

Supplemental Table S5. The overlapped genes between PagLBD21 DAP-seq target genes an

| genes | seqnames | start | end | width | strand | score | blockCount | thick | sta |
|----------------|----------|----------|----------|-------|--------|-------|------------|-------|-----|
| Potri.001Chr01 | | 5594344 | 5594619 | 276 | * | 196 | 132 | | 3 |
| Potri.001Chr01 | | 6611503 | 6611833 | 331 | * | 188 | 173 | | 4 |
| Potri.001Chr01 | | 7165158 | 7165391 | 234 | * | 199 | 135 | | 4 |
| Potri.001Chr01 | | 9531364 | 9531614 | 251 | * | 214 | 116 | | 4 |
| Potri.001Chr01 | | 13980531 | 13980772 | 242 | * | 197 | 115 | | 3 |
| Potri.001Chr01 | | 22029190 | 22029426 | 237 | * | 207 | 152 | | 3 |
| Potri.001Chr01 | | 34316537 | 34316817 | 281 | * | 208 | 161 | | 4 |
| Potri.001Chr01 | | 43036833 | 43037117 | 285 | * | 277 | 129 | | 4 |
| Potri.001Chr01 | | 47358494 | 47358780 | 287 | * | 179 | 177 | | 3 |
| Potri.002Chr02 | | 3653603 | 3653899 | 297 | * | 190 | 168 | | 3 |
| Potri.002Chr02 | | 6295734 | 6295952 | 219 | * | 175 | 112 | | 5 |
| Potri.002Chr02 | | 11789392 | 11789598 | 207 | * | 173 | 105 | | 4 |
| Potri.003Chr03 | | 13104122 | 13104423 | 302 | * | 185 | 110 | | 3 |
| Potri.003Chr03 | | 19295246 | 19295480 | 235 | * | 223 | 158 | | 4 |
| Potri.003Chr03 | | 19296783 | 19297030 | 248 | * | 242 | 115 | | 4 |
| Potri.004Chr04 | | 6269750 | 6269989 | 240 | * | 286 | 120 | | 5 |
| Potri.004Chr04 | | 6955127 | 6955418 | 292 | * | 193 | 129 | | 4 |
| Potri.004Chr04 | | 11934926 | 11935188 | 263 | * | 178 | 109 | | 4 |
| Potri.004Chr04 | | 12333541 | 12333764 | 224 | * | 204 | 83 | | 4 |
| Potri.004Chr04 | | 19238127 | 19238356 | 230 | * | 185 | 108 | | 3 |
| Potri.005Chr05 | | 4185325 | 4185527 | 203 | * | 298 | 99 | | 3 |
| Potri.005Chr05 | | 23601924 | 23602134 | 211 | * | 175 | 116 | | 4 |
| Potri.005Chr05 | | 24083689 | 24083920 | 232 | * | 197 | 79 | | 4 |
| Potri.006Chr06 | | 1628583 | 1628791 | 209 | * | 312 | 82 | | 5 |
| Potri.006Chr06 | | 4496009 | 4496255 | 247 | * | 253 | 119 | | 3 |
| Potri.006Chr06 | | 4530595 | 4530921 | 327 | * | 185 | 179 | | 3 |
| Potri.006Chr06 | | 6538315 | 6538566 | 252 | * | 232 | 88 | | 4 |
| Potri.006Chr06 | | 19624832 | 19625138 | 307 | * | 237 | 171 | | 3 |
| Potri.007Chr07 | | 2418046 | 2418260 | 215 | * | 216 | 120 | | 4 |
| Potri.007Chr07 | | 3252335 | 3252665 | 331 | * | 545 | 163 | | 3 |
| Potri.007Chr07 | | 12706167 | 12706396 | 230 | * | 335 | 122 | | 5 |
| Potri.008Chr08 | | 3222318 | 3222538 | 221 | * | 174 | 134 | | 3 |
| Potri.008Chr08 | | 8631360 | 8631653 | 294 | * | 236 | 164 | | 4 |
| Potri.008Chr08 | | 10457420 | 10457640 | 221 | * | 208 | 110 | | 4 |
| Potri.009Chr09 | | 5494478 | 5494708 | 231 | * | 181 | 81 | | 4 |
| Potri.009Chr09 | | 11366307 | 11367012 | 706 | * | 262 | 578 | | 4 |
| Potri.009Chr09 | | 11403385 | 11403734 | 350 | * | 314 | 158 | | 4 |
| Potri.009Chr09 | | 11793301 | 11793562 | 262 | * | 187 | 135 | | 4 |
| Potri.010Chr10 | | 1975920 | 1976129 | 210 | * | 200 | 125 | | 3 |
| Potri.010Chr10 | | 11849113 | 11849384 | 272 | * | 208 | 95 | | 4 |
| Potri.010Chr10 | | 19930641 | 19930935 | 295 | * | 169 | 138 | | 3 |
| Potri.011Chr11 | | 280384 | 280607 | 224 | * | 180 | 119 | | 5 |
| Potri.012Chr12 | | 1770217 | 1770546 | 330 | * | 204 | 177 | | 4 |
| Potri.012Chr12 | | 12872671 | 12872880 | 210 | * | 303 | 116 | | 3 |
| Potri.014Chr14 | | 735918 | 736142 | 225 | * | 181 | 133 | | 4 |
| Potri.014Chr14 | | 7117836 | 7118097 | 262 | * | 315 | 119 | | 6 |
| Potri.015Chr15 | | 2635540 | 2635772 | 233 | * | 180 | 104 | | 4 |
| Potri.015Chr15 | | 4009026 | 4009277 | 252 | * | 233 | 123 | | 4 |
| Potri.015Chr15 | | 11995780 | 11996031 | 252 | * | 170 | 129 | | 4 |
| Potri.017Chr17 | | 363315 | 363550 | 236 | * | 223 | 106 | | 5 |
| Potri.017Chr17 | | 2579352 | 2579643 | 292 | * | 185 | 138 | | 3 |

