

Gene	Primer Name	Primer Sequence
<i>At5g10760</i>	pRNAi-1-5'cl pRNAi-1-3'cl	CACCCTCGAGTCTAGAGCTAAAAGTGGAATCACACT C CGGAGGAAGGGAGGCAGTAAGACGAGAAGCCCAGC AACAC
<i>At5g10770</i>	pRNAi-70- 5'cl pRNAi-70- 3'cl	GTGTTGCTGGGCTTCTCGTCTTACTGCCTCCCTTCT CCG CGAATTCAAGCTTCGAACCAAGCTCCACGACG
<i>AED1</i>	pAED1-5'cl pAED1-3'cl	CACCGAGAGTAAGAGGGAGGTT ACAACCATTGGGAGCAAAAC
<i>AED1</i>	pAED1-5'q pAED1-5'q	ATTATGCTTTGCGTATGTCTCAATTGG GGACTCCACACGTGCTTGATCG
<i>At5g10770</i>	p10770-5'q p10770-3'q	CGATGGAGCTCAAGAAAGAGAGACTGA GCGAGCCTGGTCGAGTCTTAGGA
<i>AED4</i>	pAED4-5'q pAED4-3'q	TCGACGTTCTCACTGAGCTACTTGGA CCACCACTTGTGCCACTGTGTTC
<i>LLP1</i>	pLLP1-5'q pLLP1-3'q	TGAGTAAACAGCAGTTACGA TGACGCCATCAGAAGCAGGA
<i>PNP-A</i>	pPNP-5'q pPNP-3'q	AGCTGCTCAAGGAAAAGCTG AATGCATCGAACCCCTGTACC
<i>PR1</i>	pPR1-5'q pPR1-3'q	CTACGCAGAACAATAAGAGGCAAC TTGGCACATCCGAGTCTCACTG
<i>PR5</i>	pPR5-5'q pPR5-3'q	ATCGGGAGATTGCAAATACG GCGTAGCTATAGGCGTCAGG
<i>AvrRpm1</i>	pAVR-5'q pAVR-3'q	CGAACTCAGCCCCTACAGAC GTCGTTCTGCAGCTGAATTG
<i>TUBULIN</i>	pTUB-5'q pTUB-3'q	GTACCTTGAAGCTTGCTAATCCTA GTCAAAGGTGCAAAACCAAC
<i>UBIQUITIN</i>	pUBI-5'q pUBI-3'q	AGATCCAGGACAAGGTATTC CGCAGGACCAAGTGAAGAGTAG

Supplemental Table S2 Primers used in this study. Primers with names ending with 'cl' were used to amplify cDNA for cloning. Primers with names ending with 'q' were used for qPCR.

Supplemental Protocol S1 – MALDI-MS parameters for protein identification in 2D gel spots

Data collection:

PMF –

Number of shots: 1200

Mass Range: 900 – 5000 m/z

MS/MS

Parent Ion Isolation Assessment –

Automatic Precursor intensity optimization – 100 shots – Peak width < 0.8 m/z

Number of shots: 300 satisfactory spectra at final laser intensity

Fragmentation:

Relative Laser Intensity Boost: 45%

Precursor Ion Suppression

Number of shots: 800

Mass range: Precursor-dependent

Baseline subtraction: Tophat

Smoothing:

PMF:Chemical Noise 0.15 m/z

MS/MS:Savistky/Golay 0.15m/z 4 cycles

Peak picking

Algorithm: SNAP

PMF: 200 peaks, sig/noise>4

MS/MS: 200 peaks, sig/noise>3

Centroid width 0.2m/z, height 90%

Mascot searching:

Number of tryptic miscleavages allowed: 1

Peptide tolerance for PMF 50 ppm 150 ppm (without post calibration)

Peptide Mass Tolerance for MS/MS precursor 0.4 Da fragments 0.4 Da

Fixed mods – Carbamidomethyl Cystein

Variable modes – Methionine Oxidation