Harvard Forest Data Archive HF456-01

Data File:

Name = hf456-01-soil-plant-microbe-data.csv
Description = soil, plant and microbe data
Rows = 204 Columns = 170
MD5 checksum = b884fab0192c883ec306b4fc368aa81c

Variables:

Transect_Lat = latitude of the transect sampled (degree)
Transect_Long = longitude of the transect sampled (degree)
Distance = distance from the forest edge of the sampling location
   (meter)
NH4i_final = ammonium concentration of the soil sample
   (microgramPerGram)
NO3i_final = nitrate concentration of the soil sample
   (microgramPerGram)
Ammonification = net soil ammonification rate
   (microgramPerGramPerDay)
Nitrification = net soil nitrification rate (microgramPerGramPerDay)
N_min = net soil nitrogen mineralization rate
   (microgramPerGramPerDay)
Al = soil total aluminum content (microgramPerGram)
As = soil total arsenic content (microgramPerGram)
B = soil total boron content (microgramPerGram)
Ba = soil total barium content (microgramPerGram)
Ca = soil total calcium content (microgramPerGram)
Cd = soil total cadmium content (microgramPerGram)
Co = soil total cobalt content (microgramPerGram)
Cr = soil total chromium content (microgramPerGram)
Cu = soil total copper content (microgramPerGram)
Fe = soil total iron content (microgramPerGram)
K = soil total potassium content (microgramPerGram)
Li = soil total lithium content (microgramPerGram)
Mg = soil total magnesium content (microgramPerGram)
Mn = soil total manganese content (microgramPerGram)
Mo = soil total molybdenum content (microgramPerGram)
Na = soil total sodium content (microgramPerGram)
Ni = soil total nickel content (microgramPerGram)
P = soil total phosphous content (microgramPerGram)
Pb = soil total lead content (microgramPerGram)
S = soil total sulfur content (microgramPerGram)
Sb = soil total antimony content (microgramPerGram)
Se = soil total selenium content (microgramPerGram)
Si = soil total silicon content (microgramPerGram)
Sr = soil total strontium content (microgramPerGram)
Tl = soil total thallium content (microgramPerGram)
V = soil total vanadium content (microgramPerGram)
Zn = soil total zinc content (microgramPerGram)

pH = soil pH (dimensionless)
soil_temp = soil temperature (celsius)
litter_depth = litter layer depth (centimeter)
O_depth = soil organic layer depth (centimeter)
soil_moisture = proportion soil water content by weight
(dimensionless)
SOM = proportion soil organic matter content by weight
(dimensionless)
prop_pine_litter = proportion of forest floor litter that is pine
litter, measured in a 20 x 20cm square above the sampling point
(dimensionless)
prop_hw_litter = proportion of forest floor litter that is hardwood
litter, measured in a 20 x 20cm square above the sampling point
(dimensionless)
total_floor_litter = total weight of forest floor litter, measured
in a 20 x 20cm square above the sampling point (gram)
pine_floor_litter = total weight of forest floor pine litter,
measured in a 20 x 20cm square above the sampling point (gram)
hw_floor_litter = total weight of forest floor hardwood litter,
measured in a 20 x 20cm square above the sampling point (gram)
Max_height = maximum height of understory vegetation (meter)
No_white_pine_seedlings = number of white pine seedlings in a in a
1m x 1m square centered around the sampling point (dimensionless)
No_oak_seedlings = number of oak seedlings in a in a 1m x 1m square
centered around the sampling point (dimensionless)
All_plants = cumulative sum of all understory plant scores
(specifically Broad_leaf_herbs, Grassy_herbs, Ferns, Shrubs,
White_pine_seedlings, Oak_seedlings, Other_tree_seedlings) using the Braun−Blanquet
method (dimensionless)
AM_basal = basal area of all arbuscular mycorrhizal trees greater
than 5cm diameter at breast height in a 10m x 10m square plot centered
between the A and B sampling points (centimeterCubed)
ECM_basal = basal area of all ectomycorrhizal trees greater than 5cm
diameter at breast height in a 10m x 10m square plot centered between the
A and B sampling points (centimeterCubed)
hw_basal = basal area of all hardwood trees greater than 5cm
diameter at breast height in a 10m x 10m square plot centered between the
A and B sampling points (centimeterCubed)
pine_basal = basal area of all white pine trees greater than 5cm
diameter at breast height in a 10m x 10m square plot centered between the
A and B sampling points (centimeterCubed)
num_stems = number of trees larger than 5cm diameter at breast
height in a 10m x 10m square plot centered between the A and B sampling
points (dimensionless)
total_basal = cumulative basal area of all trees greater than 5cm
diameter at breast height in a 10m x 10m square plot centered between the
A and B sampling points (centimeterCubed)
ECM_AM = ratio of ectomycorrhizal:arbuscular mycorrhizal tree basal
area of all trees greater than 5cm diameter at breast height in a 10m
x 10m square plot centered between the A and B sampling points
(dimensionless)

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no_pine_saplings = number of white pine saplings smaller than 5cm
   diameter at breast height in a 10m x 10m square plot centered between the
   A and B sampling points (dimensionless)
no_oak_saplings = number of oak saplings smaller than 5cm diameter
   at breast height in a 10m x 10m square plot centered between the A
   and B sampling points (dimensionless)
PO4 = soil phosphate concentration (microgramPerGram)
PO4_release = net soil phosphate release or uptake rate
   (microgramPerGramPerDay)
root_density = root density in the top 10.2cm of soil
   (gramPerCentimeterCubed)
ECM_abundance = relative abundance of ectomycorrhizal fungi in
   high-throughput amplicon sequence data (dimensionless)
SAP_abundance = relative abundance of saprotrophic fungi in
   high-throughput amplicon sequence data (dimensionless)
soilSAP_abundance = relative abundance of soil saprotrophic fungi in
   high-throughput amplicon sequence data (dimensionless)
AM_abundance = relative abundance of arbuscular mycorrhizal fungi in
   high-throughput amplicon sequence data (dimensionless)
root_endophyte_abundance = relative abundance of root endyphytic
   fungi in high-throughput amplicon sequence data (dimensionless)
contact_expl = relative abundance of contact exploration type
   ectomycorrhizal fungi in high-throughput amplicon sequence data (dimensionless)
short_dist_expl = relative abundance of short distance exploration
   type ectomycorrhizal fungi in high-throughput amplicon sequence data
   (dimensionless)
med_dist_expl = relative abundance of medium distance exploration
   type ectomycorrhizal fungi in high-throughput amplicon sequence data
   (dimensionless)
long_dist_expl = relative abundance of long distance exploration
   type ectomycorrhizal fungi in high-throughput amplicon sequence data
   (dimensionless)
mat_expl = relative abundance of mat exploration typeectomycorrhizal
   fungi in high-throughput amplicon sequence data (dimensionless)
Nitrifier_abundance = relative abundance of nitrifying bacteria in
   high-throughput amplicon sequence data (dimensionless)
Decomposer_abundance = relative abundance of decomposer bacteria
   (summed cellulolytic, lignolytic, and chitinolytic bacteria) in
   high-throughput amplicon sequence data (dimensionless)
Cellulolytic_abundance = relative abundance of cellulolytic bacteria
   in high-throughput amplicon sequence data (dimensionless)
Lignolytic_abundance = relative abundance of lignolytic bacteria in
   high-throughput amplicon sequence data (dimensionless)
Chitinolytic_abundance = relative abundance of chitinolytic bacteria
   in high-throughput amplicon sequence data (dimensionless)
Copiotroph_abundance = relative abundance of copiotrophic bacteria
   in high-throughput amplicon sequence data (dimensionless)
Oligotroph_abundance = relative abundance of oligotrophic bacteria
   in high-throughput amplicon sequence data (dimensionless)
Ndecomp_EC_abund = relative abundance of chitinase gene copies in
   the bacterial community estimated from amplicon sequence data
   (dimensionless)
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oxidation_EC_abund = relative abundance of oxidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
celluloseDecomp_EC_abund = relative abundance of cellulose decomposition gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
carbDecomp_EC_abund = relative abundance of carbohydrate decomposition gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
Pdecomp_EC_abund = relative abundance of phosphatase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
peptidase_EC_abund = relative abundance of peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
Ndecomp_GO_abund = relative abundance of chitinase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
oxidation_GO_abund = relative abundance of oxidase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
celluloseDecomp_GO_abund = relative abundance of cellulose decomposition gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
carbDecomp_GO_abund = relative abundance of carbohydrate decomposition gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
orgNuptake_GO_abund = relative abundance of organic nitrogen uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
PO4uptake_GO_abund = relative abundance of phosphatase uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
nitrification_GO_abund = relative abundance of nitrification gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
NH4uptake_GO_abund = relative abundance of ammonium gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
Pdecomp_GO_abund = relative abundance of phosphatase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
peptidase_GO_abund = relative abundance of peptidase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
ECM_Ndecomp_GO = relative abundance of ectomycorrhizal chitinase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_Ndecomp_GO = relative abundance of saprotrophic fungal chitinase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)

ECM_orgNuptake_GO = relative abundance of ectomycorrhizal organic nitrogen uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_orgNuptake_GO = relative abundance of saprotrophic fungal organic nitrogen uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
ECM_PO4uptake_GO = relative abundance of ectomycorrhizal phosphate uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_PO4uptake_GO = relative abundance of saprotrophic fungal phosphate uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
ECM_NH4uptake_GO = relative abundance of ectomycorrhizal ammonium uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_NH4uptake_GO = relative abundance of saprotrophic fungal ammonium uptake gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
ECM_Pdecomp_GO = relative abundance of ectomycorrhizal phosphatase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_Pdecomp_GO = relative abundance of saprotrophic fungal phosphatase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
ECM_peptidase_GO = relative abundance of ectomycorrhizal peptidase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
SAP_peptidase_GO = relative abundance of saprotrophic fungal peptidase gene copies in the fungal community estimated from amplicon sequence data (dimensionless)
Oligotroph_Ndecomp_EC = relative abundance of oligotrophic bacterial chitinase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
chitinolytic_Ndecomp_EC = relative abundance of chitinolytic bacterial chitinase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
cellulolytic_Ndecomp_EC = relative abundance of cellulolytic bacterial chitinase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
lignolytic_Ndecomp_EC = relative abundance of lignolytic bacterial chitinase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
Oligotroph_Pdecomp_EC = relative abundance of oligotrophic bacterial phosphatase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
Oligotroph_peptidase_EC = relative abundance of oligotrophic bacterial peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
chitinolytic_peptidase_EC = relative abundance of chitinolytic bacterial peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)

cellulolytic_peptidase_EC = relative abundance of cellulolytic bacterial peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
lignolytic_peptidase_EC = relative abundance of lignolytic bacterial peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
copiotroph_peptidase_EC = relative abundance of copiotrophic bacterial peptidase gene copies in the bacterial community estimated from amplicon sequence data (dimensionless)
peptidase_phosphatase_top_fun_abundance = relative abundance of top 3 fungal genera contributing most peptidase and phosphatase genes (dimensionless)
Ndecomp_top_fun_abundance = relative abundance of top 3 fungal genera contributing most chitinase and peptidase genes (dimensionless)
chitinase_top_bac_abundance = relative abundance of top 3 bacterial genera contributing most chitinase genes (dimensionless)
peptidase_top_bac_abundance = relative abundance of top 3 bacterial genera contributing most peptidase genes (dimensionless)
NPdecomp_top_bac_abundance = relative abundance of top 3 bacterial genera contributing most phosphatase genes (dimensionless)
fun_amm_neg_module_abundance = cumulative relative abundance of fungal taxa in low ammonification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
fun_nitr_pos_module_abundance = cumulative relative abundance of fungal taxa in high nitrification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
fun_nitr_neg_module_abundance = cumulative relative abundance of fungal taxa in low nitrification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
fun_pmin_pos_module_abundance = cumulative relative abundance of fungal taxa in high phosphate change module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
fun_pmin_neg_module_abundance = cumulative relative abundance of fungal taxa in low phosphate change module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_amm_pos_module_abundance = cumulative relative abundance of bacterial taxa in high ammonification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_amm_neg_module_abundance = cumulative relative abundance of bacterial taxa in low ammonification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_nitr_pos_module_abundance = cumulative relative abundance of bacterial taxa in high nitrification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_nitr_neg_module_abundance = cumulative relative abundance of bacterial taxa in low nitrification module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_pmin_pos_module_abundance = cumulative relative abundance of bacterial taxa in high phosphate change module as identified by Weighted Gene Network Correlation Analysis (dimensionless)
bac_pmin_neg_module_abundance = cumulative relative abundance of bacterial taxa in low phosphate change module as identified by Weighted Gene Network Correlation Analysis (dimensionless)

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Nitrosomonodaceae_abundance = relative abundance of bacteria in the
   Nitrosomonodaceae family in high−throughput amplicon sequence data (dimensionless)
bac_richness = bacterial richness in high−throughput amplicon
   sequence data (dimensionless)
bac_shannon = bacterial shannon diversity in high−throughput
   amplicon sequence data (dimensionless)
fun_richness = fungal richness in high−throughput amplicon sequence
   data (dimensionless)
fun_shannon = fungal shannon diversity in high−throughput amplicon
   sequence data (dimensionless)
bac_evenness = bacterial evenness in high−throughput amplicon
   sequence data (dimensionless)
fun_evenness = fungal evenness in high−throughput amplicon sequence
   data (dimensionless)
edaphic_PC1 = first principal component of a Principal Coordinates
   Analysis encompassing all soil abiotic variables: pH, soil_temp,
   litter_depth, O_depth, soil_moisture, SOM (dimensionless)
bac_copy_number = copy numbers of the v4 16S DNA region per 1ul DNA
   extract as measured by quantitative PCR (dimensionless)
ITS_copy_number = copy numbers of the ITS2 DNA region per 1ul DNA
   extract as measured by quantitative PCR (dimensionless)
fun_amm_pos_module_abundance = cumulative relative abundance of
   fungal taxa in high ammonification module as identified by Weighted Gene
   Network Correlation Analysis (dimensionless)
Cmetabolism_EC_abund = relative abundance of central carbon
   metabolism gene copies in the bacterial community estimated from amplicon
   sequence data (dimensionless)
denitrification_EC_abund = relative abundance of denitrification
   gene copies in the bacterial community estimated from amplicon
   sequence data (dimensionless)
soil_temp2022 = soil temperature in 2022 (celsius)
soil_moisture2022 = proportion soil water content by weight in 2022
   (dimensionless)
Copiotroph_Ndecomp_EC = relative abundance of copiotrophic bacterial
   chitinase gene copies in the bacterial community estimated from amplicon
   sequence data (dimensionless)
Copiotroph_Pdecomp_EC = relative abundance of copiotrophic bacterial
   phosphatase gene copies in the bacterial community estimated from amplicon
   sequence data (dimensionless)
Nitrifiers_nitrification_EC = relative abundance of nitrifying
   bacterial nitrification gene copies in the bacterial community estimated
   from amplicon sequence data (dimensionless)
Copios_nitrification_EC = relative abundance of copiotrophic
   bacterial nitrification gene copies in the bacterial community estimated
   from amplicon sequence data (dimensionless)
soil_percN = soil total percent nitrogen (dimensionless)
soil_percC = soil total percent carbon (dimensionless)
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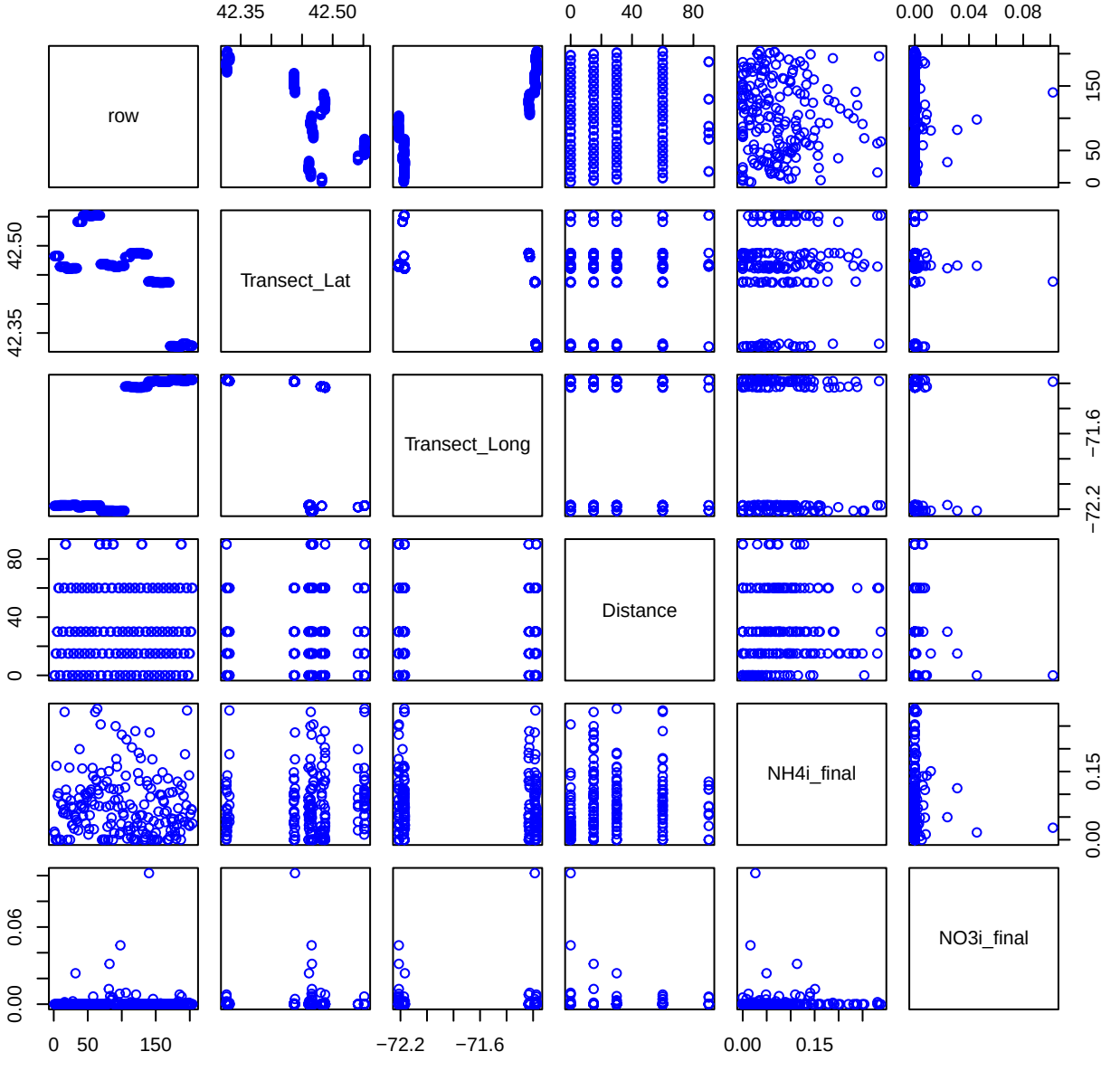
Variable	Min	Median	Mean	Max	NAs
Transect_Lat	42.327	42.466	42.456	42.552	0
Transect_Lon	−72.214	−72.167	−71.702	−71.173	0
Distance	0.000	30.000	30.000	90.000	0
NH4i_final	0.000	0.064	0.075	0.288	14
NO3i_final	0.000	0.000	0.002	0.102	14
Ammonificati	0.000	19.204	21.684	118.917	75
Nitrificatio	0.000	0.155	0.944	9.104	69
N_min	0.095	18.936	21.999	118.972	75
Al	518.600	6658.000	7641.431	24300.000	61
As	0.000	2.780	6.098	119.200	61
B	0.000	2.130	2.108	7.090	61
Ba	10.280	48.010	76.449	515.600	61
Ca	185.600	1303.000	1928.125	10540.000	61
Cd	0.000	0.000	0.428	5.930	61
Co	0.000	2.770	4.034	23.870	61
Cr	1.070	10.380	14.018	63.450	61
Cu	7.010	29.230	33.542	118.100	61
Fe	729.700	8613.000	10204.087	29720.000	61
K	276.600	674.900	1180.768	9104.000	61
Li	0.000	1.520	2.739	15.260	61
Mg	259.100	1059.000	1982.583	13210.000	61
Mn	16.650	167.200	266.889	1396.000	61
Mo	0.274	1.120	1.192	4.370	61
Na	46.600	226.100	250.764	1627.000	61
Ni	1.910	9.280	10.902	30.430	61
P	334.900	848.800	967.708	3344.000	61
Pb	2.130	51.980	94.736	638.700	61
S	211.200	1175.000	1182.270	2447.000	61
Sb	0.000	1.480	1.438	4.320	61
Se	−1.610	2.700	2.593	9.210	61
Si	290.000	1404.000	1571.901	3123.000	61
Sr	2.060	12.280	18.233	122.500	61
Tl	0.000	0.000	0.353	12.590	61
V	2.430	25.070	29.898	91.270	61
Zn	13.330	49.670	60.300	352.000	61
pH	2.930	4.190	4.272	6.850	3
soil_temp	14.900	19.444	19.744	25.000	21
litter_depth	0.000	2.000	2.133	7.000	1
O_depth	0.000	6.000	6.795	20.000	1
soil_moistur	0.175	0.535	0.516	0.831	1
SOM	0.055	0.486	0.487	0.960	4
prop_pine_li	0.000	0.010	0.304	1.018	10
prop_hw_litt	0.001	0.979	0.703	1.049	10
total_floor_	0.013	0.053	0.061	0.229	10
pine_floor_l	0.000	0.000	0.014	0.092	10
hw_floor_lit	0.000	0.023	0.026	0.168	10
Max_height	0.031	0.416	0.464	1.822	0
No_white_pin	0.000	0.000	0.157	4.000	0
No_oak_seedl	0.000	0.000	0.270	7.000	0

