Correction: Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene

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There are data and labeling errors in Figure 3. In the original Figure 3, the gel image for Os07g06970 is incorrect. It is a duplicate of the image for Os01g40290. The new Figure 3 contains the correct image. Also, the original Figure 3 was generated using Locus IDs from Release 5.0 of the Rice Genome Annotation Project. Relative to Release 7.0, used for all other reporting in the article, one of these Locus IDs, Os10g38495, is obsolete. It has been updated in the new Figure 3 to the corresponding Release 7.0 Locus ID, Os10g38489. The remaining Locus IDs are the same in Release 5.0 and Release 7.0 and unchanged in the new Figure 3.

Please see the corrected Figure 3 here. The legend remains unchanged.
There is an error in Figure 2, Table S1, Table S6, and Table S9. Release 7.0 Locus ID recorded for data associated with probe set Os.46631.1.S1_x_at is Os07g29750 and is incorrect. Os.46631.1.S1_x_at does not represent Os07g29750. The correct Locus ID for Os.46631.1.S1_x_at is the paralog Os10g39840. Os10g39840 is unchanged from Release 5.0 to Release 7.0 and appears correctly in Figure 3. Os07g29750 should be replaced with Os10g39840 in Figure 2, Table S1, and Table S4, in each of which it occurs exactly once.

There is additional information to add to Table S9. Primers used to amplify Os10g39840 (to generate the corresponding data in Figure 3) are (5’ to 3’) forward primer CCGATCAGGAGGTACGAGAAGAAGG and reverse primer GCACGCCTCAACTACAAATTGC.

There are two errors in Table 1 and Table S7. Os10g38489, unlike Os10g38640, is a predicted target, displaying a candidate EBE for Tal1b of Xoc. Os10g38489 with associated data is added to the corrected Table 1 and corrected Table S7. Os07g29750 is incorrectly included in Table 1 and Table S7 as a predicted target of Xoc Table. Based on the probeset that correctly maps to Os07g29750, OsAffx16482.1.S1_x_at, Os07g29750 is not differentially expressed in any pairwise comparison, and therefore would not be considered a predicted target, despite its candidate EBE for Table. Os07g29750 is removed from the new Table 1 and Table S7. It is not be replaced in these tables with Os10g39840 because Os10g39840 displays no candidate EBE for any Xoc TAL effector. There is therefore no net change in the total number of predicted targets.

The corrected Table 1 can be seen here.

