Harvard Forest Data Archive HF431−01

Data File:

Name = hf431−01−temp−acclimation.csv
Description = temperature acclimation data 2019
Rows = 77  Columns = 66
MD5 checksum = 23ca110c3c668e19007c083e4c94593d

Variables:

WarmingDuration = warming duration of soil, number of years
   (dimensionless)
TOC = total organic carbon measured by rock−eval pyrolysis in
   percent per g dry soil (dimensionless)
I_index = thermal lability index (dimensionless)
R_index = thermal stability index (dimensionless)
pct_moisture_content = percent moisture content (dimensionless)
pct_water_content = percent water content (dimensionless)
LOI_pct = loss on ignition in % (dimensionless)
MBC = microbial biomass carbon − ug C g soil (microgramPerGram)
DOC_ug_g_soil = dissolved organic carbon − ug C g soil
   (microgramPerGram)
DOC_MBC = ratio of DOC to MBC (dimensionless)
Respiration_20C = respiration at 20C − ug C g soil hour
   (microgramPerGramPerHour)
CUERespiration = respiration when measuring CUE − ug C g soil hour
   (microgramPerGramPerHour)
MassSpecRespiration = respiration divided by MBC (dimensionless)
BG_intercept = betaglucosidase intercept calculated from temperature
   sensitivity curve (dimensionless)
BG_a_SE = betaglucosidase "a component" standard deviation
   calculated from temperature sensitivity curve (dimensionless)
BG_TS = betaglucosidase temperature sensitivity (dimensionless)
BG_b_SE = betaglucosidase "b component" standard deviation
   calculated from temperature sensitivity curve (dimensionless)
NAG_intercept = N−acetylglucosaminidase intercept calculated from
   temperature sensitivity curve (dimensionless)
NAG_a_SE = N−acetylglucosaminidase "a component" standard deviation
   calculated from temperature sensitivity curve (dimensionless)
NAG_TS = N−acetylglucosaminidase temperature sensitivity
   (dimensionless)
NAG_b_SE = N−acetylglucosaminidase "b component" standard deviation
   calculated from temperature sensitivity curve (dimensionless)
Ecoplate_k = growth parameter (dimensionless)
Ecoplate_k_se = standard deviation of the of maximum carrying
   capacity measured using Biolog Ecoplate and calculated with the
   growthcurver package (dimensionless)
Ecoplate_k_p = p value of maximum carrying capacity when significant
   growth is measured
using Biolog Ecoplate and calculated with the
   growthcurver package (dimensionless)

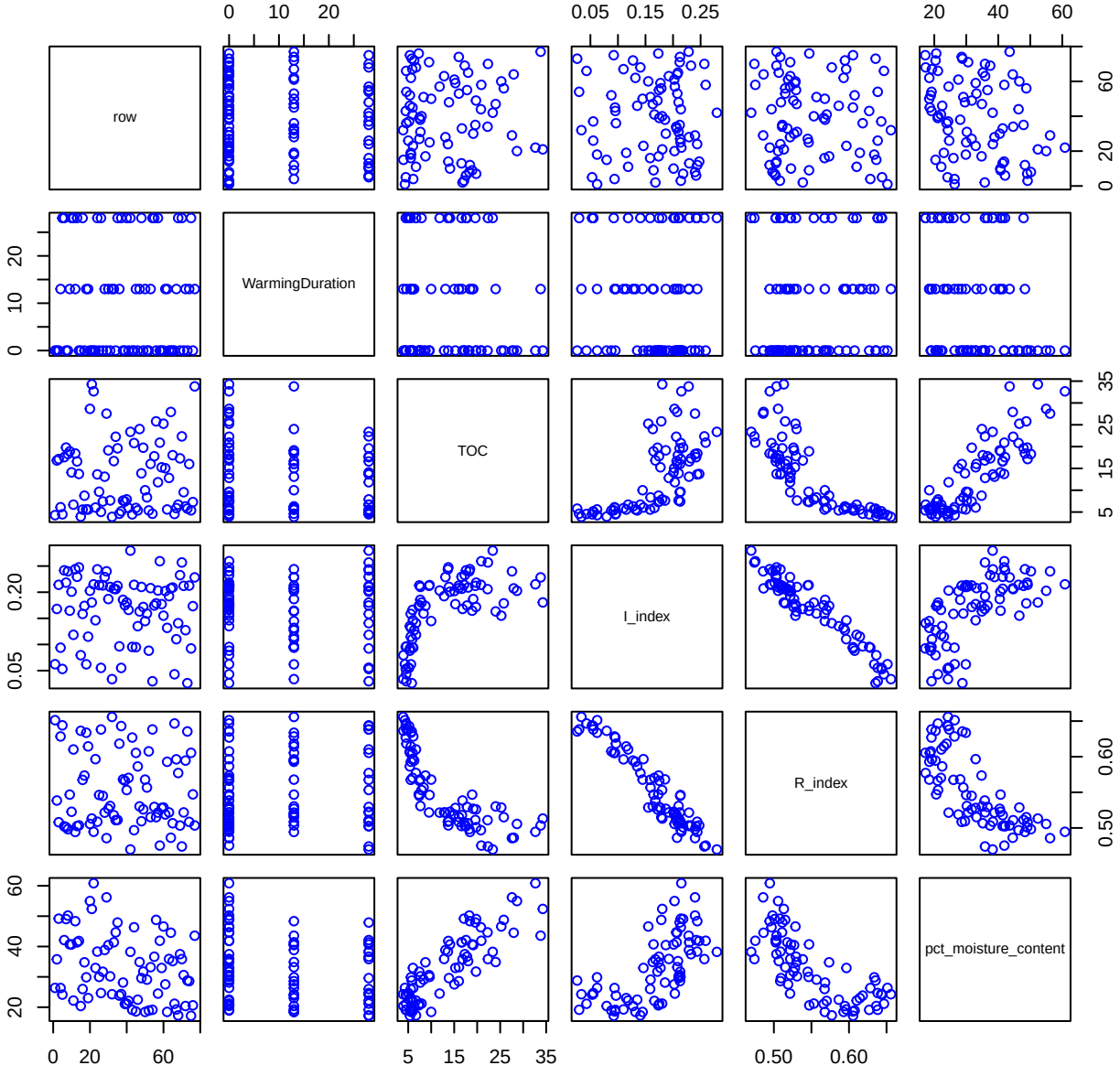
Ecoplate_n0 = estimated growth rate at time zero (the intercept) calculated with the growthcurver package measured with Biolog Ecoplate (dimensionless)
Ecoplate_r = growth rate (dimensionless)
Ecoplate_r_se = standard deviation of the growth rate calculated with the growthcurver package measured with Biolog Ecoplate (dimensionless)
Ecoplate_r_p = p value of growth rate when significant growth is measured using Biolog Ecoplate and calculated with the growthcurver package (dimensionless)
Ecoplate_auc_l = area under the curve calculated with the growthcurver package measured with Biolog Ecoplate (dimensionless)
Ecoplate_t_mid = time needed to reach half−max of optical density calculated with the growthcurver package with Biolog Ecoplate (dimensionless)
X16S_rRNA_nbc_g_dry_soil = real time qPCR from 16S rRNA gene − number of copies per g dry soil (dimensionless)
ITS_nbc_g_dry_soil = real time qPCR from ITS gene − number of copies per g dry soil (dimensionless)
F_B_ratio = fungal to bacterial ratio (dimensionless)
RespirationSum = sum of respiration measurements performed under each temperature − ug C g dry soil (microgramPerGramPerHour)
Respiration_TS = respiration temperature sensitivity (dimensionless)
resp_slope_SEexp = standard deviation calculated from temperature sensitivity curve of respiration (dimensionless)
resp_Exp_intercept = respiration intercept calculated from temperature sensitivity curve (dimensionless)
resp_Exp_intercept_SE = standard deviation of the respiration intercept calculated from temperature sensitivity curve of respiration (dimensionless)
Ecoplate_Bray_axis1 = axis 1 from ecoplate growth data (dimensionless)
Ecoplate_Bray_axis2 = axis 2 from ecoplate growth data (dimensionless)
BG = betaglucosidase enzyme activity at 20Celsius (dimensionless)
NAG = N−acetylglucosaminidase enzyme activity at 20Celsius (dimensionless)
OX = oxidative enzyme activity at 20Celsius (dimensionless)
Growth = growth measured at 20Celsius − ug C g dry soil hour (microgramPerGramPerHour)
CUE = carbon use efficiency − % (dimensionless)
NMDS_RockEval_Axis1 = axis 1 from SOM thermal analysis (dimensionless)
NMDS_RockEval_Axis2 = axis 2 from SOM thermal analysis (dimensionless)
PC1_metabol = axis 1 from principal coordinate analysis from metabolomics (dimensionless)
PC2_metabol = axis 2 from principal coordinate analysis from metabolomics (dimensionless)
PC3_metabol = axis 3 from principal coordinate analysis from metabolomics (dimensionless)