Variable	Min	Median	Mean	Max	NAs
All_plants	1.000	4.000	4.618	12.000	0
AM_basal	0.000	18.653	77.321	547.469	2
ECM_basal	0.000	267.968	304.295	934.611	2
hw_basal	0.000	230.845	247.656	693.986	2
pine_basal	0.000	0.000	134.446	860.766	2
num_stems	1.000	6.000	6.525	16.000	2
total_basal	29.190	346.413	384.845	1048.179	2
ECM_AM	0.002	16.330	134.741	935.611	2
no_pine_sapl	0.000	1.000	4.838	62.000	6
no_oak_sapli	0.000	7.000	12.909	207.000	6
PO4	0.000	0.148	1.330	10.574	21
PO4_release	−0.211	0.000	−0.007	0.195	89
root_density	0.345	3.088	3.417	10.581	14
ECM_abundanc	0.000	0.653	0.586	0.933	28
SAP_abundanc	0.038	0.196	0.251	0.929	28
soilSAP_abun	0.031	0.139	0.188	0.904	28
AM_abundance	0.000	0.000	0.002	0.046	28
root_endophy	0.000	0.000	0.001	0.090	28
contact_expl	0.000	0.223	0.284	0.807	28
short_dist_e	0.000	0.015	0.063	0.574	28
med_dist_exp	0.000	0.145	0.219	0.871	28
long_dist_ex	0.000	0.002	0.015	0.250	28
mat_expl	0.000	0.000	0.009	0.381	28
Nitrifier_ab	0.000	0.000	0.003	0.038	13
Decomposer_a	0.013	0.031	0.036	0.133	13
Cellulolytic	0.005	0.016	0.018	0.074	13
Lignolytic_a	0.000	0.006	0.009	0.125	13
Chitinolytic	0.006	0.023	0.027	0.078	13
Copiotroph_a	0.189	0.291	0.297	0.462	13
Oligotroph_a	0.000	0.104	0.103	0.208	13
Ndecomp_EC_a	0.150	0.540	0.576	1.380	13
oxidation_EC	0.230	0.520	0.548	1.050	13
celluloseDec	0.180	0.680	0.733	1.940	13
carbDecomp_E	0.090	0.380	0.415	1.150	13
Pdecomp_EC_a	0.220	0.530	0.562	1.270	13
peptidase_EC	1.500	3.000	3.153	6.090	13
Ndecomp_GO_a	0.130	1.078	1.045	2.057	28
oxidation_GO	0.200	1.924	1.890	3.650	28
celluloseDec	0.386	3.730	3.669	6.835	28
carbDecomp_G	0.304	2.536	2.721	6.562	28
orgNuptake_G	0.239	1.498	1.514	5.980	28
PO4uptake_GO	0.009	0.043	0.073	0.444	28
nitrificatio	0.208	2.286	2.517	7.481	28
NH4uptake_GO	0.020	0.247	0.269	0.982	28
Pdecomp_GO_a	1.030	10.479	10.114	19.728	28
peptidase_GO	0.213	1.866	1.838	4.798	28
ECM_Ndecomp_	0.000	0.640	0.599	0.979	28
SAP_Ndecomp_	0.020	0.314	0.345	0.940	28
ECM_orgNupta	0.000	0.779	0.700	0.976	28
SAP_orgNupta	0.013	0.168	0.230	0.840	28
ECM_PO4uptak	0.000	0.672	0.605	0.969	28

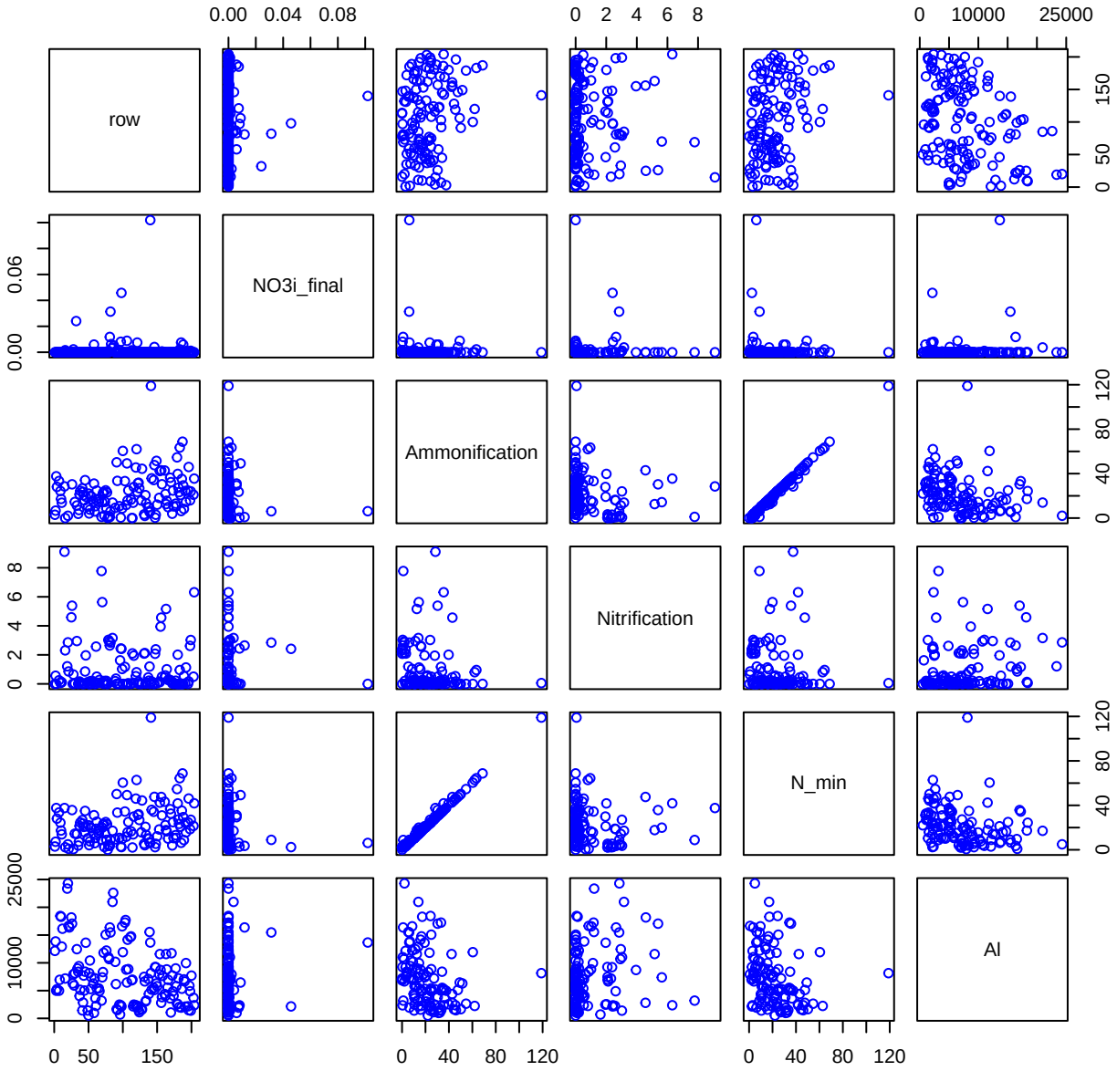
Variable	Min	Median	Mean	Max	NAs
SAP_PO4uptak	0.025	0.256	0.329	0.951	28
ECM_NH4uptak	0.000	0.770	0.689	0.980	28
SAP_NH4uptak	0.014	0.186	0.262	0.913	28
ECM_Pdecomp_	0.000	0.721	0.654	0.963	28
SAP_Pdecomp_	0.028	0.228	0.290	0.901	28
ECM_peptidas	0.000	0.742	0.665	0.971	28
SAP_peptidas	0.023	0.209	0.273	0.899	28
Oligotroph_N	0.000	0.319	0.264	0.818	13
chitinolytic	0.000	0.000	0.027	0.510	13
cellulolytic	0.000	0.000	0.020	0.510	13
lignolytic_N	0.000	0.000	0.020	0.510	13
Oligotroph_P	0.000	0.315	0.250	0.649	13
Oligotroph_p	0.000	0.084	0.089	0.300	13
chitinolytic	0.000	0.000	0.020	0.294	13
cellulolytic	0.000	0.000	0.024	0.312	13
lignolytic_p	0.000	0.000	0.024	0.312	13
copiotroph_p	0.111	0.343	0.367	0.747	13
peptidase_ph	0.000	0.242	0.295	0.848	28
Ndecomp_top_	0.001	0.289	0.320	0.851	28
chitinase_to	0.000	0.145	0.145	0.277	13
peptidase_to	0.000	0.163	0.164	0.293	13
NPdecomp_top	0.000	0.187	0.185	0.325	13
fun_amm_neg_	0.026	0.447	0.464	0.898	28
fun_nitr_pos	0.051	0.721	0.684	0.973	28
fun_nitr_neg	0.001	0.338	0.353	0.874	28
fun_pmin_pos	0.026	0.559	0.519	0.938	28
fun_pmin_neg	0.024	0.463	0.475	0.961	28
bac_amm_pos_	0.019	0.505	0.500	0.620	13
bac_amm_neg_	0.148	0.553	0.552	0.710	13
bac_nitr_pos	0.148	0.629	0.624	0.768	13
bac_nitr_neg	0.000	0.391	0.386	0.468	13
bac_pmin_pos	0.021	0.241	0.240	0.307	13
bac_pmin_neg	0.048	0.529	0.523	0.683	13
Nitrosomonod	0.000	0.000	0.003	0.038	13
bac_richness	72.000	418.000	420.791	763.000	13
bac_shannon	3.500	5.364	5.356	6.073	13
fun_richness	52.000	114.500	123.097	246.000	28
fun_shannon	1.022	2.982	2.933	4.562	28
bac_evenness	0.818	0.892	0.890	0.935	13
fun_evenness	0.248	0.625	0.612	0.831	28
edaphic_PC1	−3.059	−0.236	0.000	3.945	26
bac_copy_num	559	2803401	7131957	42688839	13
ITS_copy_num	1526	1706683	2754471	19890239	13
fun_amm_pos_	0.007	0.387	0.397	0.897	28
Cmetabolism_	5.850	12.550	13.136	25.080	13
denitrificat	0.010	0.050	0.053	0.230	13
soil_temp202	59.000	64.000	64.069	77.000	0
soil_moistur	0.032	0.287	0.307	0.824	3
Copiotroph_N	0.032	0.100	0.150	0.776	13
Copiotroph_P	0.026	0.232	0.353	0.892	13
Nitrifiers_n	0.000	0.000	0.001	0.056	13

Variable	Min	Median	Mean	Max	NAs
Copios_nitri	0.041	0.219	0.270	0.786	13
soil_percN	0.201	1.154	1.168	3.811	63
soil_percC	3.794	25.545	26.860	83.677	63

