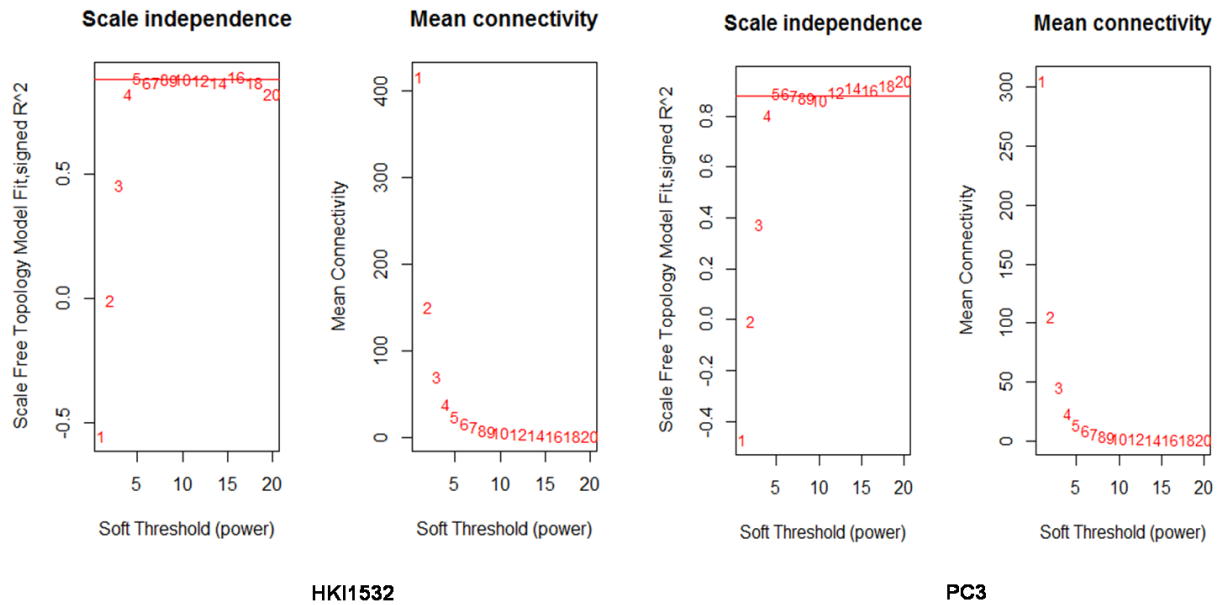
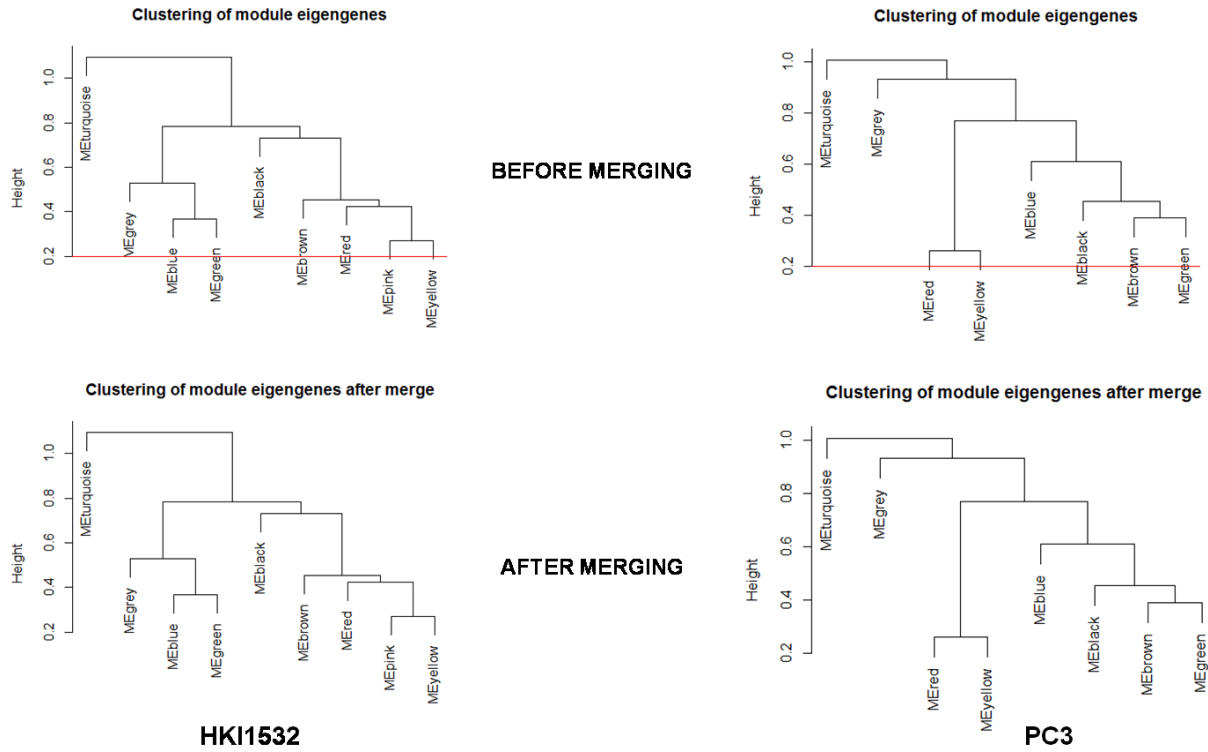


Functional interactions of drought-responsive genes indentified through genome-wide expression assay in maize



Supplementary Figure. S1. Analysis of network topology for various soft-thresholding powers.



Supplementary Figure. S2. Clustering of module eigenvectors (ME) of the co-expression networks comprising nine and eight modules for HKI1532 and PC3 respectively.

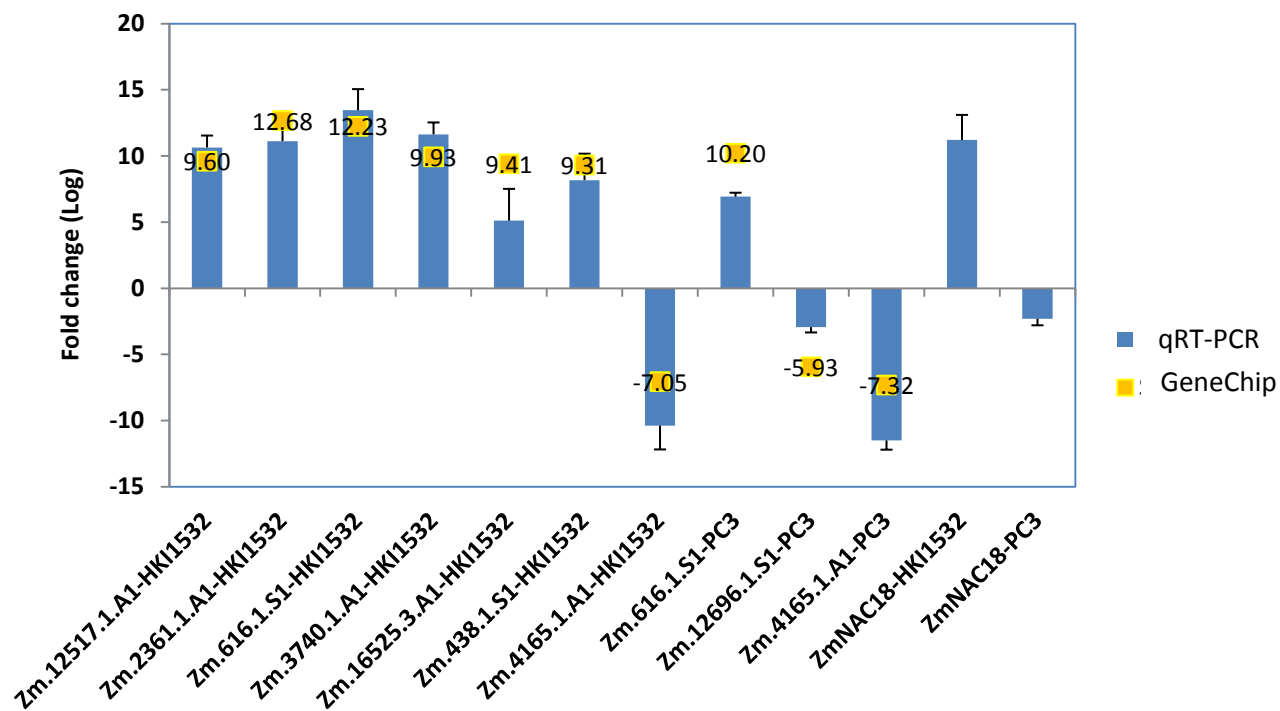
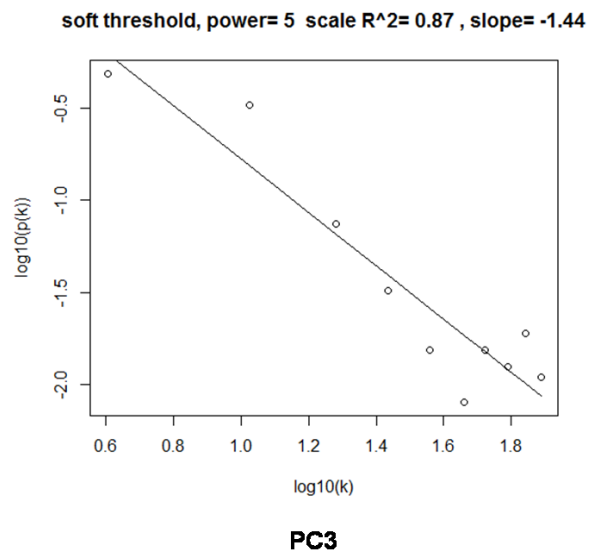
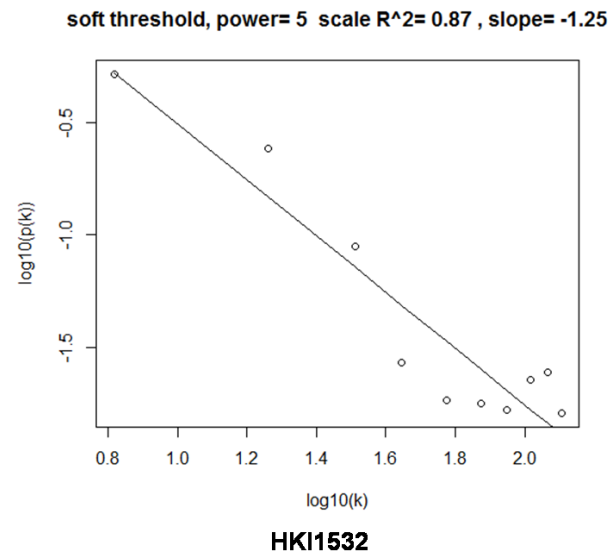


