**Table S1 – Marker genes used for cell type annotation.**

|  |  |  |  |
| --- | --- | --- | --- |
| Name | Gene ID | Cell type | Reference |
| *COMT* | Zm00001d049541 | Exodermis | Capellades et al. [1] |
| *ZmAP1* | Zm00001d002897 | Epidermis | Teichmann et al. [2] |
| *ZmST1;1* | Zm00001d028162 | Epidermis | Hopkins et al. [3] |
| *ZmRCP1* | Zm00001d041984 | Root cap | Matsuyama et al. [4] |
| *ZmRCP2* | Zm00001d052527 | Root cap | Matsuyama et al. [4] |
| *zmGRP4* | Zm00001d004728 | Root cap | Johnson et al. [5] |
| *ZmGRP6* | Zm00001d004730 | Root cap | Johnson et al. [5] |
| *Zm109* | Zm00001d004725 | Root cap | Ponce et al. [6] |
| *phyA2* | Zm00001d013402 | Root cap | Johnson et al. [5] |
| *ZRP2* | Zm00001d031909 | Cortex | Held et al. [7] |
| *RGG144* | Zm00001d026163 | Cortex | Bassani et al. [8] |
| *IVR2* | Zm00001d014947 | Cortex | Kim et al. [9] |
| *ZRP3* | Zm00001d047117 | Cortex | John et al. [10] |
| *ZmGlu1* | Zm00001d023994 | Cortex | Brzobohatý et al. [11] |
| *ZmACO20* | Zm00001d052136 | CC\* | Geisler-Lee et al. [12] |
| *ZmACO35* | Zm00001d018211 | CC | Geisler-Lee et al. [12] |
| *ZmAPL* | Zm00001d015407 | Protophloem sieve element | Bonke et al. [13] |
| *ZmLRD3* | Zm00001d047837 | Protophloem sieve element | Ingram et al. [14] |
| *RGG279* | Zm00001d013568 | Stele | Bassani et al. [8] |
| *LAC18* | Zm00001d052324 | Stele | Marcon et al. [15] |
| *NP\_001050672* | Zm00001d040257 | Stele | Saleem et al. [16] |
| *hemoglobin* | Zm00001d048020 | MZ\*\* | Trevisan et al. [17] |
| *ZmAMT1;3* | Zm00001d017249 | MZ | Gu et al. [18] |
| *ZmPIN9* | Zm00001d043179 | MZ | Yu et al. [19] |
| *CASP4* | Zm00001d003418 | Endodermis | Roppolo et al. [20] |
| *CASP3* | Zm00001d018029 | Endodermis | Roppolo et al. [20] |
| *CASP1* | Zm00001d044816 | Endodermis | Roppolo et al. [20] |
| *CASP5* | Zm00001d025613 | Endodermis | Roppolo et al. [20] |
| *CASP2* | Zm00001d001779 | Endodermis | Roppolo et al. [20] |
| *RTH6* | Zm00001d030121 | Root hair | Li et al. [21] |
| *ZmLRL5* | Zm00001d045107 | Root hair | Wang et al. [22] |
| *RTH5* | Zm00001d042961 | Root hair | Nestler et al. [23] |

\*,Companion cells (CC) associated with the protophloem.

\*\* MZ, meristematic zone.

**Table S2 – Oligonucleotide used for FISH assay.**

|  |  |  |
| --- | --- | --- |
| Gene ID | Cell-type | Oligonucleotide |
| Zm00001d049916 | Stele | GCAGCAUACAUACAUGCGUGAAAUCAACAAGGAA |
| Zm00001d052842 | Exodermis | UCGACCUGACGCUCCCAACUCCAAAAGUGAAAAAAGA |
| Zm00001d043344 | CC | CCAUUGUUGCUCUGCGUGGAGUUGUCGUUCGUU |
| Zm00001d032883 | MZ | GGUGACCGAUCAGGAUGUUUGCUGCGGGAAU |
| Zm00001d041611 | Epidermis | GGGCAAGCAGGAGGACGAAGGCAGCAGUU |
| Zm00001d051478 | Pericycle | GCCGCCGAGUUGGACGAAGACAGUGGUGUG |
| Zm00001d049606 | Protophloem\_sieve | CGUCCAGGGCUAAAACCACUACGCAGACCAGAAU |
| Zm00001d003418 | Endodermis | GGAUUCUUGCUUGCGGUUCCAGAUGUGAGUG |
| Zm00001d026163 | Cortex | GCGAACAUCACUAGGCUAACGGCCAGGA |

**Table S3 – Summary of scRNAseq in maize root tips.**

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Treatment | Total reads | Number of cells | Mean reads per cell | Median genes per cell | Total genes detected | Median UMI counts per cell\* |
| Nitrate+ | 591,938,997 | 3790 | 156,184 | 896 | 26,481 | 1568 |
| Nitrate- | 542,055,474 | 3426 | 158,218 | 944 | 26,412 | 1635 |

\*UMI, unique molecular identifier.

**Table S4 – Number and percentage of cells for each cell type among nitrate+ and nitrate-.**

|  |  |  |  |
| --- | --- | --- | --- |
| Cell-type | Total | Nitrate+ | Nitrate- |
| Exodermis | 479 (7.5%) | 269 (8.0%) | 210 (7.0%) |
| Endodermis | 148 (2.3%) | 61 (1.8%) | 87 (2.9%) |
| Cortex | 2705 (42.5%) | 1410 (42.1%) | 1295 (42.9%) |
| Stele | 1451 (22.8%) | 646 (19.3%) | 805 (26.6%) |
| CC | 475 (7.5%) | 208 (6.2%) | 267 (8.8%) |
| Pericycle | 164 (2.6%) | 125 (3.7%) | 39 (1.3%) |
| Protophloem\_sieve | 160 (2.5%) | 78 (2.3%) | 82 (2.7%) |
| Epidermis | 358 (5.6%) | 259 (7.7%) | 99 (3.3%) |
| MZ | 274 (4.3%) | 182 (5.4%) | 92 (3%) |
| Root hair | 136 (2.1%) | 93 (2.8%) | 43 (1.4%) |
| Root cap | 19 (0.3%) | 17 (0.5%) | 2 (0.1%) |

CC, companion cells; MZ, meristematic zone.