| | | | | | | |
|--------------------|----------|----------|-------|-----|-----|---|
| Potri.017Chr17 | 9634484 | 9634763 | 280 * | 179 | 201 | 4 |
| Potri.017Chr17 | 10937777 | 10937996 | 220 * | 216 | 129 | 4 |
| Potri.017Chr17 | 13004792 | 13005061 | 270 * | 208 | 157 | 3 |
| Potri.018Chr18 | 772358 | 772608 | 251 * | 170 | 156 | 3 |
| Potri.019Chr19 | 11801277 | 11801588 | 312 * | 281 | 145 | 5 |
| Potri.019Chr19 | 15371466 | 15371738 | 273 * | 195 | 142 | 3 |
| Potri.T02scaffold_ | 174244 | 174485 | 242 * | 188 | 105 | 5 |
| Potri.T11scaffold_ | 37809 | 38018 | 210 * | 221 | 101 | 3 |

id DEGs in L36

| thick. | endthick. | widstart_pos | end_pos | feature_s | insideFea | distancet | shortestD | fromOverl |
|--------|-----------|--------------|----------|-----------|-----------|-----------|-----------|-----------|
| 19 | 17 | 5594633 | 5596573 | + | upstream | -289 | 14 | NearestLo |
| 18 | 15 | 6608926 | 6610764 | - | upstream | -739 | 739 | NearestLo |
| 19 | 16 | 7162074 | 7164172 | - | upstream | -986 | 986 | NearestLo |
| 21 | 18 | 9532286 | 9534455 | - | downstrea | 3091 | 672 | NearestLo |
| 19 | 17 | 13976442 | 13981566 | - | inside | 1035 | 794 | NearestLo |
| 20 | 18 | 22029049 | 22033651 | - | inside | 4461 | 141 | NearestLo |
| 20 | 17 | 34316929 | 34319074 | + | upstream | -392 | 112 | NearestLo |
| 27 | 24 | 43033549 | 43041023 | + | inside | 3284 | 3284 | NearestLo |
| 17 | 15 | 47355398 | 47356346 | - | upstream | -2148 | 2148 | NearestLo |
| 19 | 17 | 3654028 | 3655628 | - | downstrea | 2025 | 129 | NearestLo |
| 17 | 13 | 6300384 | 6304858 | + | upstream | -4650 | 4432 | NearestLo |
| 17 | 14 | 11792508 | 11794803 | + | upstream | -3116 | 2910 | NearestLo |
| 18 | 16 | 13105319 | 13107221 | + | upstream | -1197 | 896 | NearestLo |
| 22 | 19 | 19294354 | 19294875 | + | downstrea | 892 | 371 | NearestLo |
| 24 | 21 | 19297875 | 19299786 | + | upstream | -1092 | 845 | NearestLo |
| 28 | 24 | 6269473 | 6273663 | + | inside | 277 | 277 | NearestLo |
| 19 | 16 | 6958715 | 6961637 | + | upstream | -3588 | 3297 | NearestLo |
| 17 | 14 | 11929544 | 11932387 | - | upstream | -2539 | 2539 | NearestLo |
| 20 | 17 | 12337842 | 12338677 | - | downstrea | 5136 | 4078 | NearestLo |
| 18 | 16 | 19238092 | 19239534 | + | inside | 35 | 35 | NearestLo |
