**Table S3. Differentially expressed genes in *rsa1-1* under salt stress as determined by microarray analysis.**

**Table S3A. Genes with increased expression in *rsa1-1* under salt stress as determined by microarray analysis.**

| AGI ID | Fold Change | P Value | Gene Description | Go Term (Biological Process) |
|---|---|---|---|---|
| AT1G15330 | 4.14 | 0.000002 | Cystathionine beta-synthase (CBS) protein | developmental processes |
| AT2G36640 | 2.29 | 0.008510 | embryonic cell protein 63 | developmental processes |
| AT2G42560 | 2.04 | 0.003709 | LEA domain-containing protein | developmental processes |
| AT3G15670 | 4.20 | 0.000018 | Late embryogenesis abundant protein (LEA) family protein | developmental processes |
| AT3G17520 | 2.09 | 0.000251 | Late embryogenesis abundant protein (LEA) family protein | developmental processes |
| AT3G22490 | 2.15 | 0.000591 | Seed maturation protein | developmental processes |
| AT3G51810 | 3.42 | 0.000012 | Stress induced protein | developmental processes |
| AT4G21020 | 2.43 | 0.000719 | Late embryogenesis abundant protein (LEA) family protein | developmental processes |
| AT4G28520 | 2.18 | 0.000998 | cruciferin 3 | developmental processes |
| AT4G36600 | 2.84 | 0.002876 | Late embryogenesis abundant (LEA) protein | developmental processes |
| AT5G44120 | 2.07 | 0.0004387 | RmlC-like cupins superfamily protein | developmental processes |
| AT5G44310 | 2.63 | 0.0013813 | Late embryogenesis abundant protein (LEA) family protein | developmental processes |
| AT1G08430 | 2.44 | 0.000033 | aluminum-activated malate transporter 1 | other biological processes |
| AT1G22690 | 2.12 | 0.000031 | Gibberellin-regulated family protein | other biological processes |
| AT1G48660 | 2.58 | 0.000017 | Auxin-responsive GH3 family protein | other biological processes |
| AT3G01570 | 2.68 | 0.000005 | Oleosin family protein | other biological processes |
| AT2G28490 | 2.05 | 0.000800 | RmlC-like cupins superfamily protein | other biological processes |
| AT2G42750 | 2.02 | 0.000537 | DNAJ heat shock N-terminal domain-containing protein | other cellular processes |
| AT3G18290 | 2.26 | 0.000017 | zinc finger protein-related | other cellular processes |
| AT1G04560 | 2.03 | 0.002847 | AWPM-19-like family protein | other cellular processes |
| AT1G33790 | 2.95 | 0.000024 | jacalin lectin family protein | other cellular processes |
| AT1G47400 | 5.10 | 0.000101 | unknown protein | other cellular processes |
| AT2G47780 | 5.11 | 0.000002 | Rubber elongation factor protein (REF) | other cellular processes |
| AT3G22640 | 3.06 | 0.007130 | cupin family protein | other cellular processes |
| AT4G36700 | 2.25 | 0.000202 | RmlC-like cupins superfamily protein | other cellular processes |
| AT4G12340 | 3.72 | 0.000000 | copper ion binding | other cellular processes |
| AT1G23020 | 2.89 | 0.000007 | ferric reduction oxidase 3 | other metabolic processes |
| AT1G48470 | 2.19 | 0.000870 | glutamine synthetase 1;5 | other metabolic processes |
| AT1G56430 | 2.03 | 0.007985 | nicotianamine synthase 4 | other metabolic processes |
| AT2G29330 | 2.68 | 0.000413 | tropinone reductase | other metabolic processes |
| AT3G21720 | 3.16 | 0.000001 | isocitrate lyase | other metabolic processes |
| AT3G48700 | 2.20 | 0.000168 | carboxyesterase 13 | other metabolic processes |

