## Supplement Tables and Figures

Table S1: Impact of substrate (loam, sand) and maize genotype (wild-type - WT, root hair defective mutant *rth3* – *rth3*) on mycorrhizal colonisation of roots 22 days after planting; numbers in brackets refer to standard error.

| | L_WT | L_*rth3* | S_WT | S_*rth3* |
|---|---|---|---|---|
| Arbuscules% | 1.0 (0.5) | 3.3 (0.9) | 3.5 (1.5) | 3.02 (0.6) |
| Hyphae% | 9.3 (2.06) | 27.3 (1.5) | 21.2 (3.6) | 26.8 (3.2) |
| Vesicles% | 0 (0) | 0.5 (0.5) | 0 (0) | 0 (0) |

Table S2: Share or root length in diameter classes > 0.5 mm for two different bulk densities in loam for root hair defective mutant *rth3* and its corresponding wild-type. Results refer to an additional experiment set up like the main experiment of this MS, for loam only with n=5.

| | L_WT | | L_*rth3* | |
|---|---|---|---|---|
| Bulk density cm $cm^{-3}$ | 1.3 | 1.45 | 1.3 | 1.45 |
| Root length in diameter classes >0.5 mm in % | 3 | 45 | 7 | 58 |

Figure S1: Impact of X-ray CT scanning on shoot and root growth of two maize genotypes (wild-type - WT, root hair defective mutant *rth3* – *rth3*) in loam (L) and sand (S) 22 days after planting. Plants were either scanned 7, 14 and 21 days after planting or were not exposed to X-ray CT at all. Mean values of six replicates are shown, error bars denote the standard error. Statistics: three-factorial ANOVA in conjunction with Tukey's HSD test. Significant differences between treatments are displayed with small letters for $p < 0.05$.

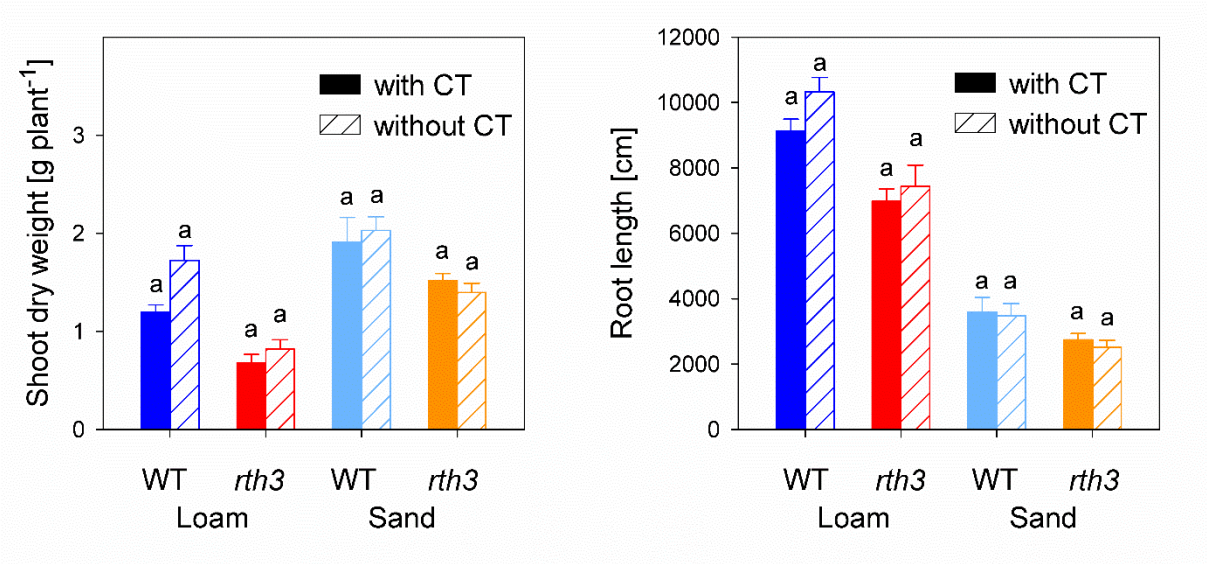



Figure S2: Root recovery with destructive sampling as compared to root recovery with non-invasive X-ray CT scanning and subsequent segmentation of roots with the algorithm Rootine 2.0. For the correlation only layers WR2 and WR3 were used (Fig. 1). The encircled values from the layer WR2 from treatment L_WT at 21 days after planting were not included in the calculation.

