**Table S1.** The putative functions (as determined by BLAST in GenBank) of the other transcript derived fragments (TDFs) responsive to the resistance of *C. metuliferus* infected with PRSV

| TDF | Size (bp) | I/C[a] | Accession number | Functional annotation | BLAST *E*-value | Restriction site[b] |
|---|---|---|---|---|---|---|
| ku2005-11 | 291 | I | BAD87519 | putative Golgi autoantigen | 2E-10 | M+M |
| ku2005-22 | 565 | I | NP565018 | oxidoreductase | 4E-48 | M+M |
| ku2005-30 | 676 | I | AAF34799 | 40S ribosomal protein S16 | 2E-66 | M+M |
| ku2005-41 | 760 | I | BAA13541 | CPRD12 protein | 6E-75 | M+M |
| ku2005-56 | 204 | I | AAA32857 | receptor-like protein kinase | 6E-5 | E+M |
| ku2005-63 | 623 | I | AAM62640 | Function unknown protein | 4E-22 | M+M |
| ku2005-81 | 393 | C | NP567449 | acid phosphatase | 3E-16 | M+M |
| ku2005-100 | 534 | C | ABA40465 | ribosomal protein S27-like protein | 5E-32 | M+M |
| ku2005-118 | 656 | I | AAS46243 | xyloglucan endotransglucosylase -hydrolase, XTH7 | 7E-100 | M+M |
| ku2500-154 | 156 | C | CAD31840 | alpha-dioxygenase | 1E-6 | E+M |
| ku2005-170 | 240 | No | CAA48140 | ubiquitin | 4E-20 | E+M |
| ku2005-175 | 461 | I | NP197655 | prephenate dehydratase | 9E-16 | M+M |
| ku2005-180 | 404 | I | BAB33421 | putative senescence-associated protein | 2E-39 | E+M |
| ku2005-181 | 619 | I | AAB37746 | expansin S1 precursor | 7E-106 | M+M |
| ku2005-232 | 522 | C | NP197857 | Function unknown protein | 2E-46 | M+M |
| ku2005-238 | 793 | I | NP194345 | transcription factor | 6E-12 | M+M |
| ku2005-243 | 468 | C | NP178175 | acetylornithine transaminase/ pyridoxal phosphate binding / transaminase | 8E-31 | M+M |
| ku2005-250 | 181 | C | MU57845 | disease resistance-responsive protein-related | 9E-68 | E+M |
| ku2005-267 | 116 | I | NP850181 | structural constituent of ribosome | 8E-4 | E+M |
| ku2005-272 | 148 | I | MU62607 | Function unknown protein | 7E-31 | E+M |
| ku2005-292 | 154 | I | AAL25650 | calcineurin-like protein | 2E-19 | E+M |
| ku2005-297 | 774 | I | NP568239 | UBP22 (UBIQUITIN-SPECIFIC PROTEASE 22) | 1E-84 | M+M |
| ku2005-314 | 284 | C | AAT77309 | Function unknown protein | 3E-21 | E+M |
| ku2005-321 | 127 | C | NP200894 | GTP-binding protein | 9E-14 | E+M |
| ku2005-336 | 318 | C | NP197501 | small GTP-binding nuclear protein; Ran-1 | 1E-17 | M+M |
| ku2005-340 | 131 | C | MU60193 | ubiquitin-protein ligase | 6E-65 | E+M |
| ku2005-345 | 145 | C | MU52543 | Function unknown protein | 8E-56 | E+M |
| ku2005-350 | 412 | C | XP482452 | Putative protein kinase | 4E-7 | M+M |
| ku2005-363 | 265 | I | NP193740 | metallopeptidase | 1E-17 | E+M |
| ku2005-365 | 292 | C | AAT77309 | Function unknown protein | 3E-23 | E+M |
| ku2005-385 | 340 | I | NP174119 | carboxy-lyase | 1E-28 | E+M |
| ku2005-394 | 386 | I | AAO24554 | Function unknown protein | 5E-38 | M+M |
| ku2005-399 | 409 | I | NP921921 | Putative protein kinase | 3E-17 | M+M |

**Table S1.** The putative functions (as determined by BLAST in GenBank) of the other transcript derived fragments (TDFs) responsive to the resistance of *C. metuliferus* infected with PRSV (continued)