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|---|---|---|---|---|
| AT5G03860 | 4.97 | 0.000000 | malate synthase | other metabolic processes |
| AT5G23020 | 2.04 | 0.0002730 | 2-isopropylmalate synthase 2 | other metabolic processes |
| AT5G01300 | 2.02 | 0.000398 | PEBP (phosphatidylethanolamine-binding protein) family protein | other metabolic processes |
| AT3G54940 | 2.05 | 0.001171 | Papain family cysteine protease | protein metabolism |
| AT5G53450 | 2.94 | 0.0000218 | OBP3-responsive gene 1 | protein metabolism |
| AT1G05680 | 2.26 | 0.000054 | Uridine diphosphate glycosyltransferase 74E2 | response to abiotic or biotic stimulus |
| AT1G32560 | 2.17 | 0.002025 | Late embryogenesis abundant protein 4-1 | response to abiotic or biotic stimulus |
| AT2G21490 | 3.73 | 0.000096 | dehydrin LEA | response to abiotic or biotic stimulus |
| AT3G14880 | 2.08 | 0.000041 | transcription factor-related | response to abiotic or biotic stimulus |
| AT3G50980 | 2.19 | 0.000054 | dehydrin xero 1 | response to abiotic or biotic stimulus |
| AT4G19690 | 6.40 | 0.000004 | iron-regulated transporter 1 | response to abiotic or biotic stimulus |
| AT5G06760 | 2.10 | 0.001487 | Late Embryogenesis Abundant 4-5 | response to abiotic or biotic stimulus |
| AT5G10140 | 4.84 | 0.0000000 | K-box region and MADS-box transcription factor family protein | response to abiotic or biotic stimulus |
| AT5G13740 | 2.05 | 0.0000623 | zinc induced facilitator 1 | response to abiotic or biotic stimulus |
| AT1G71400 | 2.37 | 0.000001 | receptor like protein 12 | response to stress |
| AT1G73120 | 2.11 | 0.000268 | unknown protein | response to stress |
| AT1G75830 | 2.14 | 0.008293 | low-molecular-weight cysteine-rich 67 | response to stress |
| AT2G15010 | 4.78 | 0.000101 | Plant thionin | response to stress |
| AT2G23110 | 2.44 | 0.000304 | Late embryogenesis abundant protein, group 6 | response to stress |
| AT3G18290 | 2.26 | 0.000017 | zinc finger protein-related | response to stress |
| AT1G03790 | 2.01 | 0.000582 | Zinc finger C-x8-C-x5-C-x3-H type family protein | transcription,DNA-dependent |
| AT3G56980 | 3.71 | 0.000019 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | transcription,DNA-dependent |
| AT5G04150 | 5.57 | 0.000009 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | transcription,DNA-dependent |
| AT4G18650 | 2.30 | 0.000496 | transcription factor-related | transcription,DNA-dependent |
| AT4G16160 | 2.34 | 0.000041 | Mitochondrial import inner membrane translocase subunit | transport |
| AT4G27140 | 12.48 | 0.000000 | seed storage albumin 1 | transport |
| AT5G01870 | 2.34 | 0.000041 | lipid-transfer protein | transport |
| AT1G02700 | 2.24 | 0.000017 | unknown protein | unknown biological processes |
| AT1G65090 | 3.28 | 0.000012 | unknown protein | unknown biological processes |
| AT1G68250 | 2.75 | 0.000118 | unknown protein | unknown biological processes |
| AT2G19320 | 2.19 | 0.000552 | unknown protein | unknown biological processes |
| AT2G21820 | 2.19 | 0.002025 | unknown protein | unknown biological processes |
| AT3G19920 | 2.20 | 0.000512 | unknown protein | unknown biological processes |
| AT5G05250 | 2.45 | 0.000357 | unknown protein | unknown biological processes |
| AT5G07330 | 2.53 | 0.0001317 | unknown protein | unknown biological processes |
| AT5G66780 | 4.49 | 0.0000069 | unknown protein | unknown biological processes |
| AT5G67370 | 2.21 | 0.0000664 | unknown protein | unknown biological processes |

