

## Supplementary Materials

Table S1. Physiochemical characteristics of the black, red and soda saline-alkali soils.

| Soil type                   | Sampling site | Lat/long          | pH   | EC<br>( $\mu\text{S m}^{-1}$ ) | soil organic matter<br>( $\text{g kg}^{-1}$ ) | total N<br>( $\text{g kg}^{-1}$ ) | total P<br>( $\text{mg kg}^{-1}$ ) | available P<br>( $\text{mg kg}^{-1}$ ) | available K<br>( $\text{mg kg}^{-1}$ ) |
|-----------------------------|---------------|-------------------|------|--------------------------------|-----------------------------------------------|-----------------------------------|------------------------------------|----------------------------------------|----------------------------------------|
| black soil (B)              | Lishu         | 43.34°N, 124.10°E | 7.56 | 77                             | 28.78                                         | 1.23                              | 1.25                               | 36.40                                  | 109.99                                 |
| red soil (R)                | Nanchang      | 116.2°N, 28.3°E   | 5.21 | 61                             | 18.45                                         | 0.79                              | 1.18                               | 34.51                                  | 159.50                                 |
| soda saline-alkali soil (S) | Dagangzi      | 45.16°N, 123.46°E | 10.4 | 1402                           | 4.11                                          | 0.29                              | 0.29                               | 10.20                                  | 66.71                                  |
| background soil             | Changchun     | 43.99°N, 125.39°E | 6.31 | 80                             | 20.61                                         | 0.65                              | 1.20                               | 30.20                                  | 88.66                                  |

Table S2. The metabarcodes of the V3-V4 regions of the bacterial 16S rRNA genes in different soil samples.

|                  | Treatments | PE Reads  | Raw Tags  | Clean Tags | Effective Tags | AvgLen(bp) | GC(%)       | Q20(%)      | Q30(%)      | Effective(%) |
|------------------|------------|-----------|-----------|------------|----------------|------------|-------------|-------------|-------------|--------------|
| Bulk soil        | B          | 79806±105 | 71712±149 | 64011±133  | 63528±163      | 459±0      | 55.39±0.035 | 96.73±0.025 | 93.63±0.060 | 79.60±0.102  |
|                  | R          | 80153±103 | 73061±292 | 65636±560  | 64925±368      | 458±0.57   | 54.58±0.122 | 96.85±0.020 | 93.89±0.056 | 81.00±0.355  |
|                  | S          | 80005±106 | 73033±133 | 65572±190  | 63684±237      | 461±0      | 53.88±0.025 | 96.82±0.025 | 93.94±0.04  | 79.6±0.399   |
| Rhizosphere soil | BGmA       | 79974±117 | 73141±223 | 66026±290  | 64412±600      | 456±0.57   | 55.12±0.045 | 96.88±0.030 | 93.92±0.060 | 80.54±0.731  |
|                  | BGmB       | 79986±148 | 73281±272 | 66348±486  | 65276±428      | 457±0      | 54.99±0.026 | 96.94±0.040 | 94.05±0.067 | 81.60±0.539  |
|                  | BGsA       | 79748±32  | 72397±519 | 64952±727  | 64273±617      | 458±0.57   | 55.17±0.021 | 96.79±0.065 | 93.77±0.114 | 80.59±0.805  |
|                  | BGsB       | 79991±190 | 72602±399 | 65293±451  | 64217±389      | 458±0      | 55.13±0.021 | 96.81±0.026 | 93.81±0.049 | 80.28±0.310  |
|                  | RGmA       | 79912±130 | 72142±443 | 64775±600  | 64190±590      | 455±0      | 55.60±0.015 | 96.83±0.030 | 93.77±0.052 | 80.32±0.608  |
|                  | RGmB       | 79807±179 | 72128±362 | 64850±507  | 64271±572      | 4550       | 55.29±0.159 | 96.88±0.028 | 93.88±0.035 | 80.53±0.535  |
|                  | RGsA       | 80063±85  | 72912±265 | 65760±362  | 65046±412      | 456±0      | 54.96±0.017 | 96.9±0.052  | 93.96±0.087 | 81.24±0.432  |
|                  | RGsB       | 80014±165 | 72929±310 | 65817±440  | 65261±439      | 456±0      | 55.15±0.173 | 96.94±0.066 | 94.00±0.096 | 81.56±0.684  |
|                  | SGmA       | 80216±198 | 73817±243 | 66644±506  | 65073±168      | 460±0.57   | 54.23±0.333 | 96.88±0.040 | 94.02±0.075 | 81.12±0.383  |
|                  | SGmB       | 79882±241 | 73396±495 | 66266±668  | 65198±684      | 461±0      | 54.56±0.01  | 96.92±0.041 | 94.08±0.076 | 81.61±0.635  |
|                  | SGsA       | 80049±187 | 73115±268 | 65554±394  | 64432±374      | 461±0      | 54.17±0.015 | 96.67±0.030 | 93.71±0.052 | 80.49±0.608  |
|                  | SGsB       | 80006±283 | 72446±254 | 64913±219  | 63500±222      | 461±0      | 53.87±0.205 | 96.70±0.058 | 93.74±0.105 | 79.37±0.370  |