Figure S3. Validation of selected DEGs from GeneChip by qRT-PCR tested in HKI1532 (Tolerant) and PC3 (Sensitive) genotypes. ZmNAC18, a previously published drought-responsive gene, is used as an external control. Genechip values are given on the label (orange).



Supplementary Figure S4. Scatter plot between the number of edges ($\log(k)$) and the probability of a node having k edges ($P(k)$).

Supplementary Table S1. Selected DEGs from GeneChip for validation by qRT-PCR.

| Probe set ID | Genotype studied | Annotation | Primer sequence | Primer T _m |
|-----------------------|------------------|---|---|-----------------------|
| Zm.12517.1.A1_at | HKI1532 | kda class iii heat shock protein | F: AGGTCACCATCGCCTAGAA R: AAAGAGCACTCCACCCATTC | 62.4 62.2 |
| Zm.2361.1.A1_at | HKI1532 | heat shock protein | F: AAGAACGTCCAGATCACCGGCTA R: ATCACTGCACACAACGGGAGTACA | 60.6 60.2 |
| Zm.616.1.S1_at | HKI1532 | tonoplast intrinsic protein | F: CGCCAGAGGACTACTAGCTTGAAA R: ACCTGATTACCGTCTCCAACACA | 57.9 61.3 |
| Zm.3740.1.A1_at | HKI1532 | kda class iv heat shock protein precursor | F: CGTCCAAGGCTGAGATGTGAATGT R: AACGGGATCAATACGCACCGGATA | 61.0 63.9 |
| Zm.16525.3.A1_x_at | HKI1532 | heat shock protein 82 | F: GTATGATCAGGTCCGCCATAG R: GTCAGAGACCACAACCTTCTC | 61.6 61.8 |
| Zm.438.1.S1_at | HKI1532 | heat shock protein 101 | F: TGTCTCTCTTTACGATCCGGTGT R: ATCTCCTCCTGGATCAGCATCTTC | 57.8 58.6 |
| Zm.4165.1.A1_at | HKI1532 | phosphoenolpyruvate carboxykinase | F: AAGAAGAACTTCGAGGTGTTTCGCC R: CGTCGTCGTCGTAATCATCTTCAC | 60.8 59.4 |
| Zm.616.1.S1_at | PC3 | tonoplast intrinsic protein | F: CGCCAGAGGACTACTAGCTTGAAA R: ACCTGATTACCGTCTCCAACACA | 57.9 61.3 |
| Zm.12696.1.S1_at | PC3 | myb family transcription expressed | F: TGCTCGATTCTTCGTCATGGAAC R: CAGCGTCACAATCAATGCGG | 61.2 60.5 |
| Zm.4165.1.A1_at | PC3 | phosphoenolpyruvate carboxykinase | F: AAGAAGAACTTCGAGGTGTTTCGCC R: CGTCGTCGTCGTAATCATCTTCAC | 60.8 59.4 |
| ZmNAC18* (Control) | HKI1532 | Drought-responsive transcription factor | F: GAAGAACGAGTGGGAGAAGATG R: ACGAGTGCGAGTGTGATTG | 62.1 62.3 |
| ZmNAC18* (Control) | PC3 | Drought-responsive transcription factor | F: GAAGAACGAGTGGGAGAAGATG R: ACGAGTGCGAGTGTGATTG | 62.1 62.3 |

*Kaliyugam S, Rinku S, Krishan K, Yadav SK, Firoz H, Nepolean T (2014). Genome-wide identification and expression pattern of drought-responsive members of the NAC family in maize. *Meta Gene* 2:407-417.

Supplementary Table S2. Drought-responsive DEGs exclusively up-regulated in HKI1532.

| Probe ID | Sequence description | log FC | Absolute FC | <i>p</i> value |
|------------------|--|-------------|-------------|----------------|
| Zm.622.1.S1_at | Tonoplast intrinsic protein | 7.532183671 | 185.1028978 | 6.35E-06 |
| Zm.19048.1.A1_at | Sorbitol transporter | 5.545369448 | 46.70060867 | 5.97E-07 |
| Zm.12135.1.A1_at | Cysteine protease 1 precursor | 4.820477483 | 28.25584605 | 3.58E-05 |
| Zm.12789.1.A1_at | Cytochrome P450 | 4.228409653 | 18.74468469 | 5.52E-07 |
| Zm.17956.1.A1_at | Ethylene responsive element binding factor 5 | 4.14001278 | 17.63063803 | 4.22E-09 |
| Zm.280.1.A1_at | luminal binding protein | 4.118441629 | 17.36898603 | 2.67E-07 |
| Zm.13983.1.S1_at | Embryo-specific protein | 3.972934156 | 15.70262835 | 4.22E-06 |
| Zm.13506.1.S1_at | Seed maturation protein | 3.894397187 | 14.87066426 | 2.82E-06 |
| Zm.395.1.S1_at | Luminal binding protein | 3.795452084 | 13.88496932 | 6.39E-08 |
| Zm.2671.1.S1_at | Transposon protein en spm sub-class | 3.616637828 | 12.26638156 | 0.000137 |
| Zm.17912.1.S1_at | Inositol phosphorylceramide synthase1 | 3.598109682 | 12.10985497 | 2.51E-05 |
| Zm.9422.1.A1_at | WRKY transcription factor 24 | 3.40291766 | 10.57743313 | 3.97E-05 |
| Zm.4089.2.S1_at | Hexose transporter | 3.066212285 | 8.375714608 | 1.62E-05 |

Table S2 (continued).