| 29 | 27 | 4182330 | 4187153 | - | inside | 1828 | 1626 | NearestLo |
| 17 | 14 | 23600307 | 23604582 | - | inside | 2658 | 1617 | NearestLo |
| 19 | 16 | 24079656 | 24082417 | - | upstream | -1272 | 1272 | NearestLo |
| 31 | 27 | 1626750 | 1628824 | - | inside | 241 | 33 | NearestLo |
| 25 | 23 | 4499695 | 4504592 | + | upstream | -3686 | 3440 | NearestLo |
| 18 | 16 | 4523335 | 4532993 | - | inside | 2398 | 2072 | NearestLo |
| 23 | 20 | 6538210 | 6541462 | - | inside | 3147 | 105 | NearestLo |
| 23 | 21 | 19616220 | 19621043 | - | upstream | -3789 | 3789 | NearestLo |
| 21 | 18 | 2415499 | 2419192 | - | inside | 1146 | 932 | NearestLo |
| 54 | 52 | 3252284 | 3254824 | - | inside | 2489 | 51 | NearestLo |
| 33 | 29 | 12704588 | 12708177 | - | inside | 2010 | 1579 | NearestLo |
| 17 | 15 | 3220515 | 3223122 | - | inside | 804 | 584 | NearestLo |
| 23 | 20 | 8631059 | 8632295 | - | inside | 935 | 301 | NearestLo |
| 20 | 17 | 10457421 | 10458550 | - | overlapEn | 1130 | 1 | NearestLo |
| 18 | 15 | 5502089 | 5508765 | + | upstream | -7611 | 7381 | NearestLo |
| 26 | 23 | 11362951 | 11367004 | - | overlapSt | 697 | 8 | NearestLo |
| 31 | 28 | 11407300 | 11410604 | + | upstream | -3915 | 3566 | NearestLo |
| 18 | 15 | 11783112 | 11788425 | - | upstream | -4876 | 4876 | NearestLo |
| 20 | 18 | 1975048 | 1979416 | - | inside | 3496 | 872 | NearestLo |
| 20 | 17 | 11844016 | 11848320 | - | upstream | -793 | 793 | NearestLo |
| 16 | 14 | 19928701 | 19931559 | + | inside | 1940 | 624 | NearestLo |
| 18 | 14 | 278846 | 281529 | - | inside | 1145 | 922 | NearestLo |
| 20 | 17 | 1772665 | 1773882 | + | upstream | -2448 | 2119 | NearestLo |
| 30 | 28 | 12868554 | 12869907 | - | upstream | -2764 | 2764 | NearestLo |
| 18 | 15 | 731206 | 735001 | - | upstream | -917 | 917 | NearestLo |
| 31 | 26 | 7118925 | 7121224 | + | upstream | -1089 | 828 | NearestLo |
| 18 | 15 | 2637644 | 2638216 | - | downstrea | 2676 | 1872 | NearestLo |
| 23 | 20 | 4011094 | 4014183 | + | upstream | -2068 | 1817 | NearestLo |
| 17 | 14 | 11994376 | 11996292 | + | inside | 1404 | 261 | NearestLo |
| 22 | 18 | 362085 | 363948 | - | inside | 633 | 398 | NearestLo |
| 18 | 16 | 2578793 | 2582511 | + | inside | 559 | 559 | NearestLo |