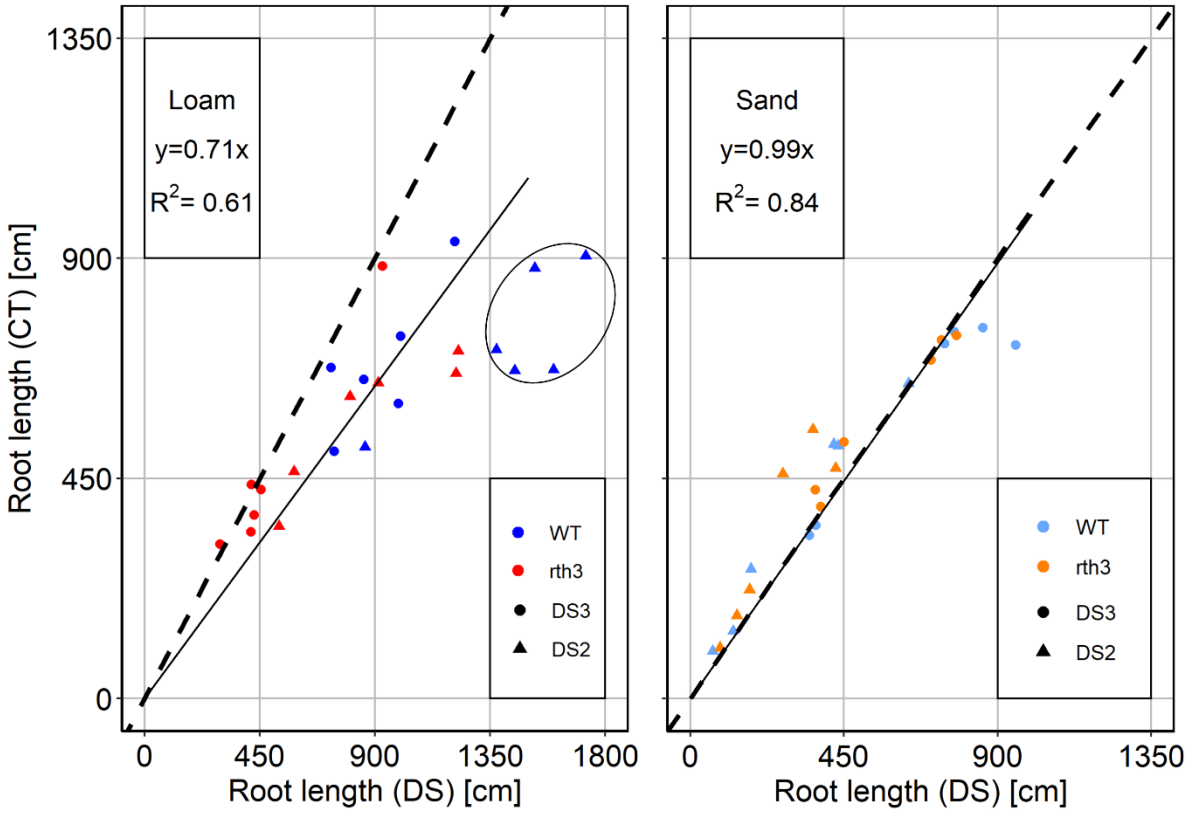



Figure S3: Change of root length density with depth for 22 days after planting for two maize genotypes (wild-type - WT, root hair defective mutant *rth3* – *rth3*) grown in loam (L) and sand (S). Data are derived from destructive sampling of soil columns in layers; n=6, bars represent standard error. The layers which correspond to the depth analysed by X-ray CT are shaded in grey. Significant differences between depths within treatments are displayed next to the bars with small letters for $p < 0.05$. Significant effects of factor between treatments within the same depth is denoted by *s* for substrate, *g* for genotype and *x* for interaction next to the graphs for $p < 0.05$.