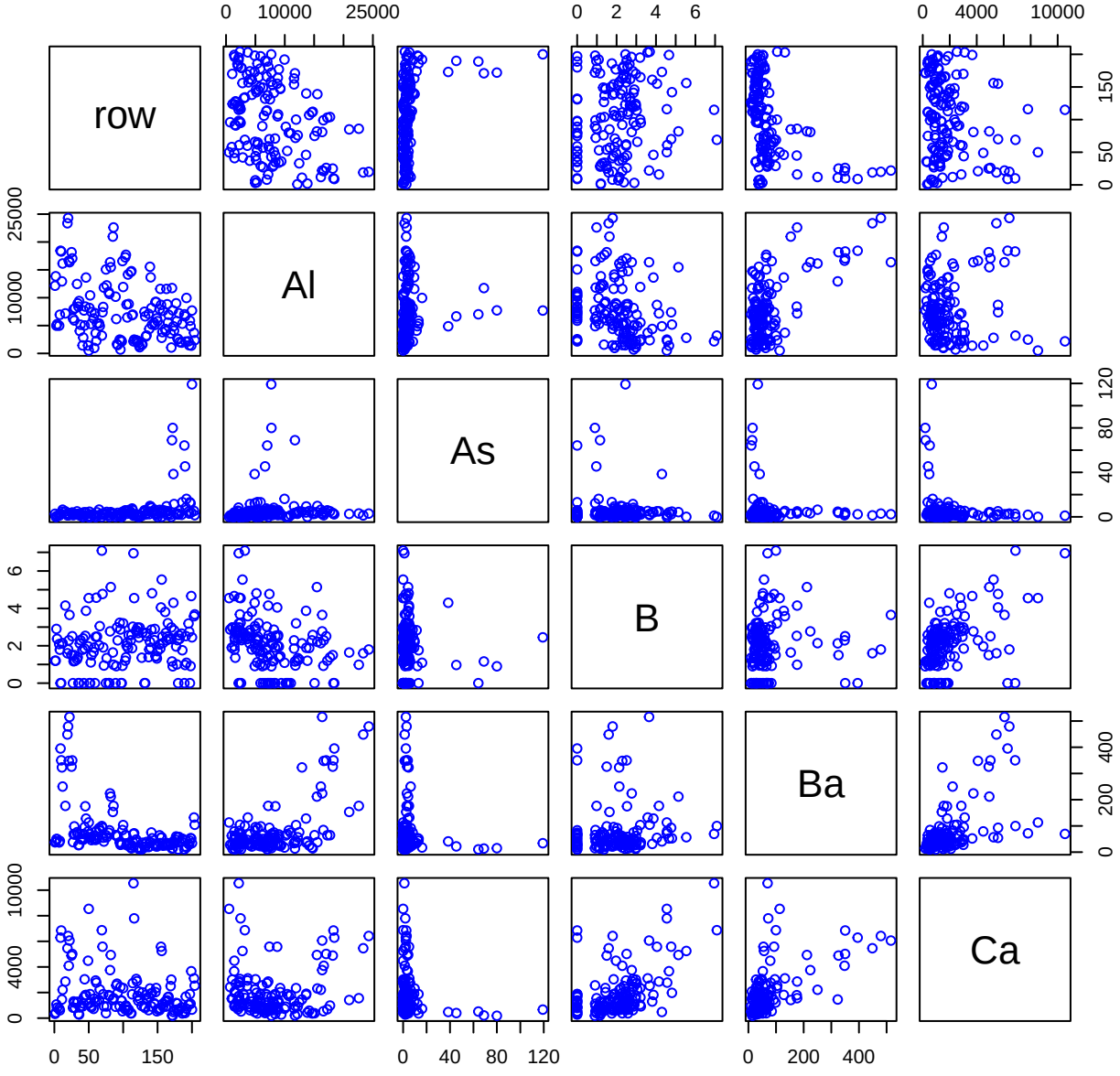
HF456−01 Plot 1



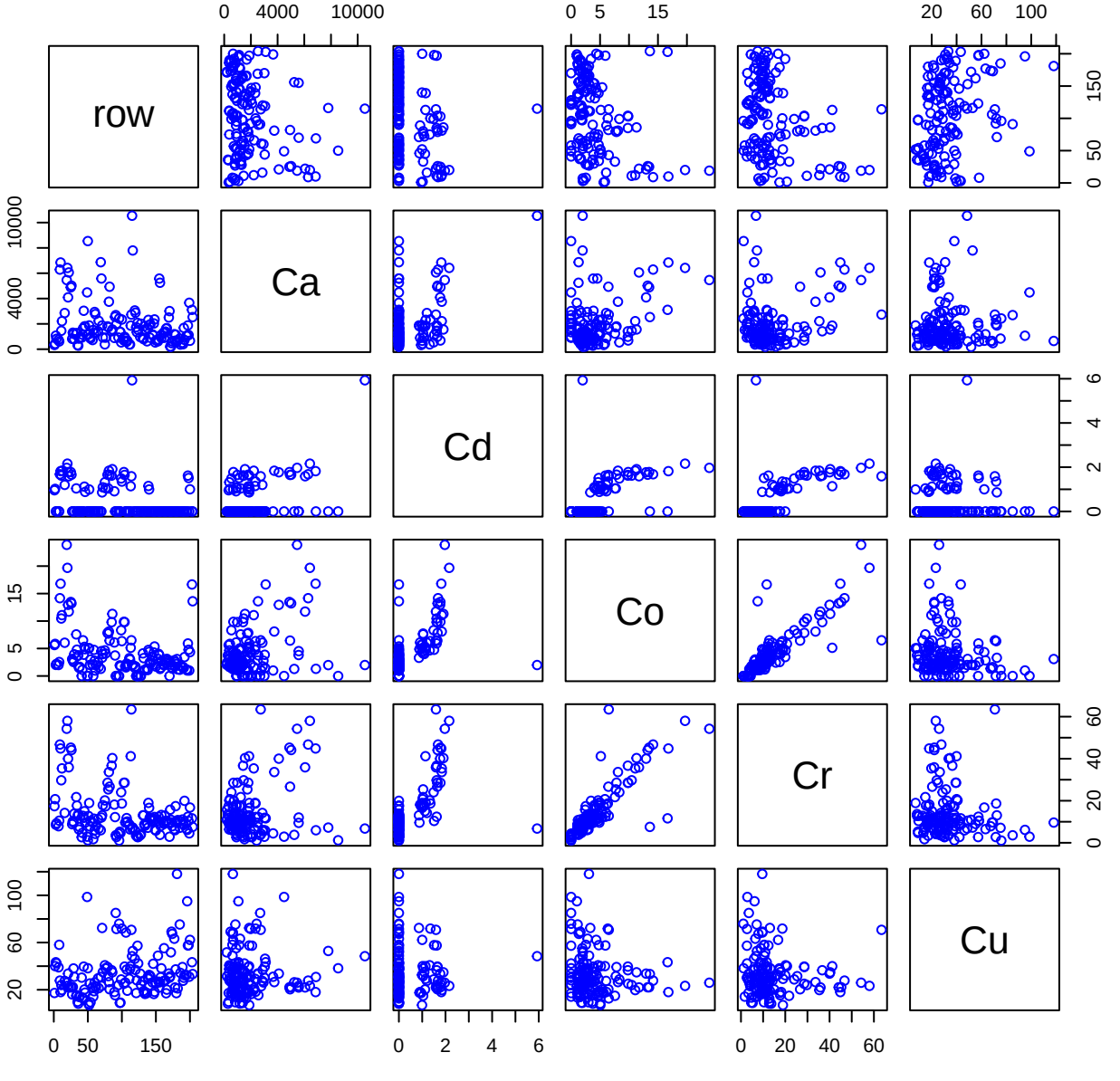
HF456−01 Plot 2



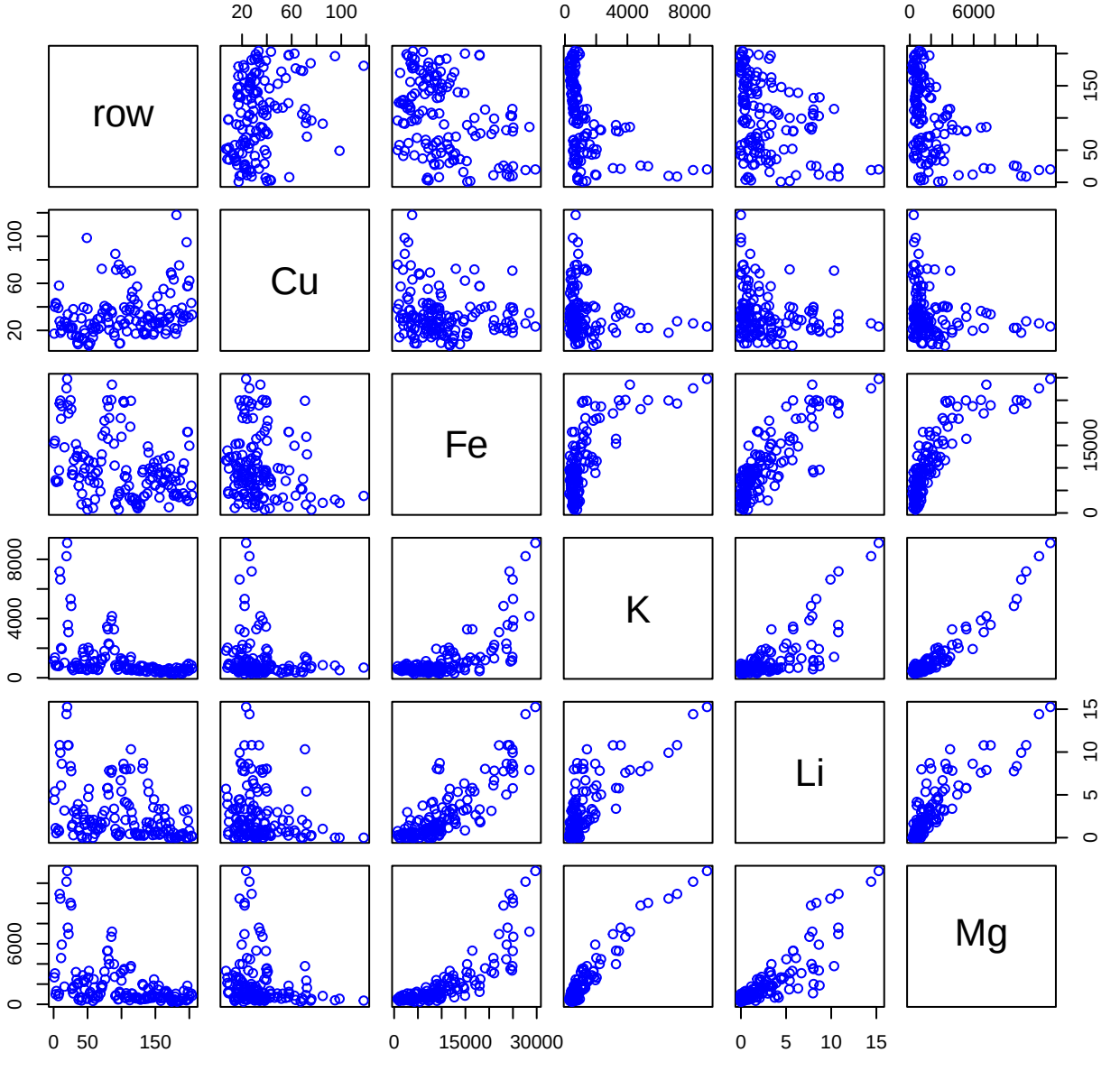
HF456−01 Plot 3



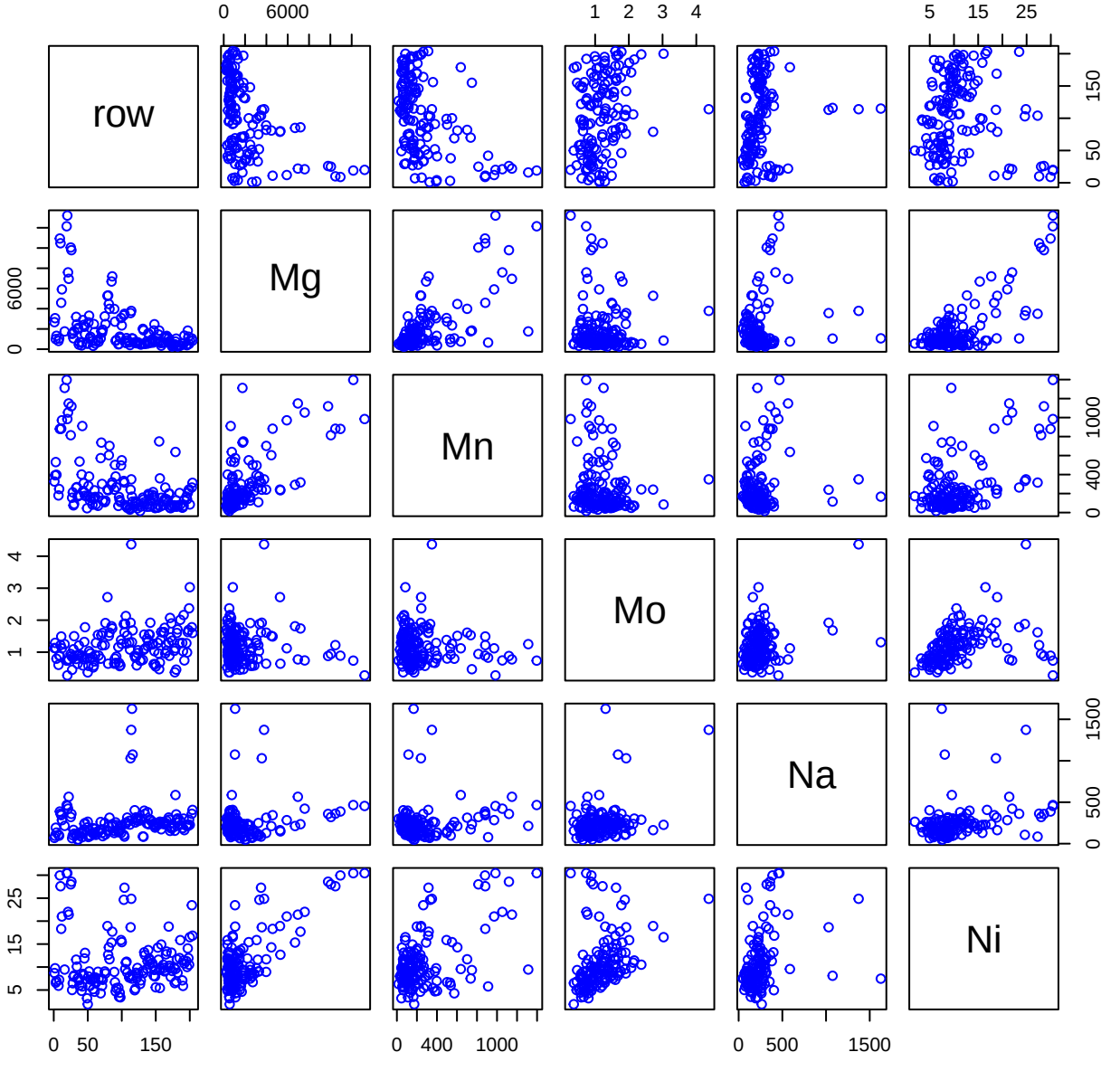
HF456−01 Plot 4



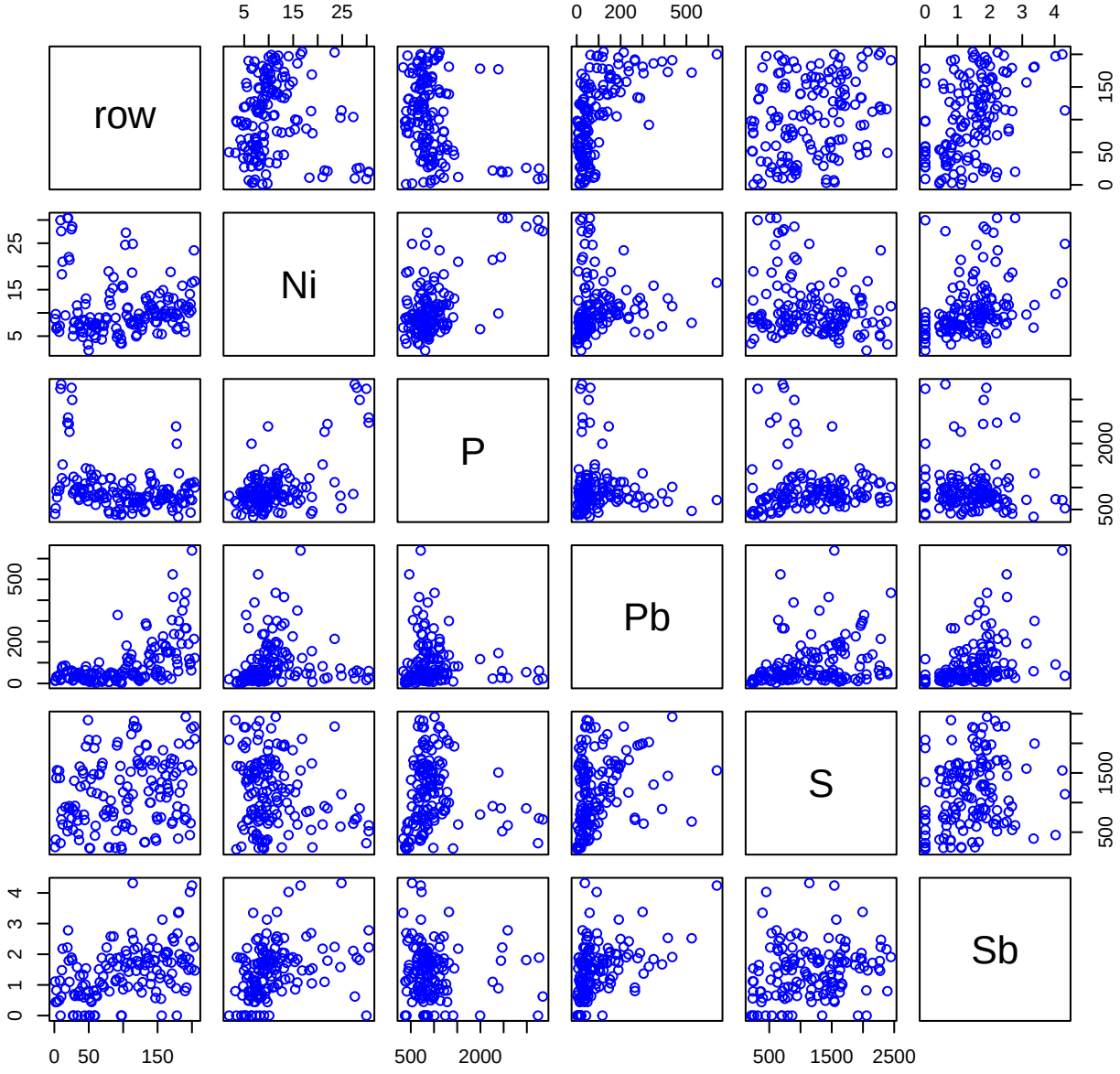
HF456−01 Plot 5



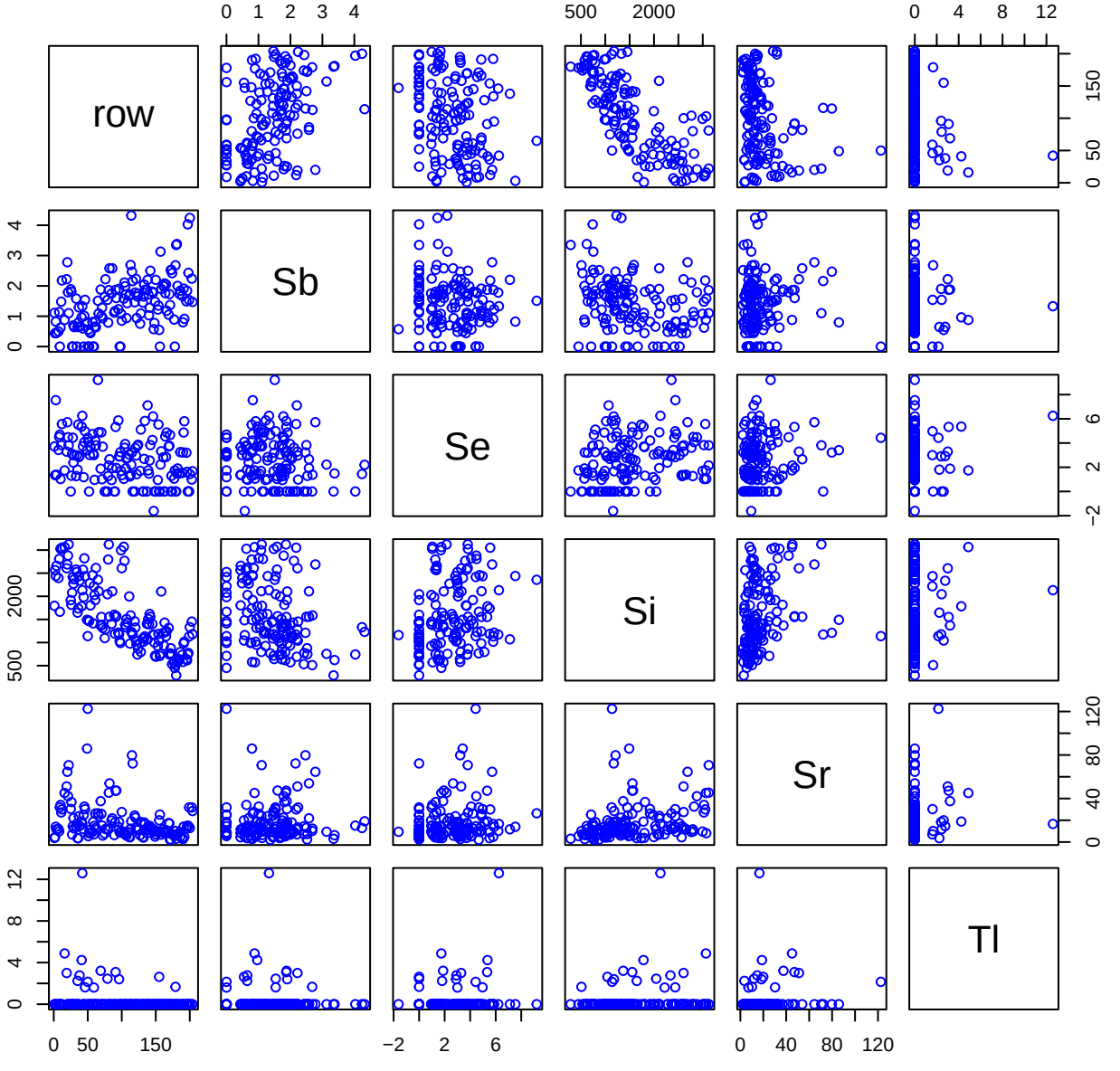
HF456−01 Plot 6