| | | | | | | | | |
|----|----|----------|----------|---|-----------|-------|------|-----------|
| 17 | 14 | 9635769 | 9638227 | + | upstream | -1285 | 1006 | NearestLo |
| 21 | 18 | 10947583 | 10953970 | + | upstream | -9806 | 9587 | NearestLo |
| 20 | 18 | 13012869 | 13015325 | + | upstream | -8077 | 7808 | NearestLo |
| 17 | 15 | 766518 | 772371 | - | overlapSt | 13 | 13 | NearestLo |
| 28 | 24 | 11796617 | 11800728 | - | upstream | -549 | 549 | NearestLo |
| 19 | 17 | 15371119 | 15377454 | + | inside | 347 | 347 | NearestLo |
| 18 | 14 | 182526 | 191285 | + | upstream | -8282 | 8041 | NearestLo |
| 22 | 20 | 28580 | 30088 | + | downstrea | 9229 | 7721 | NearestLo |

| logFC | logCPM | PValue | FDR | OX. WT | LLJGY. A | LLJGY. B | LLJGY. C | LLJGY. M |
|----------|----------|----------|----------|--------|----------|----------|----------|----------|
| -0.57569 | 4.831037 | 0.000181 | 0.009396 | -1 | 523 | 371 | 434 | 262 |
| 0.861806 | 4.542708 | 6.10E-09 | 1.98E-06 | 1 | 199 | 231 | 211 | 313 |
| 0.886539 | 4.177162 | 1.57E-07 | 3.14E-05 | 1 | 157 | 167 | 168 | 308 |
| -0.79283 | 4.083285 | 4.34E-08 | 1.05E-05 | -1 | 286 | 256 | 288 | 159 |
| 0.432116 | 5.133544 | 0.000788 | 0.029531 | 1 | 360 | 410 | 389 | 458 |
| -0.37485 | 7.09345 | 0.00049 | 0.02034 | -1 | 2302 | 1879 | 1854 | 1374 |
| -0.84924 | 6.274699 | 4.63E-08 | 1.10E-05 | -1 | 1354 | 1225 | 1301 | 684 |
| 0.731313 | 4.44416 | 2.06E-08 | 5.72E-06 | 1 | 222 | 196 | 218 | 312 |
| -1.1439 | 2.932477 | 1.25E-06 | 0.000174 | -1 | 107 | 152 | 139 | 61 |
| -1.40571 | 0.45553 | 0.000515 | 0.021046 | -1 | 17 | 25 | 26 | 7 |
| -1.48547 | 1.312806 | 1.42E-06 | 0.000193 | -1 | 53 | 33 | 47 | 17 |
| -1.35071 | 2.892329 | 3.58E-11 | 1.99E-08 | -1 | 129 | 120 | 156 | 50 |
| -0.63878 | 3.297433 | 0.001102 | 0.03764 | -1 | 163 | 169 | 127 | 80 |
| 0.482309 | 5.807377 | 0.000102 | 0.006109 | 1 | 739 | 516 | 576 | 738 |
| 0.727536 | 4.582709 | 0.000147 | 0.008053 | 1 | 324 | 156 | 229 | 398 |
| 0.830755 | 5.922182 | 8.48E-11 | 4.46E-08 | 1 | 538 | 576 | 583 | 792 |
| -0.53103 | 3.695942 | 0.000524 | 0.021309 | -1 | 205 | 199 | 186 | 109 |
| 0.392011 | 6.149288 | 0.000576 | 0.022931 | 1 | 795 | 752 | 844 | 954 |
| -1.08339 | 1.585227 | 6.70E-05 | 0.004491 | -1 | 56 | 52 | 42 | 27 |
| -0.36646 | 7.261809 | 0.001098 | 0.037536 | -1 | 2193 | 2285 | 2250 | 1588 |