Axis1_metabol = axis 1 from Bray curtis analysis from metabolomic (dimensionless)
Axis2_metabol = axis 2 from Bray curtis analysis from metabolomic (dimensionless)
PCOA_Axis1 = axis 1 from SOM thermal analysis from principal coordinate analysis (dimensionless)
PCOA_Axis2 = axis 2 from SOM thermal analysis from principal coordinate analysis (dimensionless)
Metabolomics_complexity = metabolomics complexity index (dimensionless)
CAZY_perRpoB = cazies per RpolB (dimensionless)
NOSC = mean nominal oxidation state (dimensionless)

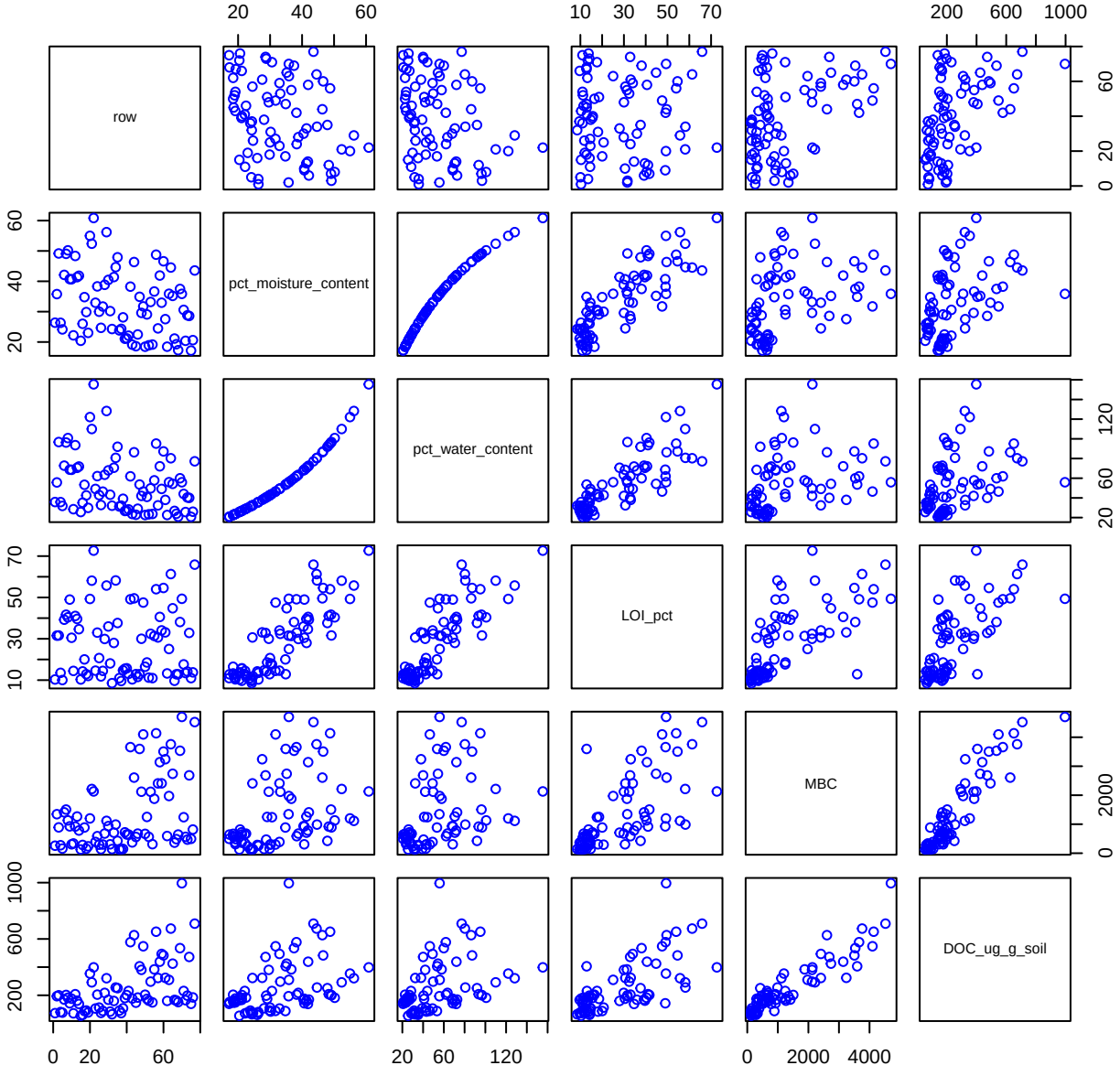
| Variable | Min | Median | Mean | Max | NAs |
|---|---|---|---|---|---|
| WarmingDurat | 0.000 | 13.000 | 10.286 | 28.000 | 0 |
| TOC | 3.900 | 12.810 | 13.342 | 34.270 | 0 |
| I_index | 0.026 | 0.179 | 0.167 | 0.280 | 0 |
| R_index | 0.470 | 0.530 | 0.552 | 0.656 | 0 |
| pct_moisture | 17.186 | 31.678 | 32.936 | 60.845 | 0 |
| pct_water_co | 20.753 | 46.365 | 53.637 | 155.392 | 0 |
| LOI_pct | 8.540 | 25.047 | 27.933 | 72.650 | 0 |
| MBC | 129.442 | 782.116 | 1312.640 | 4700.018 | 0 |
| DOC_ug_g_soi | 54.524 | 183.723 | 250.556 | 995.752 | 0 |
| DOC_MBC | 0.099 | 0.235 | 0.274 | 0.730 | 0 |
| Respiration_ | 0.144 | 1.031 | 1.212 | 4.770 | 0 |
| CUERespirati | 0.168 | 1.075 | 1.305 | 5.544 | 1 |
| MassSpecResp | 0.000 | 0.001 | 0.001 | 0.004 | 0 |
| BG_intercept | 4.669 | 6.419 | 6.342 | 8.263 | 0 |
| BG_a_SE | 0.040 | 0.242 | 0.264 | 0.594 | 0 |
| BG_TS | 0.031 | 0.064 | 0.064 | 0.091 | 0 |
| BG_b_SE | 0.002 | 0.012 | 0.014 | 0.033 | 0 |
| NAG_intercep | 3.594 | 6.239 | 6.090 | 8.872 | 0 |
| NAG_a_SE | 0.071 | 0.241 | 0.328 | 1.232 | 0 |
| NAG_TS | 0.025 | 0.061 | 0.062 | 0.109 | 0 |
| NAG_b_SE | 0.004 | 0.012 | 0.017 | 0.063 | 0 |
| Ecoplate_k | 0.461 | 0.829 | 0.812 | 1.099 | 0 |
| Ecoplate_k_s | 0.013 | 0.028 | 0.028 | 0.044 | 0 |
| Ecoplate_k_p | 0.000 | 0.000 | 0.000 | 0.000 | 0 |
| Ecoplate_n0 | 0.001 | 0.012 | 0.015 | 0.039 | 0 |
| Ecoplate_r | 0.023 | 0.034 | 0.035 | 0.055 | 0 |
| Ecoplate_r_s | 0.001 | 0.003 | 0.003 | 0.005 | 0 |
| Ecoplate_r_p | 0.000 | 0.000 | 0.000 | 0.000 | 0 |
| Ecoplate_auc | 45.376 | 524.954 | 387.415 | 871.025 | 0 |
| Ecoplate_t_m | 74.820 | 118.180 | 119.456 | 164.868 | 0 |
| X16S_rRNA_nb | 1861523557 | 23956235503 | 3129935575110900000000 | | 0 |
| ITS_nbc_g_dr | 2126201 | 318483229 | 572756339 | 2562062850 | 0 |
| F_B_ratio | 0.001 | 0.013 | 0.016 | 0.062 | 0 |
| RespirationS | 0.994 | 7.395 | 8.594 | 32.842 | 0 |
| Respiration_ | 0.071 | 0.098 | 0.097 | 0.114 | 0 |
| resp_slope_S | 0.001 | 0.008 | 0.008 | 0.015 | 0 |
| resp_Exp_int | −3.654 | −1.919 | −2.124 | −0.472 | 0 |
| resp_Exp_int | 0.025 | 0.154 | 0.153 | 0.301 | 0 |
| Ecoplate_Bra | −0.193 | −0.008 | −0.010 | 0.187 | 0 |
| Ecoplate_Bra | −0.333 | 0.027 | 0.010 | 0.134 | 1 |
| BG | 182.401 | 1565.238 | 2683.048 | 11614.265 | 0 |
| NAG | 33.320 | 1658.417 | 2514.587 | 10285.483 | 0 |
| OX | 0.002 | 0.016 | 0.031 | 0.199 | 0 |
| Growth | 0.002 | 0.469 | 0.787 | 4.779 | 0 |
| CUE | 1.555 | 37.141 | 37.135 | 77.692 | 0 |
| NMDS_RockEva | −0.007 | 0.002 | 0.000 | 0.006 | 0 |
| NMDS_RockEva | −0.004 | 0.000 | −0.000 | 0.003 | 0 |
| PC1_metabol | −7.705 | −0.246 | −0.047 | 5.181 | 0 |
| PC2_metabol | −3.627 | −0.627 | −0.095 | 4.269 | 0 |

