## Supplemental Information

**Table S1** - List of targeted KEGG ortholog enzymes

| Functional role | Enzyme name | EC number | KEGG orthology number |
|---|---|---|---|
| PRESENT IN SAMPLES | | | |
| Arabinoside degradation | arabinogalactan endo-beta-1,4-galactanase | 3.2.1.89 | K01224 |
| | arabinan endo-1,5-alpha-L-arabinanase | 3.2.1.99 | K06113 |
| Cellulose degradation | cellulase | 3.2.1.4 | K01179 |
| | beta-glucosidase | 3.2.1.21 | K01188, K05349, K05350 |
| | cellulose 1,4-beta-cellobiosidase (CBH) | 3.2.1.91 | K01225 |
| Chitin degradation | chitinase (NAG) | 3.2.1.14 | K01183 |
| | bifunctional chitinase/lysozyme | 3.2.1.14 & 3.2.1.17 | K13381 |
| Nitrogen mobilization | leucyl aminopeptidase (LAP) | 3.4.11.1 | K01255 |
| | urease | 3.5.1.5 | K01427, K01428, K01429, K01430, K14048 |
| Lignin degradation | tyrosinase (phenol oxidase) | 1.14.18.1 | K00505 |
| Pectin degradation | polygalacturonase | 3.2.1.15 | K01184 |
| | alpha-L-rhamnosidase | 3.2.1.40 | K05989 |
| Phosphate mobilization | alkaline phosphatase (AP) | 3.1.3.1 | K01077, K01113 |
| | acid phosphatase (AP) | 3.1.3.2 | K01078, K01093, K09474, K03788, K14379 |
| Superoxides | superoxide dismutase | 1.15.1.1 | K00518, K04564, K04565 |
| | superoxide reductase | 1.15.1.2 | K05919 |
| Xylan degradation | xylan 1,4-beta-xylosidase | 3.2.1.37 | K01198 |
| NOT FOUND IN ANY SAMPLES | | | |
| | polyphenol oxidase | 1.10.3.1 | K00422 |
| | peroxidase | 1.11.1.7 | K00430 |

| | | |
|---|---|---|
| fructan beta-fructosidase | 3.2.1.80 | K03332 |
| laccase (oxidoreductase) | 1.10.3.2 | K05909 |
| eosinophil peroxidase | 1.11.1.7 | K10788 |
| cytosol aminopeptidase | 3.4.11.1 & 3.4.11.5 | K11142 |
| peroxiredoxin 6, 1-Cys peroxiredoxin | 1.11.1.7, 1.11.1.15, & 3.1.1.- | K11188 |
| lactoperoxidase | 1.11.1.7 | K12550 |
| low molecular weight phosphotyrosine protein phosphatase | 3.1.3.2 3.1.3.48 | K14394 |
| lysophosphatidic acid phosphatase type 6 | 3.1.3.2 | K14395 |
| acid phosphatase | 3.1.3.2 | K14410 |
| beta-D-xylosidase 4 | 3.2.1.37 | K15920 |

**Linear Regressions of bacterial abundance and gene abundance to soil C and N content**

Bacterial relative abundance (from most abundant phylum to least abundant)