| 1.574129 | 8.183179 | 9.66E-35 | 2.07E-30 | 1 | 2256 | 1831 | 1644 | 5083 |
| -0.81174 | 2.05911 | 0.000321 | 0.014773 | -1 | 76 | 61 | 62 | 28 |
| -0.72692 | 3.806899 | 0.000199 | 0.010165 | -1 | 214 | 227 | 230 | 161 |
| -1.33382 | 0.308012 | 0.001074 | 0.037077 | -1 | 26 | 20 | 14 | 9 |
| -1.01221 | 1.676076 | 0.00064 | 0.02506 | -1 | 61 | 48 | 49 | 31 |
| -0.44256 | 5.182526 | 0.001113 | 0.037852 | -1 | 674 | 473 | 489 | 322 |
| 0.398711 | 8.035484 | 0.001092 | 0.037453 | 1 | 3401 | 2368 | 3108 | 3606 |
| -0.38945 | 8.085736 | 0.000235 | 0.011615 | -1 | 4050 | 4065 | 3896 | 2746 |
| 0.924785 | 3.357035 | 1.93E-07 | 3.72E-05 | 1 | 94 | 81 | 98 | 179 |
| 0.825414 | 2.160488 | 0.000365 | 0.01624 | 1 | 38 | 35 | 49 | 60 |
| 0.579898 | 4.28217 | 9.36E-05 | 0.005716 | 1 | 214 | 169 | 223 | 295 |
| 0.353074 | 7.892937 | 0.001375 | 0.043948 | 1 | 2667 | 2820 | 2643 | 2963 |
| 0.776973 | 10.20572 | 4.96E-08 | 1.16E-05 | 1 | 13053 | 11655 | 9380 | 20509 |
| -0.66442 | 3.230829 | 9.30E-05 | 0.005702 | -1 | 170 | 145 | 127 | 74 |
| 0.663261 | 3.844056 | 0.000128 | 0.007221 | 1 | 136 | 172 | 121 | 208 |
| -0.7956 | 2.217801 | 0.000284 | 0.013415 | -1 | 80 | 70 | 72 | 27 |
| -0.42169 | 5.289645 | 0.000997 | 0.035168 | -1 | 606 | 582 | 553 | 408 |
| 0.426847 | 7.105002 | 0.000452 | 0.019326 | 1 | 1729 | 1340 | 1529 | 1690 |
| -0.77616 | 2.012043 | 0.001211 | 0.040141 | -1 | 81 | 59 | 51 | 30 |
| -0.97079 | 4.153341 | 3.96E-10 | 1.79E-07 | -1 | 296 | 324 | 288 | 145 |
| 0.488105 | 3.947327 | 0.001198 | 0.039872 | 1 | 184 | 158 | 156 | 223 |
| -0.92493 | 2.100934 | 0.000181 | 0.009403 | -1 | 63 | 60 | 87 | 30 |
| -0.88689 | 3.038988 | 4.51E-06 | 0.000501 | -1 | 123 | 144 | 139 | 65 |
| -1.00703 | 2.186514 | 0.000483 | 0.020161 | -1 | 56 | 67 | 104 | 38 |
| -0.7715 | 6.525677 | 3.11E-05 | 0.00244 | -1 | 1481 | 1328 | 1715 | 884 |
| -1.48352 | 2.996196 | 8.04E-08 | 1.76E-05 | -1 | 107 | 183 | 154 | 61 |
| 0.785063 | 2.410629 | 0.00122 | 0.040267 | 1 | 54 | 44 | 51 | 92 |
| -1.93473 | 2.126491 | 2.45E-12 | 1.81E-09 | -1 | 72 | 106 | 79 | 22 |
| -1.12086 | 3.074609 | 0.000165 | 0.00871 | -1 | 243 | 94 | 110 | 72 |
| -1.35149 | 2.40108 | 4.06E-07 | 6.91E-05 | -1 | 107 | 103 | 76 | 49 |
| 0.490713 | 4.650171 | 7.18E-05 | 0.004733 | 1 | 303 | 253 | 257 | 331 |