| Variable | Min | Median | Mean | Max | NAs |
|---|---|---|---|---|---|
| PC3_metabol | −2.184 | −0.174 | −0.085 | 1.458 | 0 |
| Axis1_metabo | −0.202 | −0.003 | 0.003 | 0.207 | 0 |
| Axis2_metabo | −0.168 | 0.008 | 0.001 | 0.149 | 0 |
| PCOA_Axis1 | −0.235 | −0.010 | 0.004 | 0.263 | 0 |
| PCOA_Axis2 | −0.119 | 0.012 | 0.002 | 0.168 | 0 |
| Metabolomics | 128.578 | 138.345 | 139.117 | 157.440 | 0 |
| CAZY_perRpoB | 921327 | 9751748 | 8624842 | 11237339 | 57 |
| NOSC | −0.366 | −0.249 | −0.237 | −0.043 | 0 |

# HF431−01 Plot 1



# HF431−01 Plot 2



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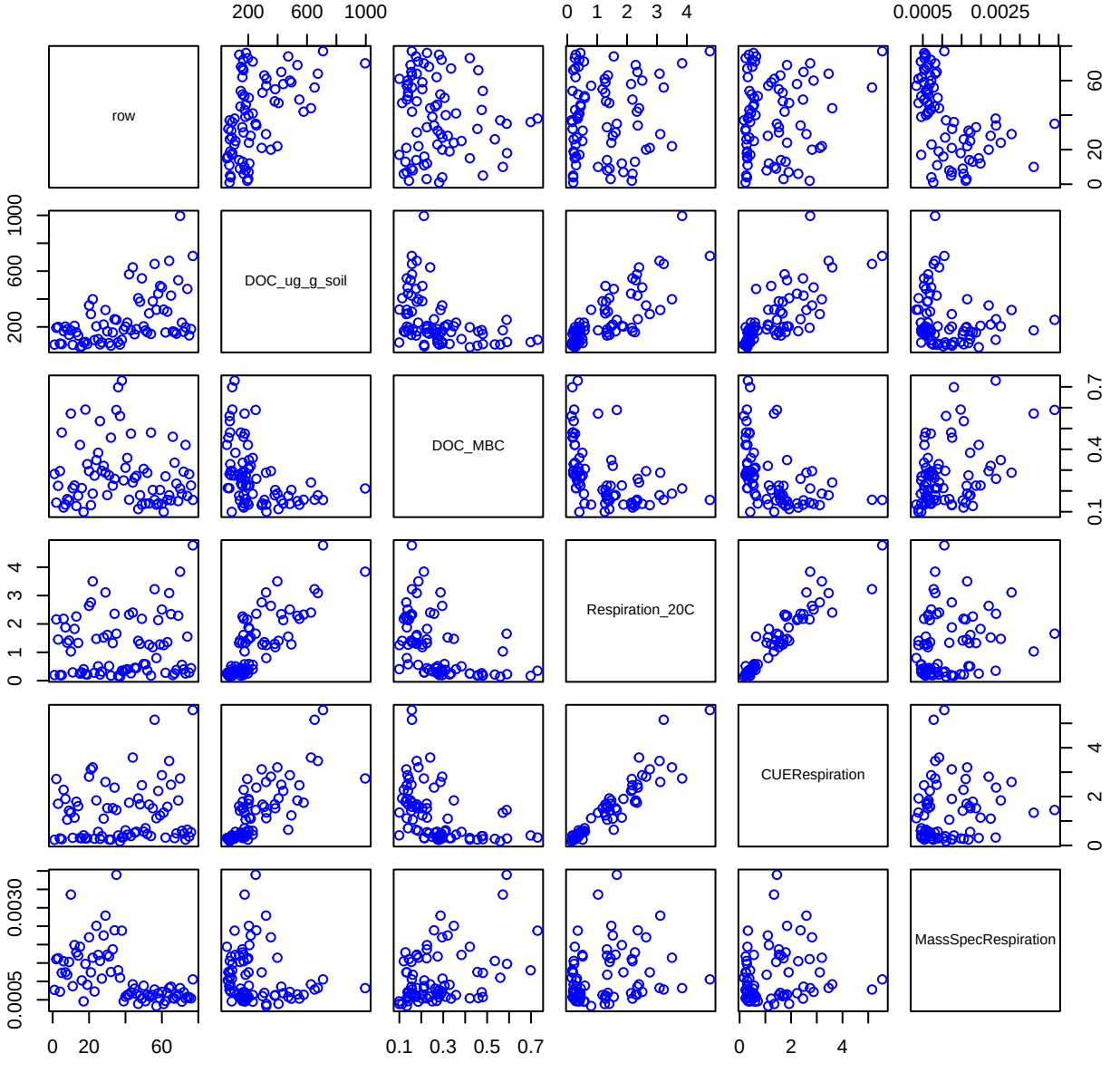