Fig. S1

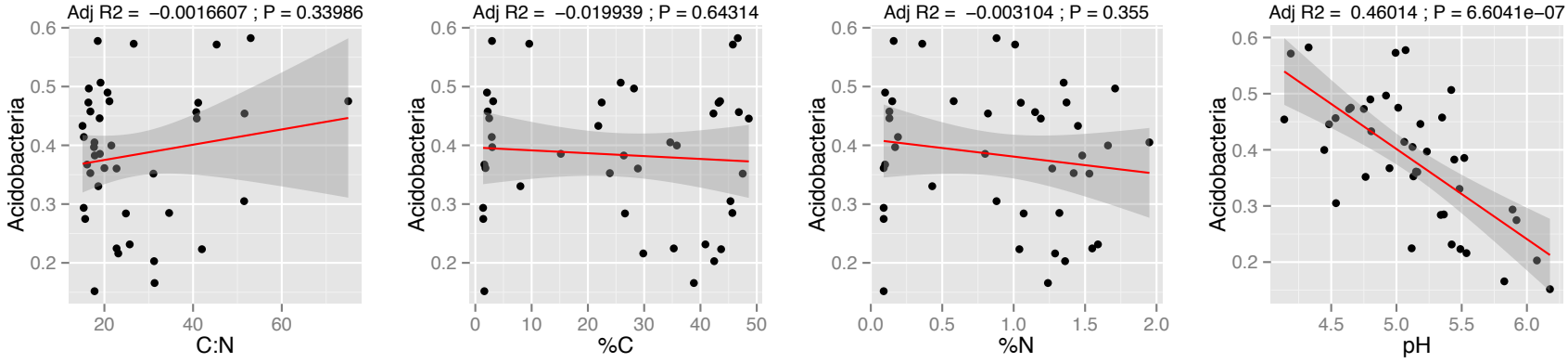



Fig. S2

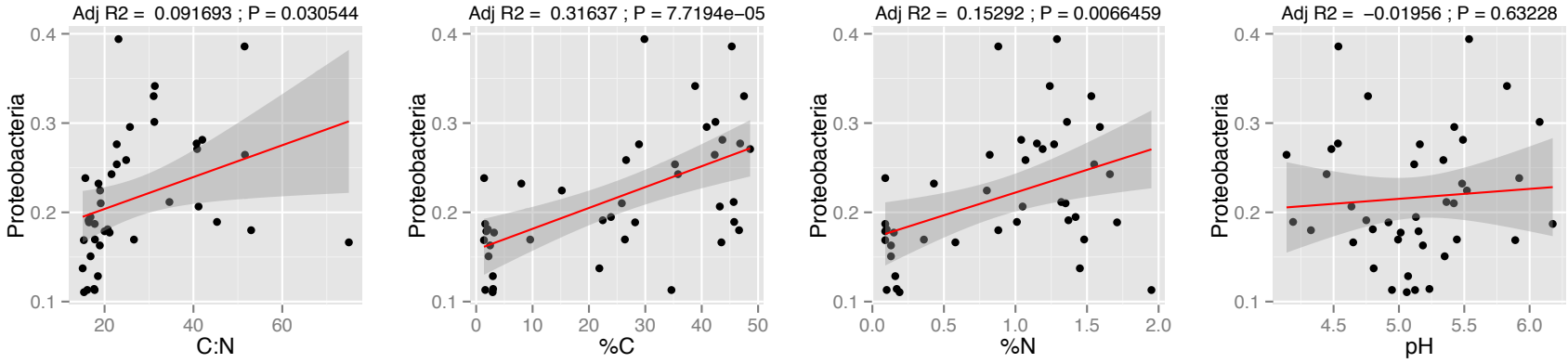


Fig. S3

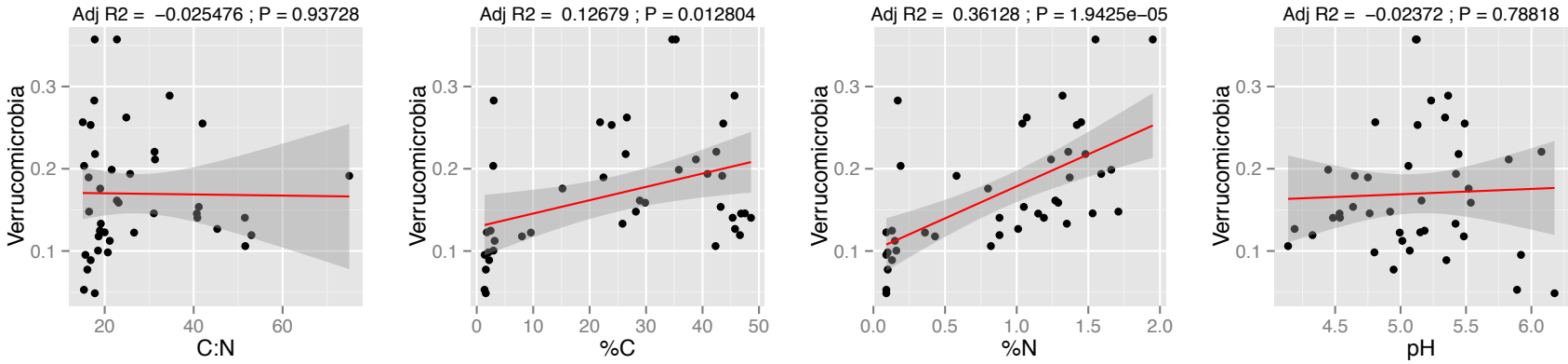

Adj R2 = −0.025476 ; P = 0.93728
Adj R2 = 0.12679 ; P = 0.012804
Adj R2 = 0.36128 ; P = 1.9425e−05