| | | | | | | | | |
|----------|----------|----------|----------|----|------|------|------|-------|
| 0.505384 | 4.041594 | 0.00031 | 0.01439 | 1 | 207 | 166 | 156 | 221 |
| 0.38167 | 7.098138 | 0.001073 | 0.03707 | 1 | 1473 | 1509 | 1649 | 1766 |
| 0.914815 | 9.743442 | 2.12E-17 | 4.55E-14 | 1 | 7821 | 7382 | 7982 | 13789 |
| -1.66886 | 0.130396 | 0.000123 | 0.006997 | -1 | 15 | 19 | 21 | 5 |
| -0.68445 | 8.091765 | 2.18E-07 | 4.12E-05 | -1 | 5460 | 3398 | 4369 | 2398 |
| 0.421916 | 6.751264 | 0.00011 | 0.006406 | 1 | 1321 | 1104 | 1175 | 1322 |
| 1.070686 | 2.31681 | 1.31E-06 | 0.000181 | 1 | 39 | 51 | 32 | 76 |
| -2.76475 | 2.736297 | 2.65E-28 | 2.27E-24 | -1 | 151 | 159 | 128 | 19 |

LLJGY.N LLJGY.O Best.hit.arabi.symarabi.defline

| | | |
|-------|--|---|
| 326 | 241 AT5G32450.1 | RNA binding (RRM/RBD/RNP motifs) family prote |
| 350 | 437 AT1G14430.1 | glyoxal oxidase-related protein |
| 305 | 237 AT4G23900.1 | Nucleoside diphosphate kinase family protein |
| 143 | 146 AT4G12350AtMYB42,Mmyb domain protein 42 | |
| 486 | 528 AT1G72480.1 | Lung seven transmembrane receptor family prot |
| 1416 | 1562 AT2G35940BLH1,EDA2BEL1-like homeodomain 1 | |
| 797 | 525 AT3G27400.1 | Pectin lyase-like superfamily protein |
| 346 | 331 AT5G54250ATCNGC4,C | cyclic nucleotide-gated cation channel 4 |
| 64 | 44 AT5G44550.1 | Uncharacterised protein family (UPF0497) |
| 5 | 12 AT1G03220.1 | Eukaryotic aspartyl protease family protein |
| 17 | 10 AT1G77760GNR1,NIA1 | nitrate reductase 1 |
| 40 | 59 AT2G37360.1 | ABC-2 type transporter family protein |
| 114 | 82 AT4G39730.1 | Lipase/lipoxygenase, PLAT/LH2 family protein |
| 767 | 884 AT1G64660ATMGL,MGL | methionine gamma-lyase |
| 331 | 356 AT1G64660ATMGL,MGL | methionine gamma-lyase |
| 1012 | 1042 AT5G17330GAD,GAD1 | glutamate decarboxylase |
| 144 | 130 AT1G66140ZFP4 | zinc finger protein 4 |
| 970 | 1019 AT5G08060.1 | |
| 16 | 23 AT3G28917MIF2 | mini zinc finger 2 |
| 1672 | 1638 AT2G16700ADF5,ATAD | actin depolymerizing factor 5 |
| 4664 | 6224 AT5G24550BGLU32 | beta glucosidase 32 |
| 42 | 36 AT4G28530anac074,NNAC | domain containing protein 74 |
| 112 | 105 AT1G19715.3 | Mannose-binding lectin superfamily protein |
| 6 | 7 AT1G22400ATUGT85A1 | UDP-Glycosyltransferase superfamily protein |
| 12 | 30 AT1G58190AtRLP9,RL | receptor like protein 9 |