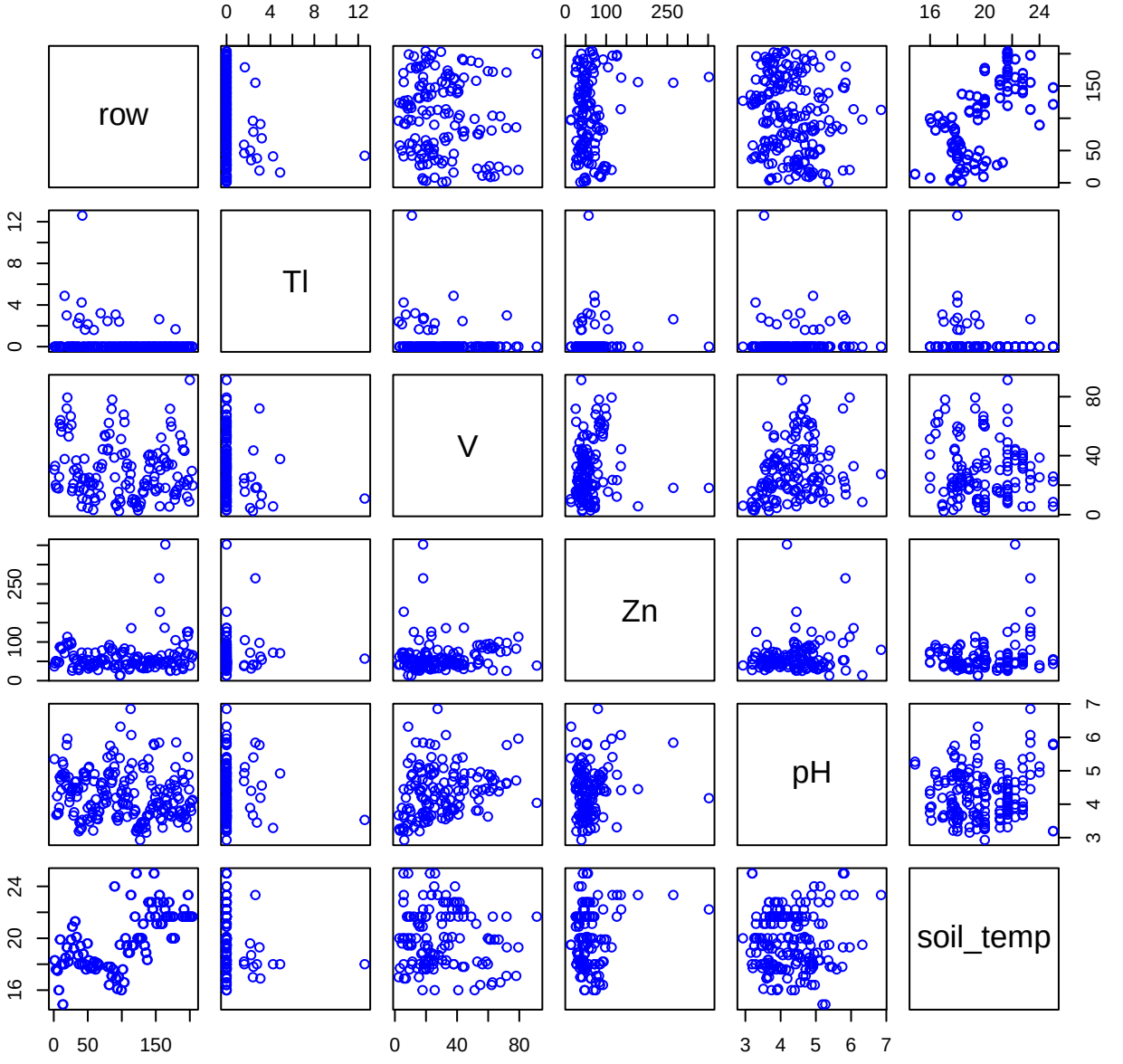
HF456−01 Plot 7



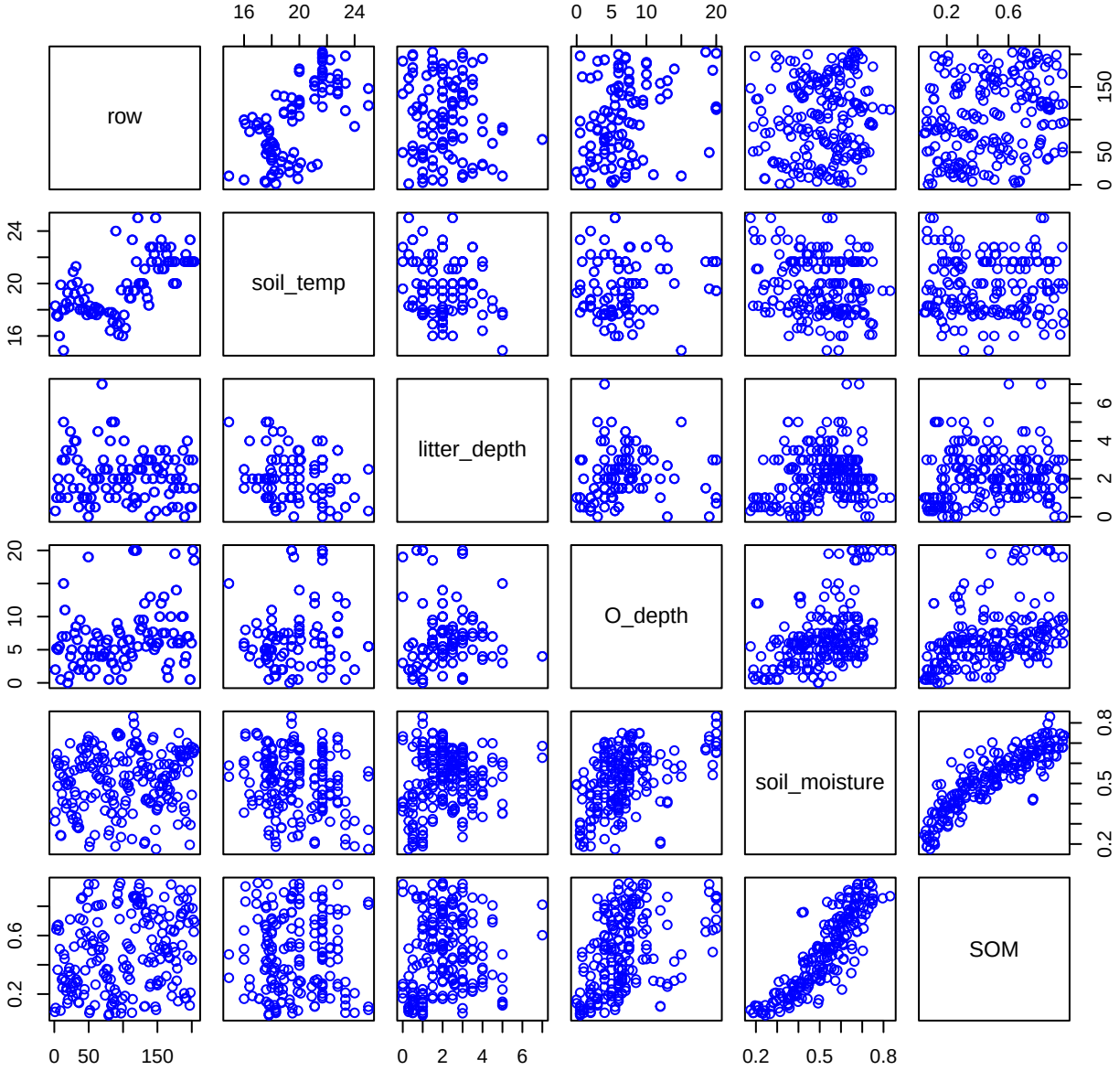
HF456−01 Plot 8



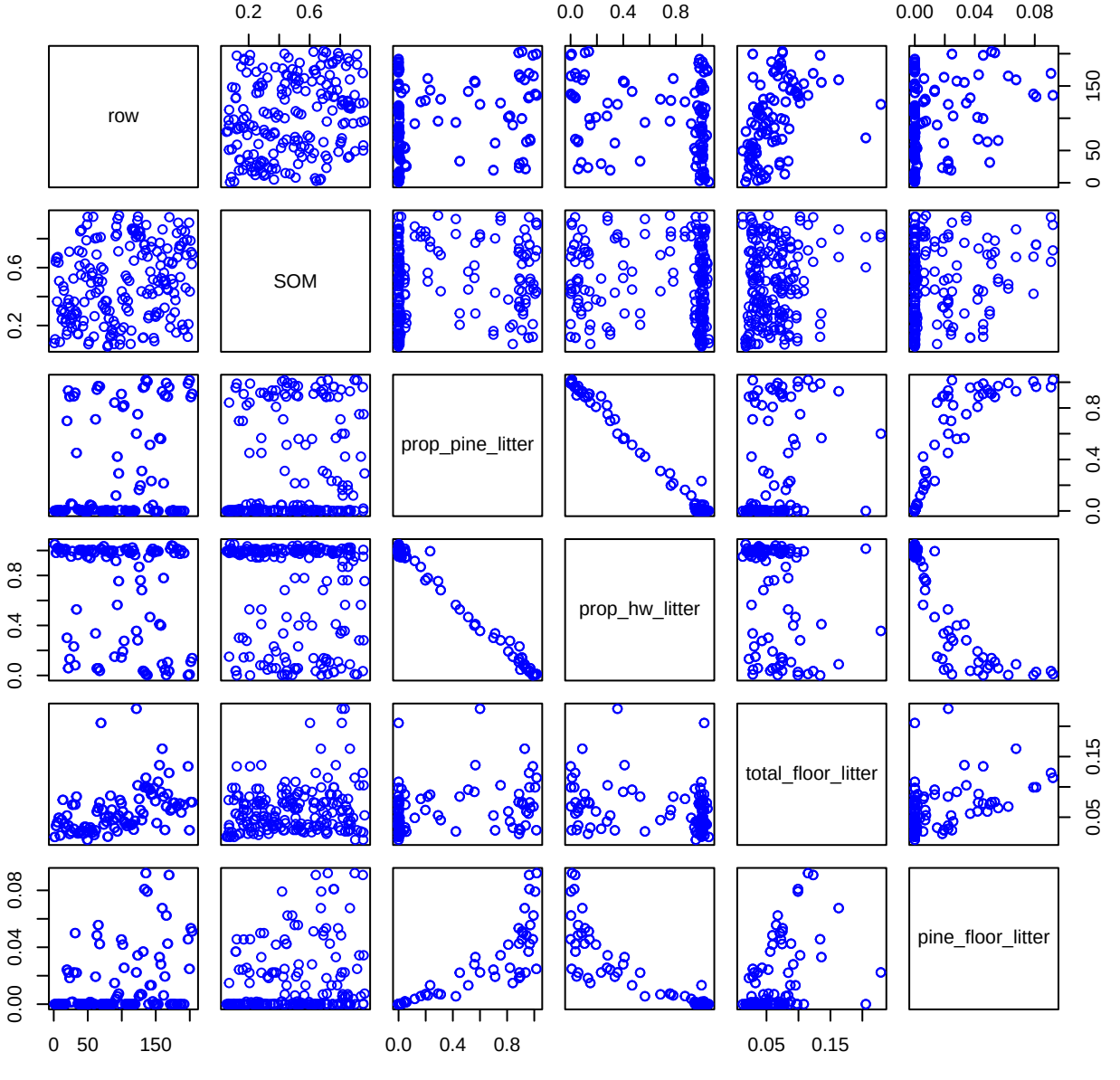
HF456−01 Plot 9



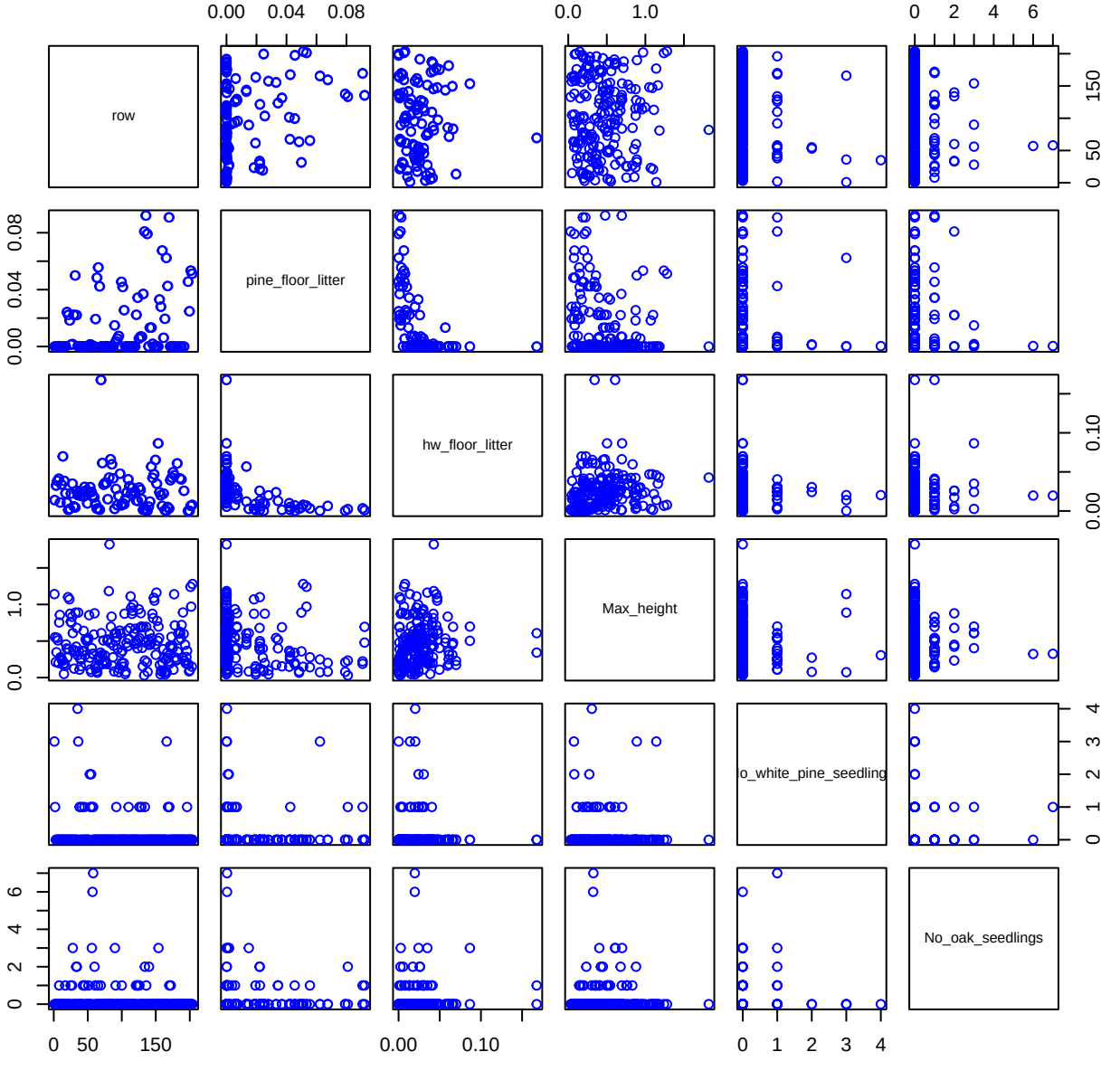
HF456−01 Plot 10



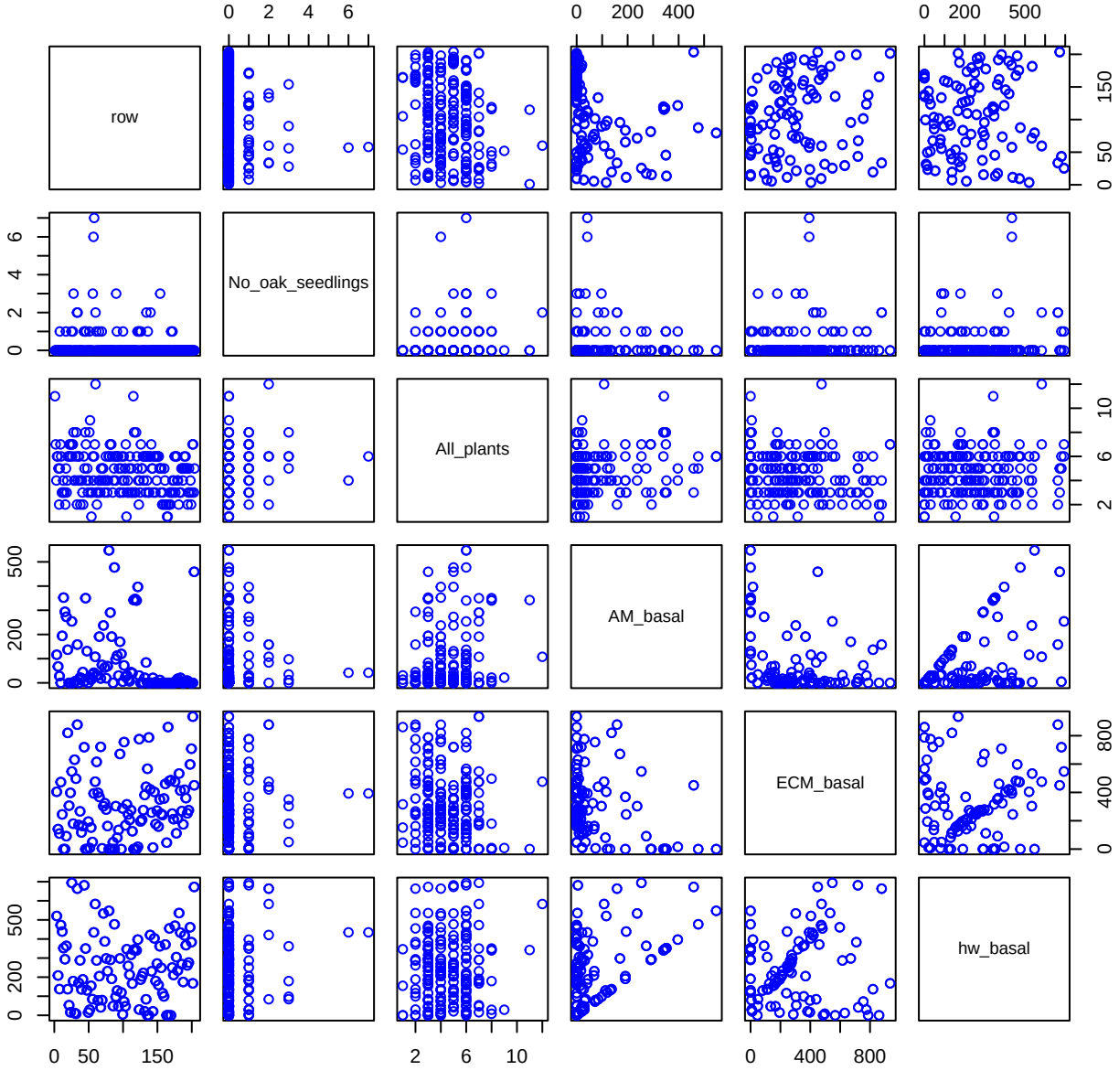
HF456−01 Plot 11



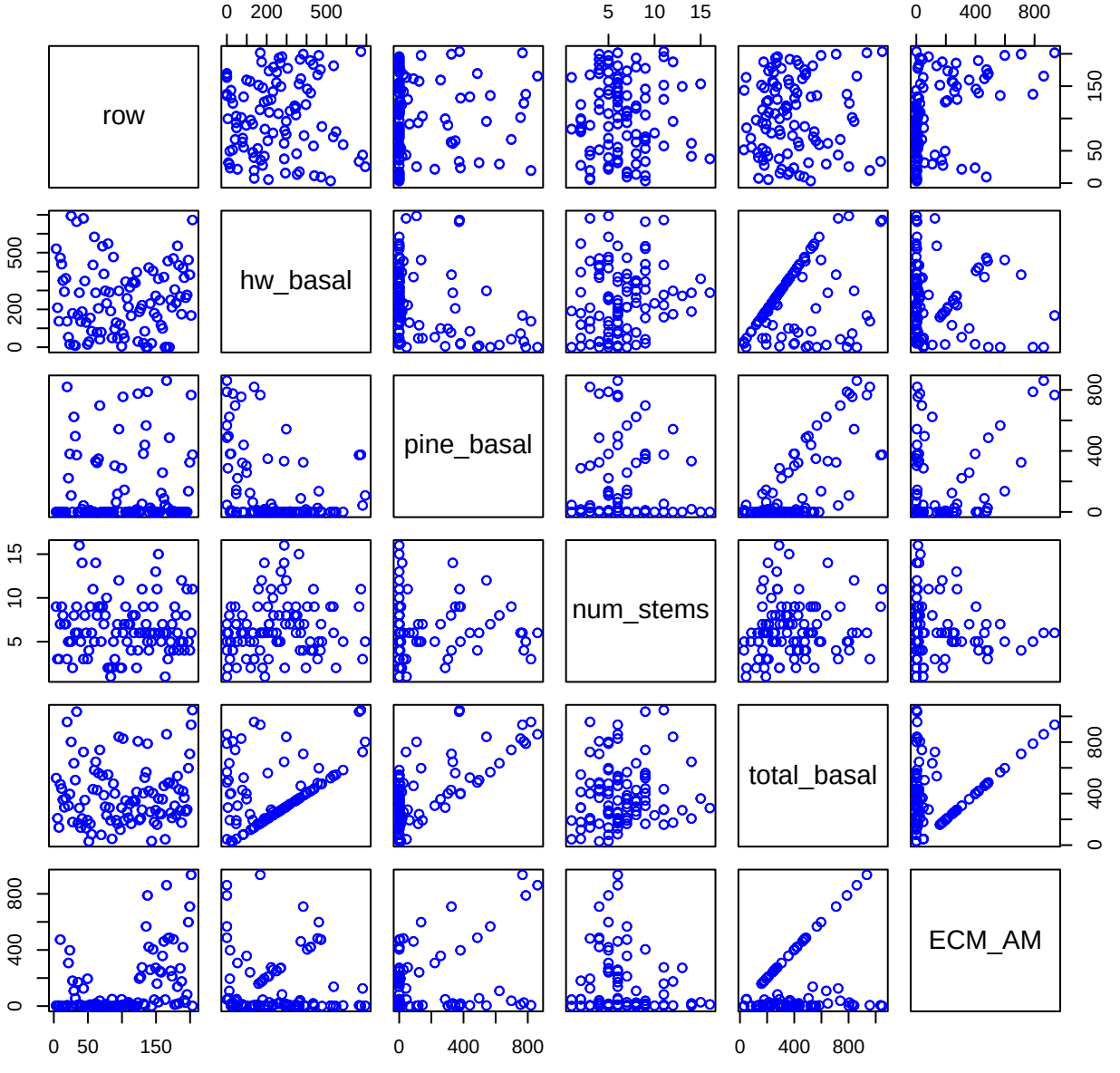
HF456−01 Plot 12



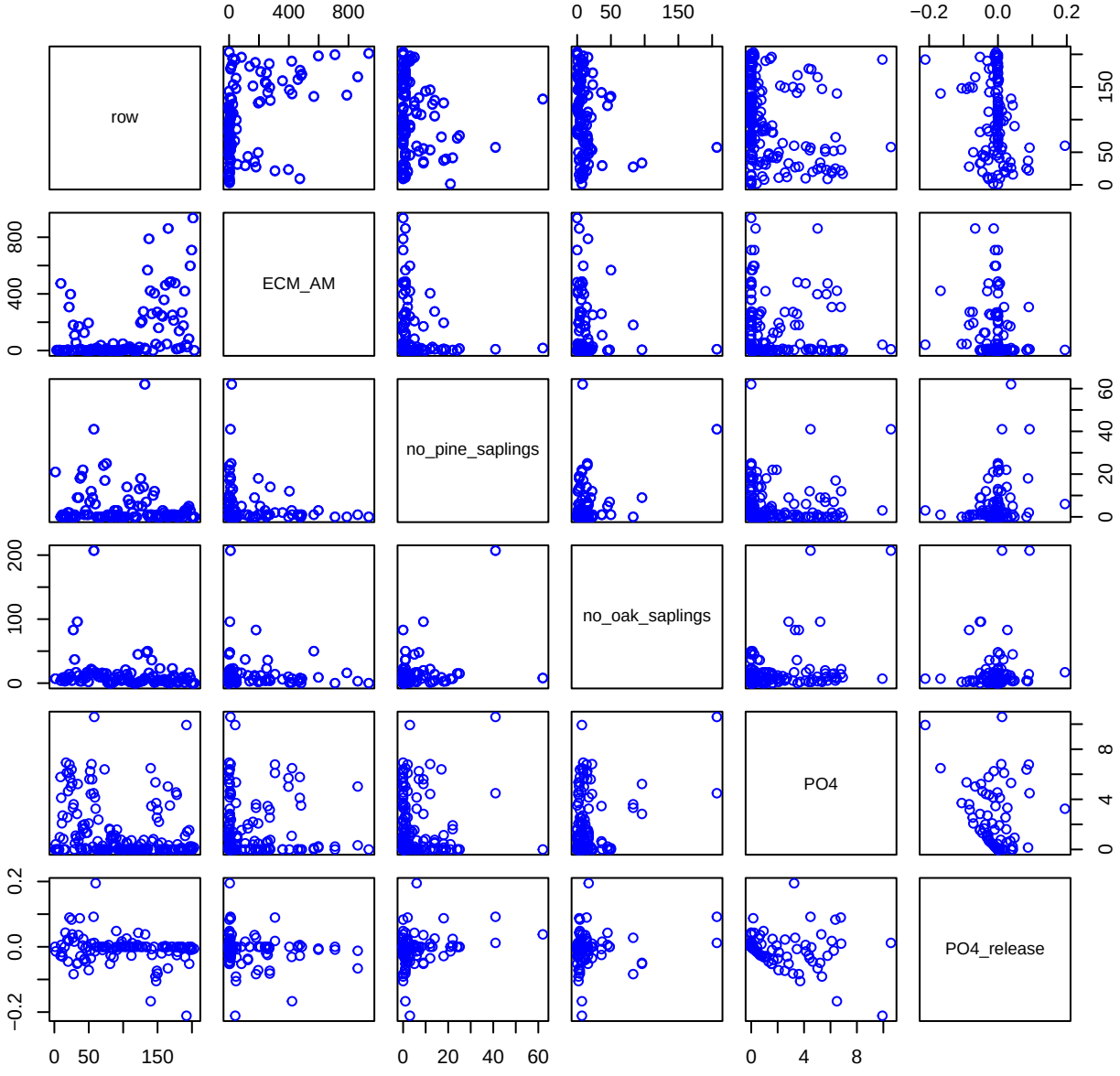