Adj R2 = −0.02372 ; P = 0.78818
Verrucomicrobia
C:N
%C
%N
pH

Fig. S4

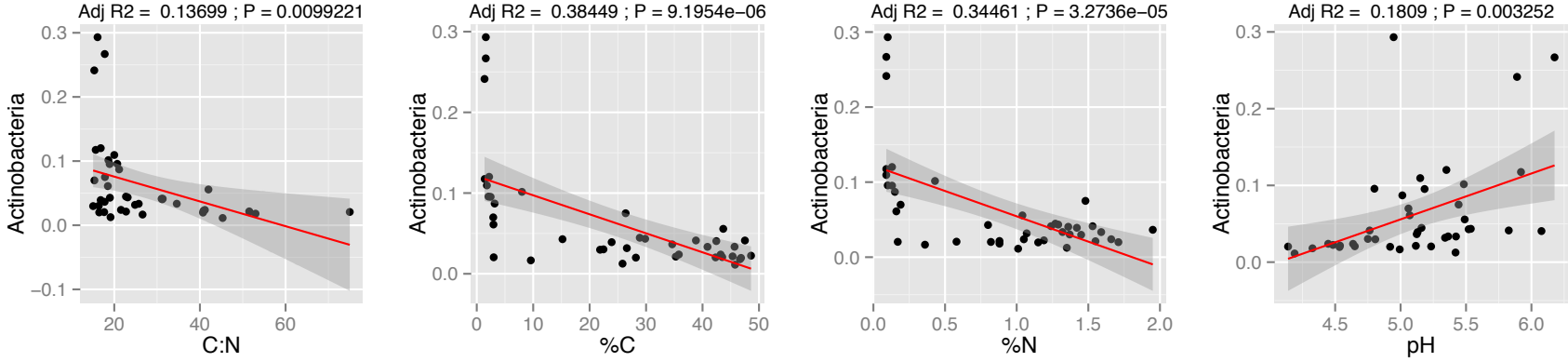

Adj R2 = 0.13699 ; P = 0.0099221
Adj R2 = 0.38449 ; P = 9.1954e−06
Adj R2 = 0.34461 ; P = 3.2736e−05
Adj R2 = 0.1809 ; P = 0.003252
Actinobacteria
C:N
%C
%N
pH