| Probe ID | Sequence description | log FC | Absolute FC | <i>p</i> value |
|------------------|---|-------------|-------------|----------------|
| Zm.2793.1.A1_at | Aldehyde dehydrogenase family 2 member mitochondrial-like | 2.987241482 | 7.929563666 | 0.000106 |
| Zm.16211.1.S1_at | Cell division protein aaa ATPase family | 2.805479082 | 6.990904283 | 5.42E-08 |
| Zm.12825.1.S1_at | Tonoplast intrinsic protein | 2.783585218 | 6.885613572 | 0.000197 |
| Zm.54.1.S1_at | Alpha amylase isozyme 3e precursor | 2.630964856 | 6.194401324 | 4.2E-06 |
| Zm.8865.1.A1_at | Integral membrane protein | 2.551747452 | 5.863440526 | 1.55E-05 |
| Zm.12796.1.A1_at | Uncharacterized conserved expressed | 2.547823296 | 5.847513537 | 1.24E-05 |
| Zm.15061.1.S1_at | Calmodulin-like protein 14 | 2.496638576 | 5.64368934 | 4.71E-06 |
| Zm.12327.1.A1_at | Heat shock transcription factor | 2.98886809 | 7.938509121 | 1.64E-08 |

Supplementary Table S3. Transcription factors unique to HKI1532 and their expression values under water stress.

| Probe ID | TF | Sequence description | log FC | Absolute FC |
|------------------|----------|--|----------|-------------|
| Zm.15542.1.S1_at | ARF | IAA9-auxin responsive aux iaa family member | 2.666122 | 6.347206295 |
| Zm.6938.1.A1_at | bHLH | | 2.85758 | 7.247982958 |
| Zm.10293.1.S1_at | bZIP | Light inducible protein cprf-2 | 2.828891 | 7.105276351 |
| Zm.3849.1.S1_at | bZIP | Glutamate decarboxylase | 4.095848 | 17.0990915 |
| Zm.16522.1.S1_at | C3H | Kh domain-containing protein | 2.379782 | 5.204579588 |
| Zm.5544.1.A1_at | C3H | Zinc finger ccch domain-containing protein 11-like | 2.430087 | 5.3892598 |
| Zm.17956.1.A1_at | ERF | Ethylene responsive element binding factor 5 | 4.140013 | 17.63063803 |
| Zm.7368.1.S1_at | ERF | Dehydration-responsive element binding protein 2c | 2.835316 | 7.136992221 |
| Zm.14048.1.A1_at | GRAS | Stearoyl-acyl-carrier protein desaturase | 2.93234 | 7.633474837 |
| Zm.12928.1.A1_at | HB-other | E3- ubiquitin protein ligase ring1-like | 2.978913 | 7.883918966 |
| Zm.16320.1.S1_at | HB-other | Protein binding protein | 3.672082 | 12.74696862 |
| Zm.5362.1.A1_at | HB-other | Rop guanine nucleotide exchange factor | 2.981591 | 7.898568637 |
| Zm.4514.1.A1_at | HD-ZIP | Homeodomain leucine zipper family IV protein | 2.752628 | 6.73943558 |

| | | | | |
|--------------------|-------------|---|----------|-------------|
| Zm.10032.1.S1_at | HSF | Heat shock factor protein 4 | 3.452248 | 10.94536587 |
| Zm.12327.1.A1_at | HSF | Protein | 2.988868 | 7.938509121 |
| Zm.15325.1.A1_at | HSF | Heat shock factor protein hsf30 | 2.68685 | 6.439059398 |
| Zm.15688.1.S1_at | HSF | | 5.270073 | 38.58779506 |
| Zm.11950.1.A1_at | LBD | Receptor like protein kinase hsl1-like | 2.951758 | 7.736914835 |
| Zm.13464.1.S1_at | LBD | ATP binding protein | 3.685086 | 12.86237845 |
| Zm.13947.3.A1_at | LBD | cipk like protein expressed | 2.738064 | 6.671742128 |
| Zm.13996.1.S1_at | LBD | Serine threonine protein kinase ht1-like | 3.256065 | 9.55373685 |
| Zm.243.1.A1_at | LBD | g-type lectin s- receptor like serine threonine protein kinase | 2.979453 | 7.886871182 |
| Zm.6021.1.A1_at | LBD | Receptor protein | 2.570086 | 5.938449094 |
| Zm.721.1.A1_at | LBD | Protein kinase pti1 | 2.555573 | 5.879009144 |
| Zm.11627.1.A1_x_at | MIKC | mads box transcription factor 26 | 3.177698 | 9.048621014 |
| Zm.8773.1.A1_at | MYB | Uncharacterized protein | 5.167537 | 35.94045447 |
| Zm.10778.1.A1_a_at | MYB_related | Glabura2 expression modulator | 3.049708 | 8.280444176 |
| Zm.18735.1.A1_at | MYB_related | Ribonucleoprotein like protein | 2.537344 | 5.805194862 |
| Zm.4251.1.S1_at | MYB_related | Protein disulfide | 3.249836 | 9.512578603 |

| | | | | |
|---------------------|-------------|--|----------|-------------|
| | | isomerase | | |
| Zm.4558.1.S1_at | MYB_related | Ectonucleotide pyrophosphatase phosphodiesterase family member | 2.75114 | 6.732487099 |
| Zm.4967.1.A1_at | MYB_related | Telomere repeat binding protein 5- like | 2.834515 | 7.13303164 |
| Zm.7870.1.S1_at | MYB_related | Protein | 4.405614 | 21.19444524 |
| Zm.10304.1.S1_at | NAC | 4 protein | 3.263138 | 9.60069243 |
| Zm.12113.1.A1_at | NAC | | 2.430397 | 5.390417005 |
| Zm.5882.1.A1_at | NAC | 4 protein | 3.850999 | 14.42999231 |
| Zm.13736.1.A1_at | NF-X1 | nf-x1-type zinc finger protein | 4.153184 | 17.7923362 |
| ZmAffx.1300.1.S1_at | SBP | | 3.850849 | 14.42849441 |
| Zm.17900.1.S1_at | TCP | Chaperone protein dnaj | 3.138252 | 8.804565395 |
| Zm.5083.1.A1_a_at | TCP | dnaj protein homolog | 4.425882 | 21.49430364 |
| Zm.5083.2.A1_x_at | TCP | dnaj protein homolog | 7.830876 | 227.6819593 |
| Zm.5083.3.A1_at | TCP | dnaj protein homolog | 7.445254 | 174.2788527 |
| Zm.10017.1.A1_at | WRKY | Wrky69- superfamily of tfs having wrky and zinc finger domains | 3.299544 | 9.846044689 |
| Zm.9422.1.A1_at | WRKY | | 3.402918 | 10.57743313 |
| Zm.8827.1.A1_at | YABBY | | 3.153776 | 8.899821159 |

Supplementary Table S4. A set of 174 selected drought-responsive genes from HKI1532 and their co-expression network groups.