Table S3. Topological properties of the co-occurrence networks constructed for the rhizosphere bacterial communities of the wild and cultivated soybeans grown in different soil suspensions.

| Ecological networks | Network size | Links | <i>avgK</i> | <i>avgCC</i> | APL   | Modularity | GD    | Diameter |
|---------------------|--------------|-------|-------------|--------------|-------|------------|-------|----------|
| BGs                 | 95           | 460   | 9.684       | 0.998        | 1.002 | 0.703      | 0.103 | 2        |
| BGm                 | 69           | 112   | 2.894       | 0.483        | 3.344 | 0.692      | 0.048 | 8        |
| RGs                 | 84           | 167   | 3.524       | 0.357        | 4.287 | 0.638      | 0.048 | 15       |
| RGm                 | 82           | 146   | 3.162       | 0.361        | 3.82  | 0.726      | 0.044 | 10       |
| SGs                 | 83           | 307   | 6.585       | 0.444        | 2.347 | 0.552      | 0.090 | 7        |
| SGm                 | 77           | 243   | 5.655       | 0.539        | 2.627 | 0.559      | 0.083 | 7        |

Note: Network size: the number of genes (i.e, nodes) in a network. Links: the number of edges in a network. *avgK*: average connectivity. *avgCC*: average clustering coefficient. APL: average path length. GD: graph density. Gs: *Glycine soja*, wild soybean; Gm, *G. max*, cultivated soybean. BGs & BGm, respective soybean cultivars grown in black soil suspension; RGs & RGm, respective soybean cultivars grown in red soil suspension; SGs & SGm, respective soybean cultivars grown in soda saline-alkali soil suspension.