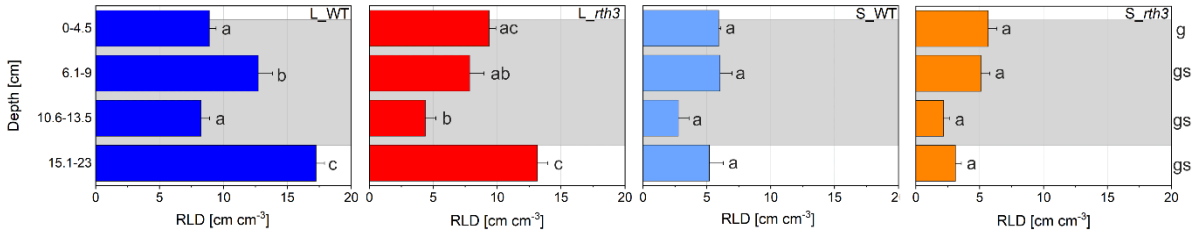



Figure S4: Root length in different root diameter classes (class width 100 µm) 22 days after planting for two maize genotypes (wild-type - WT, root hair defective mutant *rth3* – *rth3*) grown on either loam (L) or sand (S). Data are derived from WinRhizo after destructive sampling of soil columns; n=6. Statistics: two-factorial ANOVA in conjunction with Tukey's HSD test was conducted for each diameter class. Significant effect of factor is denoted by *s* for substrate, *g* for genotype and *x* for interaction, for $p > 0.05$ no letter is displayed. The inset shows proportion of laterals roots versus thick axial roots, i.e. assuming that roots diameter classes < 200 µm comprise laterals only; root diameter classes > 500 µm comprise thick axial roots only. Mean values of six replicates are shown, error bars denote the standard error. Statistics: three-factorial ANOVA in conjunction with Tukey's HSD test. Significant differences between treatments are displayed with small letters for $p < 0.05$.

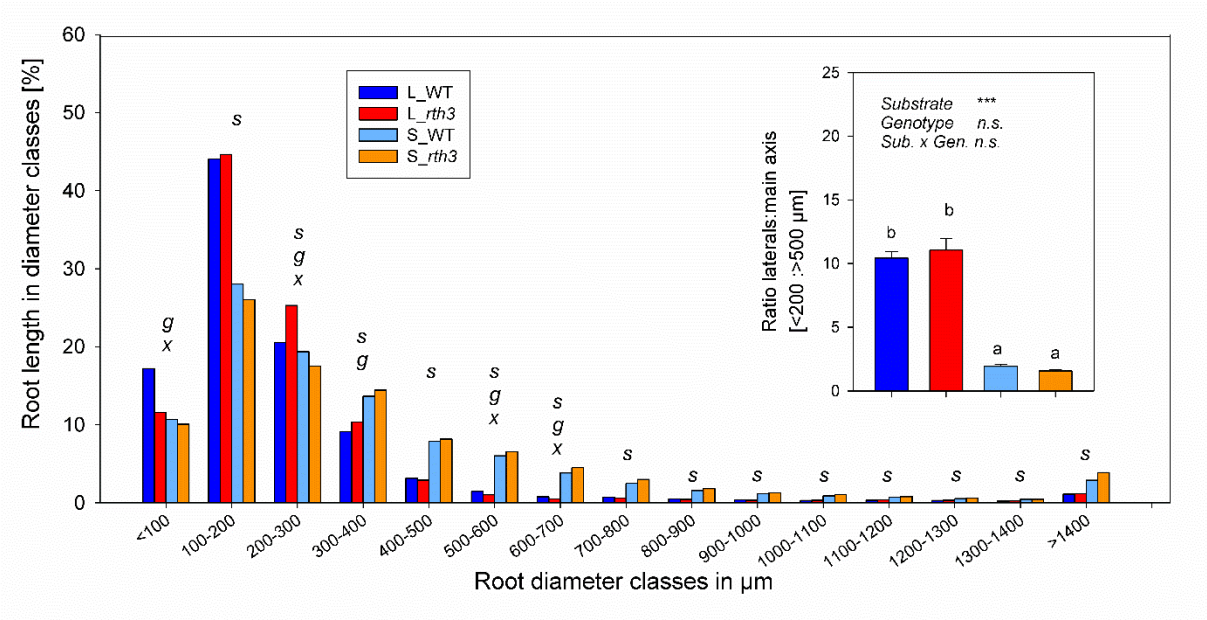



Figure S5: 3D rendering of root networks 7 days after planting for all replicates of each treatment. The primary root and all laterals connected to it are depicted in red; seminal roots in grey.