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|---------------------|--|--|----------------|------------|-------|
| Zm.10017.1.A1_at | WRKY | WRKY | 9.8460 | up | G1 |
| Zm.10304.1.S1_at | NAC | NAC | 9.6007 | up | G1 |
| Zm.12113.1.A1_at | NAC | NAC | 5.3904 | up | G1 |
| Zm.12327.1.A1_at | HSF | HSF | 7.9385 | up | G1 |
| Zm.16211.1.S1_at | ERF | ERF | 6.9909 | up | G1 |
| Zm.17956.1.A1_at | AP2 | AP2 | 17.6306 | up | G1 |
| Zm.18735.1.A1_at | MYB_related | MYB_related | 5.8052 | up | G1 |
| Zm.4558.1.S1_at | MYB_related | MYB_related | 6.7325 | up | G1 |
| Zm.5112.1.A1_at | atpase subunit 8 | ATPase | 7.9600 | up | G1 |
| Zm.5882.1.A1_at | NAC | NAC | 14.4300 | up | G1 |
| Zm.7368.1.S1_at | AP2 | AP2 | 7.1370 | up | G1 |
| Zm.7870.1.S1_at | MYB_related | MYB_related | 21.1944 | up | G1 |
| Zm.8773.1.A1_at | MYB | MYB | 35.9405 | up | G1 |
| Zm.8865.1.A1_at | WRKY | WRKY | 5.8634 | up | G1 |
| Zm.9422.1.A1_at | WRKY | WRKY | 10.5774 | up | G1 |
| ZmAffx.1219.1.S1_s_ | atp synthase | ATP_synthase | 8.7593 | up | G1 |
| at | subunit alpha | | | | |
| ZmAffx.1300.1.S1_at | SBP | SBP | 14.4285 | up | G1 |
| ZmAffx.1401.1.S1_at | atpase subunit 8 | ATPase | 22.6600 | up | G1 |
| ZmAffx.1474.1.S1_s_ | atpase subunit 9 | ATPase | 18.6416 | up | G1 |
| at | | | | | |
| Zm.10383.4.S1_a_at | NF-YB | NF-YB | 5.6872 | up | G1 |
| Zm.11645.1.A1_at | ring-h2 zinc finger protein atl6-like | Ring_H2_ZnFP | 16.5903 | up | G1 |
| Zm.11783.1.A1_at | MYB_related | MYB_related | 25.2762 | up | G1 |
| Zm.13603.1.S1_at | WRKY | WRKY | 10.8794 | up | G1 |
| Zm.13801.1.S1_at | ERF | ERF | 6.0215 | up | G1 |
| Zm.2629.1.S1_at | bZIP | bZIP | 9.5268 | up | G1 |
| Zm.2807.1.A1_at | zf-C2H2_6 | C2H2 | 16.8529 | up | G1 |
| Zm.4838.1.A1_at | NAC | NAC | 10.5986 | up | G1 |
| Zm.5212.1.S1_at | ERF | ERF | 5.0598 | up | G1 |
| Zm.5979.1.A1_at | MYB_related | MYB_related | 22.6368 | up | G1 |
| Zm.6938.1.A1_at | bHLH | bHLH | 7.2480 | up | G1 |
| Zm.7780.1.A1_at | abscisic acid 8 - hydroxylase | ABA-8H | 9.1029 | up | G1 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|------------------|---|--|----------------|------------|-------|
| Zm.8972.1.S1_at | AP2 | AP2 | 136.1449 | up | G1 |
| Zm.9463.1.A1_at | ERF | ERF | 31.6441 | up | G1 |
| Zm.9645.1.S1_at | MYB_related | MYB_related | 5.0466 | up | G1 |
| Zm.9930.1.A1_at | Similar to Absciscic stress ripening protein 1 ef hand family protein | ASR_protein | 31.2614 | up | G1 |
| Zm.11848.1.A1_at | Pkinase | EF_hand_4 | 29.6250 | up | G2 |
| Zm.11950.1.A1_at | calcium-dependent protein kinase | Pkinase | 7.7369 | up | G2 |
| Zm.12648.1.A1_at | Pkinase | CDPK | 6.8351 | up | G2 |
| Zm.13464.1.S1_at | Pkinase | Pkinase | 12.8624 | up | G2 |
| Zm.13947.3.A1_at | Pkinase | Pkinase | 6.6717 | up | G2 |
| Zm.13996.1.S1_at | Pkinase_Tyr | Pkinase_Tyr | 9.5537 | up | G2 |
| Zm.15061.1.S1_at | efhand | efhand | 5.6437 | up | G2 |
| Zm.168.1.A1_at | receptor-like protein kinase | Pkinase | 11.1913 | up | G2 |
| Zm.17842.1.S1_at | EF_hand_5 | EF_hand_5 | 5.0894 | up | G2 |
| Zm.5761.1.A1_at | EF_hand_5 | EF_hand_5 | 13.1971 | up | G2 |
| Zm.6021.1.A1_at | Pkinase | Pkinase | 5.9384 | up | G2 |
| Zm.721.1.A1_at | protein kinase ptl1 | protein_kinase | 5.8790 | up | G2 |
| Zm.9675.1.A1_at | signalling.G-proteins | G-proteins | 16.5283 | up | G2 |
| Zm.10267.1.A1_at | Similar to Calmodulin-like protein | Calmodulin | 44.6102 | up | G2 |
| Zm.10480.1.S1_at | EF_hand_5 | EF_hand_5 | 7.6222 | up | G2 |
| Zm.1162.1.S1_at | ef-hand calcium binding | Efhand_Ca | 10.5453 | up | G2 |
| Zm.11745.1.A1_at | mitogen-activated protein kinase kinase kinase a-like calcium binding protein | MAPKKK-like | 41.5661 | up | G2 |
| Zm.12139.1.A1_at | with ef-hand motif | Efhand_Ca | 23.9415 | up | G2 |
| Zm.1442.2.S1_at | EF_hand_5 | EF_hand_5 | 6.3463 | up | G2 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|--------------------|--|--|----------------|------------|-------|
| Zm.15379.1.A1_at | mitogen-activated protein kinase-like | MAPK | 6.4221 | up | G2 |
| Zm.17723.1.S1_at | EF_hand_3 | EF_hand_3 | 10.6374 | up | G2 |
| Zm.352.1.S1_at | calmodulin | calmodulin | 12.5478 | up | G2 |
| Zm.5036.1.A1_at | protein kinase | protein_kinase | 7.8306 | up | G2 |
| Zm.5299.1.S1_at | protein_kinase | protein_kinase | 9.0731 | up | G2 |
| Zm.6367.1.S1_at | acc synthase | ACC_synthase | 26.9101 | up | G2 |
| ZmAffx.777.1.A1_at | serine threonine- specific protein kinase npk15-like | Pkinase_Tyr | 5.7526 | up | G2 |
| Zm.12842.1.A1_at | glycolate oxidase | glycolate_oxydase | -10.2520 | down | G3 |
| Zm.1332.1.S1_at | atp synthase protein i | ATP_synthase | -11.5518 | down | G3 |
| Zm.16683.1.S1_at | chlorophyll a b- binding protein type ii | chl_A-B_BP | -5.3993 | down | G3 |
| Zm.2601.1.S1_at | glyceraldehyde-3- phosphate | G3PD | 10.3605 | up | G3 |
| Zm.3449.1.S1_at | atp synthase delta chain | ATP_synthase | -6.1518 | down | G3 |
| Zm.3895.2.A1_at | PS.lightreaction.phot osystem II. PSII polypeptide subunits | PSII | -6.4430 | down | G3 |
| Zm.5828.1.A1_at | phosphoglycerate kinase | PGK | -7.9285 | down | G3 |
| Zm.6763.1.S1_at | ribulose- - bisphosphate carboxylase | RuBisCo | -6.3449 | down | G3 |
| Zm.7091.1.A1_at | oxygenase small subunit chlorophyll a-b binding protein cp24 | chl_A-B_BP | -5.8528 | down | G3 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|--------------------|--|--|----------------|------------|-------|
| Zm.10401.1.S1_at | PS.photorespiration. glycolate oxydase | glycolate_oxydase | -7.9978 | down | G3 |
| Zm.1088.1.S1_at | atp synthase gamma chain | ATP_synthase | -85.9131 | down | G3 |
| Zm.13239.2.A1_at | chlorophyll a-b binding protein 2 | chl_A-B_BP | -6.3594 | down | G3 |
| Zm.18297.1.S1_at | fructose- - bisphosphatase | FBPase | -90.5095 | down | G3 |
| Zm.12134.3.A1_a_at | granule-bound starch synthase | Stach_synthase | 7.7288 | up | G4 |
| Zm.18317.1.A1_at | sucrose phosphate synthase | SPS | 8.7263 | up | G4 |
| Zm.54.1.S1_at | alpha-amylase isozyme 3e precursor | Alpha-amylase | 6.1944 | up | G4 |
| Zm.299.1.S1_a_at | malate synthase | malate_synthase | 11.1339 | up | G4 |
| Zm.3762.1.A1_at | beta-amylase | beta-amylase | 63.8023 | up | G4 |
| Zm.3883.1.S1_at | beta-amylase | beta-amylase | 10.7594 | up | G4 |
| Zm.409.1.S1_at | cell wall invertase | invertase | 13.0407 | up | G4 |
| Zm.8365.1.A1_at | hexokinase 1 | hexokinase_1 | 7.6251 | up | G4 |
| Zm.12825.1.S1_at | tonoplast intrinsic protein | TIP3-1 | 6.8856 | up | G5 |
| Zm.171.1.A2_at | voltage-dependent anion channel | VDAC | -13.1264 | down | G5 |
| Zm.622.1.S1_at | tonoplast intrinsic protein | TIP | 185.1029 | up | G5 |
| Zm.13050.1.A1_at | integral membrane single c2 domain protein | IMP | 6.7528 | up | G5 |
| Zm.2959.1.S1_at | AWPM-19 | AWPM-19 | 136.2445 | up | G5 |
| Zm.3906.1.A1_at | na ⁺ h ⁺ antiporter | Na ⁺ _H ⁺ _antiporter | 19.0454 | up | G5 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|-------------------|--|--|----------------|------------|-------|