Fig. S5

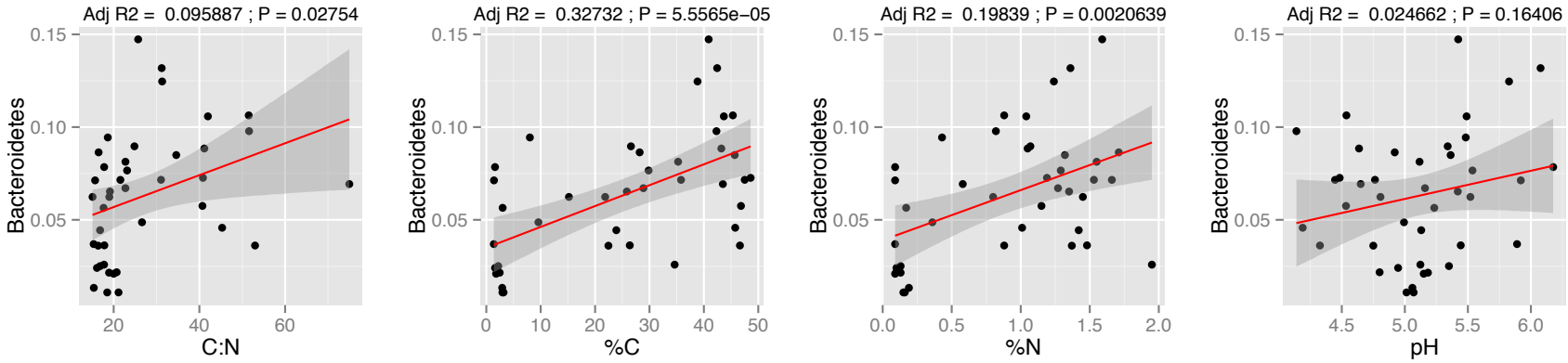
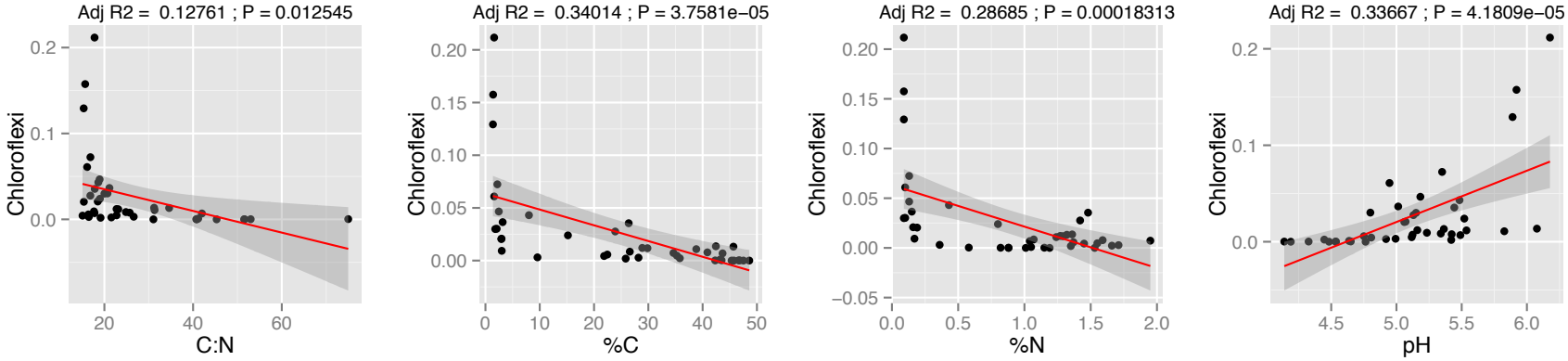

Adj R2 = 0.095887 ; P = 0.02754
Adj R2 = 0.32732 ; P = 5.5565e−05
Adj R2 = 0.19839 ; P = 0.0020639
Adj R2 = 0.024662 ; P = 0.16406
Bacteroidetes
C:N
%C
%N
pH

Fig. S6


Adj R2 = 0.12761 ; P = 0.012545
Adj R2 = 0.34014 ; P = 3.7581e−05
Adj R2 = 0.28685 ; P = 0.00018313
Adj R2 = 0.33667 ; P = 4.1809e−05
Chloroflexi
C:N
%C
%N
pH