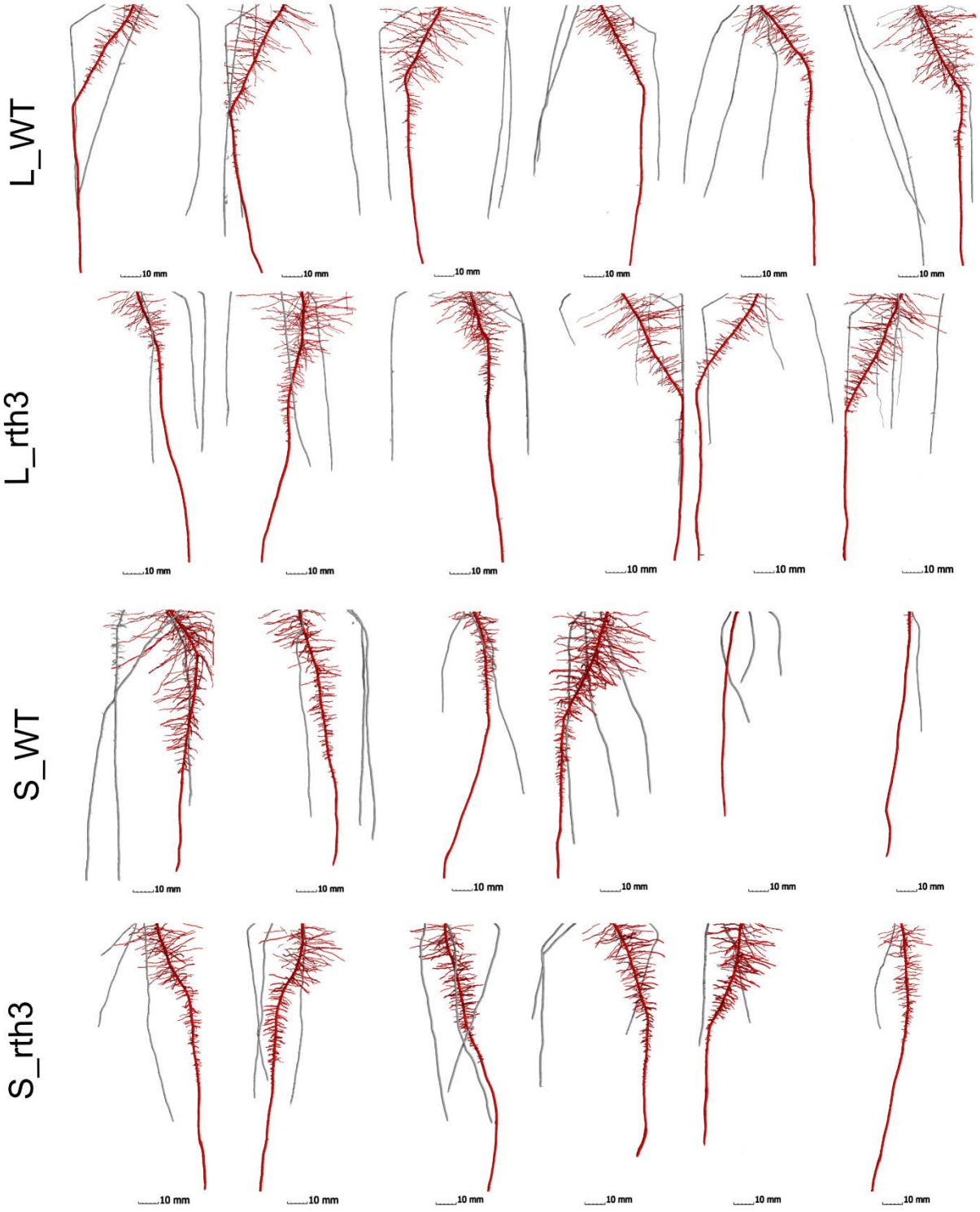



Figure S6: Change of RVF with time for different root length scenarios. Scenarios were calculated based on root system architecture of the treatment S_WT. Values for root hair length = 0 correspond to extent of P depletion zone of 1.8 mm (see Fig. 9).