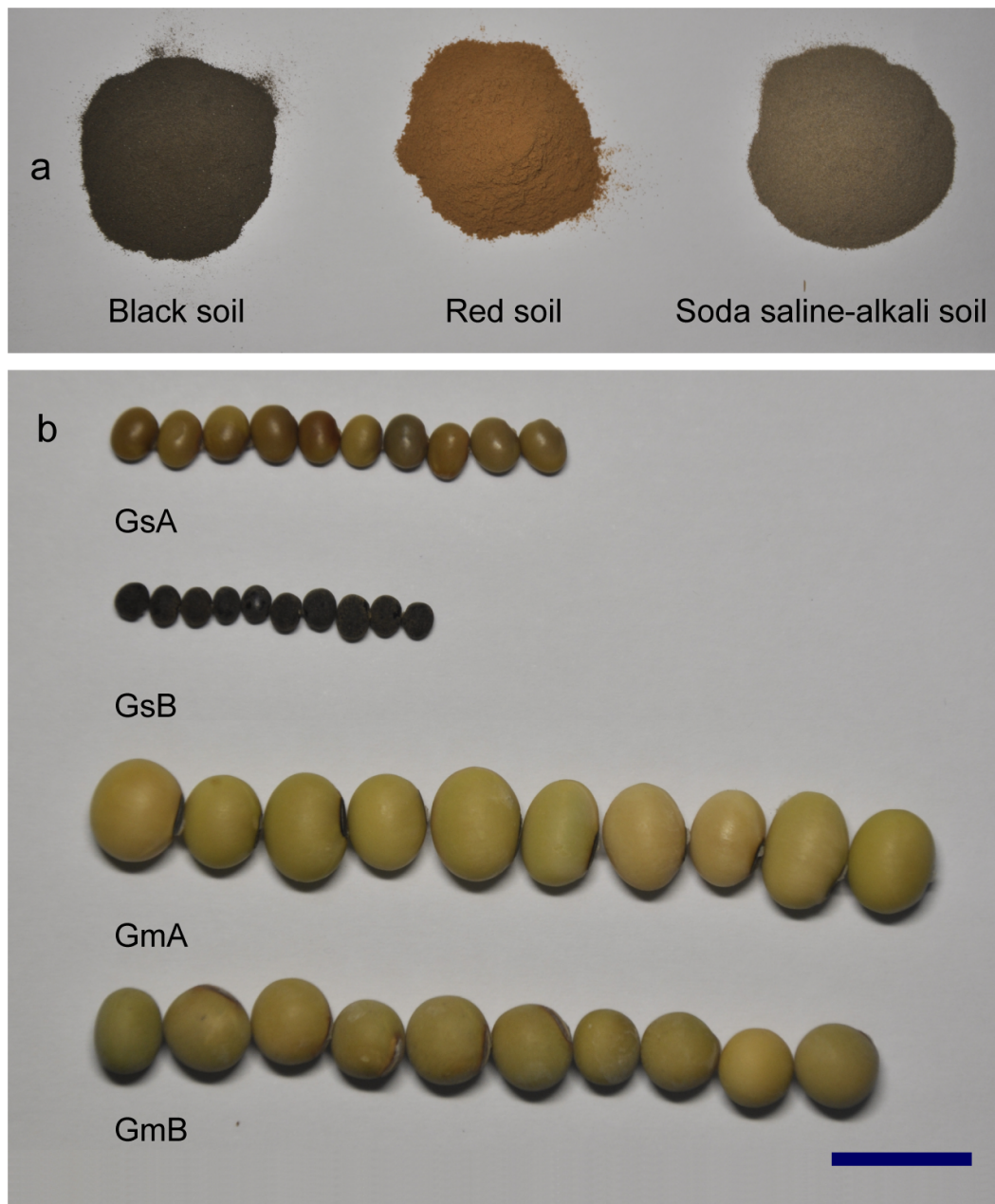


Figure S1. The morphological appearance of the a) soil types, and b) cultivars of the wild and the cultivated soybean seeds. The description of the soil types is shown in Table S1. The wild soybean (ZYQ95 (GsA) and 01-289 (GsB)) possessed brown (GsA) or black (GsB) coloured seed coat; while the seed coat of the cultivated soybean (Williams 82 (GmA) and Zhonghuang (GmB)) are yellow. The scale bar = 1cm.