HF456−01 Plot 13



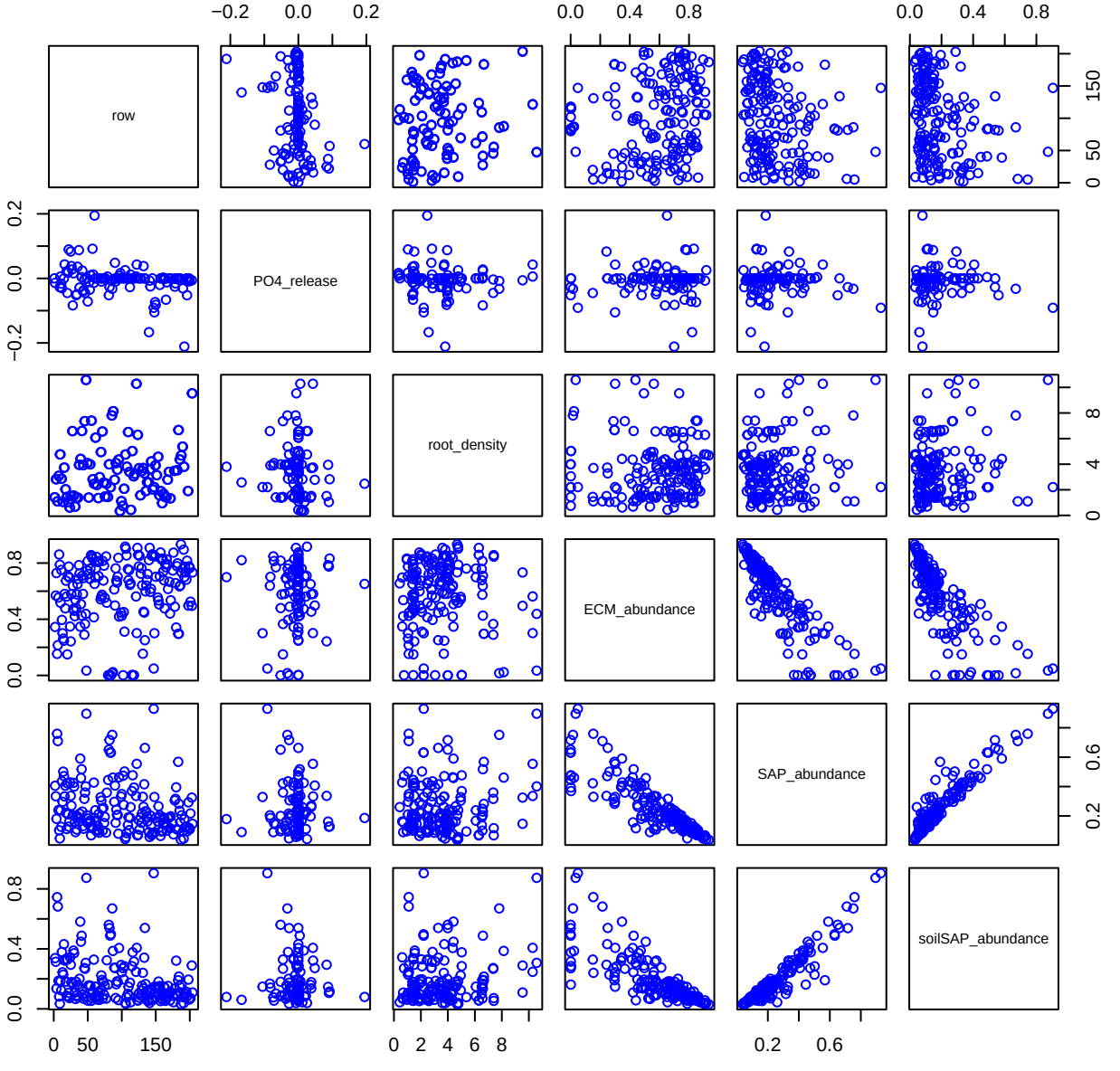
HF456−01 Plot 14



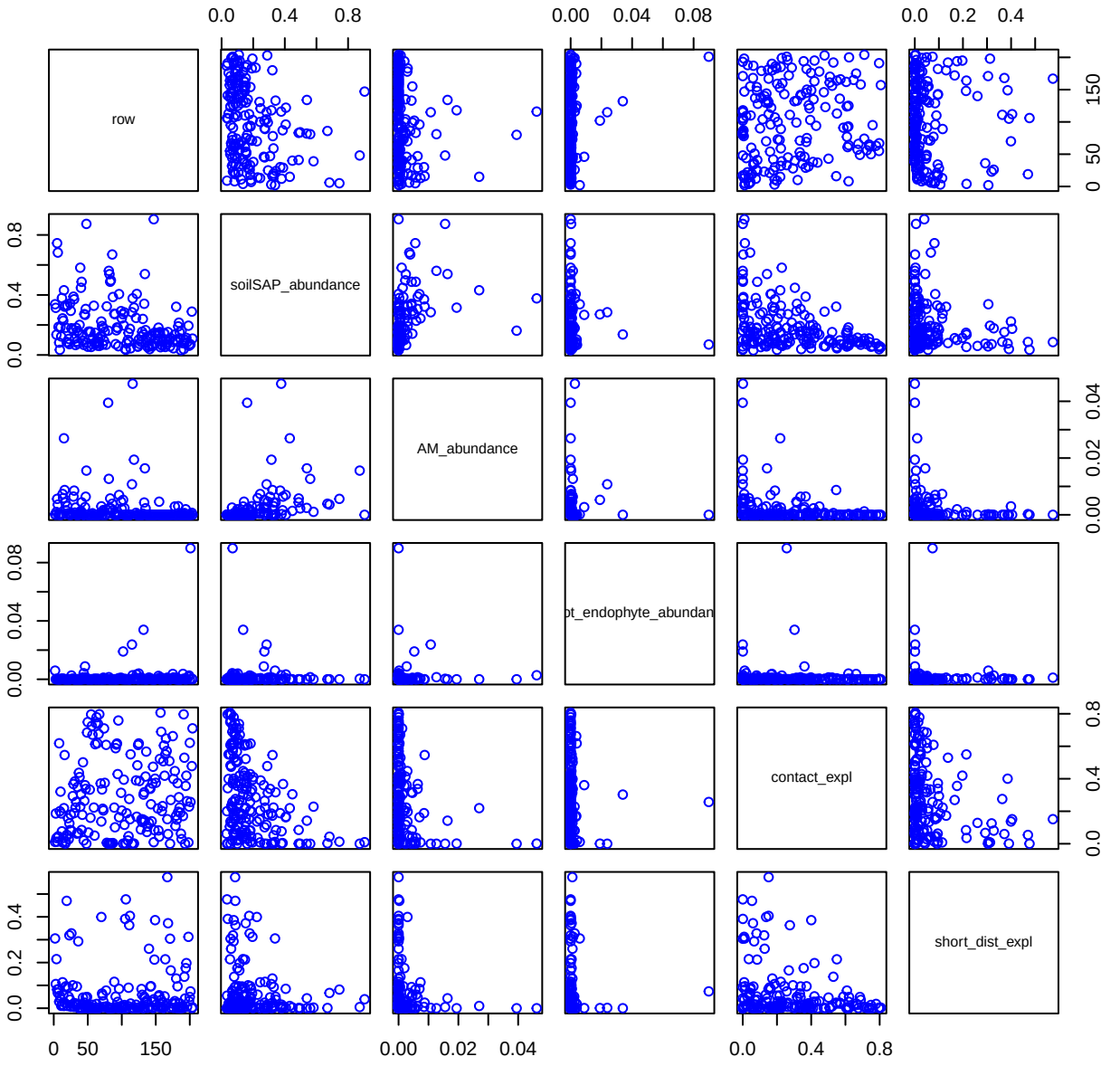
HF456−01 Plot 15



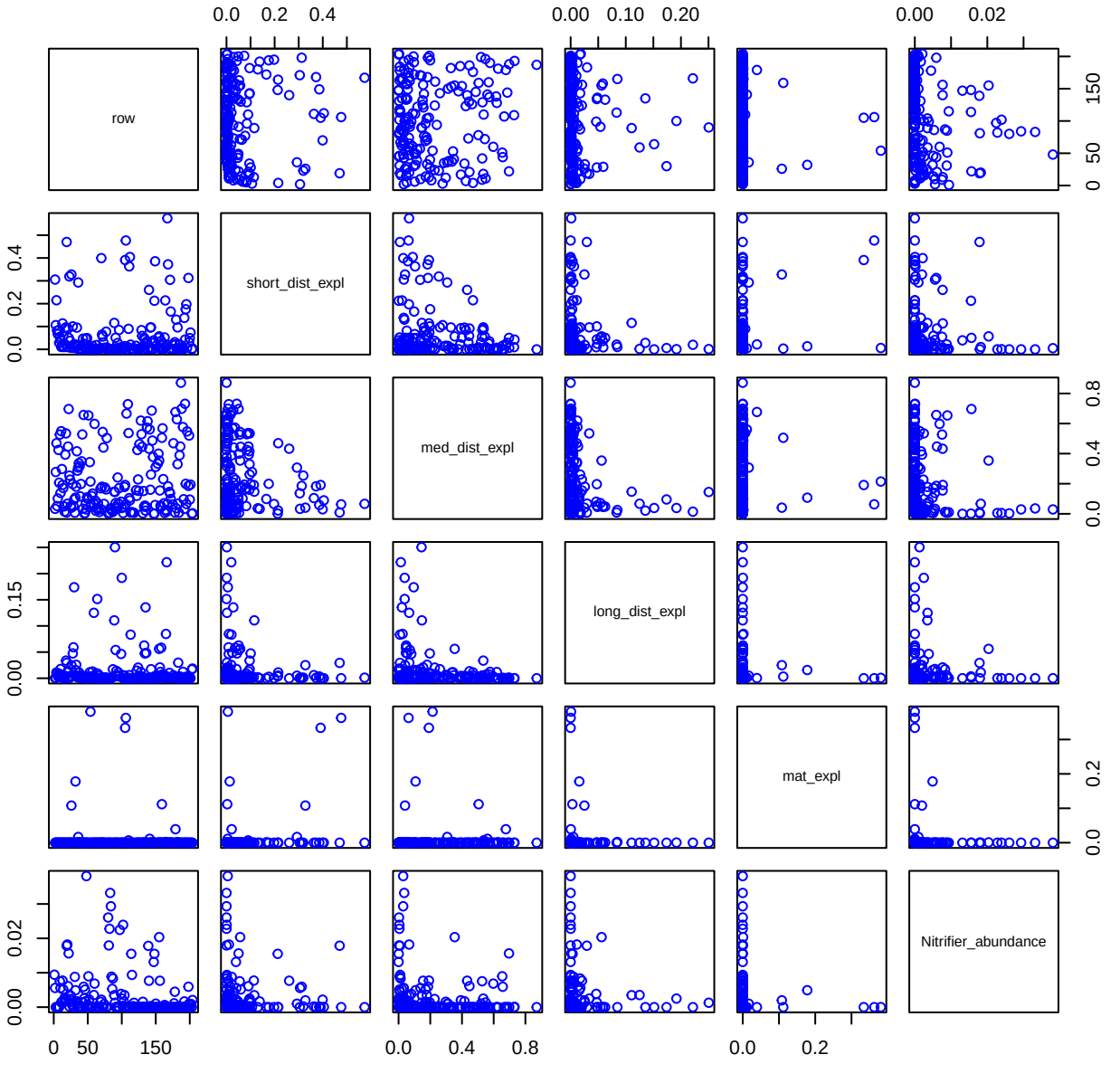
HF456−01 Plot 16



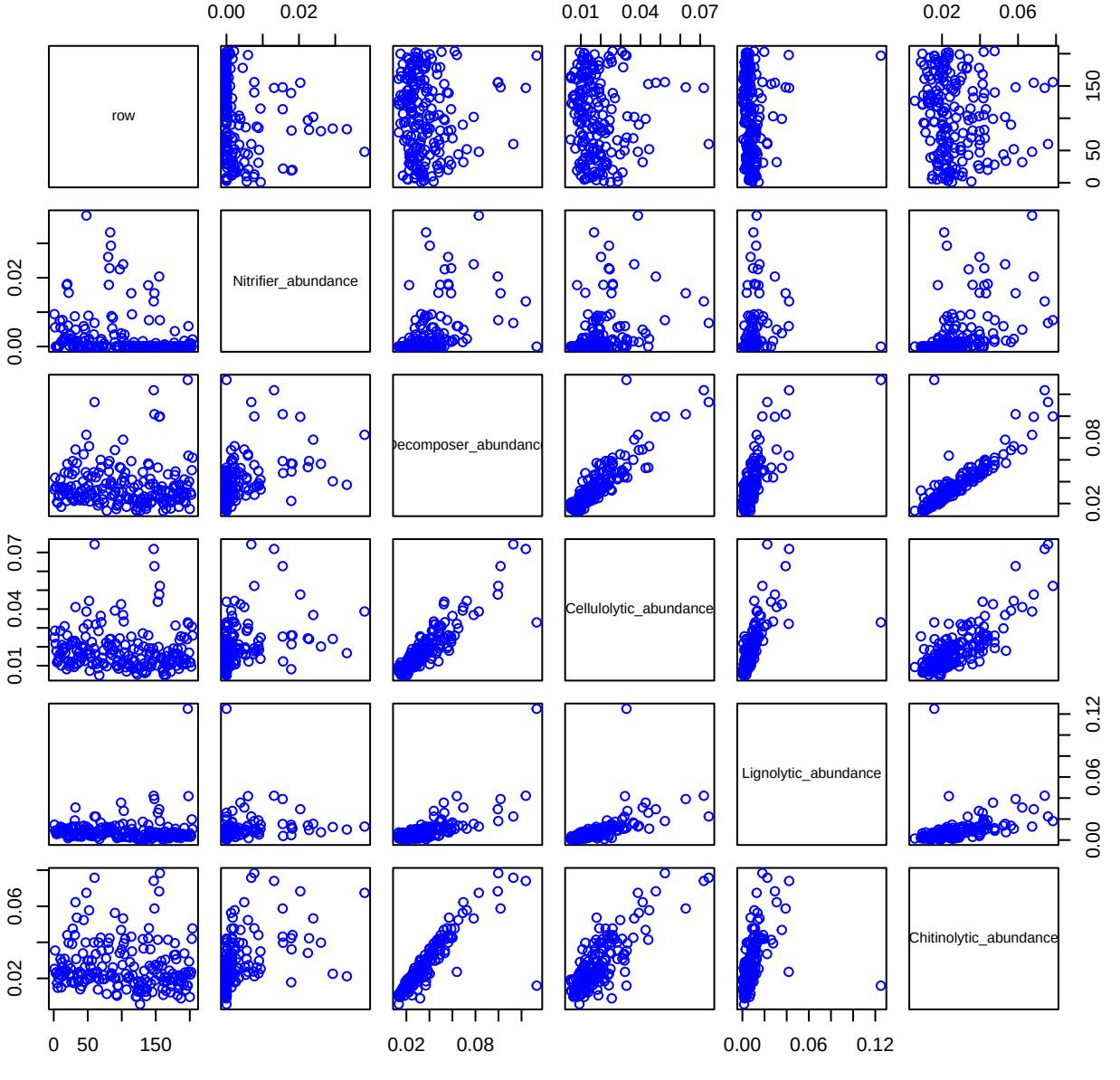
HF456−01 Plot 17



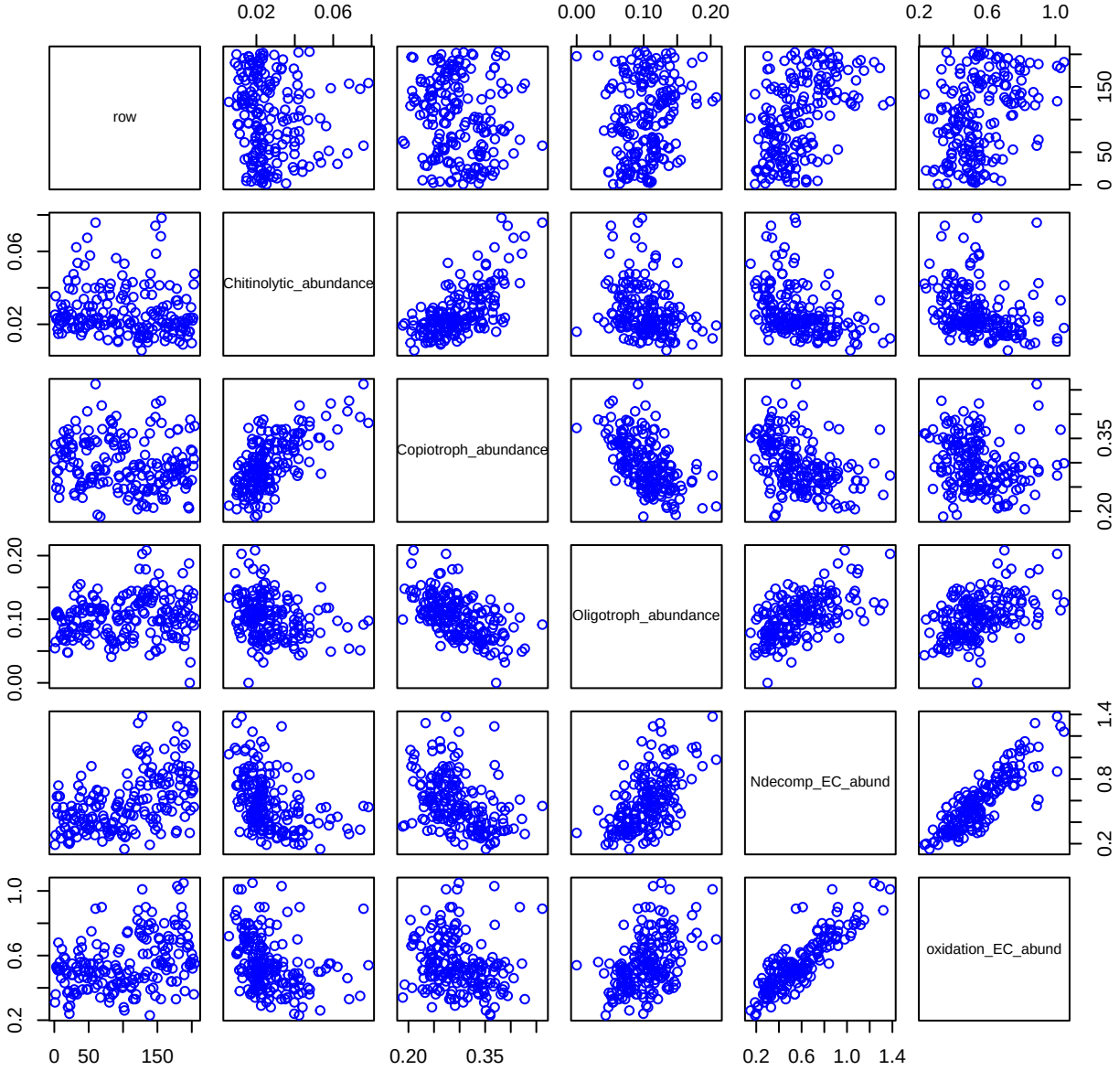
HF456−01 Plot 18



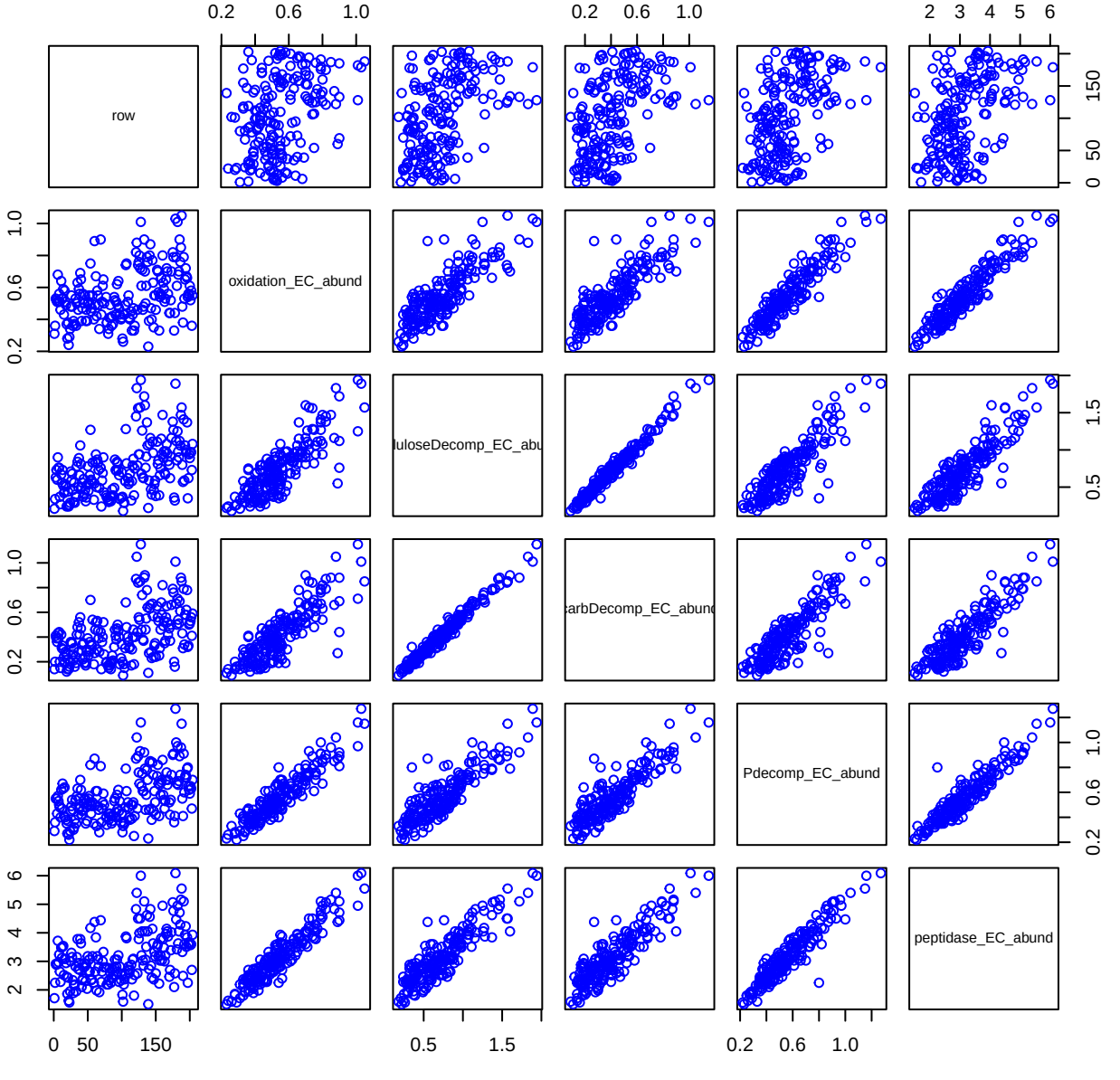