There is an additional error in Figure 2 and Table S1, that is also in Table S4. In Figure 2, Table S1, and Table S4, the Release 7.0 Locus ID recorded for data associated with probe set Os.46631.1.S1_x_at is Os07g29750 and is incorrect. Os.46631.1.S1_x_at does not represent Os07g29750. The correct Locus ID for Os.46631.1.S1_x_at is the paralog Os10g39840. Os10g39840 is unchanged from Release 5.0 to Release 7.0 and appears correctly in Figure 3. Os07g29750 should be replaced with Os10g39840 in Figure 2, Table S1, and Table S4, in each of which it occurs exactly once.
| TAL effector | Target Locus ID | Probe set ID(s) | Fold change 2-96h Xoc | Fold change Mock-Xoc 96h | q (Mock-Xoc) | EBE Score | EBE rel. score | EBE to TLS | EBE to TATA box | EBE to Y patch | Induced by | Description |
|--------------|----------------|----------------|----------------------|-------------------------|-------------|-----------|-------------|-----------|---------------|---------------|------------|-------------|
| Tal4a        | 01g27210 Os.7911.1.51_at | 1.63 1.66 1.8E-01 | 29.22 2.85 341 253 143 -50 | none | + | Glutathione S-transferase, putative, expressed |
| Tal6         | 01g31220 Os.6438.1.51_a at Os.6438.2.51_x at | 1.48 1.53 1.52 8.0E-02 1.7E-02 | 18.75 2.38 685 157 152 | none | 33 | - | + | Expressed protein |
| Tal2d        | 01g51040 Os.53457.1.51_at | 2.30 2.23 1.9E-01 | 14.32 2.19 324 527 | none | -328 | 0 | + | Transmembrane protein 16K, putative, expressed |
| Tal9b        | 01g51040 Os.53457.1.51_at | 2.30 2.23 1.9E-01 | 14.07 2.81 275 18 | 0 | -299 | none | - | + | Transmembrane protein 16K, putative, expressed |
| Tal2g        | 01g52130 Os.41841.1.51_at | 13.00 9.59 1.3E-06 | 13.94 1.97 77 427 | 58 28 | none | - | + | Sulfate transporter, putative, expressed |
| Tal3b        | 01g53220 Os.35681.1.51_at | 3.50 4.12 2.2E-06 | 17.72 2.92 611 146 | -5 | -137 | none | nd | nd | HSF-type DNA-binding domain containing protein, expressed |
| Tal6         | 02g14770 Os.2450.1.51_a at Os.2450.3.51_x at | 1.88 1.85 1.77 1.55 1.3E-02 6.8E-02 | 18.48 2.35 569 92 | 48 | -70 | -37 | + | Phosphoenolpyruvate carboxylase, putative, expressed |
| Tal11a       | 02g15290 Os.56119.1.51_at | 1.72 4.93 4.1E-07 | 20.15 3.18 582 422 | none | -288 | none | + | VQ domain containing protein, putative, expressed |
| Tal5a        | 02g15290 Os.56119.1.51_at | 1.72 4.93 4.1E-07 | 23.32 1.88 107 148 | 30 | -3 | -180 | - | VQ domain containing protein, putative, expressed |
| Tal7         | 02g15710 Os.Affx.2629.1.51_at | 5.70 5.52 8.4E-02 | 15.75 1.94 265 951 | none | 150 | 434 | nd | nd | Plastocyanin-like domain containing protein, putative, expressed |
| Tal3b        | 02g34970 Os.47735.1.51_at | 9.07 5.31 4.0E-07 | 15.33 2.53 75 110 | 29 | -282 | none | - | + | No apical meristem protein, putative, expressed |
| Tal2a        | 02g43760 Os.1349.1.51_at Os.Affx.2950.1.51_s_at | 1.25 1.23 1.45 1.32 1.7E-03 5.3E-03 | 15.87 1.75 21 521 | none | -334 | -5 | nd | + | Ubiquitin carboxyl-terminal hydrolase, family 1, putative, expressed |
| Tal7         | 02g43760 Os.1349.1.51_at Os.Affx.2950.1.51_s_at | 1.25 1.23 1.45 1.32 1.7E-03 5.3E-03 | 16.45 2.03 547 628 | 341 | 17 | 117 | + | Ubiquitin carboxyl-terminal hydrolase, family 1, putative, expressed |
Table 1. Cont.