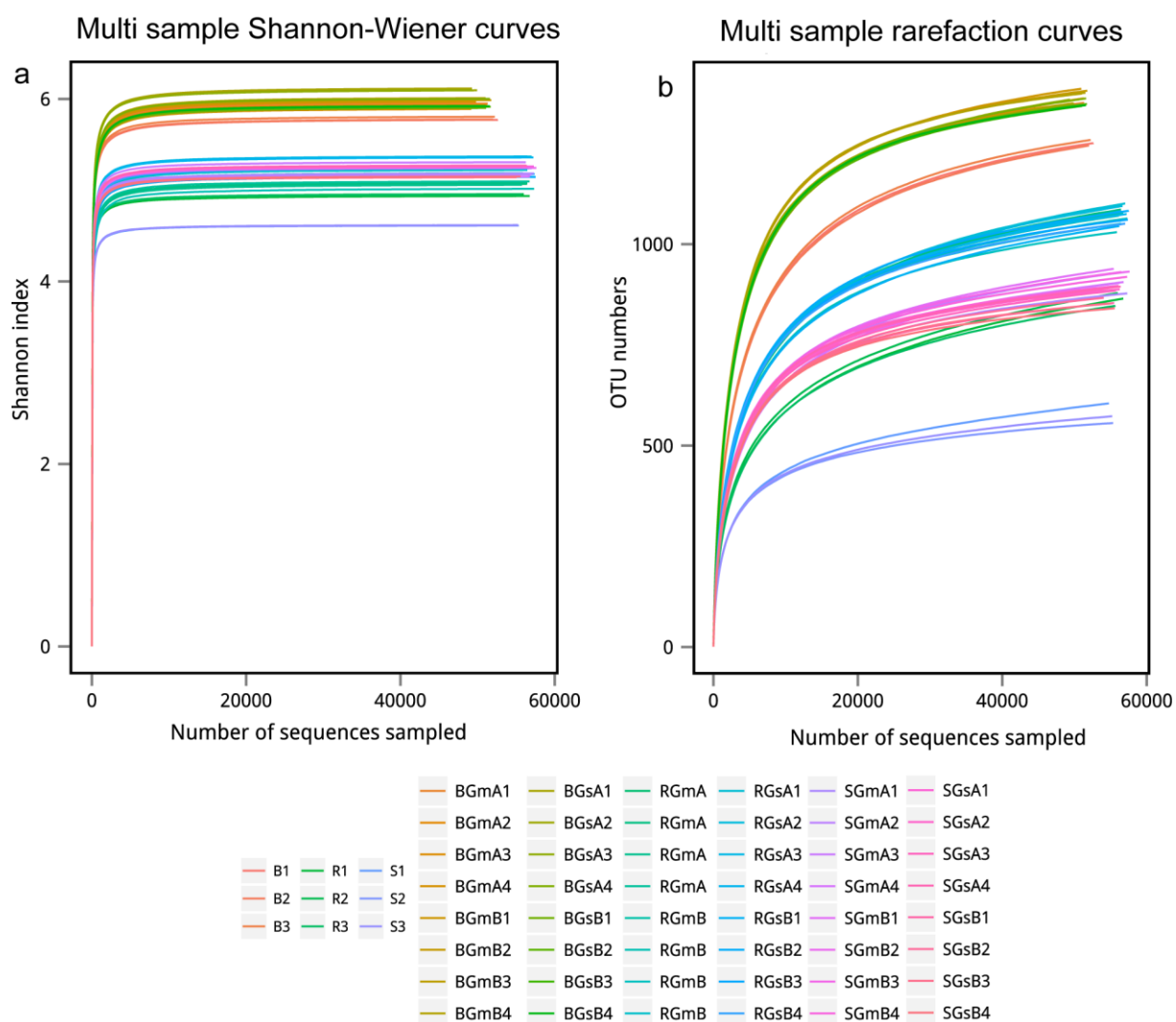


Figure S2. The a) Shannon-Wiener and b) rarefaction curves showing the relationship between sequencing depth and bacterial community diversity in each soil samples. Gs: *Glycine soja*, wild soybean; Gm, *G. max*, cultivated soybean. GsA, cultivar ZYQ95 of *G. soja*; GsB, cultivar 01-289 of *G. soja*; GmA, cultivar williams 82 of *G. max*; GmB, cultivar Zhonghuang of *G. max*. BGsA, BGsB, BGmA & BGmB, respective soybean cultivars grown in black soil suspension; RGsA, RGsB, RGmA & RGmB, respective soybean cultivars grown in red soil suspension; SGsA, SGsB, SGmA & SGmB, respective soybean cultivars grown in soda saline-alkali soil suspension. B1-3, R1-3 and S-3 represent bulk soils inoculated with black, red and soda saline-alkali soil suspensions, respectively.