HF456−01 Plot 19



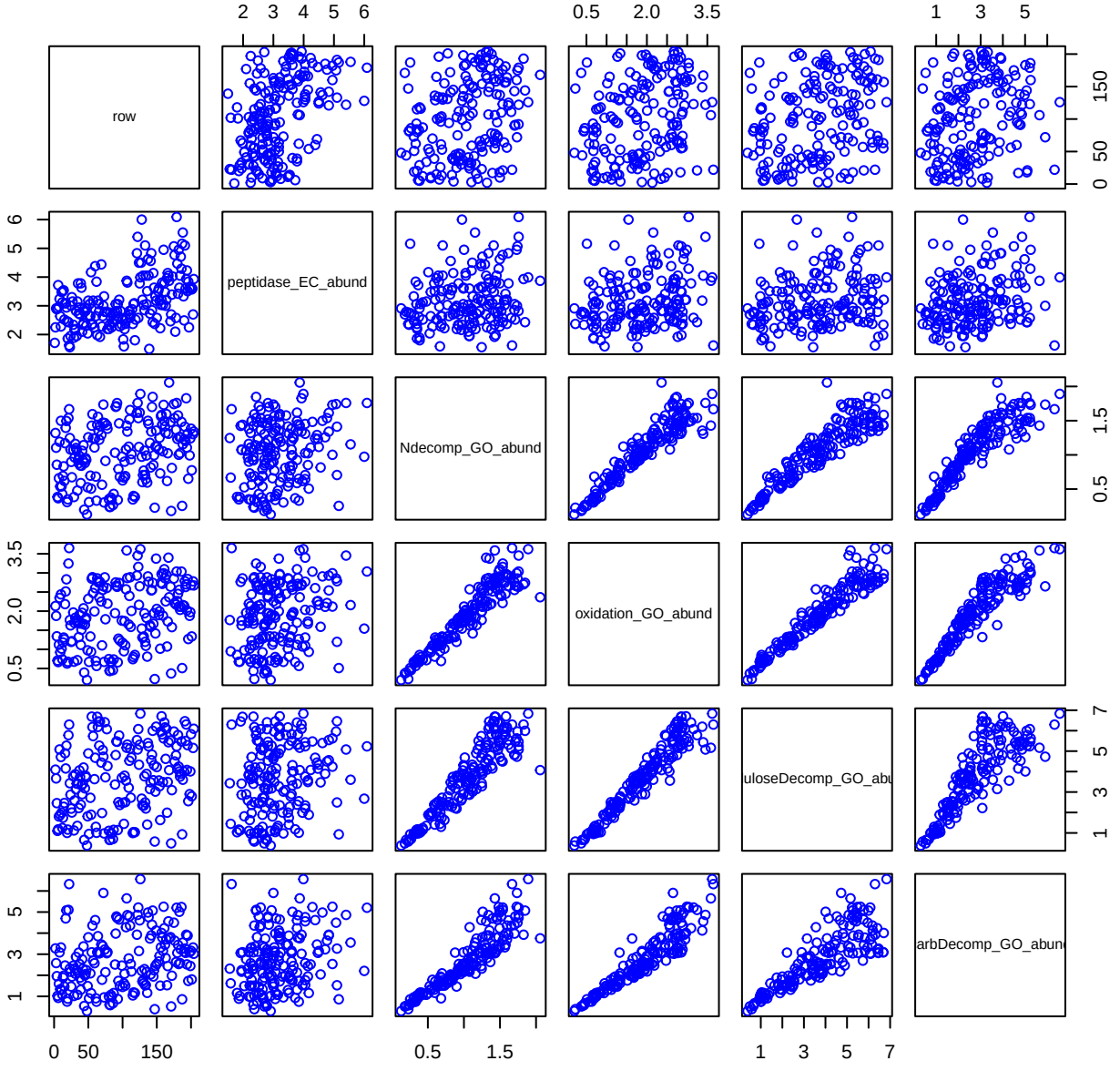
HF456−01 Plot 20



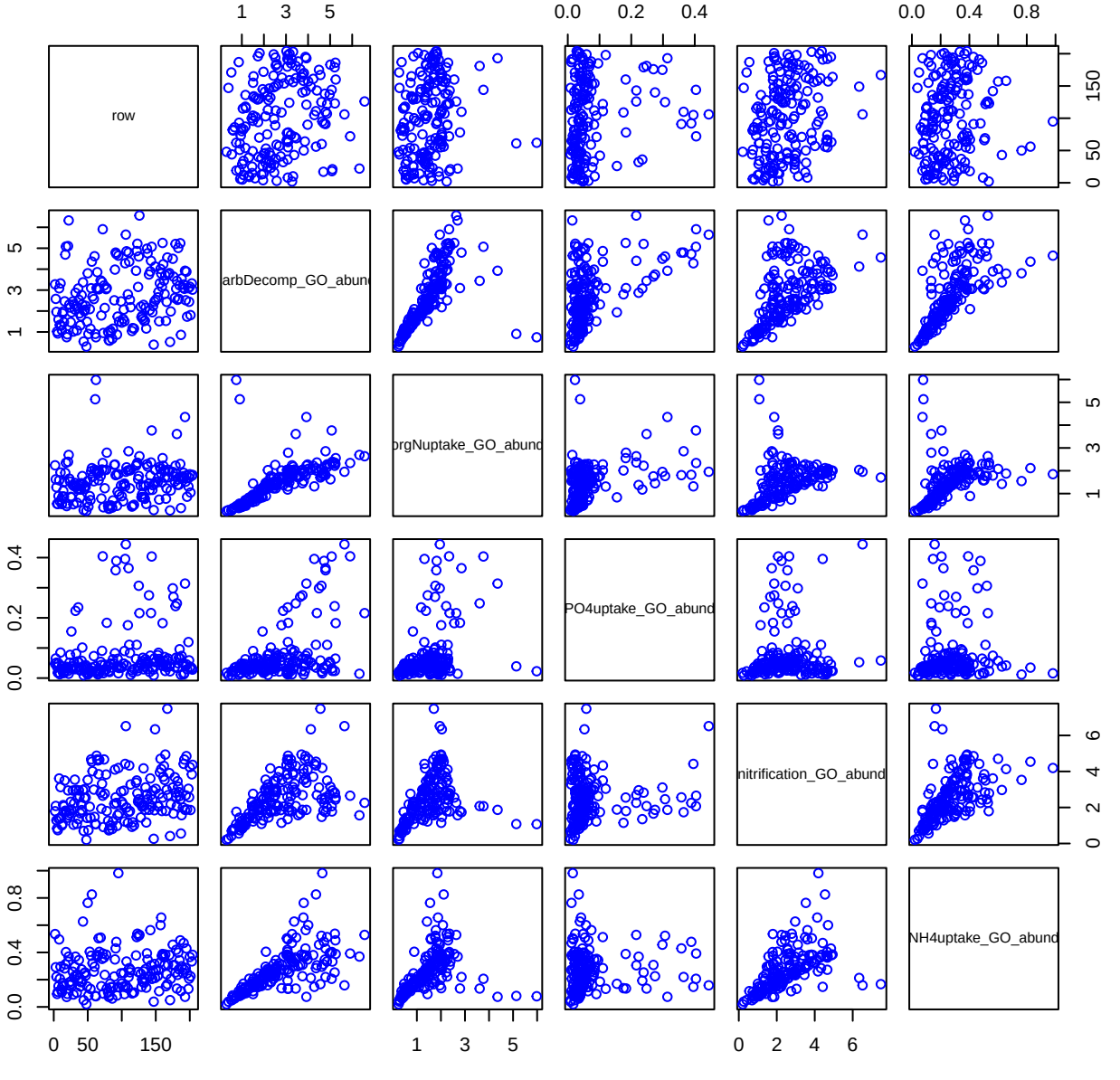
HF456−01 Plot 21



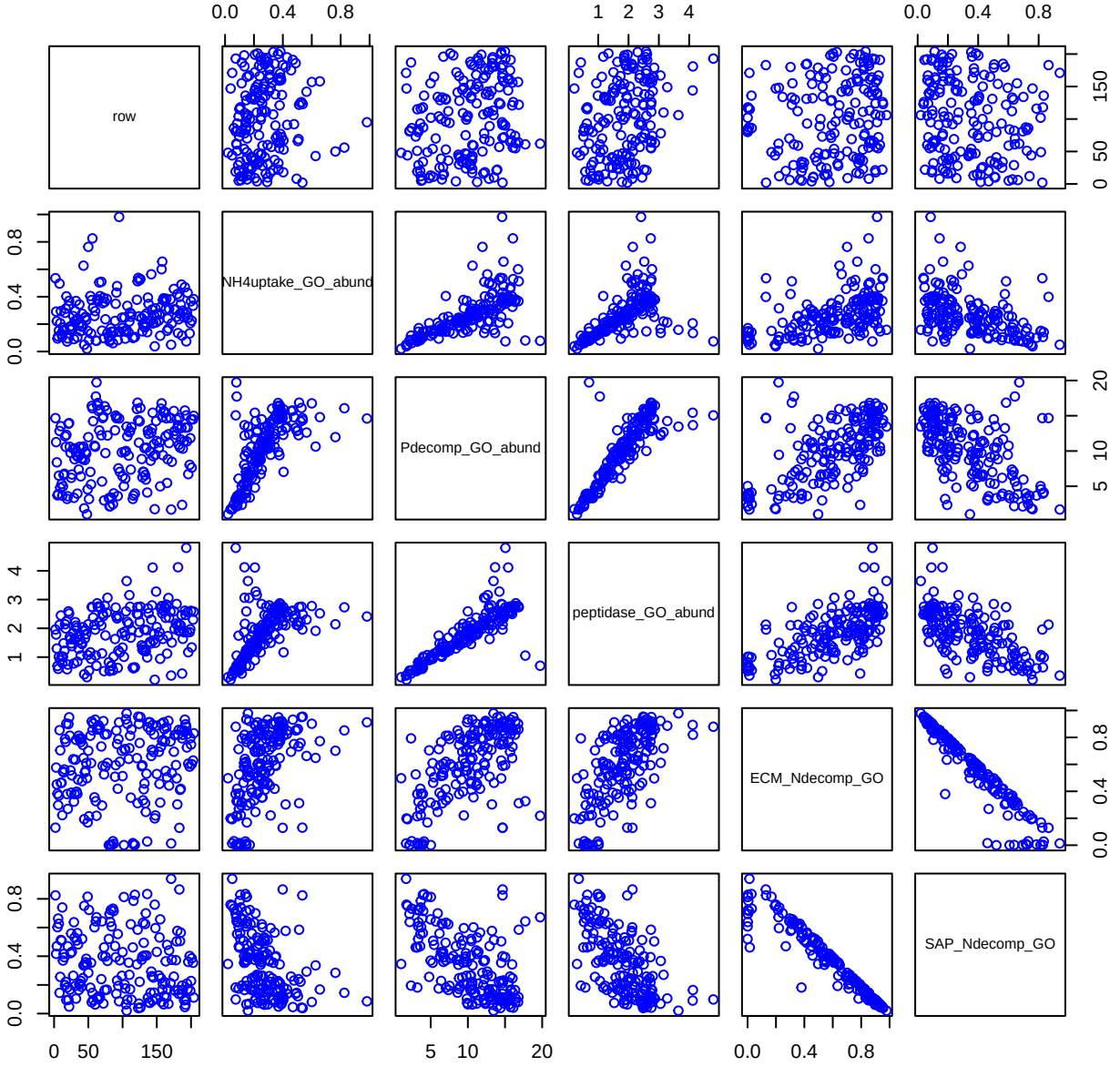
HF456−01 Plot 22



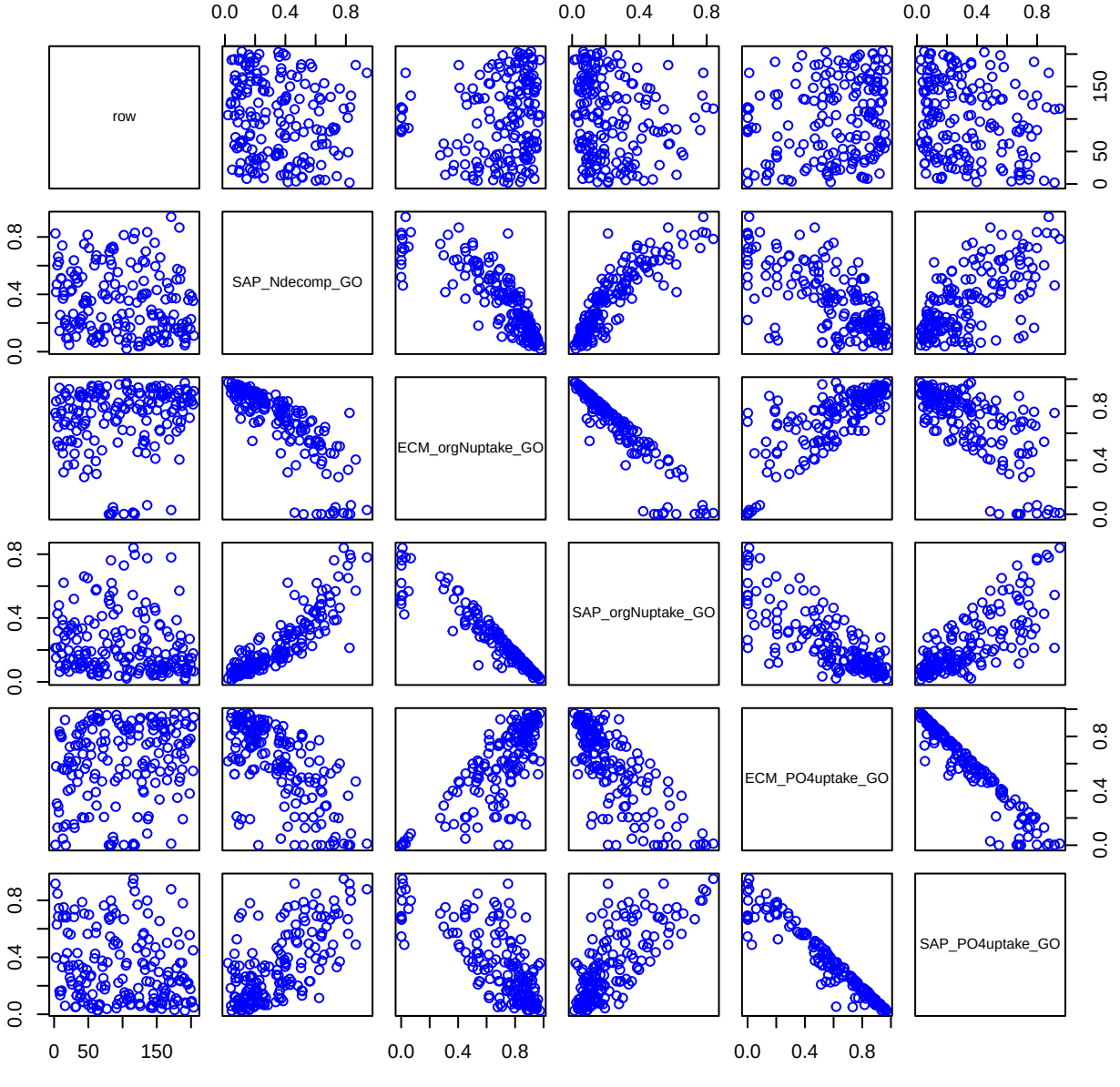
HF456−01 Plot 23



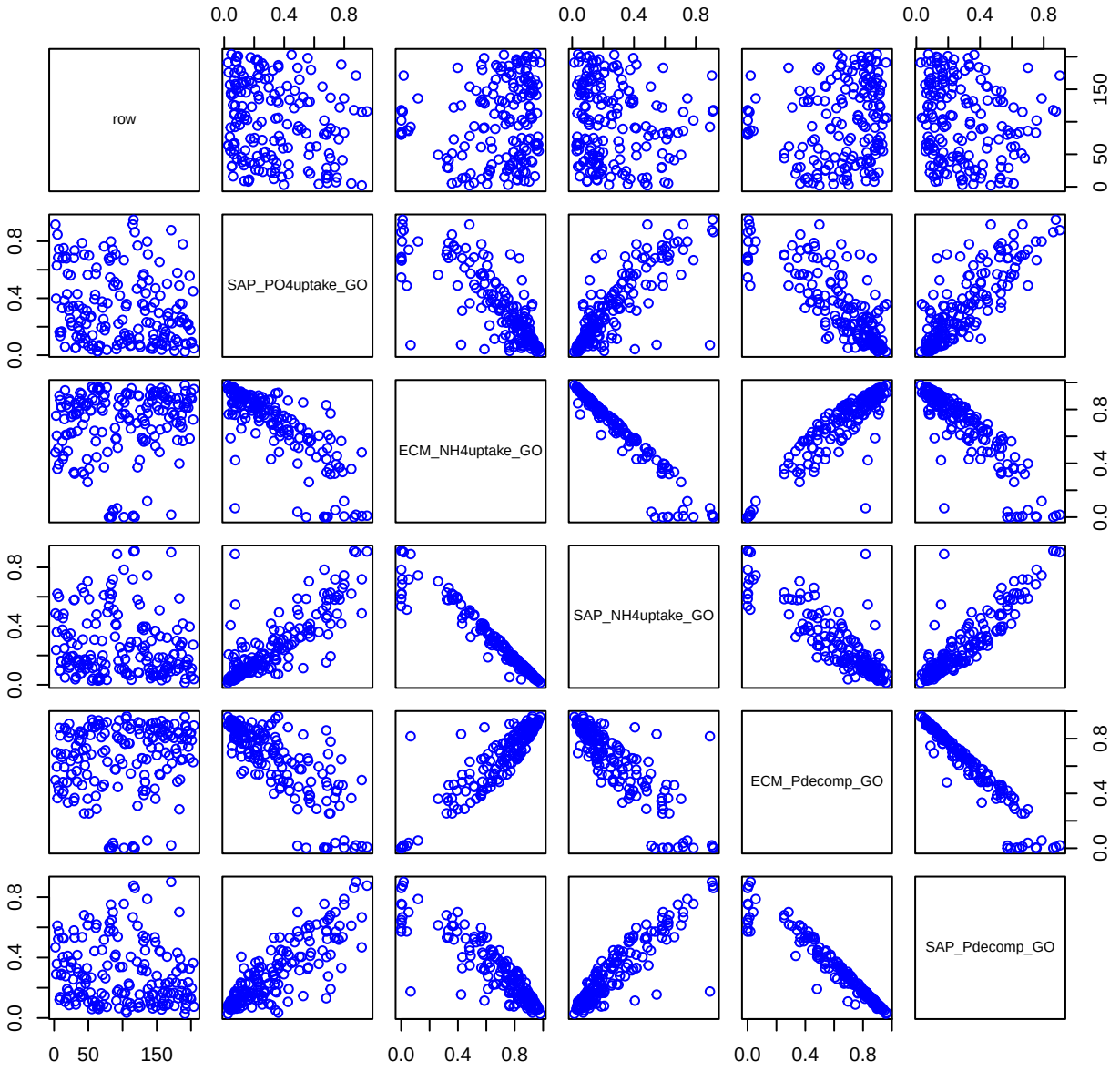
HF456−01 Plot 24



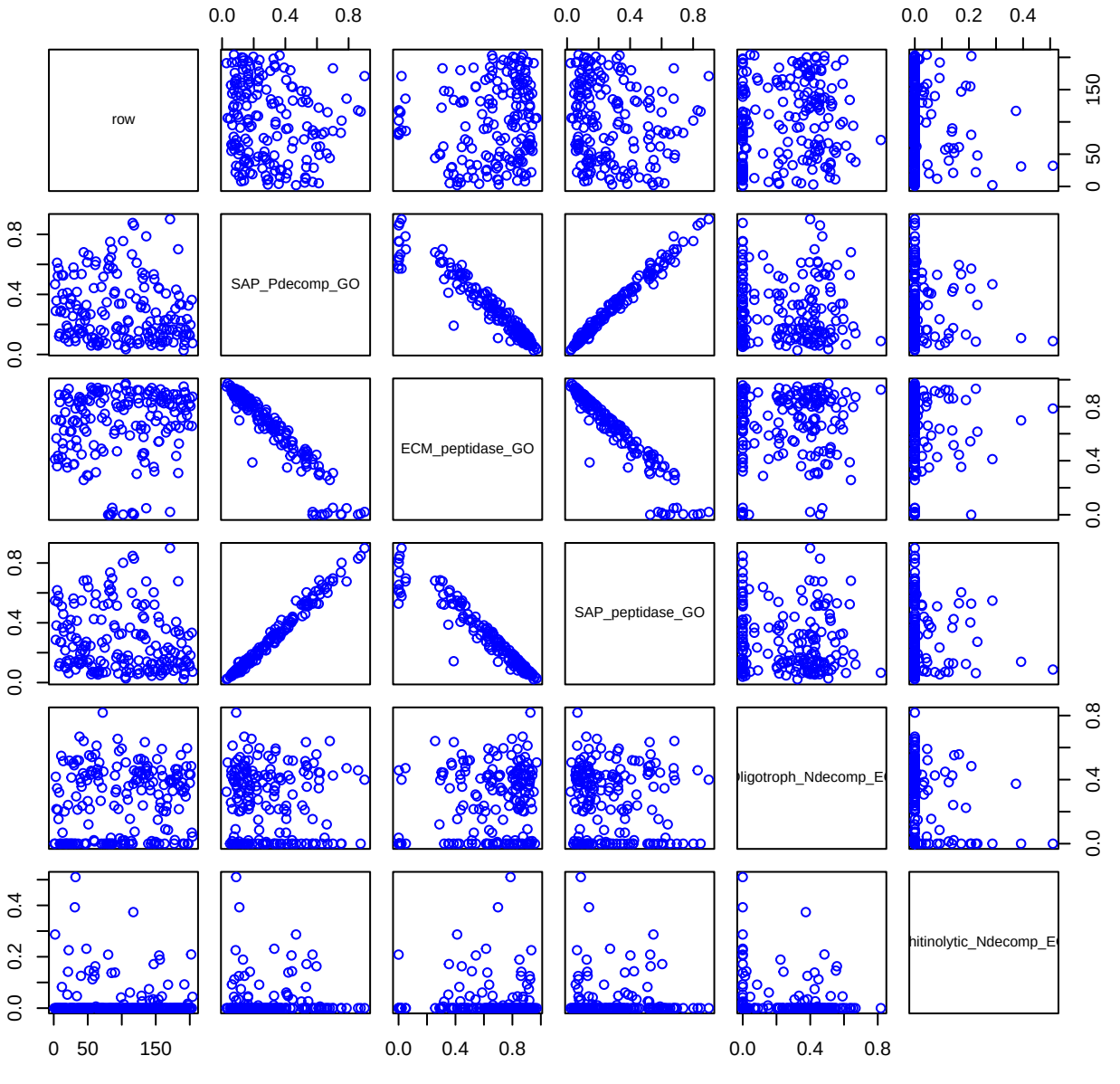