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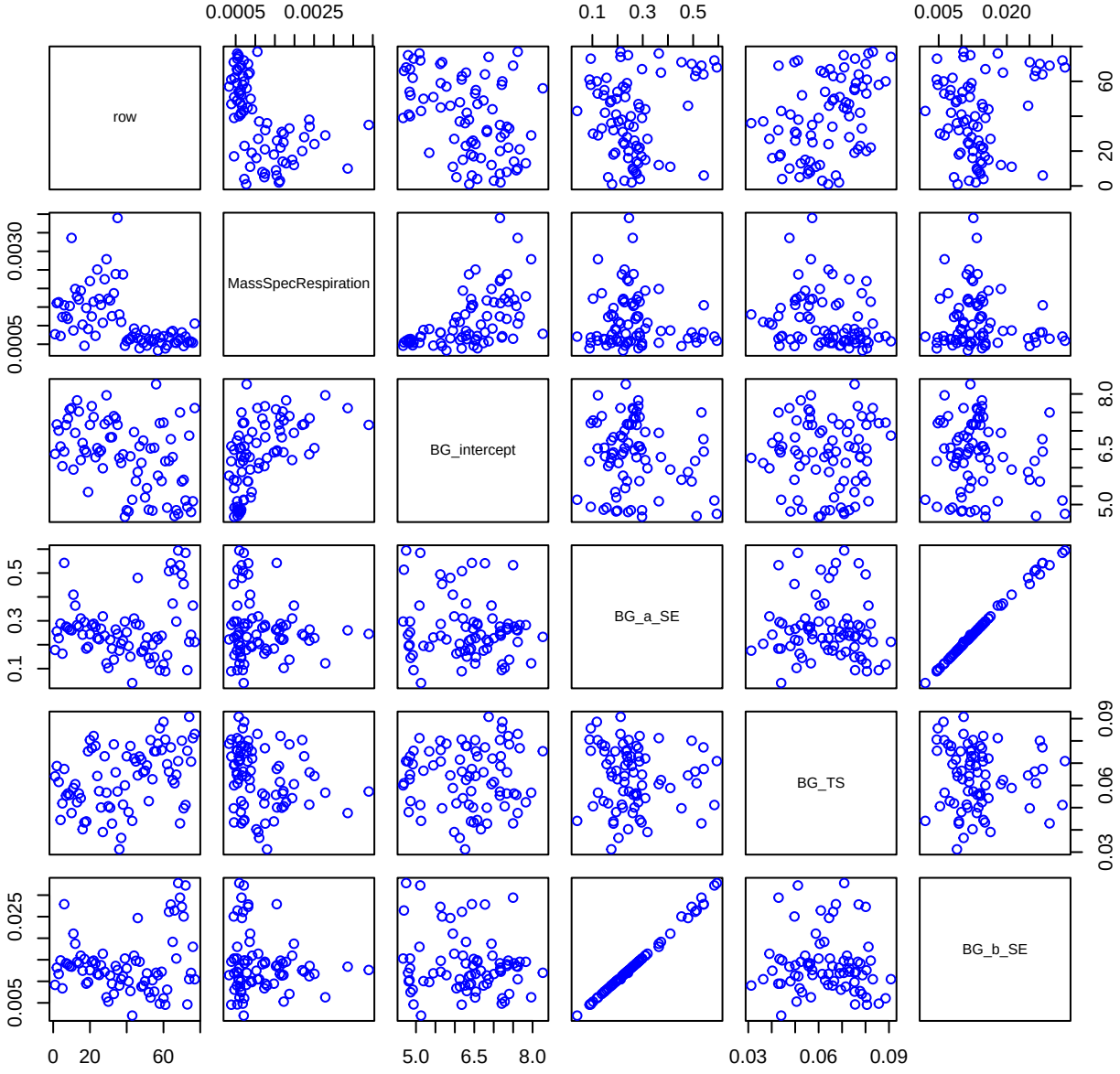

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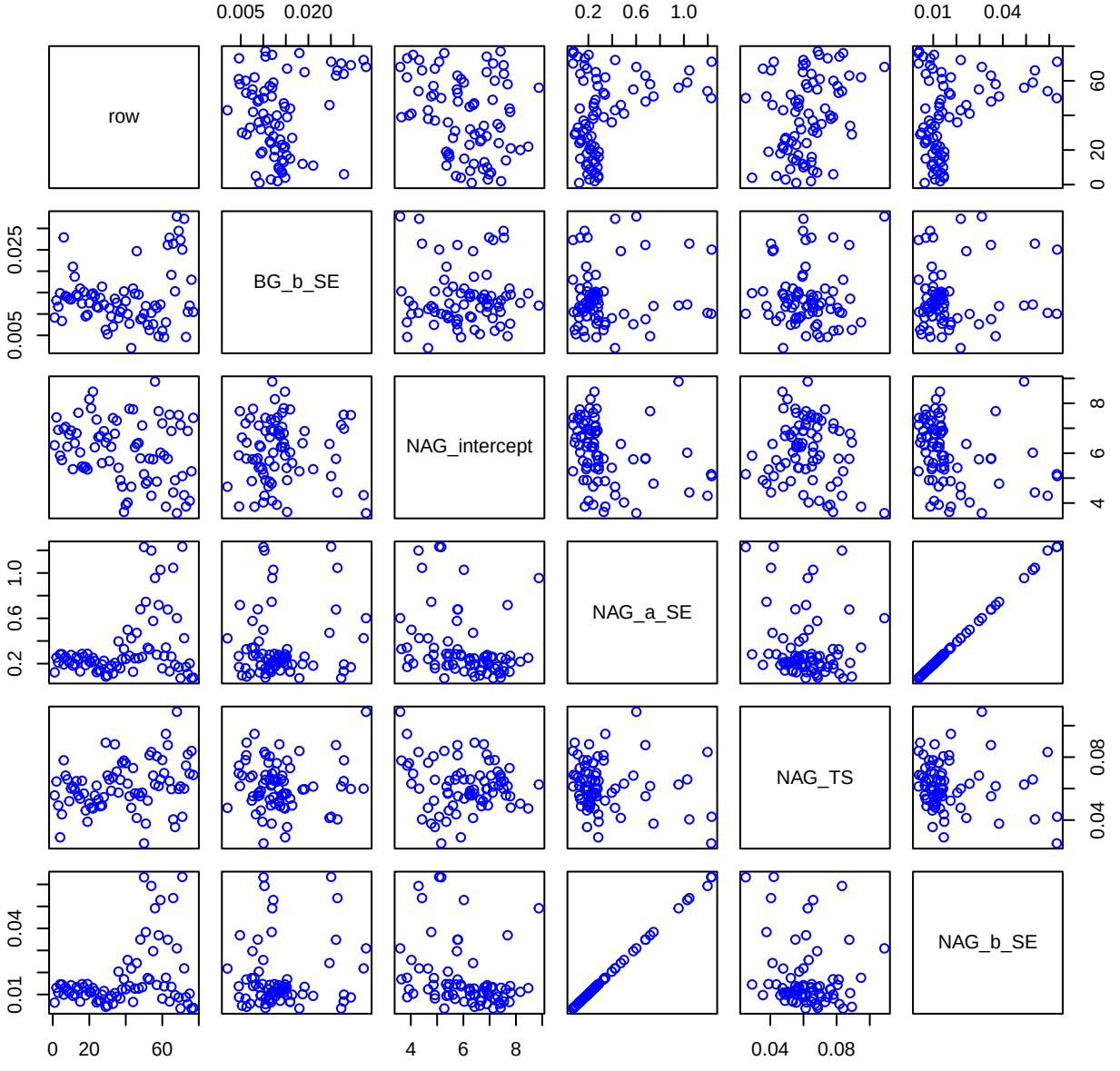