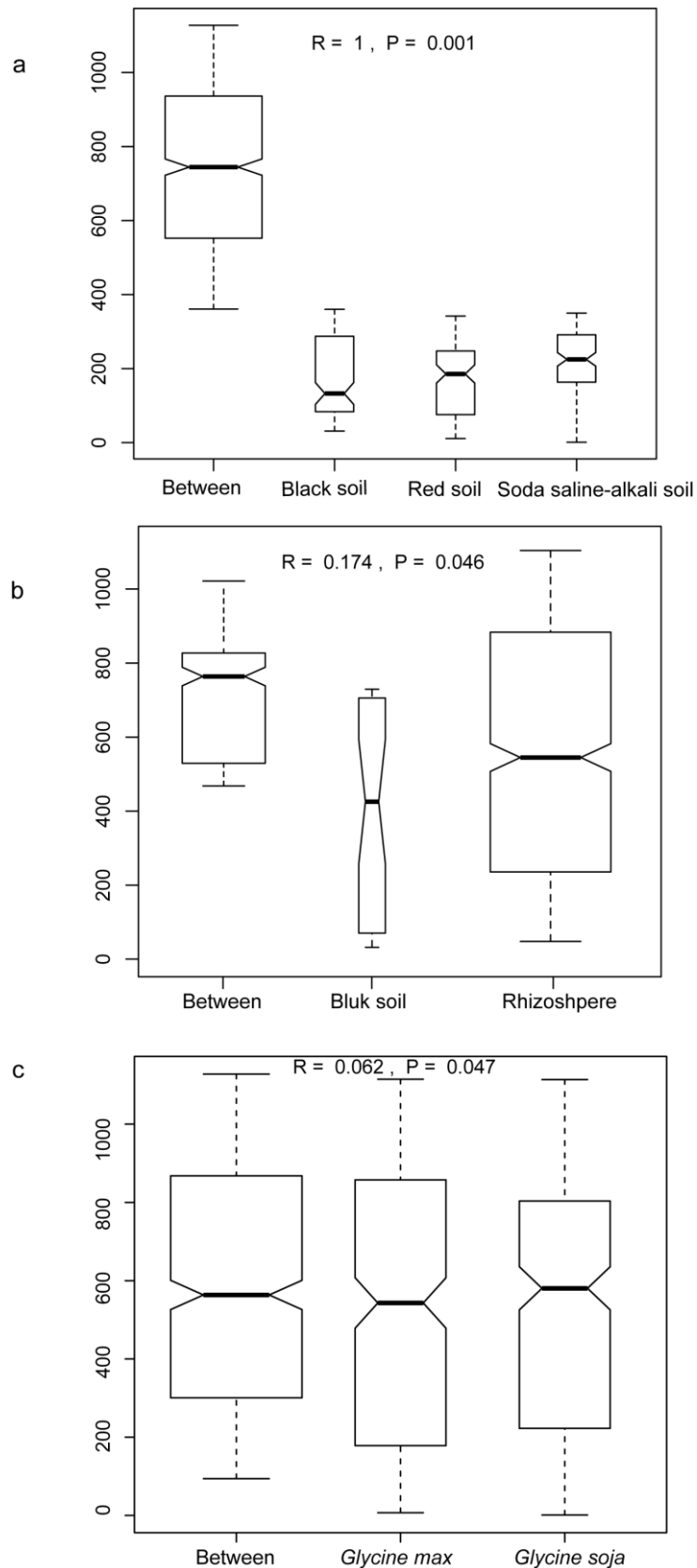


Figure S3. The analysis of similarity (ANOSIM) test showing the bacterial community dissimilarity between soil samples from different a) soil suspensions (black, red and soda saline-alkali soils), b) soil fractions (bulk and rhizosphere), and c) soybean species (*Glycine max* and *G. soja*).