HF456−01 Plot 25



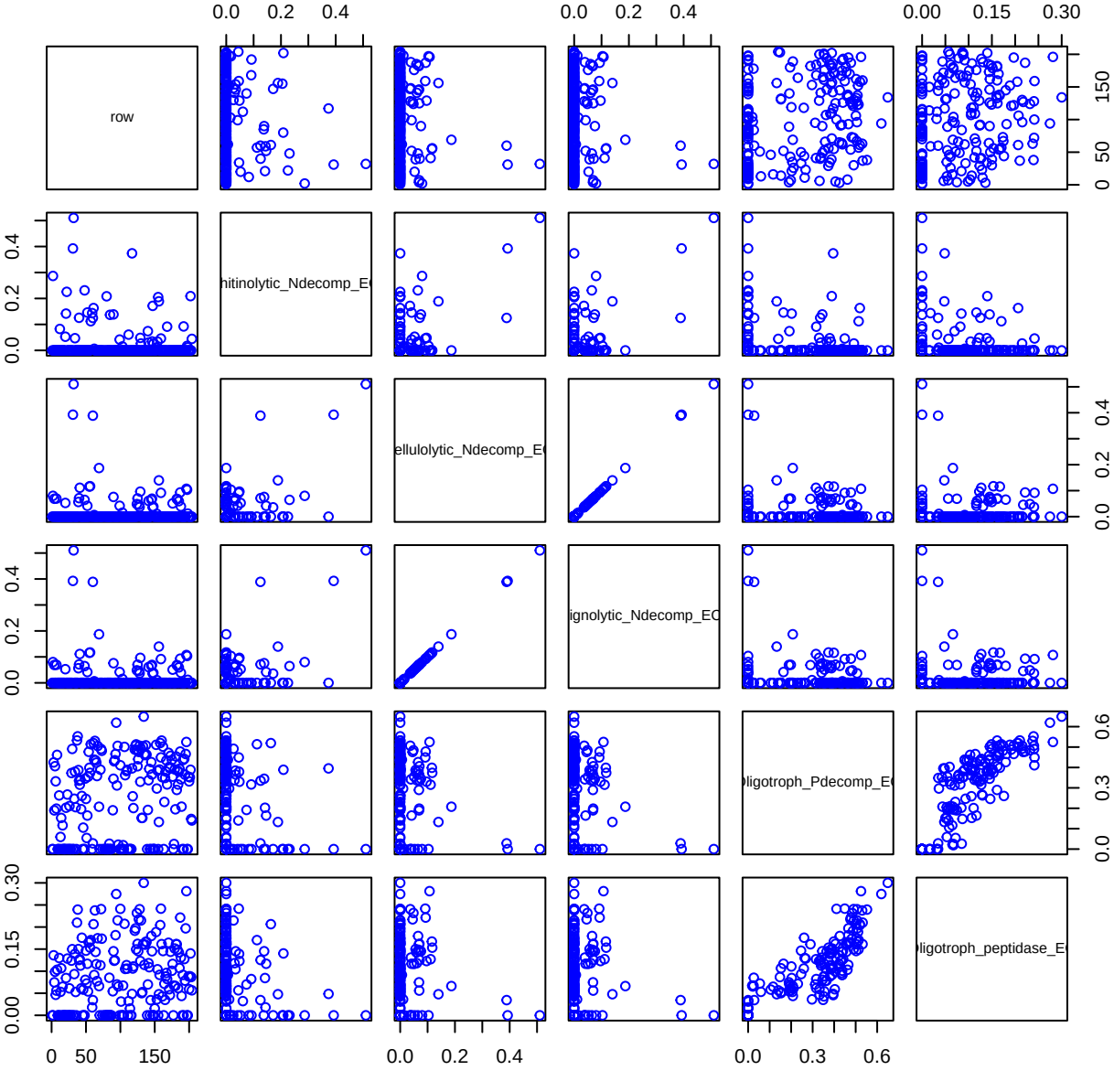
HF456−01 Plot 26



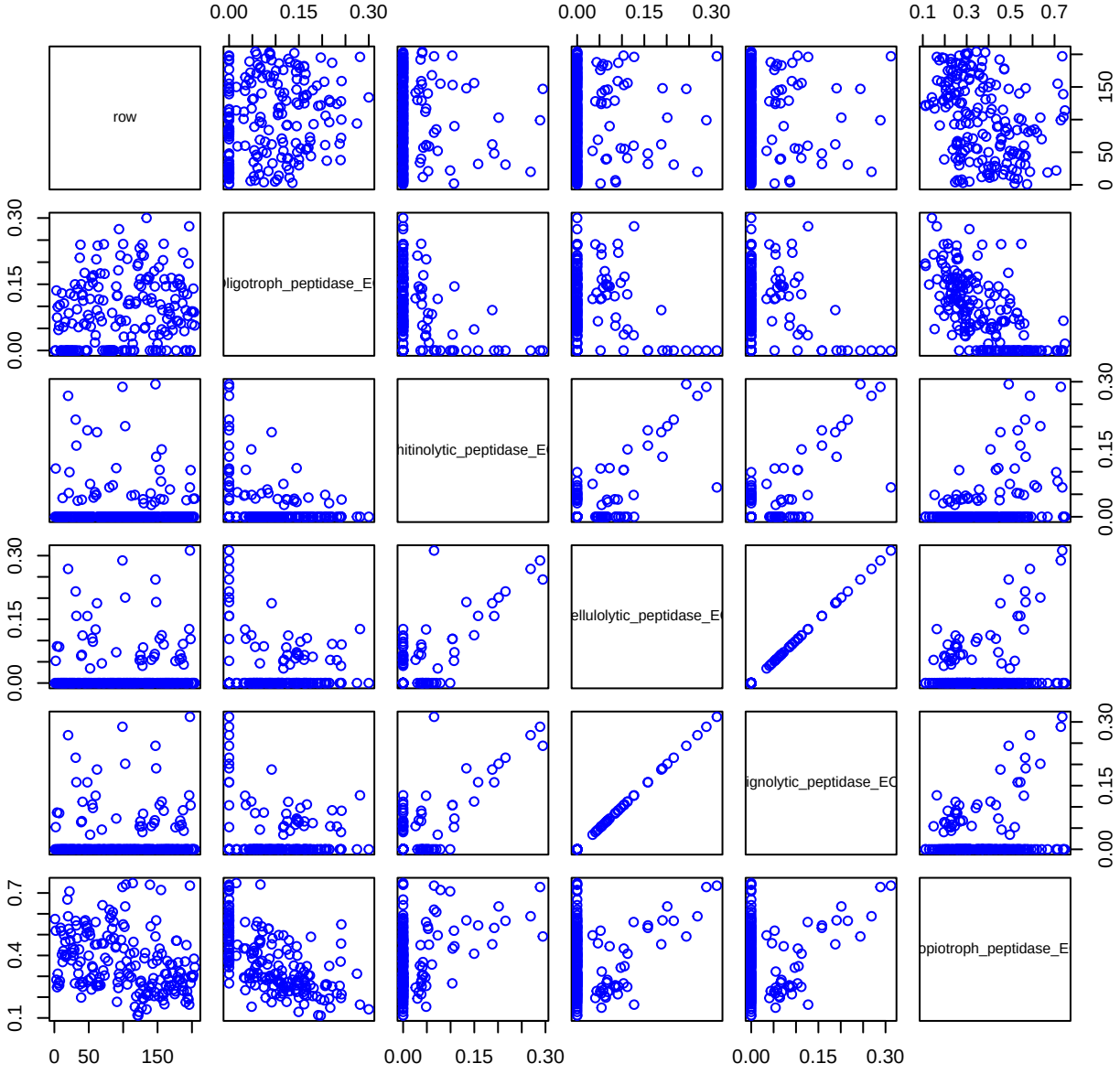
HF456−01 Plot 27



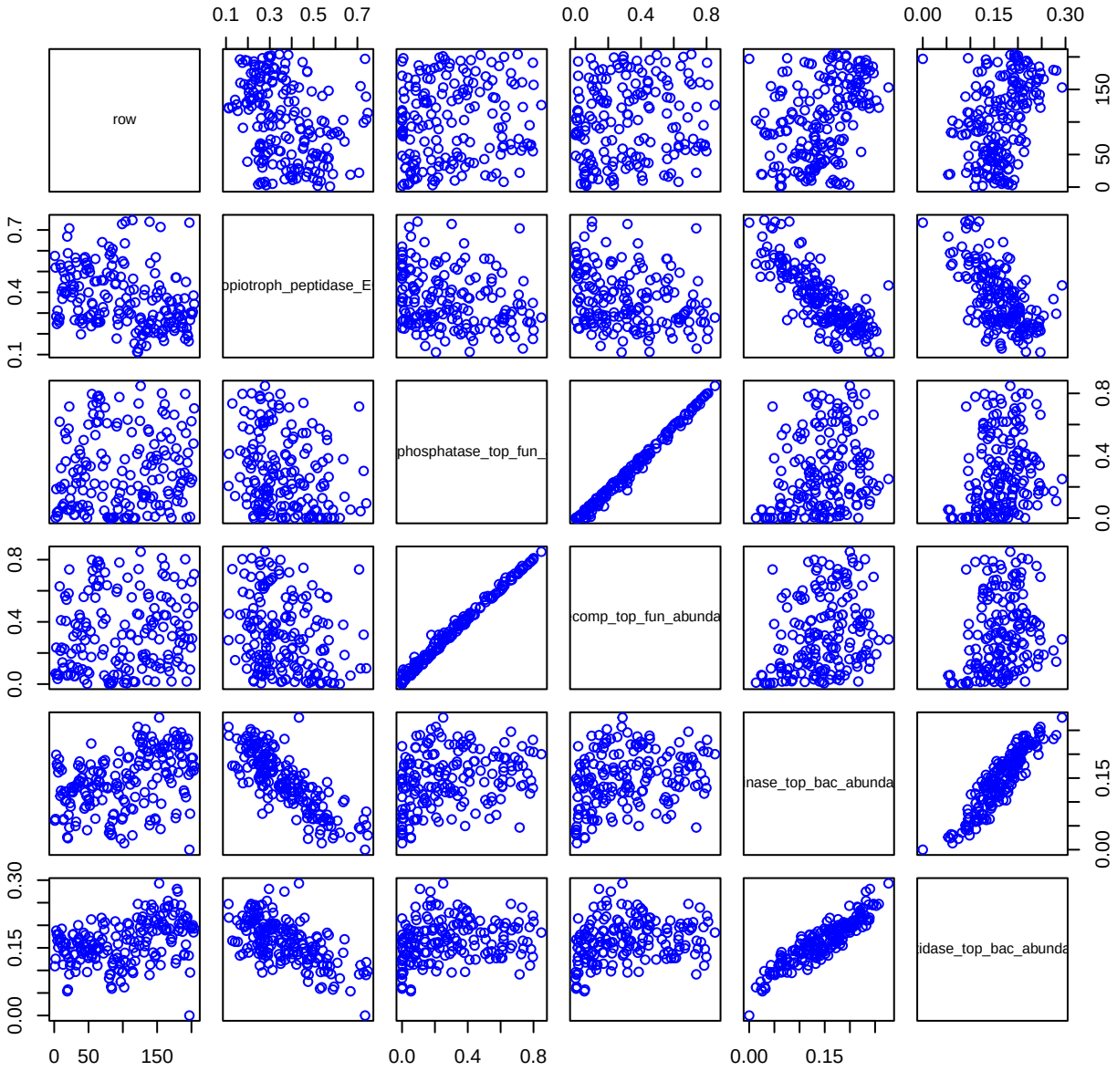
HF456−01 Plot 28



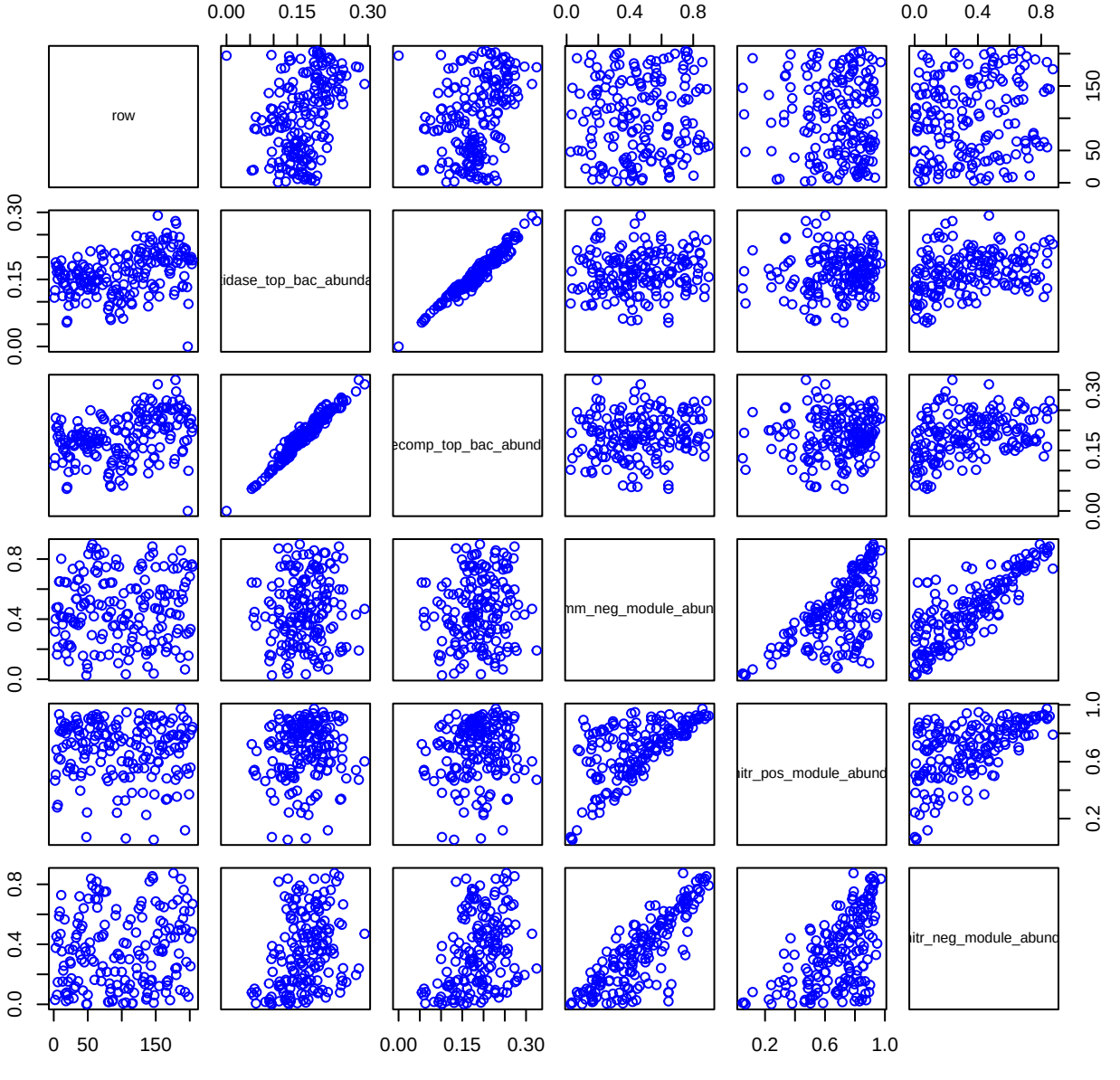
HF456−01 Plot 29



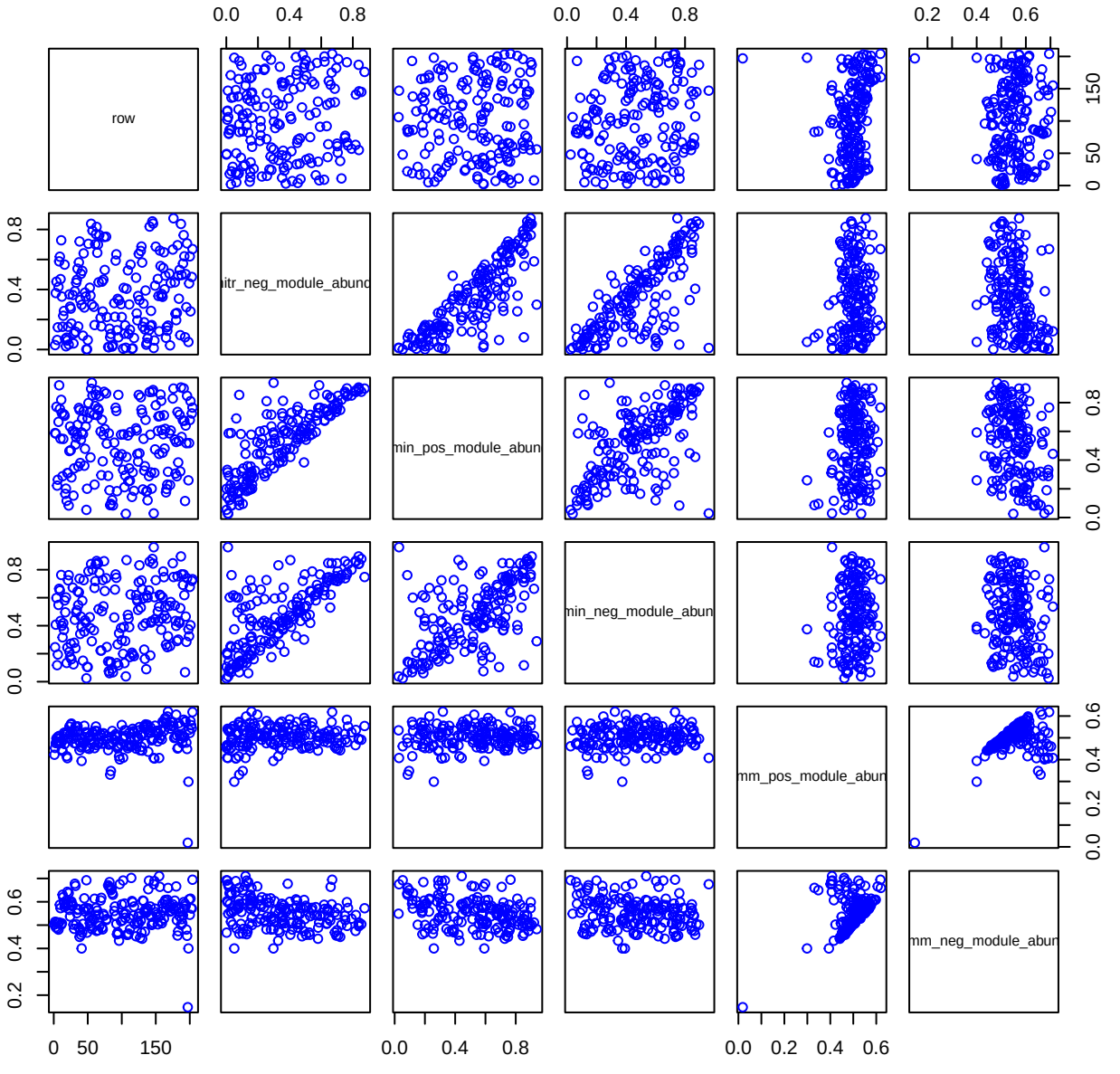
HF456−01 Plot 30



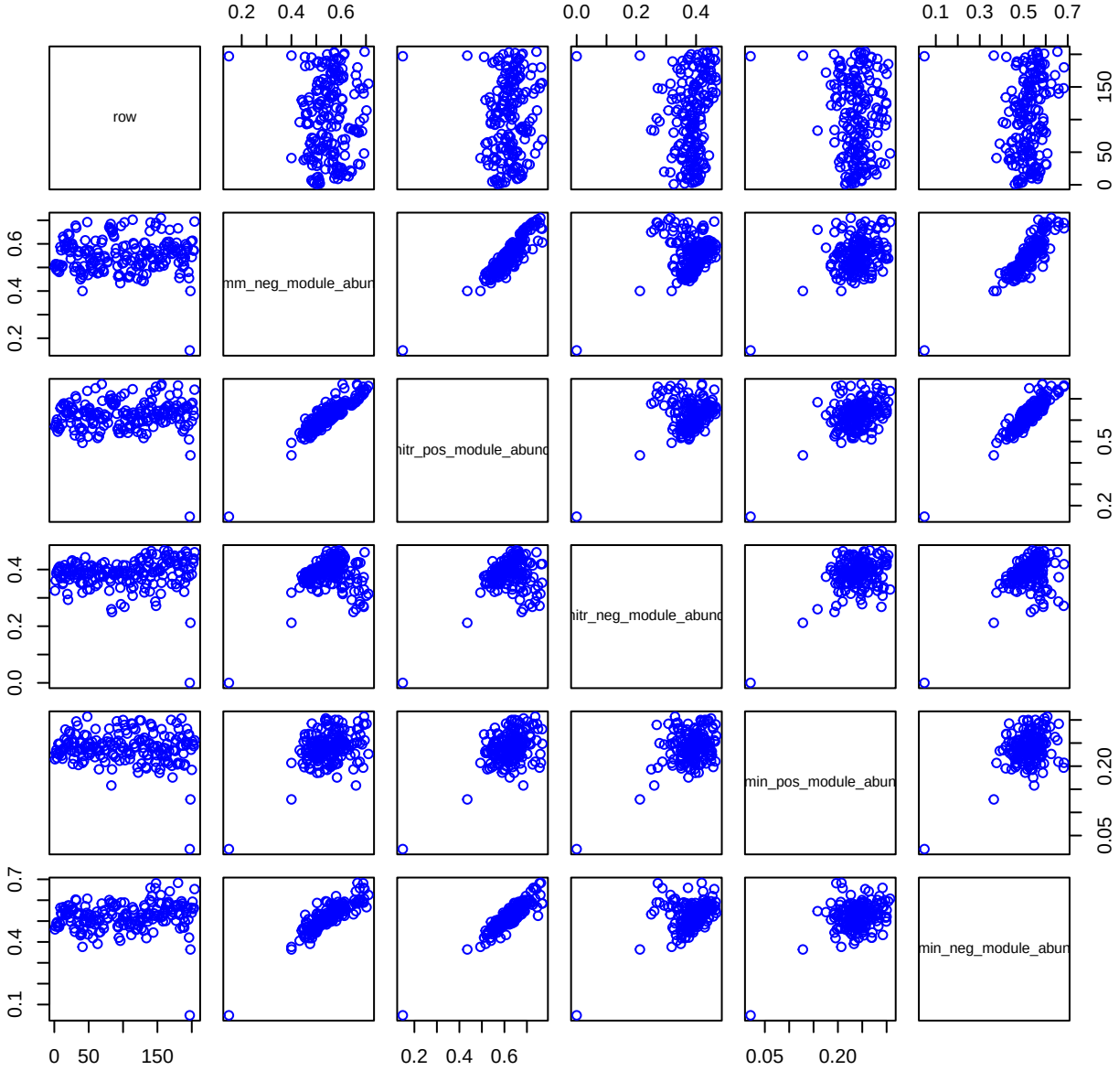