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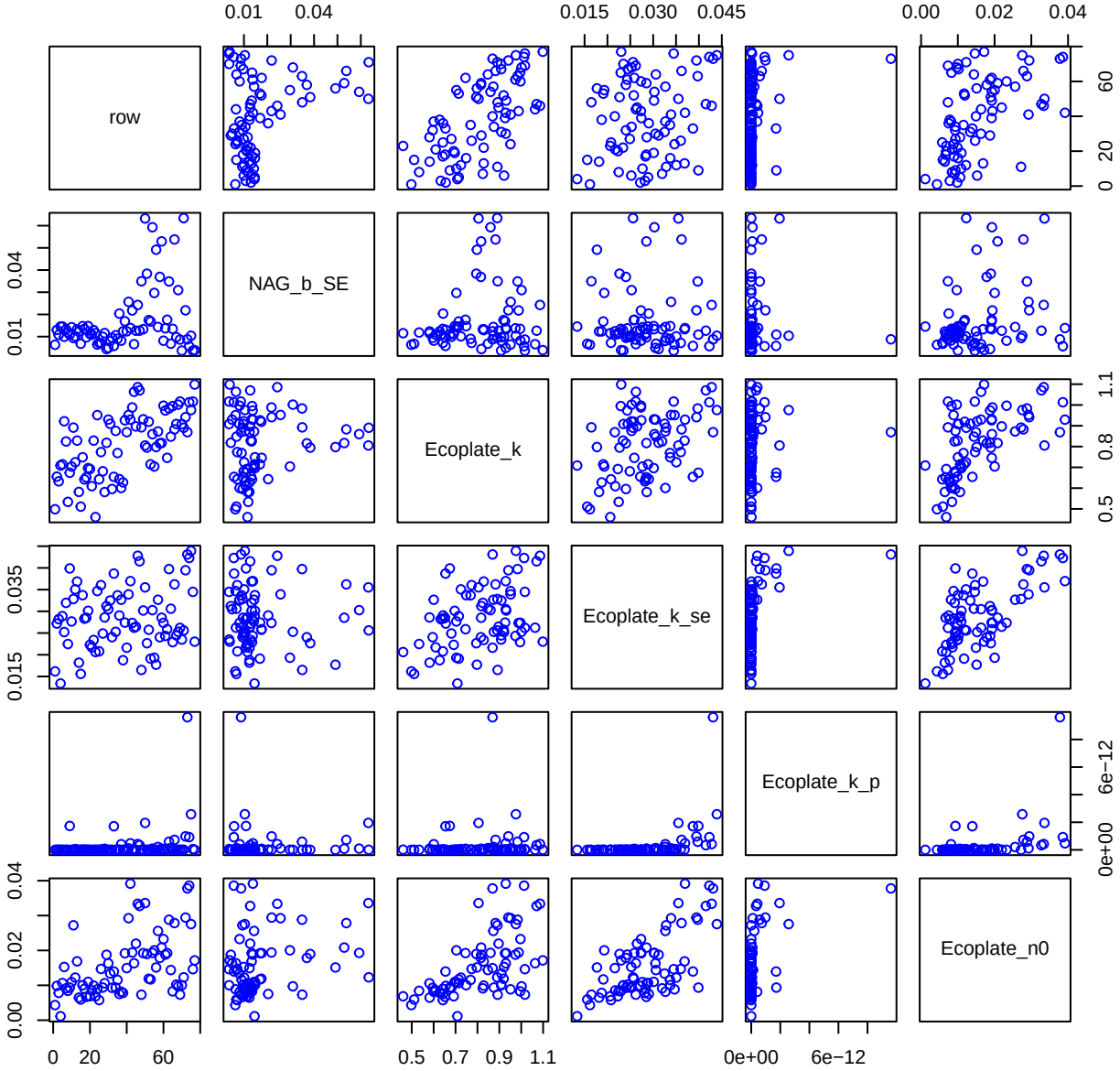

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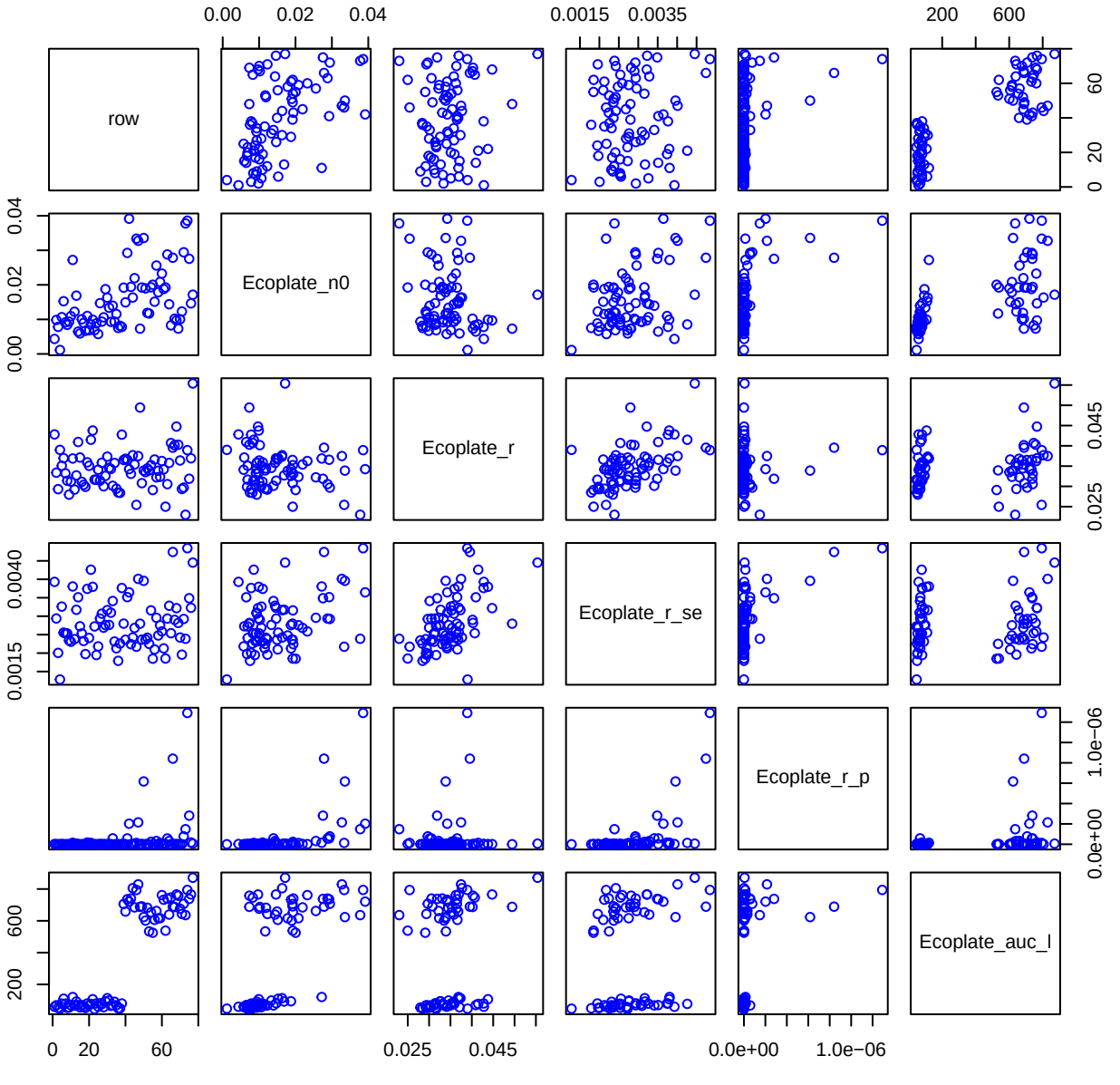