Enzyme gene abundance

Fig. S7

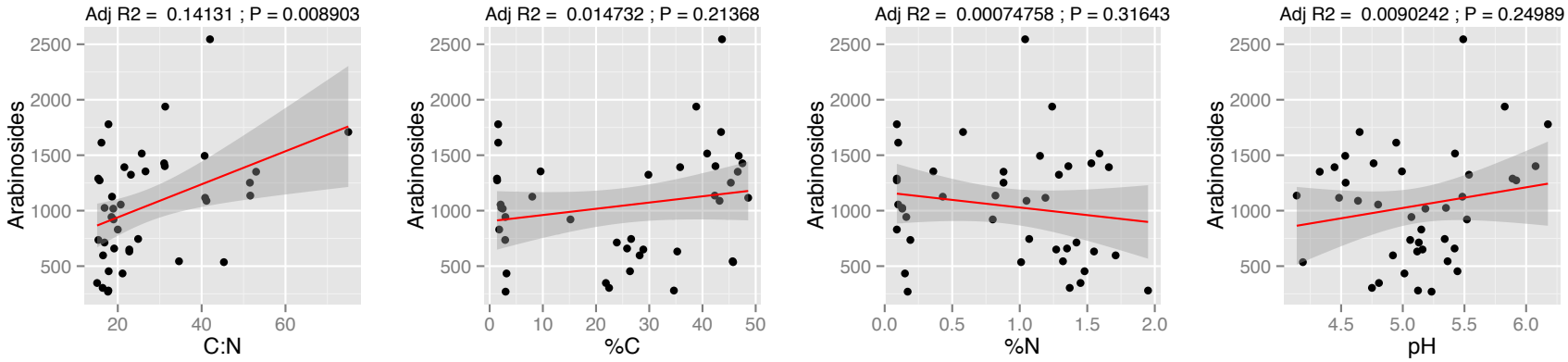



Fig. S8

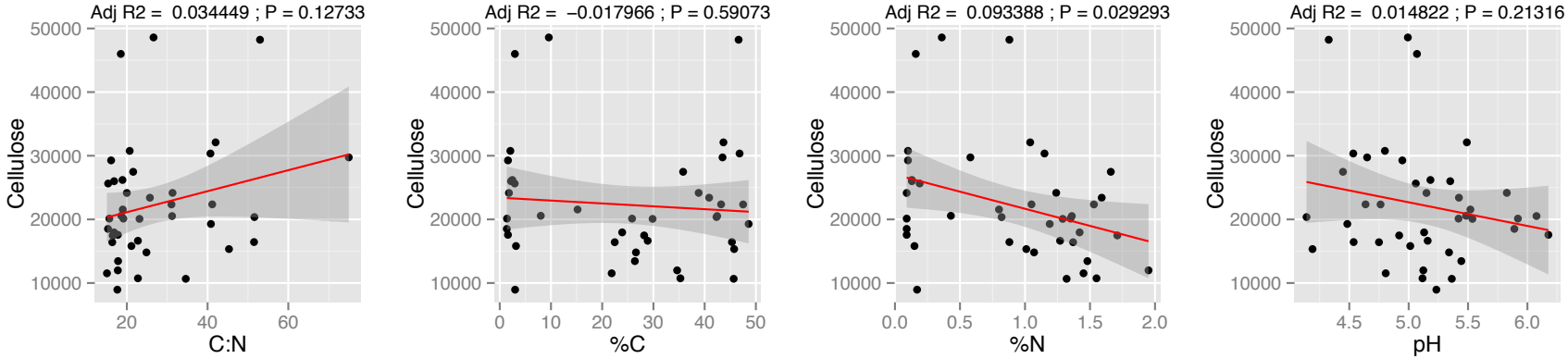


Fig. S9

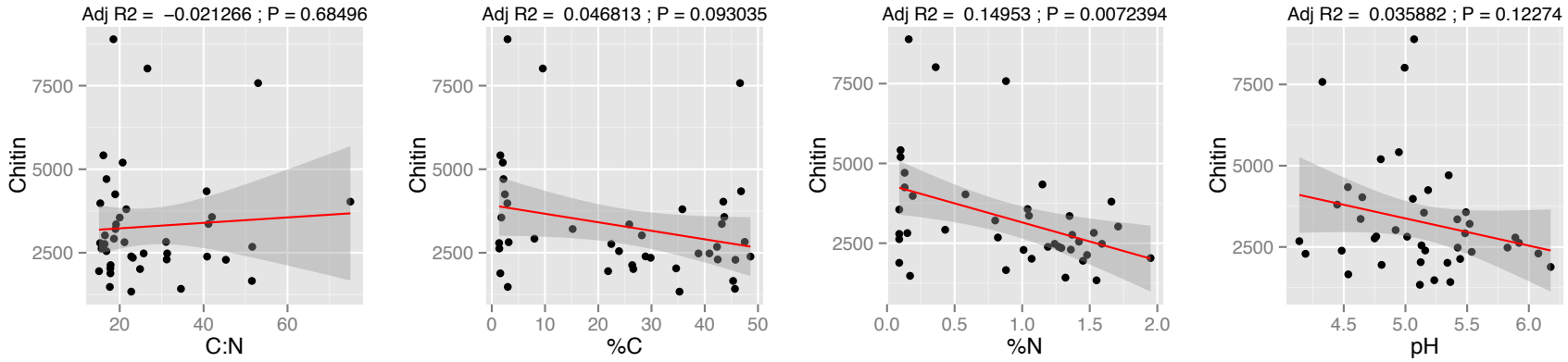