HF456−01 Plot 31



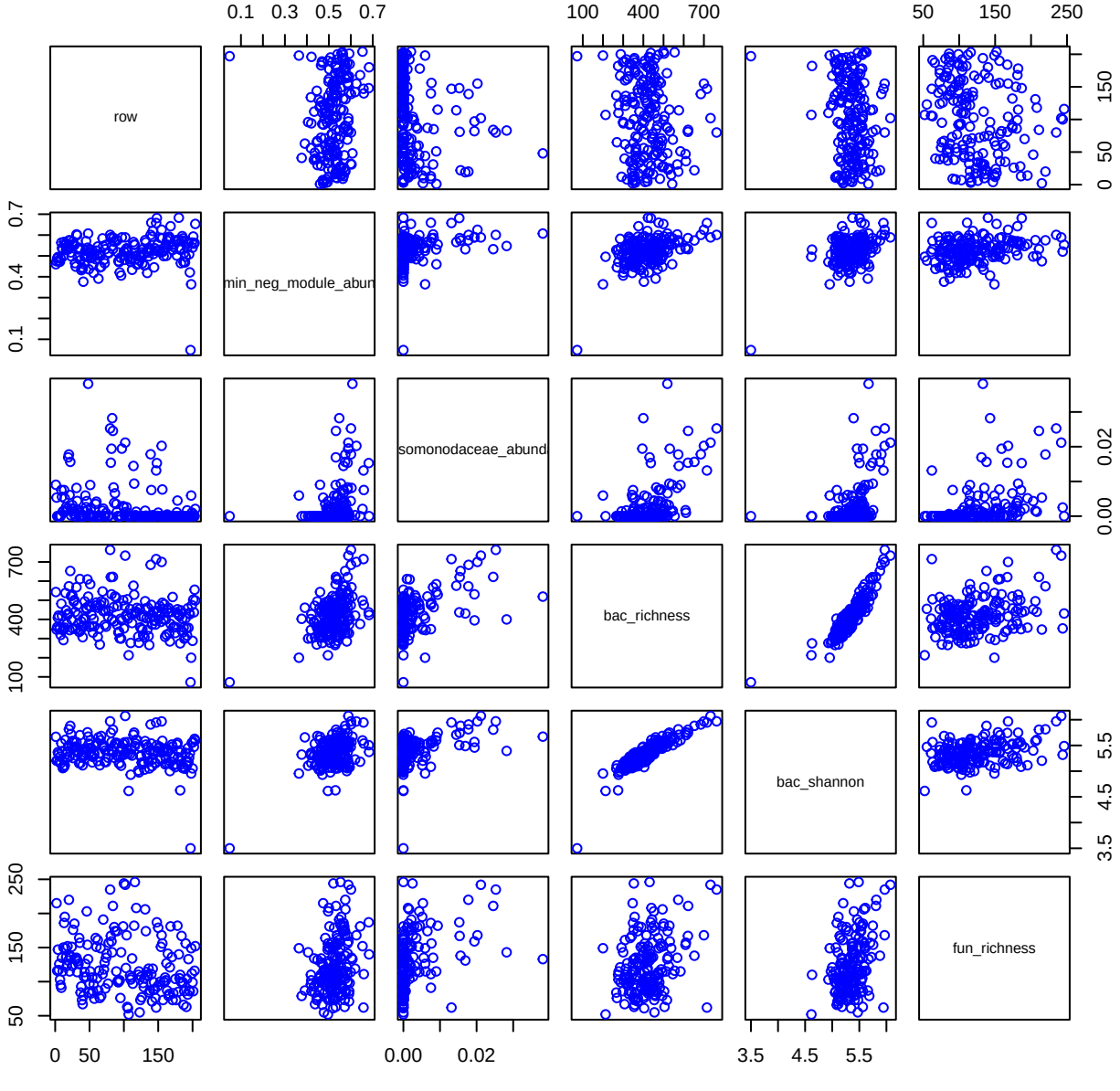
HF456−01 Plot 32



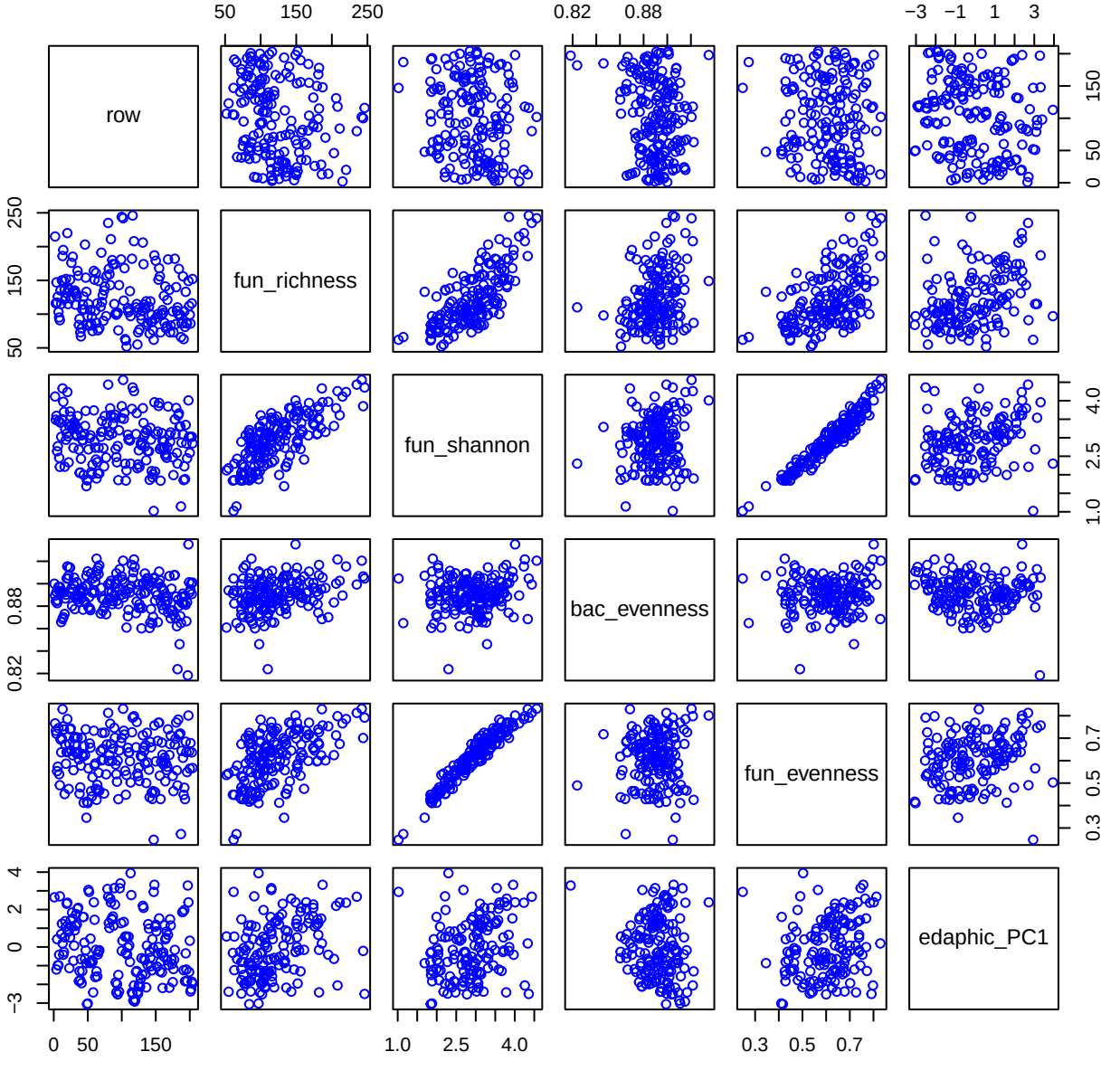
HF456−01 Plot 33



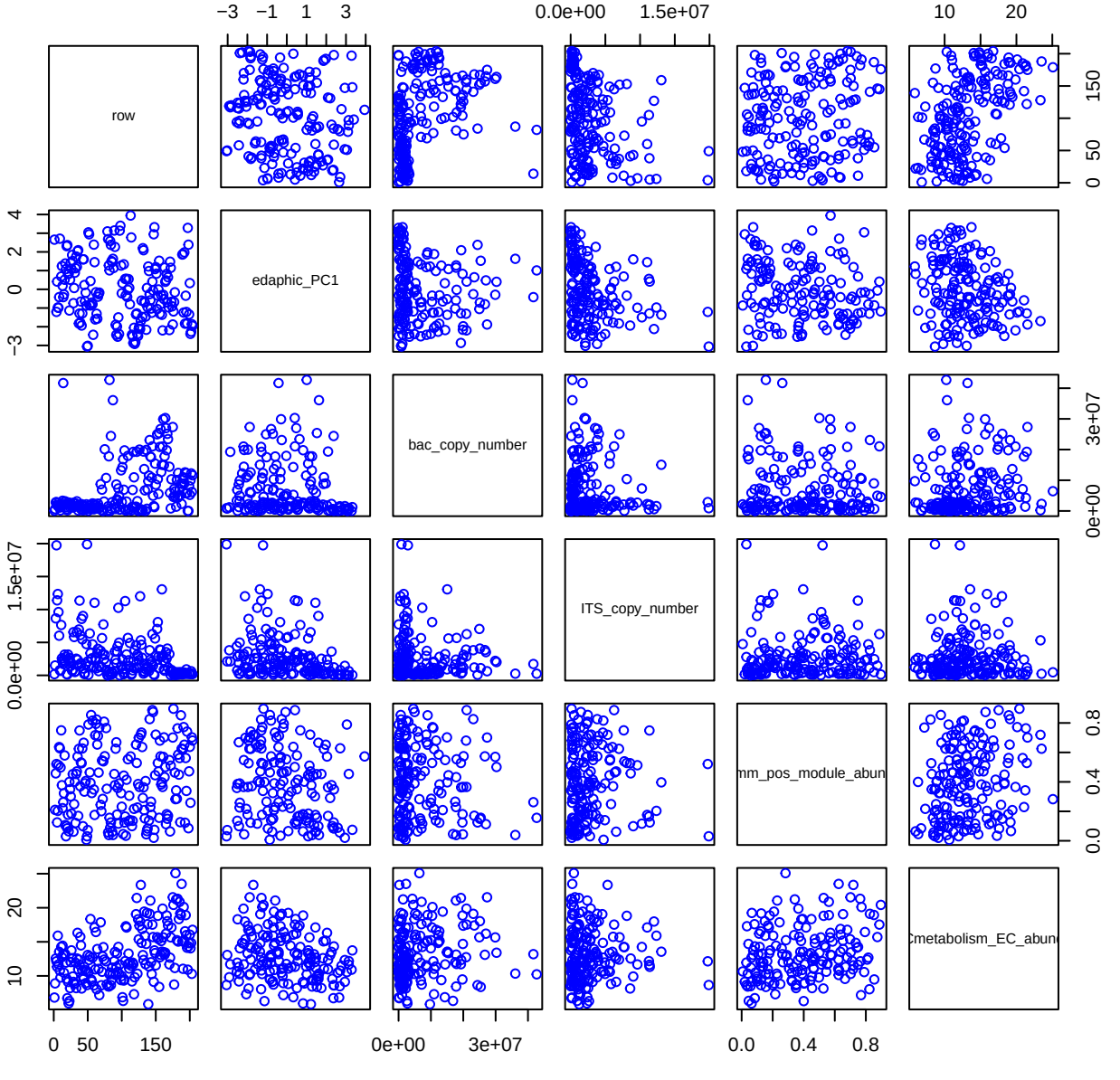
HF456−01 Plot 34



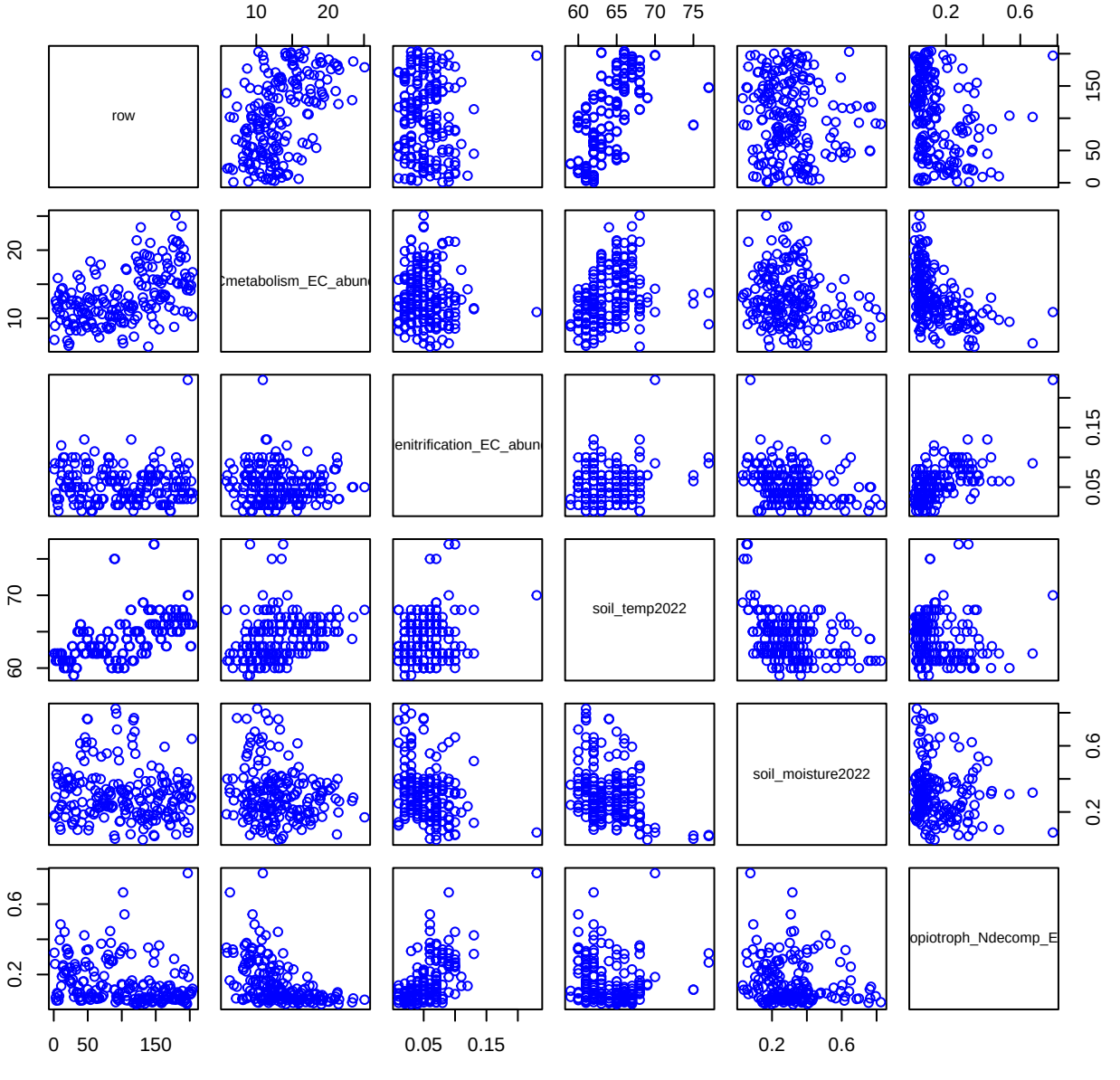
HF456−01 Plot 35



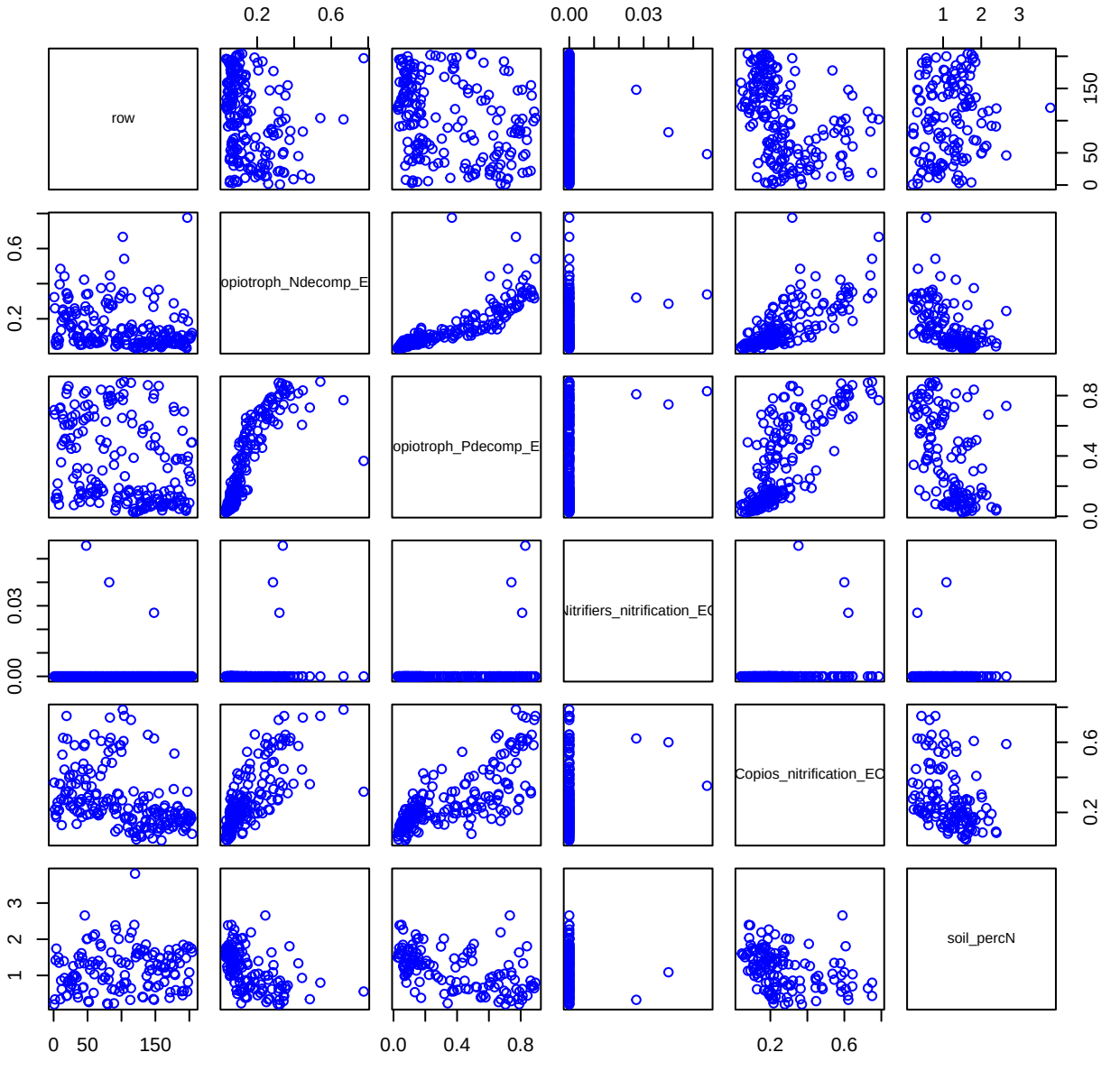
HF456−01 Plot 36



HF456−01 Plot 37



HF456−01 Plot 38



HF456−01 Plot 39