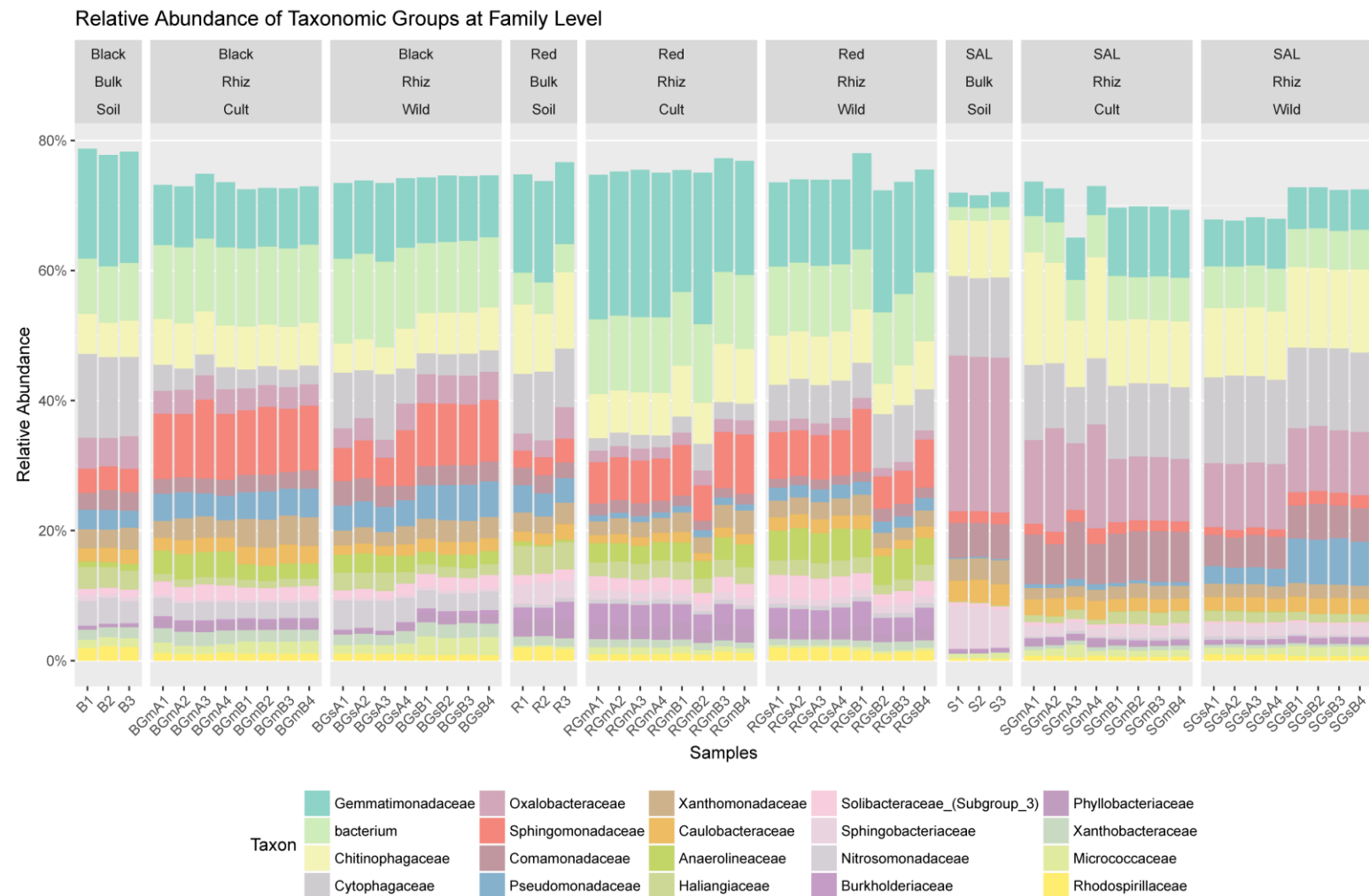


Figure S4. The relative abundance of bacterial families in a) bulk soil, and b-c) rhizosphere soils, including that of cultivated soybeans (b) and wild soybeans (c). The x-axis is labelled with sample ID. The grey bars represent unclassified proportion of OTUs at the family level. SAL: soda saline-alkali soil; Rhiz: rhizosphere soil; Bulk: bulk soil; Cult: cultivated soybean (*G. max*); Wild: wild soybean (*G. soja*).