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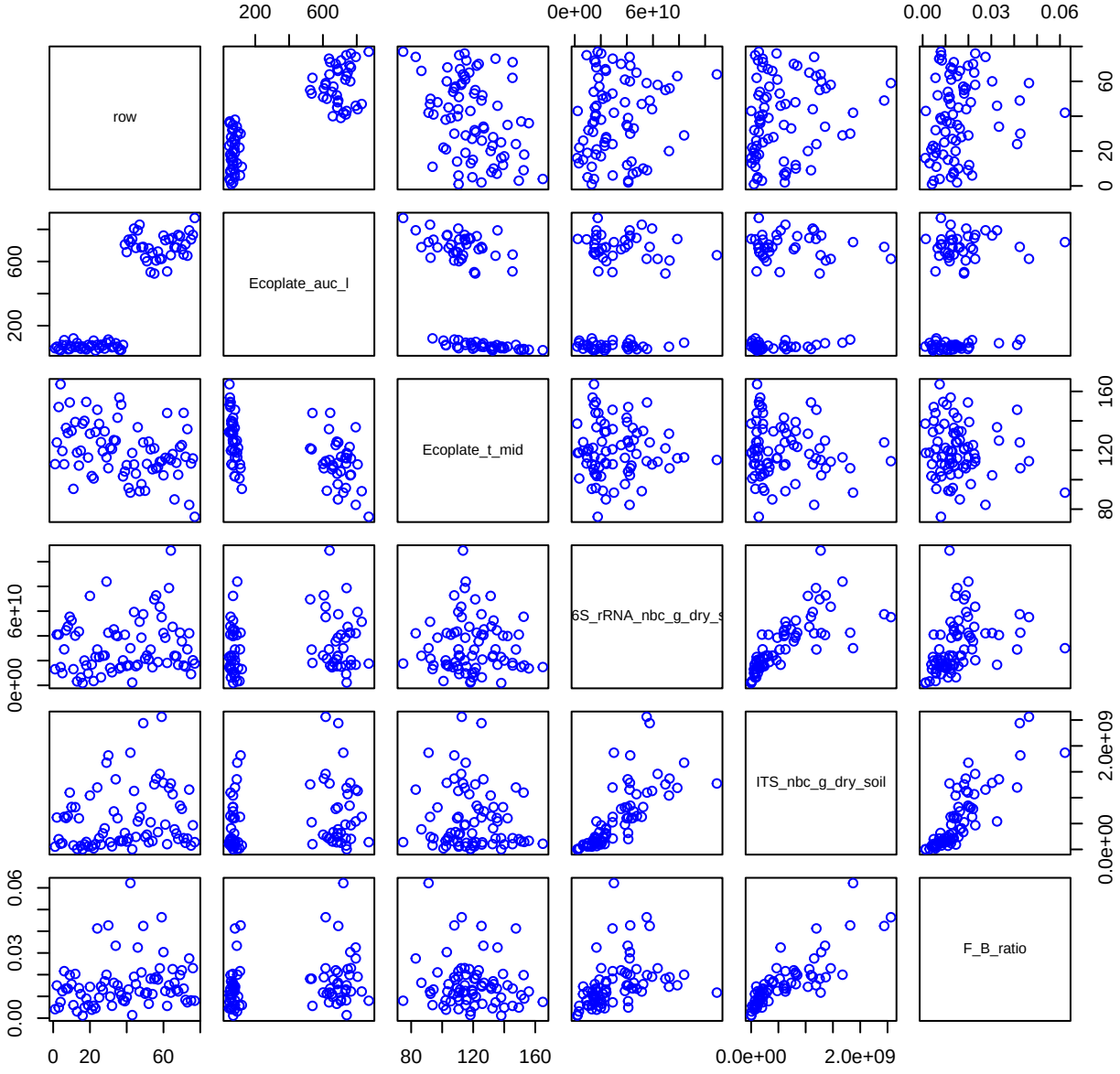

