            | AE      | AF   | AG   | AH   | BE   | BF   | BG   | BH   | CE | CF   | CG   | CH   | DE   | DF   | DG   | DH   |
| Phenylalanine, tyrosine and tryptophan biosynthesis | ko00400    | /       | /    | /    | /    | /    | /    | /    | /    | /  | /    | /    | /    | /    | /    | /    | 0.02 |
| Glycolysis / Gluconeogenesis                        | ko00010    | /       | /    | /    | /    | /    | 0.03 | /    | /    | /  | /    | /    | /    | /    | /    | /    | /    |
| Biosynthesis of amino acids                         | ko01230    | /       | /    | /    | /    | 0.01 | 0.04 | 0.05 | 0.02 | /  | /    | /    | /    | /    | /    | /    | /    |
| Citrate cycle (TCA cycle)                           | ko00020    | /       | /    | /    | /    | 0.05 | /    | /    | /    | /  | /    | /    | /    | 0.03 | /    | 0.04 | /    |
| Glycerolipid metabolism                             | ko00561    | /       | /    | /    | /    | /    | /    | /    | /    | /  | /    | /    | /    | /    | 0.04 | /    | /    |
| Lysine degradation                                  | ko00310    | /       | /    | /    | /    | /    | /    | /    | /    | /  | /    | /    | /    | /    | /    | /    | 0.04 |
| Biosynthesis of antibiotics                         | ko01130    | /       | /    | /    | /    | /    | 0.01 | /    | 0.05 | /  | /    | /    | /    | 0.01 | /    | /    | 0.02 |
| Photosynthesis                                      | ko00195    | /       | /    | /    | /    | /    | /    | /    | /    | /  | 0.02 | /    | /    | /    | /    | /    | /    |
| Arginine and proline metabolism                     | ko00330    | /       | /    | /    | /    | /    | /    | /    | /    | /  | /    | /    | /    | 0.03 | /    | /    | 0.04 |
| Flavone and flavonol biosynthesis                   | ko00944    | /       | 0.03 | 0.03 | 0.03 | /    | 0.03 | 0.02 | 0.02 | /  | 0.03 | 0.03 | 0.03 | /    | 0.02 | 0.03 | 0.02 |
| Monobactam biosynthesis                             | ko00261    | /       | /    | /    | /    | /    | /    | /    | 0.04 | /  | /    | /    | 0.05 | /    | /    | /    | /    |
| Lysine biosynthesis                                 | ko00300    | /       | /    | /    | /    | /    | /    | /    | 0.05 | /  | /    | /    | /    | /    | /    | /    | /    |

**Table S4.**Correlation analysis betweenPGW and gene expression levels in aminoacidmetabolism.

|                      | PGW     | BraA06g024290.3<br>C | BraA07g031850.3C | BraA07g035330.3C | BraA10g021330.3C | BraA06g014310.3C | BraA03g041700.3C |
|----------------------|---------|----------------------|------------------|------------------|------------------|------------------|------------------|
| PGW                  | 1       |                      |                  |                  |                  |                  |                  |
| BraA06g024290.3<br>C | -0.023  | 1                    |                  |                  |                  |                  |                  |
| BraA07g031850.3<br>C | -0.070  | 0.399                | 1                |                  |                  |                  |                  |
| BraA07g035330.3<br>C | -0.043  | 0.631**              | 0.647**          | 1                |                  |                  |                  |
| BraA10g021330.3<br>C | -0.234  | 0.120                | 0.356            | 0.400            | 1                |                  |                  |
| BraA06g014310.3<br>C | 0.550*  | 0.255                | -0.017           | -0.080           | -0.141           | 1                |                  |
| BraA03g041700.3<br>C | -0.515* | 0.154                | 0.355            | 0.385            | 0.256            | -0.708**         | 1                |

\*\*.: correlation is significant at the 0.01 level, \*: correlation is significant at the 0.05 level.PGW: plant gross weight.