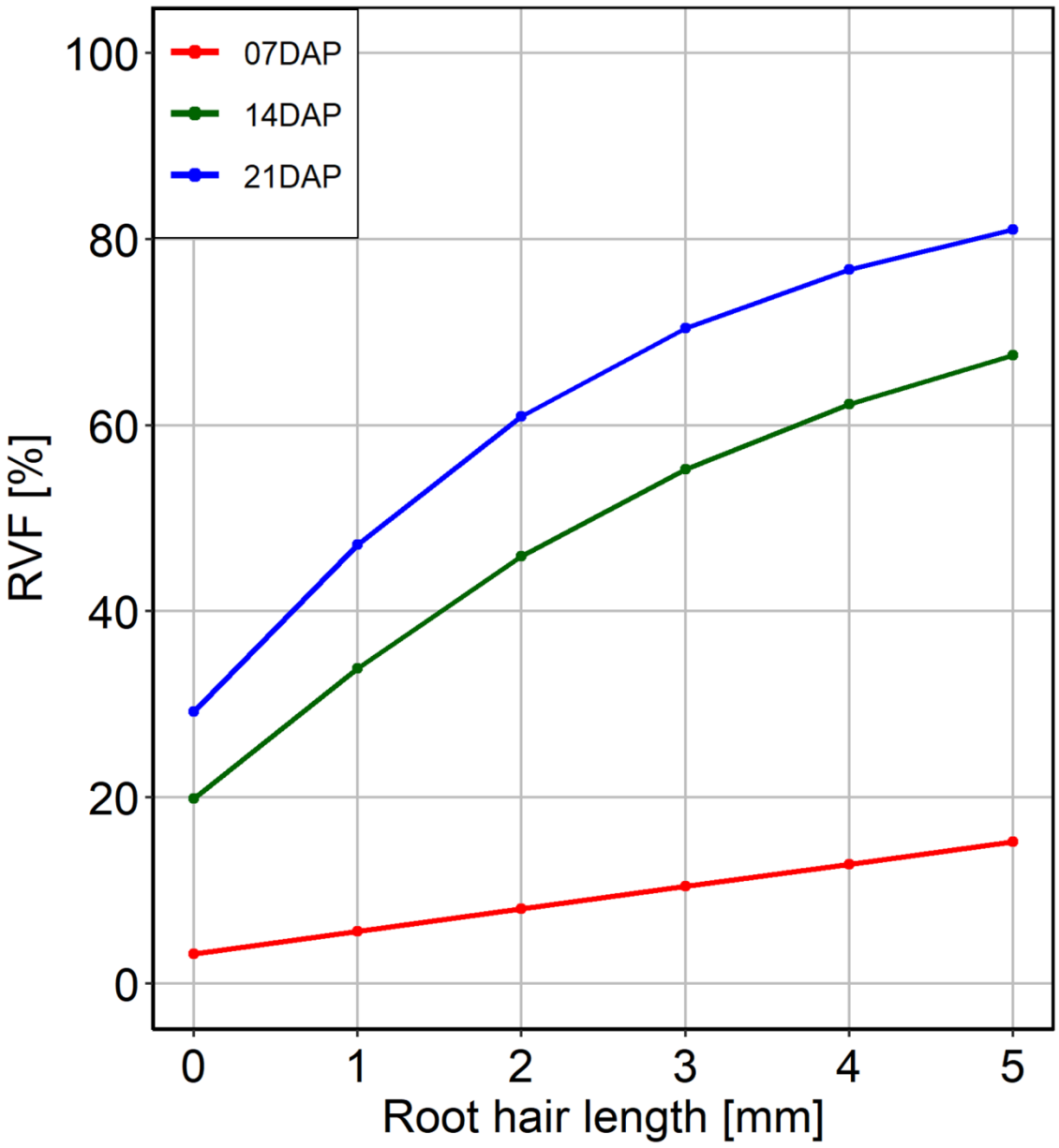
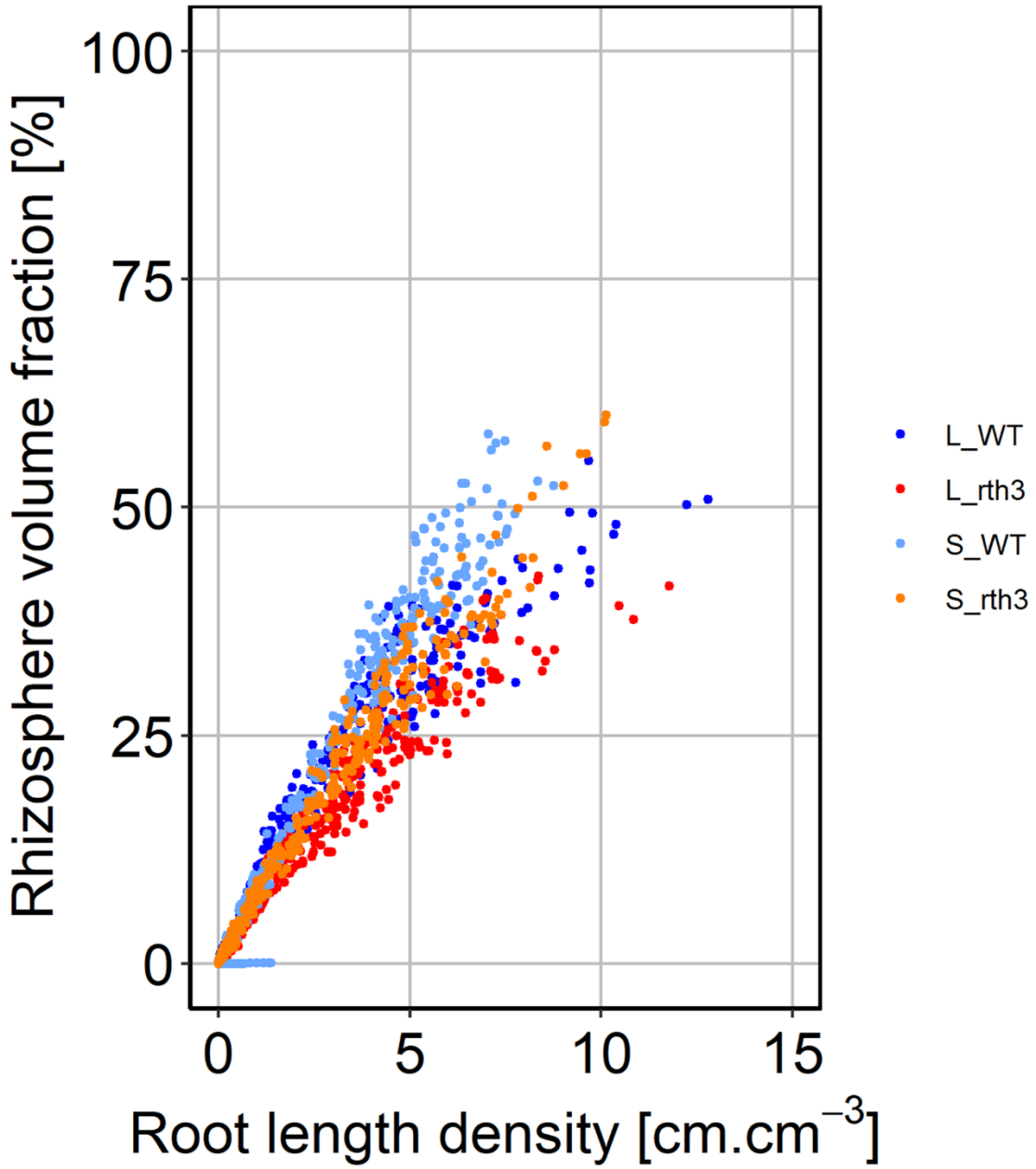



Figure S7: Scatter plot of RVF versus RLD for all time points and treatments across all depths. Different colours indicate the different treatments. Rhizosphere volume fraction is determined assuming a typical rhizosphere extent for P depletion of < 1.8 mm, plus 0.24 mm for hair length in WT.


Rhizosphere volume fraction [%]
100
75
50
25
0
0
5
10
15
Root length density [cm.cm$^{-3}$]
L_WT
L_rth3
S_WT
S_rth3