| **TDF** | **Size (bp)** | **I/C**[a] | **Accession number** | **Functional annotation** | **BLAST *E*-value** | **Restriction site**[b] |
|---|---|---|---|---|---|---|
| ku2005-409 | 735 | I | MU54137 | transferase | 1E-150 | M+M |
| ku2005-418 | 207 | C | AAK93736 | putative cysteinyl-tRNA synthetase | 1E-12 | M+M |
| ku2005-423 | 181 | I | MU54308 | 60S ribosomal protein L13A (RPL13aD) | 9E-28 | E+M |
| ku2005-432 | 511 | I | NP001030956 | RPS15 (RIBOSOMAL PROTEIN S15) | 2E-39 | M+M |
| ku2005-440 | 207 | I | 1710320A | Photosystem I 20 kD protein | 1E-22 | E+M |
| ku2005-445 | 651 | I | CAB72464 | protein-tyrosine-phosphatase-like protein | 2E-46 | M+M |
| ku2005-449 | 592 | I | XP450905 | putative annexin | 4E-63 | M+M |
| ku2005-457 | 189 | C | NP179688 | Function unknown protein | 5E-10 | E+M |
| ku2005-462 | 659 | C | BAD95352 | bZIP-like protein | 2E-20 | M+M |
| ku2005-481 | 735 | C | NP195540 | transferase, transferring glycosyl groups | 1E-32 | M+M |
| ku2005-482 | 543 | I | NP566542 | Function unknown protein | 2E-7 | M+M |
| ku2005-483 | 349 | I | NP172512 | Function unknown protein | 8E-39 | M+M |
| ku2005-509 | 181 | I | MU44891 | CA1 (CARBONIC ANHYDRASE 1) | 2E-72 | E+M |
| ku2005-510 | 114 | C | MU53888 | carbonate dehydratase | 4E-32 | E+M |
| ku2005-512 | 228 | I | MU43461 | NtEIG-A1 | 7E-23 | E+M |
| ku2005-515 | 176 | I | MU62474 | Function unknown protein | 2E-16 | E+M |
| ku2005-517 | 109 | I | MU47871 | bundle-sheath defective protein 2 family/bsd2 family | 2E-36 | E+M |
| ku2005-524 | 300 | C | MU51610 | Function unknown protein | 1E-112 | M+M |
| ku2005-529 | 480 | I | NP918587 | putative 33kDa oxygen evolvingprotein of photosystem II | 4E-27 | M+M |
| ku2005-544 | 224 | I | P08474 | Ribulose bisphosphate carboxylase small chain (RuBiSco) | 2E-20 | E+M |
| ku2005-554 | 11109 | I | AAM73656 | AER, auxin and ethylene cross-talk marker | 1E-13 | M+M |
| ku2005-561 | 872 | C | AAD11808 | syntaxin-related protein Nt-syr1 | 3E-57 | M+M |
| ku2005-567 | 200 | C | MU47813 | ATBI1 (BAX INHIBITOR 1) | 2E-75 | E+M |
| ku2005-570 | 636 | I | CAD87534 | putative xyloglucan endotransglycosylase | 2E-102 | M+M |
| ku2005-571 | 1165 | C | MU60959 | AER | 0 | M+M |
| ku2005-573 | 991 | C | NP196696 | catalytic | 9E-41 | M+M |
| ku2005-574 | 677 | C | NP177209 | Kinase | 3E-101 | M+M |
| ku2005-577 | 863 | C | MU43308 | syntaxin-related protein Nt-syr1 | 0 | M+M |
| ku2005-582 | 527 | I | MU47524 | thioredoxin h | 0 | M+M |
| ku2005-591 | 585 | I | CAB61890 | acetohydroxy acid isomeroreductase | 8E-96 | M+M |

**Table S1.** The putative functions (as determined by BLAST in GenBank) of the other transcript derived fragments (TDFs) responsive to the resistance of *C. metuliferus* infected with PRSV (continued)

| **TDF** | **Size (bp)** | **I/C**[a] | **Accession number** | **Functional annotation** | **BLAST *E*-value** | **Restriction site**[c] |
|---|---|---|---|---|---|---|
| ku2005-17 | 99 | C | | No significant similarity match | | E+M |
| ku2005-27 | 130 | I | | No significant similarity match | | E+M |
| ku2005-46 | 487 | C | | No significant similarity match | | M+M |
| ku2005-51 | 386 | I | | No significant similarity match | | M+M |
| ku2005-59 | 109 | C | | No significant similarity match | | E+M |
| ku2005-86 | 483 | C | | No significant similarity match | | M+M |
| ku2005-91 | 384 | I | | No significant similarity match | | M+M |
| ku2005-105 | 172 | I | | No significant similarity match | | E+M |
| ku2005-123 | 346 | ND | | No significant similarity match | | M+M |
| ku2005-128 | 249 | I | | No significant similarity match | | E+M |
| ku2005-137 | 251 | C | | No significant similarity match | | E+M |
| ku2005-141 | 342 | I | | No significant similarity match | | E+M |
| ku2005-149 | 136 | C | | No significant similarity match | | E+M |
| ku2005-189 | 448 | C | | No significant similarity match | | M+M |
| ku2005-227 | 479 | C | | No significant similarity match | | M+M |
| ku2005-252 | 133 | I | | No significant similarity match | | E+M |
| ku2005-262 | 111 | I | | No significant similarity match | | E+M |
| ku2005-317 | 170 | I | | No significant similarity match | | E+M |
| ku2005-380 | 430 | I | | No significant similarity match | | M+M |
| ku2005-404 | 196 | I | | No significant similarity match | | E+M |
| ku2005-417 | 303 | C | | No significant similarity match | | E+M |
| ku2005-427 | 722 | I | | No significant similarity match | | M+M |
| ku2005-435 | 678 | C | | No significant similarity match | | M+M |
| ku2005-500 | 439 | C | | No significant similarity match | | M+M |
| ku2005-519 | 93 | C | | No significant similarity match | | E+M |

[a] The transcription of TDFs is induced by virus infection (I) or constitutive (C) in *C. metuliferus*.
ND means non-detectable.

[b] The TDFs contain either restriction enzyme site of *EcoR* I or *Mse* I at the both ends.