| TAL effector | Target Locus ID | Probe set ID(s) | Fold change 2-96h Xoc | Fold change Mock-Xoc 96h | q (Mock-Xoc) | EBE Score | EBE rel. score | EBE rank | EBE to TLS | EBE to TXS | EBE to TATA box | EBE to Y patch | Induced by | Description |
|--------------|-----------------|----------------|-----------------------|-------------------------|-------------|-----------|-------------|---------|-----------|-----------|----------------|--------------|-----------|-------------|
| Tal3c        | 02g47660 Os.7751.1.51_at | 2.25 | 2.24 | 1.9E-03 | 10.93 | 1.92 | 53 | 140 | -63 | -98 | none | - | + | Basic helix-loop-helix, putative, expressed |
| Tal4c        | 02g47660 Os.7751.1.51_at | 2.25 | 2.24 | 1.9E-03 | 24.73 | 3.01 | 434 | 367 | 310 | -25 | none | + | - | Basic helix-loop-helix, putative, expressed |
| Tal2c        | 03g03034 Os.10510.1.51_at Os.32171.1.51_x_at | 1.49 | 1.26 | 3.11 | 2.83 | 1.1E-02 | 6.8E-02 | 19.55 | 1.83 | 0 | 142 | 114 | -779 | 6 | - | + | Flavonol synthase/flavanone 3-hydroxylase, putative, expressed |
| Tal3b        | 03g03034 Os.10510.1.51_at Os.32171.1.51_x_at | 1.49 | 1.26 | 3.11 | 2.83 | 1.1E-02 | 6.8E-02 | 16.73 | 2.76 | 258 | 759 | 567 | none | none | + | - | Flavonol synthase/flavanone 3-hydroxylase, putative, expressed |
| Tal11a       | 03g05370 OsAff.24978.1.51_at | 10.98 | 13.02 | 5.2E-04 | 17.39 | 2.74 | 307 | 798 | 331 | 526 | none | + | - | Expressed protein |
| Tal3c        | 03g07540 OsAff.3165.1.51_at | 6.33 | 3.84 | 3.6E-02 | 12.33 | 2.17 | 350 | 248 | 99 | -625 | none | - | + | bHLH family protein, putative, expressed |
| Tal7         | 03g25490 Os.34992.2.51_at | 2.10 | 2.02 | 3.8E-05 | 16.32 | 2.01 | 494 | 199 | 30 | -363 | 9 | + | - | Cytochrome P450 72A1, putative, expressed |
| Tal4a        | 03g37840 Os.20541.1.51_at | 2.24 | 1.96 | 2.2E-04 | 15.58 | 1.52 | 0 | 362 | 151 | -3 | none | - | + | Potassium transporter, putative, expressed |
| Tal2d        | 04g49194 Os.17316.1.51_at | 22.42 | 10.49 | 3.9E-07 | 8.22 | 1.26 | 0 | 101 | 26 | -715 | none | - | + | Naringenin-2-oxoglutarate 3-dioxygenase, putative, expressed |
| Tal3a        | 05g12450 OsAff.26856.1.51_at | 1.81 | 1.34 | 2.3E-01 | 16.07 | 2.01 | 294 | 446 | 315 | none | none | + | - | Hydroquinone glucosyltransferase, putative, expressed |
| Tal3b        | 05g27590 Os.57186.1.51_at | 2.40 | 4.42 | 3.4E-08 | 11.40 | 1.88 | 2 | 103 | 33 | -1 | none | - | + | Wound-induced protein WI12, putative, expressed |
| Tal11b       | 06g14750 OsAff.15432.1.51_at | 1.29 | 1.30 | 2.0E-01 | 12.44 | 2.77 | 129 | 313 | 195 | 160 | -15 | + | - | Phosphatidylinositol-4-phosphate 5-Kinase family protein, putative, expressed |
| Tal1c        | 06g14750 OsAff.15432.1.51_at | 1.29 | 1.30 | 2.0E-01 | 12.00 | 2.44 | 256 | 178 | 47 | none | none | + | - | Phosphatidylinositol-4-phosphate 5-Kinase family protein, putative, expressed |
| TAL effector | Target Locus ID<sup>b</sup> | Probeset ID(s) | Fold change 2-96h Xoc<sup>c</sup> | Fold change Mock-Xoc 96h<sup>d</sup> | q<sup>e</sup>(Mock-Xoc)<sup>f</sup> | EBE Score<sup>g</sup> | EBE rel. score<sup>h</sup> | EBE rank<sup>i</sup> | EBE to TLS<sup>j</sup> | EBE to TXS<sup>k</sup> | EBE to TATA box<sup>l</sup> | EBE to Y patch<sup>m</sup> | Induced by | Description |