**Table S3B. Genes with reduced expression in *rsa1-1* under salt stress as determined by microarray analysis.**

| AGI ID | Fold Change | P Value | Gene Description | Go Term (Biological Process) |
|---|---|---|---|---|
| AT1G59840 | 5.34 | 0.000000 | cofactor assembly of complex C | cell organization and biogenesis |
| AT2G45220 | 2.91 | 0.000007 | Plant invertase/pectin methylesterase inhibitor superfamily | cell organization and biogenesis |
| AT4G01630 | 2.07 | 0.000069 | expansin A17 | cell organization and biogenesis |
| AT1G11190 | 2.58 | 0.000054 | bifunctional nuclease i | DNA or RNA metabolism |
| AT1G45474 | 3.39 | 0.000000 | photosystem I light harvesting complex gene 5 | electron transport or energy pathways |
| AT2G05510 | 2.10 | 0.000130 | Glycine-rich protein | other biological processes |
| AT2G16005 | 2.55 | 0.004500 | MD-2-related lipid recognition domain-containing protein | other biological processes |
| AT2G33790 | 3.95 | 0.000000 | arabinogalactan protein 30 | other biological processes |
| AT5G23830 | 2.74 | 0.000012 | MD-2-related lipid recognition domain-containing protein | other biological processes |
| AT1G21100 | 2.48 | 0.000632 | O-methyltransferase family protein | other cellular processes |
| AT3G09220 | 2.16 | 0.000035 | laccase 7 | other cellular processes |
| AT1G05660 | 2.87 | 0.000066 | Pectin lyase-like superfamily protein | other metabolic processes |
| AT1G14120 | 2.37 | 0.002630 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | other metabolic processes |
| AT1G30700 | 2.49 | 0.000049 | FAD-binding Berberine family protein | other metabolic processes |
| AT1G50560 | 2.16 | 0.000109 | cytochrome P450, family 705, subfamily A, polypeptide 25 | other metabolic processes |
| AT2G36690 | 2.08 | 0.000189 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | other metabolic processes |
| AT3G13784 | 2.09 | 0.001985 | cell wall invertase 5 | other metabolic processes |
| AT3G25830 | 2.71 | 0.001655 | terpene synthase-like sequence-1,8-cineole | other metabolic processes |
| AT3G43670 | 2.60 | 0.000133 | Copper amine oxidase family protein | other metabolic processes |
| AT3G46700 | 2.13 | 0.000591 | UDP-Glycosyltransferase superfamily protein | other metabolic processes |
| AT4G13310 | 2.82 | 0.000005 | cytochrome P450, family 71, subfamily A, polypeptide 20 | other metabolic processes |
| AT4G39120 | 5.96 | 0.000000 | myo-inositol monophosphatase like 2 | other metabolic processes |
| AT5G04120 | 3.04 | 0.000206 | Phosphoglycerate mutase family protein | other metabolic processes |
| AT5G17530 | 3.68 | 0.000000 | phosphoglucosamine mutase family protein | other metabolic processes |
| AT5G24140 | 2.03 | 0.001785 | squalene monooxygenase 2 | other metabolic processes |
| AT5G28510 | 2.98 | 0.000000 | beta glucosidase 24 | other metabolic processes |
| AT5G42580 | 2.29 | 0.002919 | cytochrome P450, family 705, subfamily A, polypeptide 12 | other metabolic processes |
| AT5G42600 | 2.69 | 0.000857 | marneral synthase | other metabolic processes |
| AT1G24610 | 2.63 | 0.000000 | Rubisco methyltransferase family protein | other metabolic processes |
| AT1G35250 | 2.23 | 0.000041 | Thioesterase superfamily protein | other metabolic processes |
| AT5G28520 | 3.87 | 0.000018 | Mannose-binding lectin superfamily protein | other metabolic processes |
| AT3G05350 | 2.52 | 0.000001 | Metallopeptidase M24 family protein | protein metabolism |
| AT3G46280 | 2.35 | 0.000048 | protein kinase-related | protein metabolism |