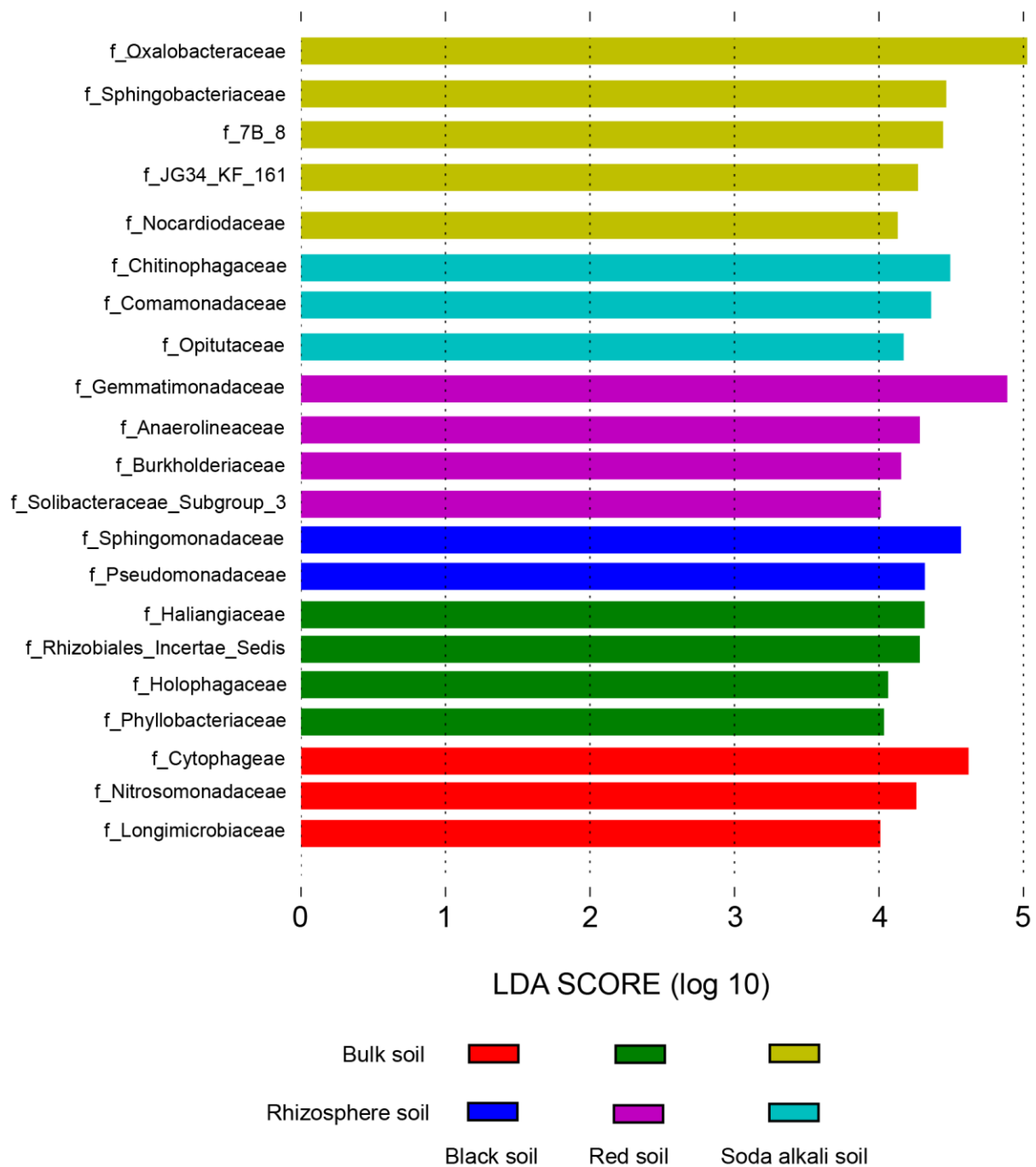


Figure S5. Bacterial families differed significantly in abundance between rhizosphere and bulk soils using the Linear Discriminant Analysis (LDA) effect size (LEfSe) method (LDA cut-off = 4). RB, RR & RS, rhizosphere soils of soybeans grown in black (RB), red (RR) and soda saline-alkali (RS) soil suspension, respectively; BB, BR & BS, bulk soils inoculated with black (BB), red (BR) and soda saline-alkali (BS) soil suspension, respectively.