|---------------|-----------------------------|----------------|---------------------------------|---------------------------------|-------------------------------|-----------------|-----------------|----------------|----------------|----------------|----------------|----------------|----------------|----------------|
| Tal2a         | 06g14750 OsAffx.15432.1.51_at | 1.29           | 1.30                            | 2.0E-01                         | 17.59                         | 1.94            | 88              | 79             | -22            | -618           | -33            | nd             | -              | Phosphatidylinositol-4-phosphate 5-Kinase family protein, putative, expressed |
| Tal4c         | 06g37080 Os.16282.1.51_at, OsAffx.15788.1.51_at | 5.54 11.84     | 7.15 9.94                       | 2.7E-10 6.3E-09                  | 14.64                         | 1.78            | 0               | 150            | 39             | -1             | none           | -              | +              | L-asorbate oxidase precursor, putative, expressed |
| Tal8          | 06g37080 Os.16282.1.51_at, OsAffx.15788.1.51_at | 5.54 11.84     | 7.15 9.94                       | 2.7E-10 6.3E-09                  | 19.92                         | 2.32            | 605             | 661            | 560            | -36            | 548            | +              | -              | L-asorbate oxidase precursor, putative, expressed |
| Tal2g         | 06g46500 Os.49496.1.51_at | 6.40           | 6.88                            | 4.3E-08                          | 14.27                         | 2.01            | 117             | 89             | 59             | -489           | -47            | -              | +              | Monocopper oxidase, putative, expressed |
| Tal11a        | 06g47950 OsAffx.15977.1, 51_s_at | 1.78           | 1.67                            | 2.8E-02                          | 16.20                         | 2.55            | 19              | 527            | none           | -328           | 0              | nd             | nd             | Tetratricopeptide-like helical, putative, expressed |
| Tal1c         | 07g06970 Os.49794.1.51_at | 2.95           | 2.27                            | 1.3E-02                          | 5.97                          | 1.22            | 0               | 216            | 24             | none           | none           | -              | +              | HEN1, putative, expressed |
| Tal3a         | 07g06970 Os.49794.1.51_at | 2.95           | 2.27                            | 1.3E-02                          | 16.21                         | 2.03            | 354             | 930            | 815            | 444            | none           | +              | -              | HEN1, putative, expressed |
| Tal4b         | 07g34510 Os.51294.1.51_at | 0.95           | 1.00                            | 2.8E-01                          | 8.88                          | 1.63            | 33              | 302            | 151            | -425           | none           | nd             | nd             | Retrotransposon protein, putative, unclassified, expressed |
| Tal3b         | 07g36430 Os.31021.1.51_at | 2.53           | 2.40                            | 2.6E-02                          | 15.78                         | 2.6             | 108             | 117            | 31             | -4             | none           | -              | +              | Expressed protein |