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|---|---|---|---|---|
| AT4G04460 | 2.16 | 0.000052 | Saposin-like aspartyl protease family protein | protein metabolism |
| AT5G04200 | 2.00 | 0.000005 | metacaspase 9 | protein metabolism |
| AT1G14960 | 2.05 | 0.016870 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | response to abiotic or biotic stimulus |
| AT1G70850 | 2.02 | 0.000142 | MLP-like protein 34 | response to abiotic or biotic stimulus |
| AT1G73330 | 2.10 | 0.000241 | drought-repressed 4 | response to abiotic or biotic stimulus |
| AT2G01520 | 2.92 | 0.001365 | MLP-like protein 328 | response to abiotic or biotic stimulus |
| AT3G01290 | 2.01 | 0.000504 | SPFH/Band 7/PHB domain-containing membrane-associated protein family | response to abiotic or biotic stimulus |
| AT3G11340 | 2.28 | 0.000010 | UDP-Glycosyltransferase superfamily protein | response to abiotic or biotic stimulus |
| AT3G15570 | 2.79 | 0.000315 | Phototropic-responsive NPH3 family protein | response to abiotic or biotic stimulus |
| AT3G26460 | 3.23 | 0.000071 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | response to abiotic or biotic stimulus |
| AT4G10250 | 2.06 | 0.000385 | HSP20-like chaperones superfamily protein | response to abiotic or biotic stimulus |
| AT4G12470 | 2.01 | 0.009553 | azelaic acid induced 1 | response to abiotic or biotic stimulus |
| AT4G12480 | 2.20 | 0.000135 | lipid-transfer protein | response to abiotic or biotic stimulus |
| AT4G14060 | 2.03 | 0.002251 | Polyketide cyclase/dehydrase and lipid transport superfamily protein | response to abiotic or biotic stimulus |
| AT5G38030 | 2.31 | 0.000023 | MATE efflux family protein | response to abiotic or biotic stimulus |
| AT5G47450 | 2.97 | 0.000009 | tonoplast intrinsic protein 2;3 | response to abiotic or biotic stimulus |
| AT5G59720 | 4.03 | 0.000001 | heat shock protein 18.2 | response to abiotic or biotic stimulus |
| AT1G52200 | 2.95 | 0.000003 | PLAC8 family protein | response to stress |
| AT1G66100 | 3.11 | 0.000128 | Plant thionin | response to stress |
| AT1G78000 | 2.00 | 0.000012 | sulfate transporter 1;2 | response to stress |
| AT2G40300 | 2.05 | 0.000034 | ferritin 4 | response to stress |
| AT5G14130 | 2.16 | 0.000017 | Peroxidase superfamily protein | response to stress |
| AT5G44910 | 2.18 | 0.000681 | Toll-Interleukin-Resistance (TIR) domain family protein | response to stress |
| AT2G39040 | 1.92 | 0.000027 | Peroxidase superfamily protein | response to stress |
| AT1G10480 | 2.18 | 0.000017 | zinc finger protein 5 | signal transduction |
| AT2G34180 | 2.19 | 0.000229 | CBL-interacting protein kinase 13 | signal transduction |
| AT1G79950 | 2.68 | 0.000104 | RAD3-like DNA-binding helicase protein | transcription,DNA-dependent |
| AT2G18370 | 2.13 | 0.000012 | lipid-transfer protein | transport |
| AT2G32270 | 2.27 | 0.000023 | zinc transporter 3 precursor | transport |
| AT2G39380 | 2.36 | 0.000007 | exocyst subunit exo70 family protein H2 | transport |
| AT3G22570 | 2.01 | 0.000026 | lipid-transfer protein | transport |
| AT3G24300 | 2.41 | 0.000026 | ammonium transporter 1;3 | transport |
| AT3G45710 | 2.16 | 0.000168 | Major facilitator superfamily protein | transport |
| AT3G58550 | 2.14 | 0.000067 | lipid-transfer protein | transport |
| AT4G12510 | 2.08 | 0.000049 | lipid-transfer protein | transport |
| AT4G12550 | 5.77 | 0.000004 | Auxin-Induced in Root cultures 1 | transport |
| AT5G46900 | 2.21 | 0.000140 | lipid-transfer protein | transport |
| AT5G60660 | 2.31 | 0.000020 | plasma membrane intrinsic protein 2;4 | transport |
| AT1G55240 | 2.40 | 0.000049 | unknown protein | unknown biological processes |

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|---|---|---|---|---|
| AT2G37750 | 2.49 | 0.000005 | unknown protein | unknown biological processes |
| AT4G03150 | 3.12 | 0.000048 | unknown protein | unknown biological processes |
| AT4G37090 | 3.03 | 0.000018 | unknown protein | unknown biological processes |
| AT5G26270 | 2.52 | 0.000047 | unknown protein | unknown biological processes |