| Zm.43.1.S1_a_at | Similar to Isoform 2 of Late embryogenesis abundant protein vacuolar proton- inorganic pyrophosphatase | LEA | 1315.5604 | up | G5 |
| Zm.6095.1.S1_at | tonoplast intrinsic protein | H_PPase | 9.5673 | up | G5 |
| Zm.616.1.S1_at | HSF | TIP | 4818.6917 | up | G5 |
| Zm.10032.1.S1_at | Late embryogenesis abundant (LEA) group 1 family protein | HSF | 10.9454 | up | G6 |
| Zm.13506.1.S1_at | HSF | LEA | 14.8707 | up | G6 |
| Zm.15325.1.A1_at | heat shock protein 90 | HSF | 6.4391 | up | G6 |
| Zm.16525.1.A1_at | protein disulfide isomerase | HSP90 | 19.4948 | up | G6 |
| Zm.4251.1.S1_at | heat shock 70 kda protein 4 | PDI | 9.5126 | up | G6 |
| Zm.4273.2.A1_at | heat shock protein 90 | HSP70 | 11.8497 | up | G6 |
| Zm.5048.6.A1_a_at | subtilisin-like protease | HSP90 | 5.1986 | up | G6 |
| Zm.5970.1.S1_at | heat shock protein sti-like | subtilisin_protease | 5.0545 | up | G6 |
| Zm.6353.1.S1_at | hsp20-like chaperone | Hsp | 8.1336 | up | G6 |
| Zm.10095.1.A1_at | heat shock cognate 70 kda protein 2 | Chaperone | 8.6478 | up | G6 |
| Zm.12227.1.S1_at | HSP20 | HSP70 | 439.1870 | up | G6 |
| Zm.12517.1.A1_at | heat-shock protein 70t-2 | HSP20 | 777.1541 | up | G6 |
| Zm.15462.1.S1_at | kda class ii heat shock protein | HSP70 | 605.6317 | up | G6 |
| Zm.16504.1.A1_at | kda class ii heat shock protein | classII_Hsp | 164.2669 | up | G6 |
| Zm.16504.2.A1_at | | classII_Hsp | 608.5566 | up | G6 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|--------------------|---|--|----------------|------------|-------|
| Zm.16505.1.A1_at | heat shock protein 90 | HSP90 | 8.9312 | up | G6 |
| Zm.16505.3.A1_at | heat shock protein 90 | HSP90 | 15.6185 | up | G6 |
| Zm.16525.2.S1_a_at | heat shock protein 90 | HSP90 | 170.3164 | up | G6 |
| Zm.16959.2.A1_at | kda class i heat shock | ClassI_Hsp | 285.0497 | up | G6 |
| Zm.1882.1.S1_at | late embryogenesis abundant protein | LEA | 6.2180 | up | G6 |
| Zm.191.1.A1_at | heat shock protein 70 | HSP70 | 416.5075 | up | G6 |
| Zm.2361.1.A1_at | kda class i heat shock protein 1 | ClassI_Hsp | 6541.7460 | up | G6 |
| Zm.2482.1.A1_at | kda class i heat shock protein 1 | ClassI_Hsp | 67.1456 | up | G6 |
| Zm.2497.1.S1_at | heat shock protein | Hsp | 120.9187 | up | G6 |
| Zm.311.1.A1_at | kda class ii heat shock protein | classII_Hsp | 248.3084 | up | G6 |
| Zm.369.1.A1_at | heat-shock protein 20 | HSP20 | 1994.3936 | up | G6 |
| Zm.3693.1.A1_at | kda class i heat shock protein 1 | Class_I_Hsp | 1868.7272 | up | G6 |
| Zm.3740.1.A1_at | kda class iv heat shock protein precursor | classIV_Hsp | 976.0863 | up | G6 |
| Zm.438.1.S1_at | heat shock protein 101 | Hsp | 635.6821 | up | G6 |
| Zm.7900.1.A1_at | atp-dependent clp protease atp-binding subunit precursor | ATP-clp_protease | 10.6947 | up | G6 |
| Zm.11660.1.A1_at | acetyl- synthetase | Acyl_CoA_ligase | 11.4370 | up | G7 |
| Zm.12135.1.A1_at | Peptidase_C1 | Peptidase_C1 | 28.2558 | up | G7 |
| Zm.12789.1.A1_at | cytochrome p450 | p450 | 18.7447 | up | G7 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|--------------------|--|--|----------------|------------|-------|
| Zm.17912.1.S1_at | inositol phosphorylceramide synthase 1 | PAP-like | 12.1099 | up | G7 |
| Zm.2671.1.S1_at | Phospholipase A2, active site domain containing protein | Phospholipase_A2 | 12.2664 | up | G7 |
| Zm.4877.1.S1_at | beta-ketoacyl-acp synthase | ACP_synthase | -5.3292 | down | G7 |
| Zm.7407.1.A1_a_at | squalene monooxygenase | squalene_MO | 8.1116 | up | G7 |
| Zm.11770.1.A1_at | Phospholipase A2, active site domain containing protein | Phospholipase_A2 | 6.2287 | up | G7 |
| Zm.12107.1.A1_at | cytochrome p450 | p450 | 32.4015 | up | G7 |
| Zm.13167.1.A1_at | phosphatidylserine synthase 2 | PSS | 6.5494 | up | G7 |
| Zm.14226.1.A1_at | cytochrome p450 | p450 | 59.8887 | up | G7 |
| Zm.15532.1.S1_at | cytochrome p450 89a2-like | p450 | 17.5465 | up | G7 |
| Zm.15540.1.S1_at | Phospholipase D alpha 1 | PhospholipaseD | 7.6308 | up | G7 |
| Zm.16251.1.A1_at | protein phosphatase 2c abi1 | PP2C | 57.5343 | up | G7 |
| Zm.17264.1.A1_a_at | cytochrome p450 81d1-like | p450 | 29.2600 | up | G7 |
| Zm.19112.1.A1_at | cytochrome p450 | p450 | 20.1450 | up | G7 |
| Zm.2032.1.S1_at | cytochrome p450 | p450 | 11.0156 | up | G7 |
| Zm.445.1.S1_at | lipoxygenase 1 | LOX1 | 11.0874 | up | G7 |
| Zm.15542.1.S1_at | iaa9 - auxin- responsive aux iaa family member | Aux_IAA | 6.3472 | up | G8 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|-------------------|--|--|----------------|------------|-------|
| Zm.1616.1.A1_at | Similar to Peroxidase BP 1 precursor flavin-containing monooxygenase | peroxidase1-like | -8.7304 | down | G8 |
| Zm.17905.1.S1_at | fmo gs-ox-like 3- like | FMO_like | 6.2131 | up | G8 |
| Zm.10676.1.S1_at | 12-oxophytodienoic acid reductase | 12-OPR | 267.2536 | up | G8 |
| Zm.14498.2.A1_at | expansin a1 xyloglucan endotransglucosylas e | expansin_a1 | 15.9133 | up | G8 |
| Zm.1527.2.A1_a_at | hydrolase protein 23 precursor xyloglucan | XET_hydrolase | 32.0586 | up | G8 |
| Zm.15456.1.A1_at | galactosyltransferase katamari1-like | XET_katamari1 | 8.8858 | up | G8 |
| Zm.704.1.S1_at | probable xyloglucan endotransglucosylas e hydrolase protein 23 | XET_hydrolase | 28.2553 | up | G8 |
| Zm.8927.1.S1_at | cell wall.cell wall proteins.AGPs | AGPs | 129.0533 | up | G8 |
| Zm.9297.1.A1_at | cell wall.cell wall proteins.AGPs | AGPs | 64.6181 | up | G8 |
| Zm.13609.1.S1_at | tonoplast dicarboxylate transporter-like | TDT | 7.7288 | up | G9 |
| Zm.14368.1.A1_at | potassium transporter hak2p | K_transporter | 11.4091 | up | G9 |
| Zm.19048.1.A1_at | sorbitol transporter | Sugar_transporter | 46.7006 | up | G9 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|--------------------|--|--|----------------|------------|-------|
| Zm.10826.1.S1_at | vacuolar amino acid transporter 1-like | AVT1 | 5.2827 | up | G9 |
| Zm.13688.1.S1_at | Similar to MtN3 protein precursor | MtN3-like | 695.3546 | up | G9 |
| Zm.16478.3.A1_a_at | abc transporter c family member 8-like | ABC_transporter | 55.6952 | up | G9 |
| Zm.19239.1.A1_at | carbohydrate transporter sugar porter transporter | CHO_transporter | 17.5054 | up | G9 |
| Zm.4089.1.S1_at | hexose transporter | hexose_transporter | 8.8766 | up | G9 |
| Zm.7545.1.A1_at | sugar transporter | sugar_transporter | 10.2086 | up | G9 |
| Zm.9995.1.A1_at | MtN3_slv | MtN3 | 6.2435 | up | G9 |
| Zm.107.1.S1_at | glutamine synthetase | Gln-synt_C | 155.4548 | up | G10 |
| Zm.16478.2.S1_at | aspartate aminotransferase | AspAT | 16.4664 | up | G10 |
| Zm.17181.1.S1_at | pyridoxal phosphate- dependent enzyme domain containing protein | PyrdxIP-dep_enz | 40.6412 | up | G10 |
| Zm.17982.1.A1_at | Amino_oxidase | Amino_oxidase | 9.3929 | up | G10 |
| Zm.5534.1.S1_at | s- adenosylmethionine decarboxylase | SAM_decarbox | 7.0383 | up | G10 |
| Zm.246.1.A1_at | glutathione s- transferase | GST | 15.1098 | up | G11 |
| Zm.2793.1.A1_at | aldehyde dehydrogenase family 2 | ADH | 7.9296 | up | G11 |
| Zm.562.1.A1_at | glutathione s- transferase gstu6 | GST | 9.1296 | up | G11 |