| 379 | 424 AT1G15740.1 | Leucine-rich repeat family protein |
| 3514 | 3793 AT2G37640ATEXP3,AT | Barwin-like endoglucanases superfamily protei |
| 2746 | 3122 AT5G17420ATCESA7,C | Cellulose synthase family protein |
| 137 | 169 AT4G36850.1 | PQ-loop repeat family protein / transmembrane |
| 79 | 64 AT2G26560PLA IIA,P | phospholipase A 2A |
| 280 | 271 AT2G04160AIR3 | Subtilisin-like serine endopeptidase family p |
| 3352 | 3453 AT5G02500AT-HSC70- | heat shock cognate protein 70-1 |
| 16798 | 17000 AT1G14930.1 | Polyketide cyclase/dehydrase and lipid transp |
| 95 | 92 AT3G22540.1 | Protein of unknown function (DUF1677) |
| 226 | 204 AT1G50450.1 | Saccharopine dehydrogenase |
| 46 | 47 AT1G20550.1 | O-fucosyltransferase family protein |
| 436 | 371 AT1G08290WIP3 | WIP domain protein 3 |
| 1787 | 2325 AT5G22740ATCSLA02, | cellulose synthase-like A02 |
| 39 | 35 AT4G21380ARK3,RK3 | receptor kinase 3 |
| 159 | 130 AT1G70260.1 | nodulin MtN21 /EamA-like transporter family p |
| 231 | 198 AT3G55330PPL1 | PsbP-like protein 1 |
| 31 | 43 AT5G38280PR5K | PR5-like receptor kinase |
| 80 | 61 AT3G24770CLE41 | CLAVATA3/ESR-RELATED 41 |
| 38 | 30 AT1G24140.1 | Matrixin family protein |
| 989 | 593 AT3G49780ATPSK3 (F | phytosulfokine 4 precursor |
| 52 | 36 AT2G46130ATWRKY43,WRKY | DNA-binding protein 43 |
| 88 | 59 AT3G28920AtHB34,HB | homeobox protein 34 |
| 23 | 18 AT3G18170.1 | Glycosyltransferase family 61 protein |
| 59 | 57 AT5G50790.1 | Nodulin MtN3 family protein |
| 27 | 28 AT3G59850.1 | Pectin lyase-like superfamily protein |
| 352 | 387 AT4G22720.1 | Actin-like ATPase superfamily protein |

| | |
|-------|--|
| 240 | 241 AT5G15150ATHB-3, AThomeobox 3 |
| 1801 | 2114 AT3G02090MPPBETA Insulinase (Peptidase family M16) protein |
| 13445 | 13700 AT1G67090RBCS1A ribulose bisphosphate carboxylase small chain |
| 6 | 5 AT2G29110ATGLR2.8, glutamate receptor 2.8 |
| 2583 | 2679 AT1G22710ATSUC2, SUsucrose-proton symporter 2 |
| 1558 | 1642 AT1G06950ATTIC110, translocon at the inner envelope membrane of |
| 82 | 83 AT4G27290.1 S-locus lectin protein kinase family protein |
| 29 | 12 AT1G24430.1 HXXXD-type acyl-transferase family protein |

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family protein

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ort superfamily protein

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chloroplasts 110