Fig. S10

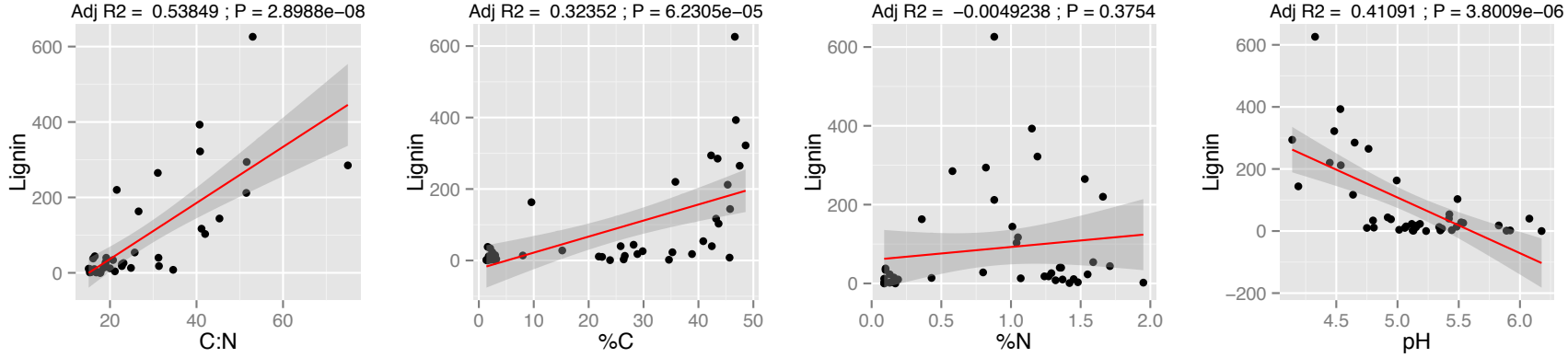


Fig. S11

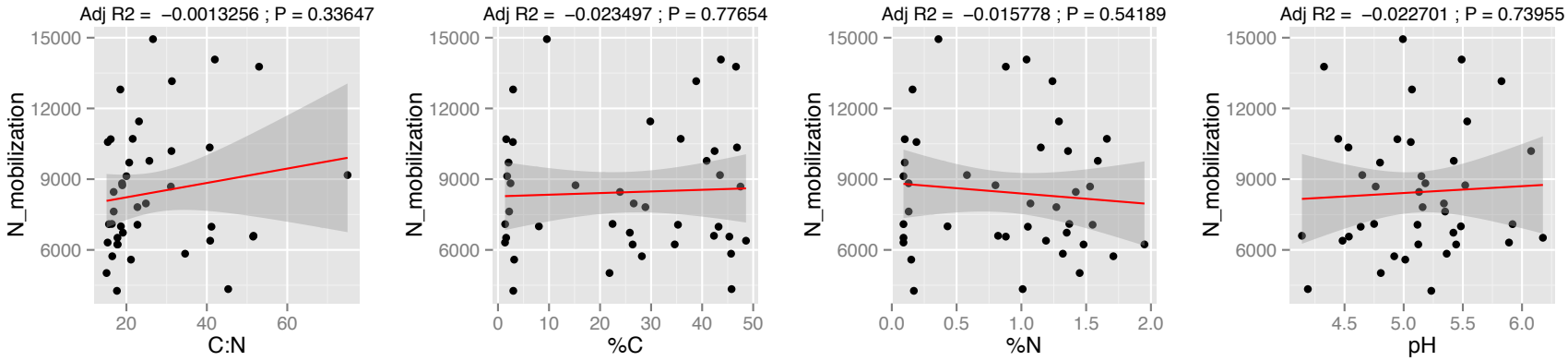



Fig. S12

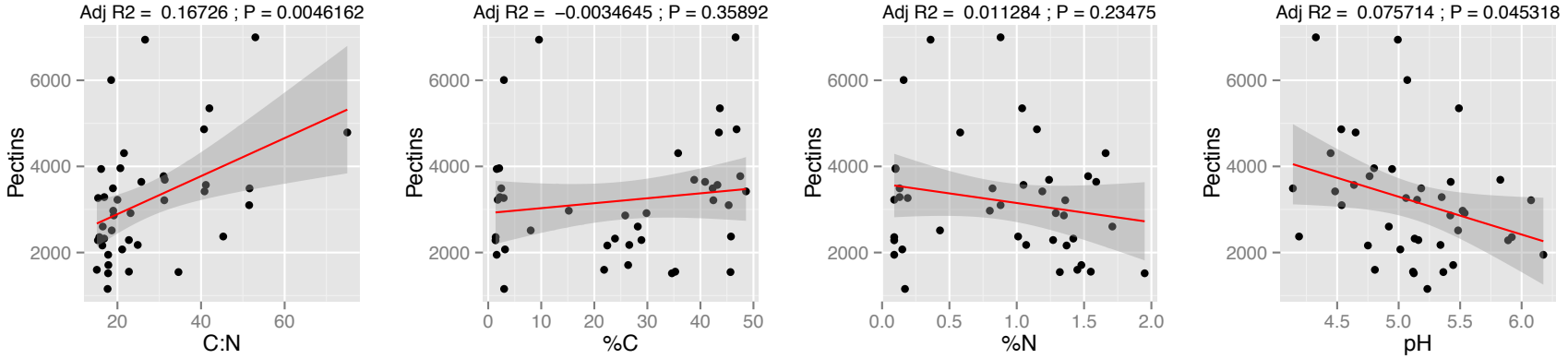


