

Table S3. List of differentially expressed hydrolase transcripts in non-mycorrhizal *M. trun*

Locus Name Mt4.0v1

AAA-type ATPase family protein
ribonuclease 1
P-loop containing nucleoside triphosphate hydrolases superfamily protein
Arginase/deacetylase superfamily protein
Minichromosome maintenance (MCM2/3/5) family protein
Glycosyl hydrolase family protein
minichromosome maintenance (MCM2/3/5) family protein
apyrase 2
Helicase protein with RING/U-box domain
pleiotropic drug resistance 12
Protein phosphatase 2C family protein
Glycosyl hydrolase family protein
Glycosyl hydrolase family protein
minichromosome maintenance (MCM2/3/5) family protein
xyloglucan endotransglucosylase/hydrolase 5
Kinesin motor family protein
Plant invertase/pectin methylesterase inhibitor superfamily
chitinase A
P-loop containing nucleoside triphosphate hydrolases superfamily protein
purple acid phosphatase 27
P-loop containing nucleoside triphosphate hydrolases superfamily protein
P-loop containing nucleoside triphosphate hydrolases superfamily protein
n/a
Subtilisin-like serine endopeptidase family protein
xyloglucan endotransglucosylase/hydrolase 16
Ribonuclease T2 family protein
Plant invertase/pectin methylesterase inhibitor superfamily
P-loop containing nucleoside triphosphate hydrolases superfamily protein
RHO-related protein from plants 9
Minichromosome maintenance (MCM2/3/5) family protein
glycosyl hydrolase 9B13
Kinesin motor family protein
Plant invertase/pectin methylesterase inhibitor superfamily
heat shock protein 101
serine carboxypeptidase-like 9
basic chitinase
type one serine/threonine protein phosphatase 4
Plant invertase/pectin methylesterase inhibitor superfamily
ATP binding microtubule motor family protein

Disease resistance protein (TIR-NBS-LRR class) family
HAL2-like
Pectin lyase-like superfamily protein
Haloacid dehalogenase-like hydrolase (HAD) superfamily protein
glycosyl hydrolase 9B15
Subtilisin-like serine endopeptidase family protein
beta glucosidase 17
Cysteine proteinases superfamily protein

catula roots under continuous potassium deprivation. Transcripts were annotated with the Mt4.0v1

Gene ID	Regulation in -K	Log ₂ ratio +K vs -K
Medtr4g077880	DOWN	-1.40847
Medtr5g040940	DOWN	-1.08022
Medtr4g114120	DOWN	-1.00446
Medtr0088s0100	DOWN	-1.00083
Medtr4g071090	DOWN	-0.855956
Medtr5g062320	DOWN	-0.828105
Medtr4g122270	DOWN	-0.817807
Medtr7g085120	DOWN	-0.797378
Medtr1g044120	DOWN	-0.773212
Medtr4g011630	DOWN	-0.77298
Medtr5g024340	DOWN	-0.768248
Medtr5g062430	DOWN	-0.758044
Medtr5g069800	DOWN	-0.756467
Medtr8g090000	DOWN	-0.736981
Medtr7g084750	DOWN	-0.731848
Medtr5g094310	DOWN	-0.725471
Medtr8g042910	DOWN	-0.724164
Medtr2g040830	DOWN	-0.717756
Medtr5g066320	DOWN	-0.694651
Medtr4g037670	DOWN	-0.693954
Medtr1g075680	DOWN	-0.692995
Medtr1g017540	DOWN	-0.671819
Medtr0002s1060	DOWN	-0.660572
Medtr7g081420	DOWN	-0.658442
Medtr3g084630	DOWN	-0.636586
Medtr5g041080	DOWN	-0.635431
Medtr4g035980	DOWN	-0.634356
Medtr7g105030	DOWN	-0.626468
Medtr6g087980	DOWN	-0.621774
Medtr4g096700	DOWN	-0.617833
Medtr1g088190	DOWN	-0.60876
Medtr3g055940	DOWN	-0.598559
Medtr2g044810	DOWN	-0.595938
Medtr4g109450	UP	0.606699
Medtr2g018630	UP	0.626348
Medtr8g074335	UP	0.627604
Medtr5g081230	UP	0.658689
Medtr4g025690	UP	0.694371
Medtr4g124650	UP	0.794908

Medtr6g076090	UP	1.01477
Medtr4g090525	UP	1.04389
Medtr3g030540	UP	1.07383
Medtr2g035440	UP	1.11761
Medtr5g010000	UP	1.12027
Medtr1g006990	UP	1.20378
Medtr3g026400	UP	1.3988
Medtr4g080360	UP	1.45599

version of *M. truncatula* genomic database (<http://jcvi.org/medicago/index.php>).