| Tal6          | 07g47790 Os.8920.1.51_at | 4.16           | 8.41                            | 3.6E-02                          | 13.38                         | 1.7             | 8               | 798            | 610            | -192           | 694            | +              | -              | AP2 domain containing protein, expressed |
| Tal4a         | 09g20220 Os.4759.1.51_at | 2.17           | 2.38                            | 4.9E-02                          | 28.93                         | 2.83            | 280             | 170            | 139            | -751           | 34             | +              | -              | Glutathione S-transferase, putative, expressed |
| Tal2d         | 09g23560 Os.5983.1.51_at | 2.19           | 5.02                            | 2.8E-01                          | 14.19                         | 2.17            | 288             | 525            | none           | none           | 93             | nd             | nd             | Dehydrogenase, putative, expressed |
| Tal6          | 09g29100 Os.18607.1.51_at | 1.64           | 1.97                            | 3.6E-02                          | 17.00                         | 2.13            | 167             | 0              | 0              | 0              | 0              | -              | +              | Cyclin, putative, expressed |
| Tal4b         | 09g32100 Os.16365.1.51_at | 3.34           | 2.45                            | 8.0E-03                          | 8.15                          | 1.5             | 16              | 270            | 84             | 21             | none           | -              | +              | Expressed protein |
| Tal11b        | 10g38489 Os.2612.1.51_at | 4.75           | 4.14                            | 4.0E-07                          | 8.75                          | 4.13            | 325             | 64             | 20             | none           | none           | nt             | nt             | glutathione S-transferase GSTU6, putative, expressed |
| TAL Effector | Target Locus ID | Probeset ID(s) | Fold change Mock-Xoc 96h<sup>4</sup> | Fold change 2-96h Xoc<sup>c</sup> | q (Mock-Xoc)<sup>a</sup> | EBE Score<sup>b</sup> | EBE rel. score<sup>b</sup> | EBE rank<sup>b</sup> | EBE to TLS<sup>1</sup> | EBE to TXS<sup>1</sup> | EBE to TATA box<sup>b</sup> | EBE to Y patch<sup>b</sup> | Induced by Tal<sup>gene knockout strain of Xoc</sup><sup>i</sup> Tal<sup>gene expression</sup><sup>iii</sup> | Description |
|-------------|----------------|----------------|-----------------------------|-----------------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------------------|----------------|
| Tal9a 11g01480 | Os.18448.1.51_s_at | OsAffx.30765.1.51_s_at | 5.42 5.74 3.94 4.17 8.2E-06 5.4E-06 | 19.71 | 2.56 206 776 621 365 | none | + | - | MYB family transcription factor, putative, expressed |
| Tal9a 12g01490 | Os.18448.1.51_at | 5.21 3.92 2.6E-05 19.71 | 2.56 205 302 191 151 | none | + | - | MYB family transcription factor, putative, expressed |
| Tal6 12g42970 | Os.11382.1.51_at | 2.31 1.65 2.2E-04 16.84 | 2.14 139 132 30 | -565 | 12 | - | + | GATA zinc finger domain containing protein, expressed |
| Tal6 12g42970 | Os.11382.1.51_at | 2.31 1.65 2.2E-04 18.27 | 2.32 411 107 5 | -590 | -13 | - | + | GATA zinc finger domain containing protein, expressed |