Fig. S13

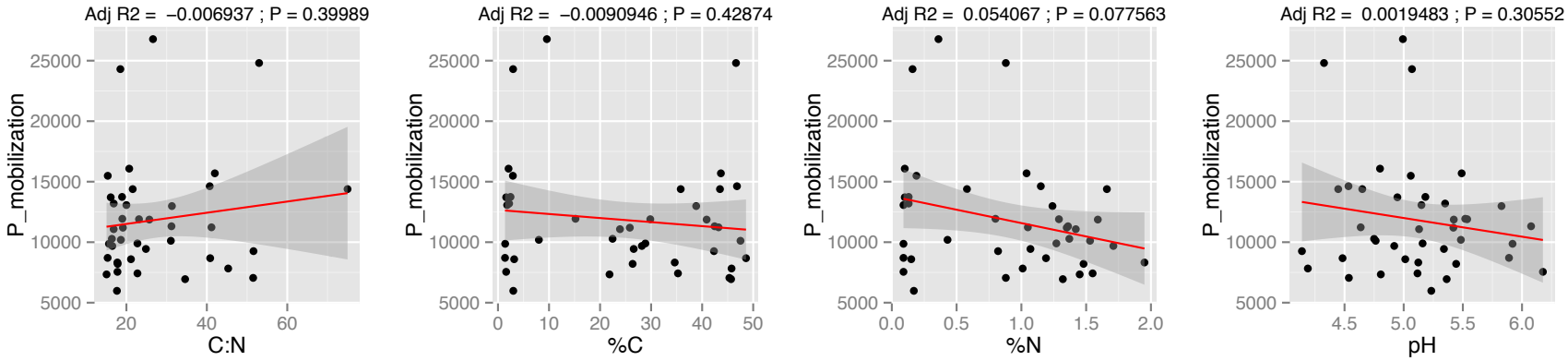



Fig. S14

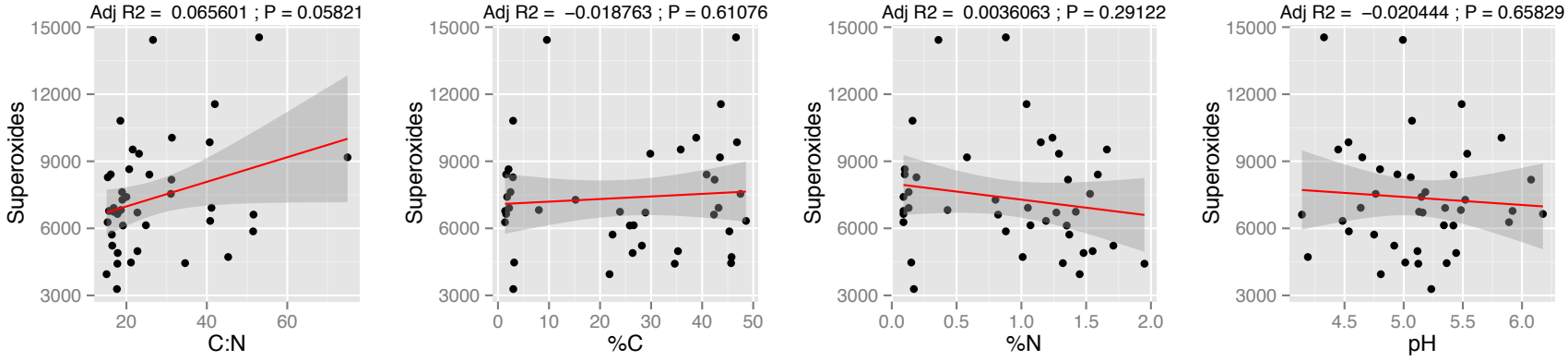
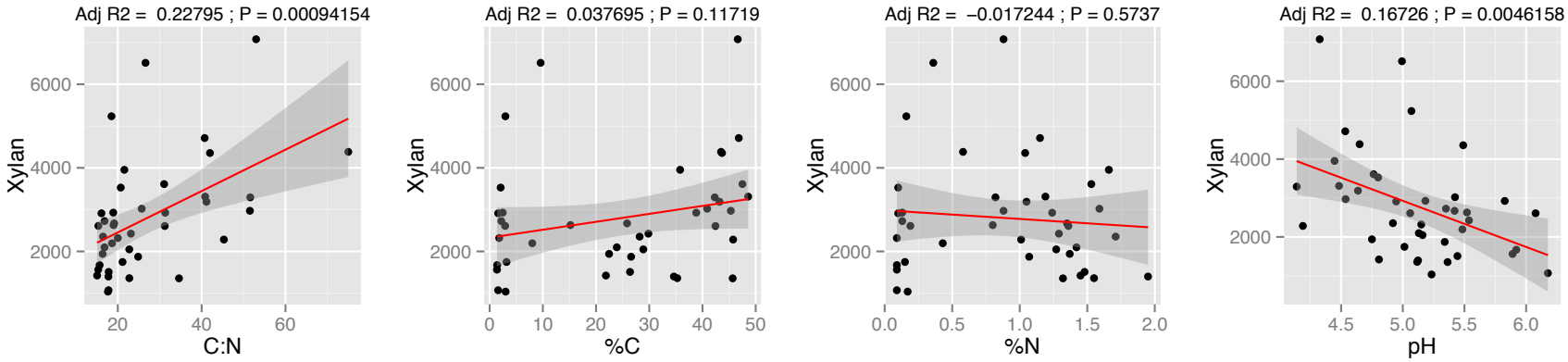


Fig. S15


Adj R2 = 0.22795 ; P = 0.00094154
Xylan
C:N
Adj R2 = 0.037695 ; P = 0.11719
%C
Adj R2 = −0.017244 ; P = 0.5737
%N
Adj R2 = 0.16726 ; P = 0.0046158
pH