Table S4 (continued).

| Probe ID | Gene | Gene symbol used in Coexpression Network | Absolute FC | Regulation | Group |
|-------------------|--|--|----------------|------------|-------|
| Zm.5873.1.S1_at | glutathione s- transferase | GST | 7.4667 | up | G11 |
| Zm.627.1.A1_at | glutathione s- transferase | GST | 9.4673 | up | G11 |
| Zm.13591.1.S1_at | probable glutathione s-transferase gstu6-like | GST | 8.0440 | up | G11 |
| Zm.1987.2.A1_at | Superoxide dismutase-3 precursor | SOD | 22.6019 | up | G11 |
| Zm.2193.1.A1_at | glutathione s- transferase gstu6 | GST | 58.1546 | up | G11 |
| Zm.3996.1.S1_at | gdp-mannose pyrophosphorylase | GMPase | 17.1766 | up | G11 |
| Zm.6203.2.A1_a_at | phospholipid hydroperoxide glutathione peroxidase | GPx | 8.4774 | up | G11 |

Supplementary Table S5. Statistical parameters of the co-expression network of genes specific to drought tolerance.

| Probe ID | Average shortest pathlength | Clustering coefficient | Closeness centrality | Degree | Neighborhood connectivity |
|-----------------------|-----------------------------|------------------------|----------------------|--------|---------------------------|
| Zm.12134.3.A1_a_at | 2.4765 | 0.6579 | 0.4038 | 20 | 32.4500 |
| Zm.12789.1.A1_at | 2.9588 | 0.7619 | 0.3380 | 7 | 17.5714 |
| Zm.12825.1.S1_at | 2.5294 | 0.6667 | 0.3953 | 15 | 30.0000 |
| Zm.12842.1.A1_at | 3.2059 | 0.9048 | 0.3119 | 7 | 16.7143 |
| Zm.16251.1.A1_at | 2.3588 | 0.5810 | 0.4239 | 23 | 30.7826 |
| Zm.721.1.A1_at | 3.0471 | 0.7143 | 0.3282 | 8 | 15.5000 |
| Zm.9995.1.A1_at | 0.0000 | 0.0000 | 0.0000 | 0 | 0.0000 |
| Zm.10304.1.S1_at | 2.7765 | 0.6800 | 0.3602 | 25 | 23.6400 |
| Zm.10826.1.S1_at | 3.2706 | 0.6667 | 0.3058 | 3 | 8.6667 |
| Zm.1162.1.S1_at | 3.4235 | 0.8889 | 0.2921 | 10 | 24.4000 |
| Zm.11645.1.A1_at | 2.5765 | 0.2924 | 0.3881 | 43 | 16.1163 |
| Zm.11783.1.A1_at | 2.8294 | 0.6341 | 0.3534 | 24 | 21.7917 |
| Zm.12107.1.A1_at | 2.7412 | 0.7574 | 0.3648 | 17 | 26.3529 |
| Zm.12113.1.A1_at | 2.8588 | 0.7333 | 0.3498 | 15 | 26.3333 |
| Zm.13591.1.S1_at | 2.8118 | 0.5000 | 0.3556 | 4 | 25.2500 |
| Zm.13609.1.S1_at | 3.2706 | 1.0000 | 0.3058 | 3 | 29.6667 |
| Zm.168.1.A1_at | 2.7941 | 0.5217 | 0.3579 | 24 | 20.0833 |
| Zm.17723.1.S1_at | 2.7176 | 0.5810 | 0.3680 | 23 | 22.0000 |
| Zm.2032.1.S1_at | 3.9353 | 0.0000 | 0.2541 | 1 | 17.0000 |
| Zm.2671.1.S1_at | 3.1059 | 0.6429 | 0.3220 | 8 | 27.2500 |
| Zm.3762.1.A1_at | 3.2765 | 0.6667 | 0.3052 | 3 | 13.3333 |
| Zm.5112.1.A1_at | 3.2235 | 0.5357 | 0.3102 | 8 | 11.7500 |
| Zm.54.1.S1_at | 3.2529 | 0.6667 | 0.3074 | 4 | 24.5000 |
| Zm.6938.1.A1_at | 2.9412 | 0.5074 | 0.3400 | 17 | 17.7059 |
| Zm.7368.1.S1_at | 3.6412 | 1.0000 | 0.2746 | 3 | 27.0000 |
| Zm.7780.1.A1_at | 3.3824 | 0.6667 | 0.2957 | 3 | 14.3333 |
| Zm.9422.1.A1_at | 2.7059 | 0.4397 | 0.3696 | 36 | 19.3889 |
| Zm.9930.1.A1_at | 2.8471 | 0.8129 | 0.3512 | 19 | 26.0000 |
| ZmAffx.1219.1.S1_s_at | 2.6824 | 0.5714 | 0.3728 | 7 | 18.5714 |
| ZmAffx.1300.1.S1_at | 2.5353 | 0.1897 | 0.3944 | 23 | 11.7826 |
| ZmAffx.1401.1.S1_at | 3.2412 | 1.0000 | 0.3085 | 5 | 17.2000 |
| ZmAffx.1474.1.S1_s_at | 3.2412 | 1.0000 | 0.3085 | 5 | 17.2000 |
| Zm.12135.1.A1_at | 2.3765 | 0.6739 | 0.4208 | 24 | 36.4167 |
| Zm.12327.1.A1_at | 3.8294 | 1.0000 | 0.2611 | 3 | 22.0000 |
| Zm.12648.1.A1_at | 3.2824 | 0.8000 | 0.3047 | 5 | 20.2000 |
| Zm.13464.1.S1_at | 2.9824 | 0.7524 | 0.3353 | 15 | 21.9333 |

Table S5 (continued).