<sup>a</sup>Expression values are from the GeneChip expression experiment; see Materials and Methods.
<sup>b</sup>Prefix “LOC_Os” is omitted.
<sup>c</sup>Fold change in transcript abundance in leaves at 96h relative to 2h after inoculation with X. oryzae pv. oryzicola BLS256 (Xoc).
<sup>d</sup>Fold change in transcript abundance in Xoc vs. mock inoculated leaves across all time points.
<sup>e</sup>Score is according to Doyle et al. [32] except that new RVDS ‘SN’ and ‘YG’, present in Tal2g, were assigned nucleotide association frequencies of ‘NN’ and ‘NG’, respectively (see text).
<sup>f</sup>EBE relative score, ratio of the observed EBE score to the best possible score for the TAL effector [32].
<sup>g</sup>EBE rank among the single best scoring sites for the TAL effector in each rice promoter [32].
<sup>h</sup>Distance in bases from the 5’ end of the EBE to the translational start site (TLS) of the target locus; a positive value indicates a location downstream of the EBE.
<sup>i</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative TATA box; a positive value indicates a location downstream of the EBE; none, putative TATA box not present.
<sup>j</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative Y patch; a positive value indicates a location downstream of the EBE; none, putative Y patch not present.
<sup>k</sup>Expression values are from the GeneChip expression experiment; see Materials and Methods.
<sup>l</sup>Prefix “LOC_Os” is omitted.
<sup>m</sup>Fold change in transcript abundance in leaves at 96h relative to 2h after inoculation with X. oryzae pv. oryzicola BLS256 (Xoc).
<sup>n</sup>Fold change in transcript abundance in Xoc vs. mock inoculated leaves across all time points.
<sup>o</sup>Score is according to Doyle et al. [32] except that new RVDS ‘SN’ and ‘YG’, present in Tal2g, were assigned nucleotide association frequencies of ‘NN’ and ‘NG’, respectively (see text).
<sup>p</sup>EBE relative score, ratio of the observed EBE score to the best possible score for the TAL effector [32].
<sup>q</sup>EBE rank among the single best scoring sites for the TAL effector in each rice promoter [32].
<sup>r</sup>Distance in bases from the 5’ end of the EBE to the translational start site (TLS) of the target locus; a positive value indicates a location downstream of the EBE.
<sup>s</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative TATA box; a positive value indicates a location downstream of the EBE; none, putative TATA box not present.
<sup>t</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative Y patch; a positive value indicates a location downstream of the EBE; none, putative Y patch not present.
<sup>u</sup>Expression values are from the GeneChip expression experiment; see Materials and Methods.
<sup>v</sup>Prefix “LOC_Os” is omitted.
<sup>w</sup>Fold change in transcript abundance in leaves at 96h relative to 2h after inoculation with X. oryzae pv. oryzicola BLS256 (Xoc).
<sup>x</sup>Fold change in transcript abundance in Xoc vs. mock inoculated leaves across all time points.
<sup>y</sup>Score is according to Doyle et al. [32] except that new RVDS ‘SN’ and ‘YG’, present in Tal2g, were assigned nucleotide association frequencies of ‘NN’ and ‘NG’, respectively (see text).
<sup>z</sup>EBE relative score, ratio of the observed EBE score to the best possible score for the TAL effector [32].
<sup>AA</sup>EBE rank among the single best scoring sites for the TAL effector in each rice promoter [32].
<sup>AB</sup>Distance in bases from the 5’ end of the EBE to the translational start site (TLS) of the target locus; a positive value indicates a location downstream of the EBE.
<sup>AC</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative TATA box; a positive value indicates a location downstream of the EBE; none, putative TATA box not present.
<sup>AD</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative Y patch; a positive value indicates a location downstream of the EBE; none, putative Y patch not present.
<sup>AE</sup>Expression values are from the GeneChip expression experiment; see Materials and Methods.
<sup>AF</sup>Prefix “LOC_Os” is omitted.
<sup>AG</sup>Fold change in transcript abundance in leaves at 96h relative to 2h after inoculation with X. oryzae pv. oryzicola BLS256 (Xoc).
<sup>AH</sup>Fold change in transcript abundance in Xoc vs. mock inoculated leaves across all time points.
<sup>AI</sup>Score is according to Doyle et al. [32] except that new RVDS ‘SN’ and ‘YG’, present in Tal2g, were assigned nucleotide association frequencies of ‘NN’ and ‘NG’, respectively (see text).
<sup>AJ</sup>EBE relative score, ratio of the observed EBE score to the best possible score for the TAL effector [32].
<sup>AK</sup>EBE rank among the single best scoring sites for the TAL effector in each rice promoter [32].
<sup>AL</sup>Distance in bases from the 5’ end of the EBE to the translational start site (TLS) of the target locus; a positive value indicates a location downstream of the EBE.
<sup>AM</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative TATA box; a positive value indicates a location downstream of the EBE; none, putative TATA box not present.
<sup>AN</sup>Distance in bases from the 5’ end of the EBE to the nearest identified putative Y patch; a positive value indicates a location downstream of the EBE; none, putative Y patch not present.
<sup>AO</sup>Expression values are from the GeneChip expression experiment; see Materials and Methods.
<sup>AP</sup>Prefix “LOC_Os” is omitted.
The corrected Table S7 can be downloaded here. The legend remains unchanged.

**Supporting Information**

Table S7. All computationally predicted targets in rice (cv. Nipponbare) of TAL effectors of *Xanthomonas oryzae* pv. oryzicola BLS256 (Xoc) and TAL effectors of *Xanthomonas oryzae* pv. oryzae PXO99A (Xoo).

(XLSX)

**Reference**

1. Cernadas RA, Doyle EL, Nino-Liu DO, Wilkins KE, Bancroft T, et al. (2014) Code-Assisted Discovery of TAL Effector Targets in Bacterial Leaf Streak of Rice Reveals Contrast with Bacterial Blight and a Novel Susceptibility Gene. PLoS Pathog 10(2): e1003972. doi:10.1371/journal.ppat.1003972