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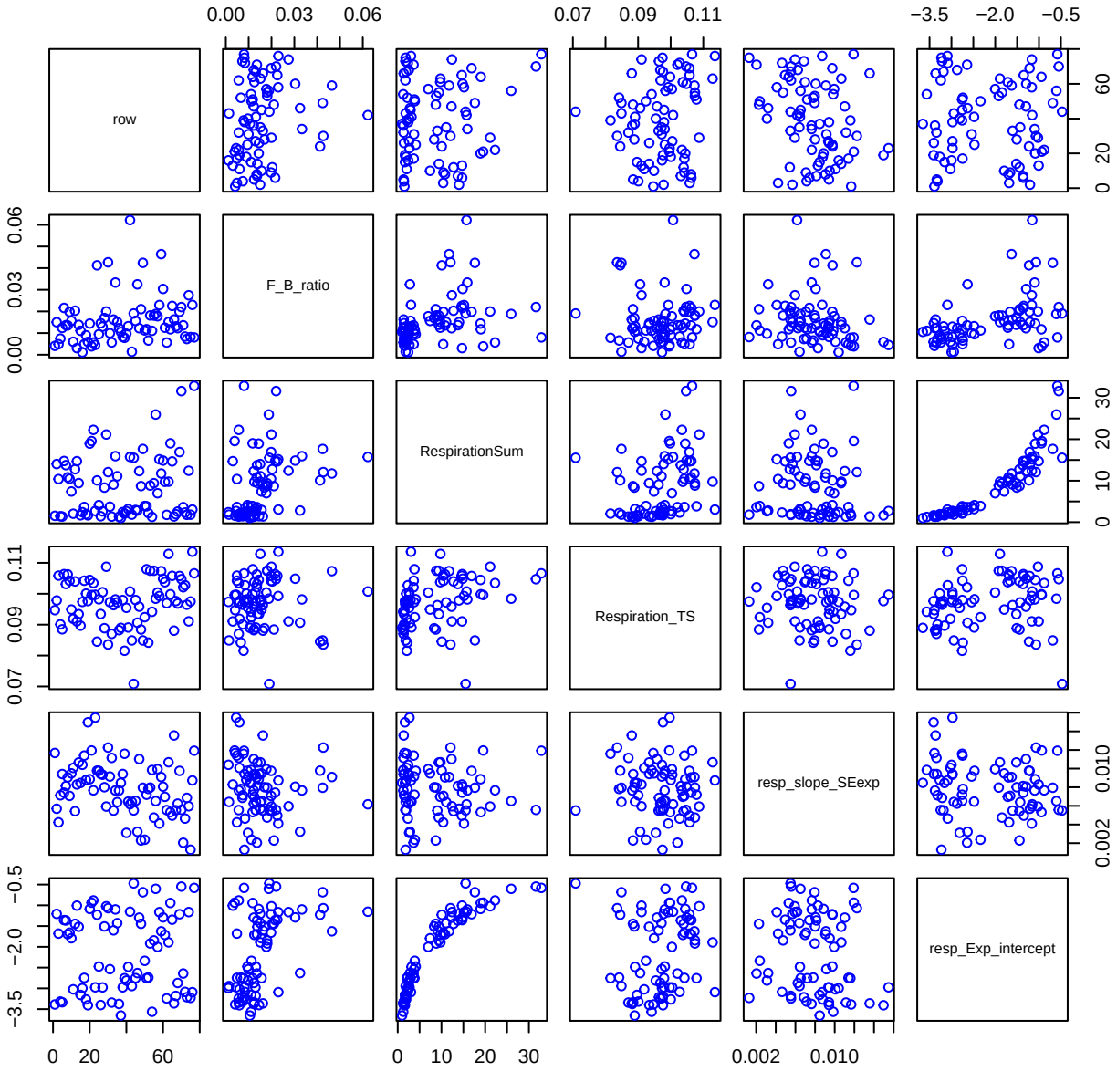
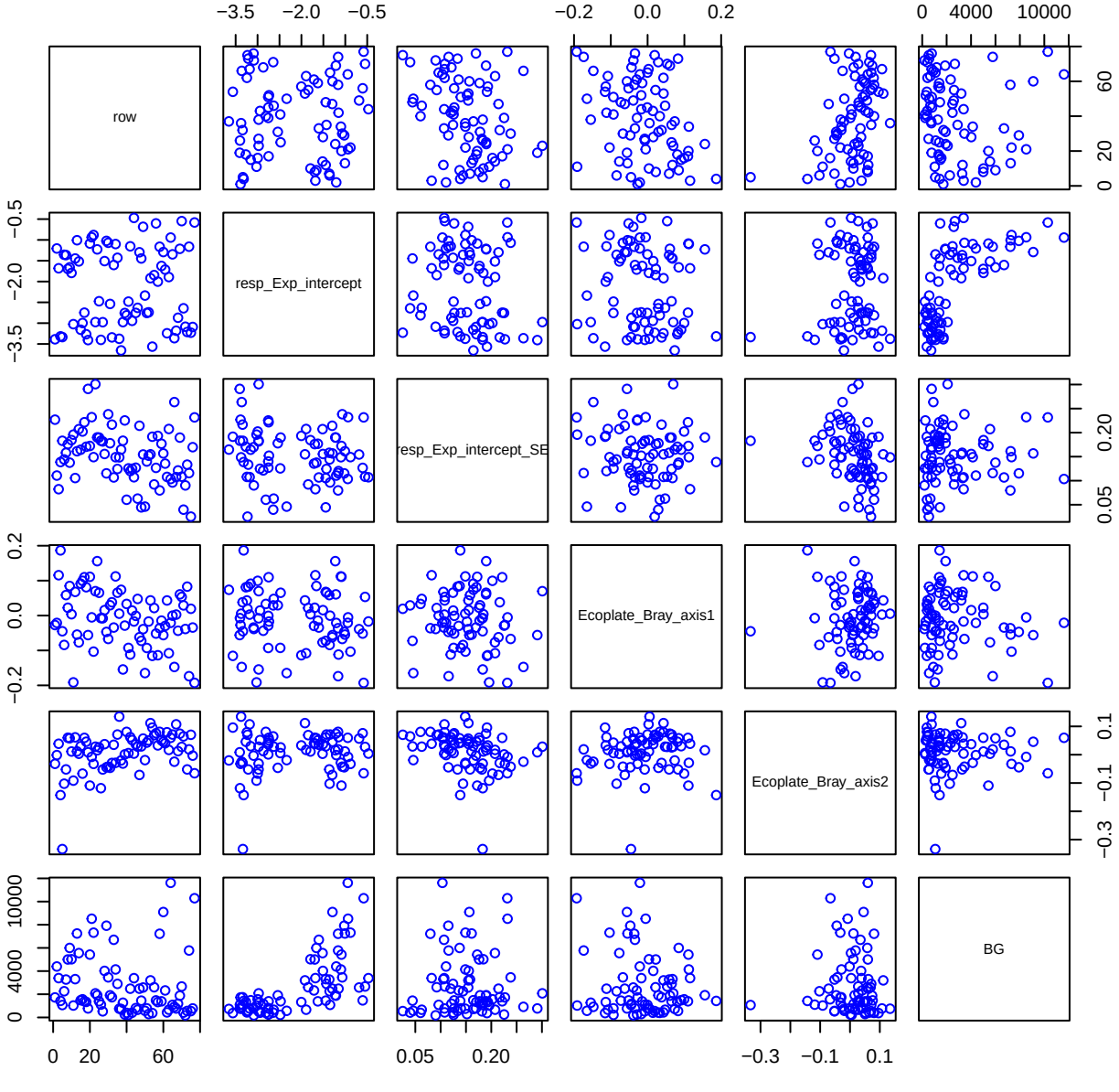
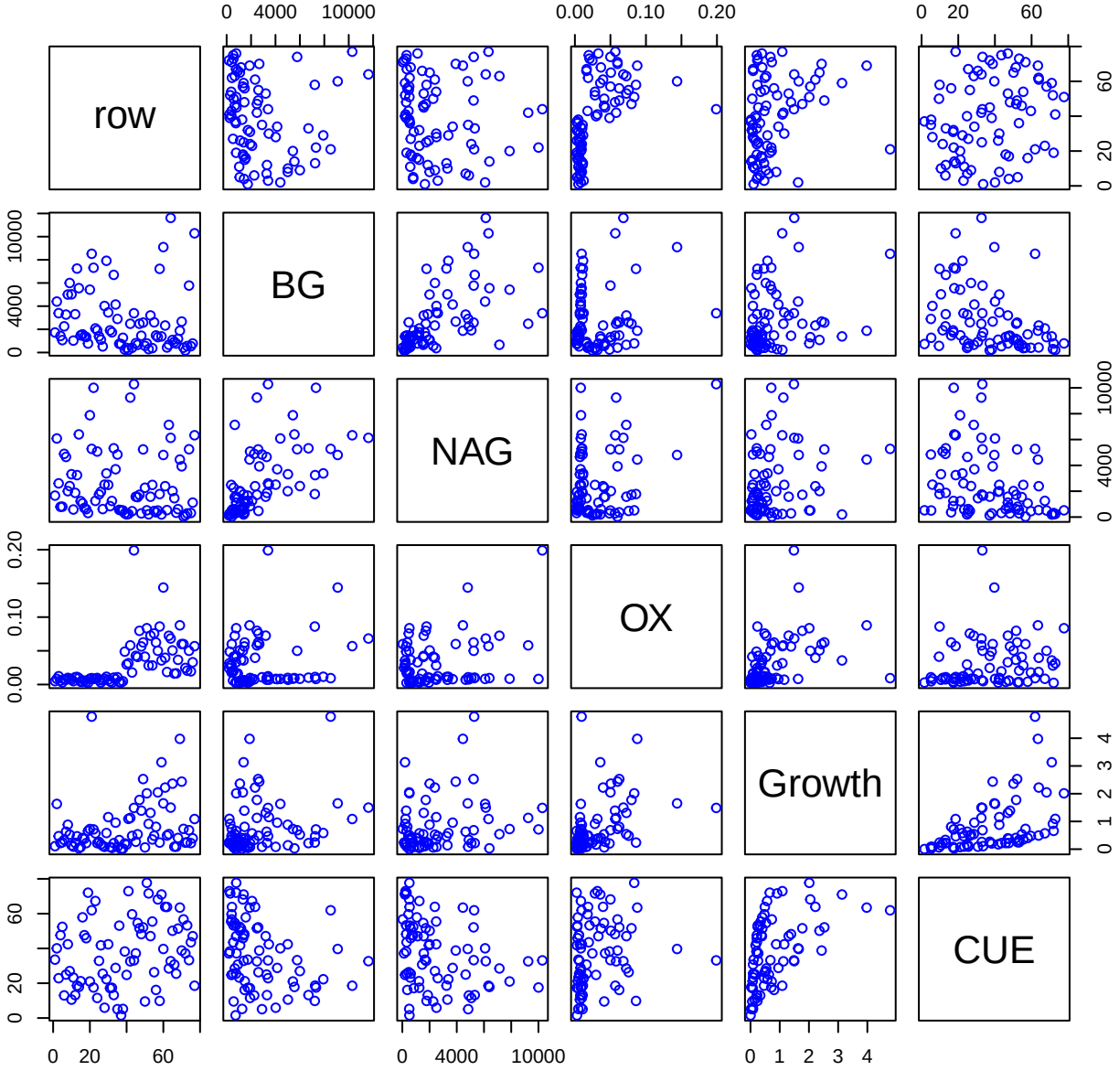