| Probe ID | Average shortest pathlength | Clustering coefficient | Closeness centrality | Degree | Neighborhood connectivity |
|--------------------|-----------------------------------|---------------------------|-------------------------|--------|------------------------------|
| Zm.13688.1.S1_at | 3.1706 | 1.0000 | 0.3154 | 3 | 33.3333 |
| Zm.13996.1.S1_at | 2.2294 | 0.4115 | 0.4485 | 40 | 27.5250 |
| Zm.14368.1.A1_at | 2.2765 | 0.5161 | 0.4393 | 32 | 31.4375 |
| Zm.14498.2.A1_at | 2.3706 | 0.4577 | 0.4218 | 28 | 23.1429 |
| Zm.1527.2.A1_a_at | 3.0000 | 0.9697 | 0.3333 | 12 | 25.0833 |
| Zm.15540.1.S1_at | 3.4824 | 1.0000 | 0.2872 | 2 | 16.5000 |
| Zm.16211.1.S1_at | 2.8647 | 0.7424 | 0.3491 | 12 | 25.0000 |
| Zm.17264.1.A1_a_at | 3.2059 | 1.0000 | 0.3119 | 2 | 29.0000 |
| Zm.2193.1.A1_at | 0.0000 | 0.0000 | 0.0000 | 0 | 0.0000 |
| Zm.2601.1.S1_at | 2.4118 | 0.6087 | 0.4146 | 23 | 27.4348 |
| Zm.3996.1.S1_at | 2.4294 | 0.6877 | 0.4116 | 23 | 36.3043 |
| Zm.5036.1.A1_at | 3.0176 | 0.9000 | 0.3314 | 5 | 29.2000 |
| Zm.5212.1.S1_at | 2.3118 | 0.5291 | 0.4326 | 28 | 29.6429 |
| Zm.5299.1.S1_at | 2.8176 | 0.7574 | 0.3549 | 17 | 24.5882 |
| Zm.5970.1.S1_at | 2.9412 | 0.5667 | 0.3400 | 21 | 19.9524 |
| Zm.6021.1.A1_at | 2.8824 | 0.4308 | 0.3469 | 23 | 18.1739 |
| Zm.6095.1.S1_at | 2.5000 | 0.6209 | 0.4000 | 18 | 24.6111 |
| Zm.7407.1.A1_a_at | 2.9294 | 0.5628 | 0.3414 | 22 | 19.2273 |
| Zm.10095.1.A1_at | 2.9353 | 0.8333 | 0.3407 | 9 | 16.3333 |
| Zm.10676.1.S1_at | 2.8471 | 0.8363 | 0.3512 | 19 | 26.2632 |
| Zm.13506.1.S1_at | 2.3941 | 0.5163 | 0.4177 | 18 | 23.7222 |
| Zm.13603.1.S1_at | 3.4588 | 1.0000 | 0.2891 | 3 | 38.3333 |
| Zm.13801.1.S1_at | 3.2765 | 1.0000 | 0.3052 | 3 | 16.3333 |
| Zm.15542.1.S1_at | 2.9941 | 0.7143 | 0.3340 | 8 | 25.6250 |
| Zm.17181.1.S1_at | 3.2588 | 1.0000 | 0.3069 | 4 | 19.0000 |
| Zm.17912.1.S1_at | 2.7294 | 0.5101 | 0.3664 | 32 | 20.7188 |
| Zm.17956.1.A1_at | 2.9059 | 0.9286 | 0.3441 | 8 | 29.1250 |
| Zm.18735.1.A1_at | 2.6706 | 0.4762 | 0.3744 | 7 | 15.8571 |
| Zm.19112.1.A1_at | 2.8235 | 0.5628 | 0.3542 | 22 | 20.6364 |
| Zm.1987.2.A1_at | 2.6529 | 0.4396 | 0.3769 | 14 | 13.0714 |
| Zm.2959.1.S1_at | 2.3000 | 0.4762 | 0.4348 | 21 | 26.0476 |
| Zm.299.1.S1_a_at | 2.5706 | 0.9273 | 0.3890 | 11 | 49.2727 |
| Zm.43.1.S1_a_at | 2.7824 | 0.5000 | 0.3594 | 12 | 12.8333 |
| Zm.445.1.S1_at | 2.8765 | 0.8485 | 0.3476 | 12 | 27.3333 |
| Zm.5534.1.S1_at | 3.9353 | 0.0000 | 0.2541 | 1 | 17.0000 |
| Zm.562.1.A1_at | 3.1353 | 0.6667 | 0.3189 | 3 | 26.0000 |

Table S5 (Continued).

| Probe ID | Average shortest pathlength | Clustering coefficient | Closeness centrality | Degree | Neighborhood connectivity |
|--------------------|-----------------------------------|---------------------------|-------------------------|--------|------------------------------|
| Zm.5882.1.A1_at | 2.7529 | 0.5862 | 0.3632 | 29 | 21.8621 |
| Zm.616.1.S1_at | 2.4000 | 0.5229 | 0.4167 | 18 | 22.6667 |
| Zm.622.1.S1_at | 2.3941 | 0.5029 | 0.4177 | 19 | 23.4211 |
| Zm.7900.1.A1_at | 2.8176 | 0.7190 | 0.3549 | 21 | 25.0000 |
| Zm.9297.1.A1_at | 2.6706 | 0.3846 | 0.3744 | 40 | 18.2750 |
| Zm.10017.1.A1_at | 2.8118 | 0.7101 | 0.3556 | 24 | 24.2500 |
| Zm.11770.1.A1_at | 2.7588 | 0.6571 | 0.3625 | 21 | 23.2857 |
| Zm.14226.1.A1_at | 2.8941 | 0.7576 | 0.3455 | 12 | 24.7500 |
| Zm.6367.1.S1_at | 2.8588 | 0.8476 | 0.3498 | 15 | 26.8667 |
| Zm.9675.1.A1_at | 3.0000 | 1.0000 | 0.3333 | 6 | 22.6667 |
| Zm.1442.2.S1_at | 2.9176 | 0.6813 | 0.3427 | 14 | 23.0000 |
| Zm.15379.1.A1_at | 4.4059 | 0.0000 | 0.2270 | 1 | 10.0000 |
| Zm.2629.1.S1_at | 2.4529 | 0.6397 | 0.4077 | 17 | 35.1765 |
| Zm.352.1.S1_at | 2.7882 | 0.6209 | 0.3586 | 18 | 22.5556 |
| Zm.5761.1.A1_at | 3.4118 | 0.5333 | 0.2931 | 10 | 14.5000 |
| Zm.6203.2.A1_a_at | 3.6353 | 1.0000 | 0.2751 | 3 | 32.6667 |
| Zm.8865.1.A1_at | 2.9294 | 0.3571 | 0.3414 | 8 | 15.2500 |
| Zm.12517.1.A1_at | 2.9000 | 0.7895 | 0.3448 | 19 | 19.0000 |
| Zm.15462.1.S1_at | 2.7118 | 0.5671 | 0.3688 | 22 | 18.5909 |
| Zm.16504.1.A1_at | 2.8529 | 0.8562 | 0.3505 | 18 | 20.5000 |
| Zm.16504.2.A1_at | 2.9118 | 0.9118 | 0.3434 | 17 | 20.1176 |
| Zm.16505.3.A1_at | 2.7941 | 0.7310 | 0.3579 | 19 | 22.0000 |
| Zm.16525.1.A1_at | 3.0647 | 0.5909 | 0.3263 | 12 | 18.0833 |
| Zm.16525.2.S1_a_at | 2.5000 | 0.4091 | 0.4000 | 12 | 36.8333 |
| Zm.16959.2.A1_at | 2.8471 | 0.8070 | 0.3512 | 19 | 19.8421 |
| Zm.191.1.A1_at | 2.3353 | 0.4933 | 0.4282 | 25 | 32.4000 |
| Zm.2361.1.A1_at | 2.9118 | 0.9118 | 0.3434 | 17 | 20.1176 |
| Zm.2497.1.S1_at | 2.9000 | 0.7895 | 0.3448 | 19 | 19.0000 |
| Zm.311.1.A1_at | 2.9118 | 0.9118 | 0.3434 | 17 | 20.1176 |
| Zm.369.1.A1_at | 2.8176 | 0.6952 | 0.3549 | 21 | 19.5238 |
| Zm.3693.1.A1_at | 2.8882 | 0.5417 | 0.3462 | 16 | 17.5625 |
| Zm.3740.1.A1_at | 3.4765 | 1.0000 | 0.2876 | 12 | 19.2500 |
| Zm.4273.2.A1_at | 2.8588 | 0.5931 | 0.3498 | 22 | 17.5909 |
| Zm.438.1.S1_at | 2.8235 | 0.7158 | 0.3542 | 20 | 19.6000 |
| Zm.5873.1.S1_at | 3.6059 | 0.8611 | 0.2773 | 9 | 19.7778 |
| Zm.5979.1.A1_at | 3.6647 | 1.0000 | 0.2729 | 2 | 21.5000 |

Table S5 (Continued).