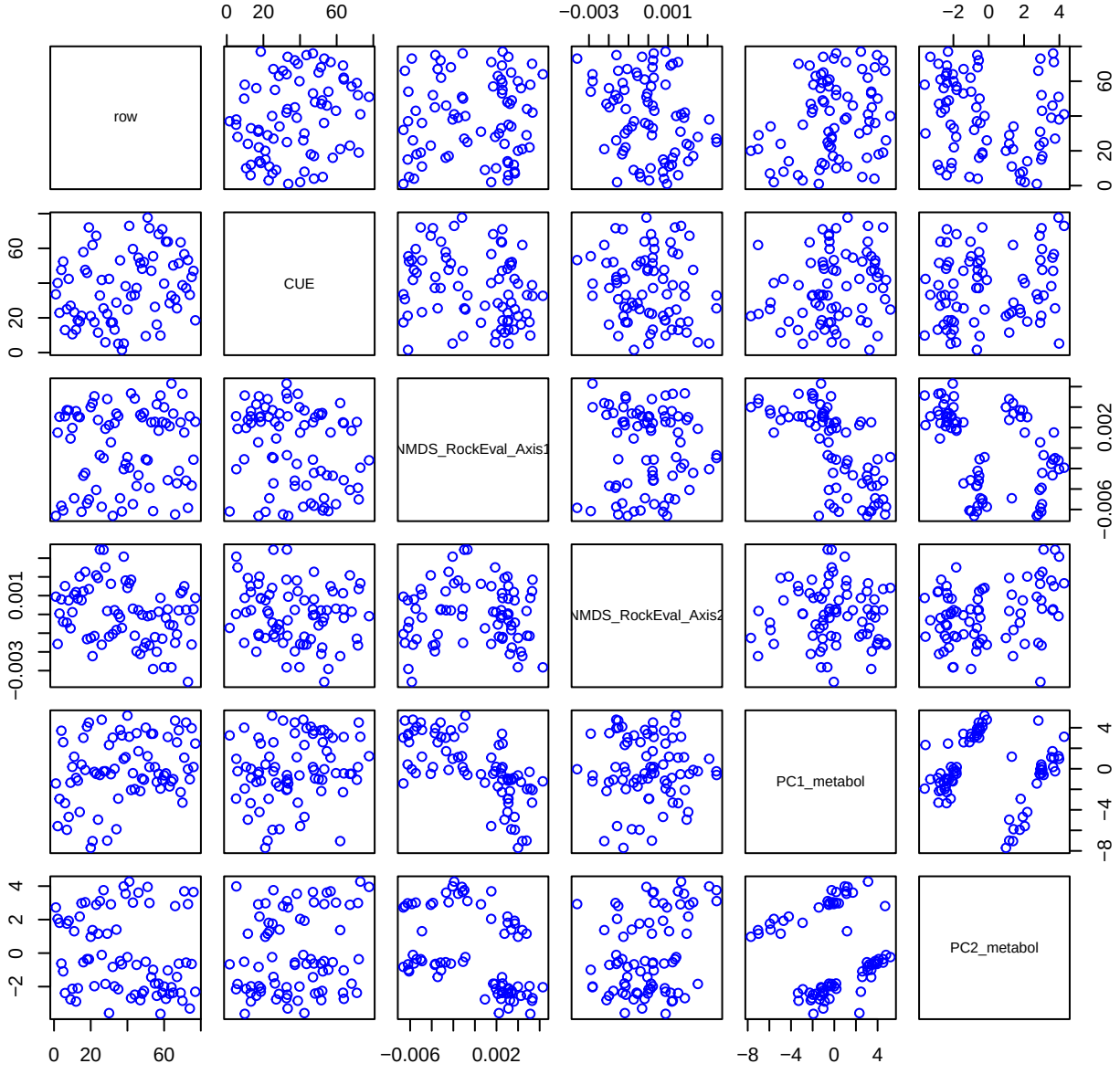
# HF431−01 Plot 10



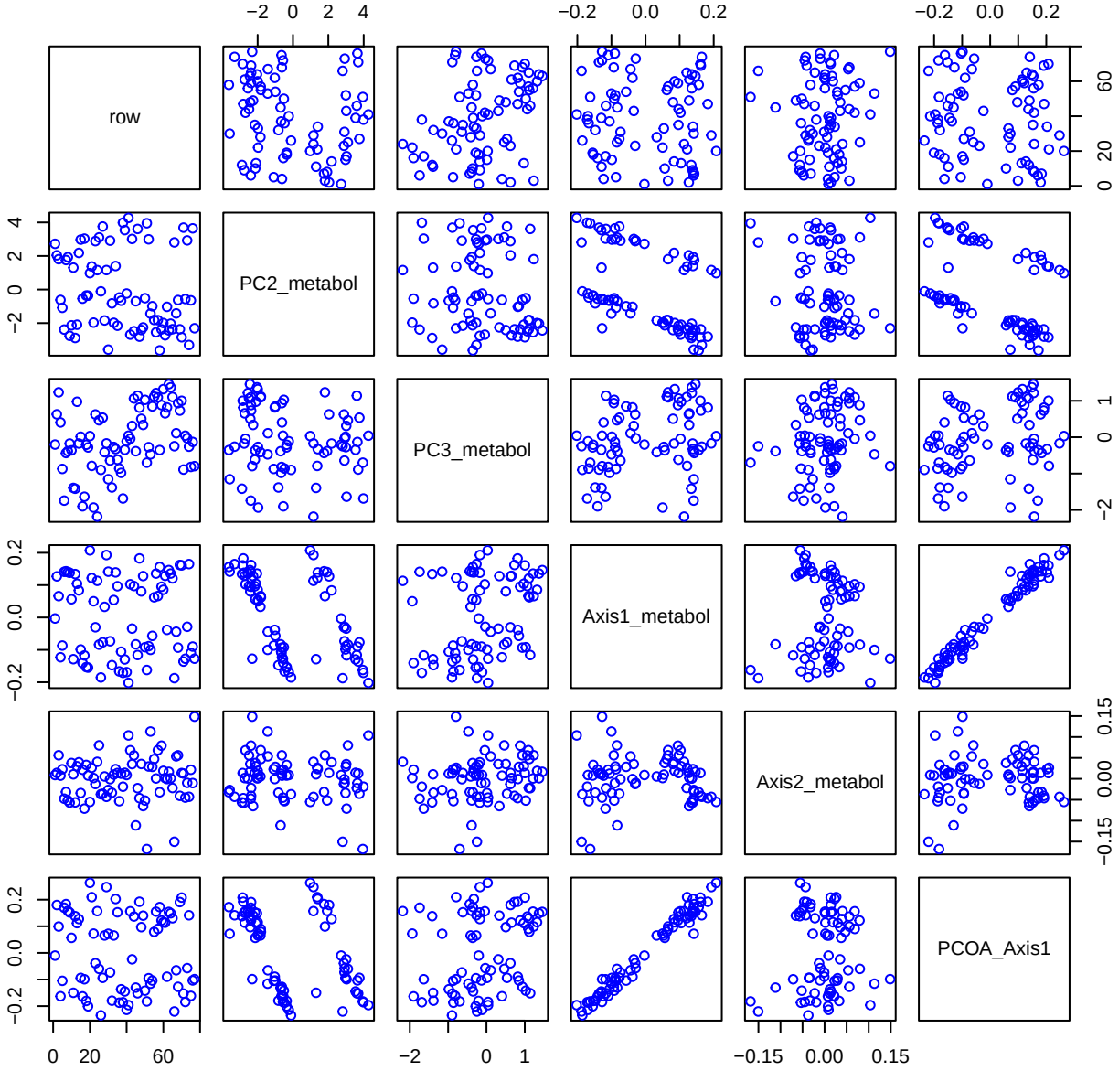
# HF431−01 Plot 11



# HF431−01 Plot 12



# HF431−01 Plot 13



# HF431−01 Plot 14