| Probe ID | Average shortest pathlength | Clustering coefficient | Closeness centrality | Degree | Neighborhood connectivity |
|--------------------|-----------------------------------|---------------------------|-------------------------|--------|------------------------------|
| Zm.6353.1.S1_at | 2.8353 | 0.4929 | 0.3527 | 27 | 21.0741 |
| Zm.7870.1.S1_at | 2.9059 | 0.7053 | 0.3441 | 20 | 18.5500 |
| Zm.10032.1.S1_at | 2.2765 | 0.5931 | 0.4393 | 22 | 30.8182 |
| Zm.10267.1.A1_at | 2.7118 | 0.5394 | 0.3688 | 29 | 21.0345 |
| Zm.10401.1.S1_at | 2.6176 | 0.9500 | 0.3820 | 16 | 40.3125 |
| Zm.10480.1.S1_at | 2.9176 | 0.8030 | 0.3427 | 12 | 23.5833 |
| Zm.107.1.S1_at | 2.7059 | 1.0000 | 0.3696 | 8 | 53.5000 |
| Zm.1088.1.S1_at | 1.8353 | 0.3091 | 0.5449 | 56 | 23.0357 |
| Zm.11660.1.A1_at | 2.7000 | 1.0000 | 0.3704 | 9 | 52.4444 |
| Zm.11745.1.A1_at | 2.4588 | 0.5000 | 0.4067 | 4 | 43.5000 |
| Zm.11848.1.A1_at | 2.9471 | 0.8667 | 0.3393 | 10 | 23.2000 |
| Zm.11950.1.A1_at | 2.3529 | 0.6397 | 0.4250 | 17 | 34.1765 |
| Zm.12139.1.A1_at | 2.3706 | 0.5556 | 0.4218 | 18 | 38.1111 |
| Zm.12227.1.S1_at | 2.6353 | 1.0000 | 0.3795 | 13 | 46.1538 |
| Zm.13050.1.A1_at | 2.7824 | 1.0000 | 0.3594 | 2 | 57.5000 |
| Zm.13167.1.A1_at | 2.7353 | 1.0000 | 0.3656 | 6 | 54.8333 |
| Zm.13239.2.A1_at | 1.9941 | 0.4061 | 0.5015 | 47 | 25.0000 |
| Zm.1332.1.S1_at | 1.8529 | 0.2887 | 0.5397 | 59 | 22.0000 |
| Zm.13947.3.A1_at | 2.5882 | 0.9231 | 0.3864 | 14 | 42.9286 |
| Zm.15325.1.A1_at | 3.8294 | 1.0000 | 0.2611 | 3 | 22.0000 |
| Zm.15456.1.A1_at | 2.2824 | 0.5365 | 0.4381 | 34 | 29.5588 |
| Zm.15532.1.S1_at | 2.2353 | 0.3942 | 0.4474 | 28 | 26.8214 |
| Zm.1616.1.A1_at | 2.4824 | 0.7879 | 0.4028 | 22 | 34.3182 |
| Zm.16478.2.S1_at | 2.3941 | 0.4815 | 0.4177 | 27 | 28.5556 |
| Zm.16478.3.A1_a_at | 2.9647 | 0.8095 | 0.3373 | 7 | 21.4286 |
| Zm.16683.1.S1_at | 1.9294 | 0.3529 | 0.5183 | 49 | 23.7959 |
| Zm.171.1.A2_at | 2.7353 | 1.0000 | 0.3656 | 6 | 54.8333 |
| Zm.17842.1.S1_at | 2.3471 | 0.5556 | 0.4261 | 19 | 37.6842 |
| Zm.17905.1.S1_at | 2.6882 | 1.0000 | 0.3720 | 11 | 49.4545 |
| Zm.17982.1.A1_at | 2.6941 | 1.0000 | 0.3712 | 10 | 52.1000 |
| Zm.18297.1.S1_at | 1.8235 | 0.3156 | 0.5484 | 56 | 23.0000 |
| Zm.18317.1.A1_at | 2.7059 | 1.0000 | 0.3696 | 8 | 53.5000 |
| Zm.1882.1.S1_at | 2.6412 | 1.0000 | 0.3786 | 12 | 48.1667 |
| Zm.19048.1.A1_at | 2.8000 | 1.0000 | 0.3571 | 4 | 53.5000 |
| Zm.19239.1.A1_at | 2.4118 | 0.6444 | 0.4146 | 10 | 34.0000 |
| Zm.246.1.A1_at | 2.6353 | 1.0000 | 0.3795 | 13 | 45.6923 |

Table S5 (Continued).

| Probe ID | Average shortest pathlength | Clustering coefficient | Closeness centrality | Degree | Neighborhood connectivity |
|--------------------|-----------------------------------|---------------------------|-------------------------|--------|------------------------------|
| Zm.2482.1.A1_at | 2.6824 | 1.0000 | 0.3728 | 12 | 47.1667 |
| Zm.2793.1.A1_at | 2.4294 | 0.8789 | 0.4116 | 20 | 38.9500 |
| Zm.2807.1.A1_at | 2.8647 | 0.6947 | 0.3491 | 20 | 22.3000 |
| Zm.3449.1.S1_at | 1.8706 | 0.3235 | 0.5346 | 54 | 23.4444 |
| Zm.3883.1.S1_at | 2.5706 | 0.6111 | 0.3890 | 9 | 44.2222 |
| Zm.3895.2.A1_at | 1.9588 | 0.3620 | 0.5105 | 52 | 24.0962 |
| Zm.3906.1.A1_at | 2.7294 | 1.0000 | 0.3664 | 5 | 54.2000 |
| Zm.4089.1.S1_at | 2.4706 | 0.6286 | 0.4048 | 15 | 41.0000 |
| Zm.409.1.S1_at | 2.6412 | 1.0000 | 0.3786 | 2 | 43.5000 |
| Zm.4838.1.A1_at | 2.3235 | 0.5238 | 0.4304 | 15 | 33.8000 |
| Zm.4877.1.S1_at | 2.6824 | 1.0000 | 0.3728 | 12 | 46.6667 |
| Zm.5828.1.A1_at | 1.8647 | 0.3111 | 0.5363 | 55 | 22.8182 |
| Zm.627.1.A1_at | 2.5529 | 0.7628 | 0.3917 | 23 | 32.0000 |
| Zm.6763.1.S1_at | 1.9882 | 0.3963 | 0.5030 | 48 | 25.0833 |
| Zm.704.1.S1_at | 2.5471 | 0.9848 | 0.3926 | 12 | 48.5833 |
| Zm.7091.1.A1_at | 2.0706 | 0.4313 | 0.4830 | 45 | 25.6444 |
| Zm.8365.1.A1_at | 2.3412 | 0.5000 | 0.4271 | 21 | 38.2381 |
| Zm.8773.1.A1_at | 2.3059 | 0.6159 | 0.4337 | 24 | 26.5000 |
| Zm.8927.1.S1_at | 0.0000 | 0.0000 | 0.0000 | 0 | 0.0000 |
| Zm.8972.1.S1_at | 2.3471 | 0.7474 | 0.4261 | 20 | 38.1500 |
| Zm.9463.1.A1_at | 2.8235 | 0.5947 | 0.3542 | 20 | 21.0000 |
| Zm.9645.1.S1_at | 2.8471 | 0.0000 | 0.3512 | 1 | 59.0000 |
| ZmAffx.777.1.A1_at | 2.5059 | 0.9810 | 0.3991 | 15 | 44.4667 |
| Zm.10383.4.S1_a_at | 2.2647 | 0.4507 | 0.4416 | 29 | 31.2759 |
| Zm.15061.1.S1_at | 3.8176 | 0.0000 | 0.2619 | 1 | 20.0000 |
| Zm.16505.1.A1_at | 2.7176 | 0.4803 | 0.3680 | 29 | 20.8621 |
| Zm.4251.1.S1_at | 2.9529 | 0.6952 | 0.3386 | 15 | 21.4000 |
| Zm.4558.1.S1_at | 2.9471 | 0.6618 | 0.3393 | 17 | 20.6471 |
| Zm.5048.6.A1_a_at | 2.9529 | 0.6857 | 0.3386 | 15 | 22.2000 |
| Zm.7545.1.A1_at | 3.0294 | 0.6667 | 0.3301 | 4 | 20.2500 |