

```
/home/kelvinli/git/AnalysisTools/Profile/SummaryTableUtilities/Select_Categories_By_PCA/Select_Categories_By_PCA.r
```

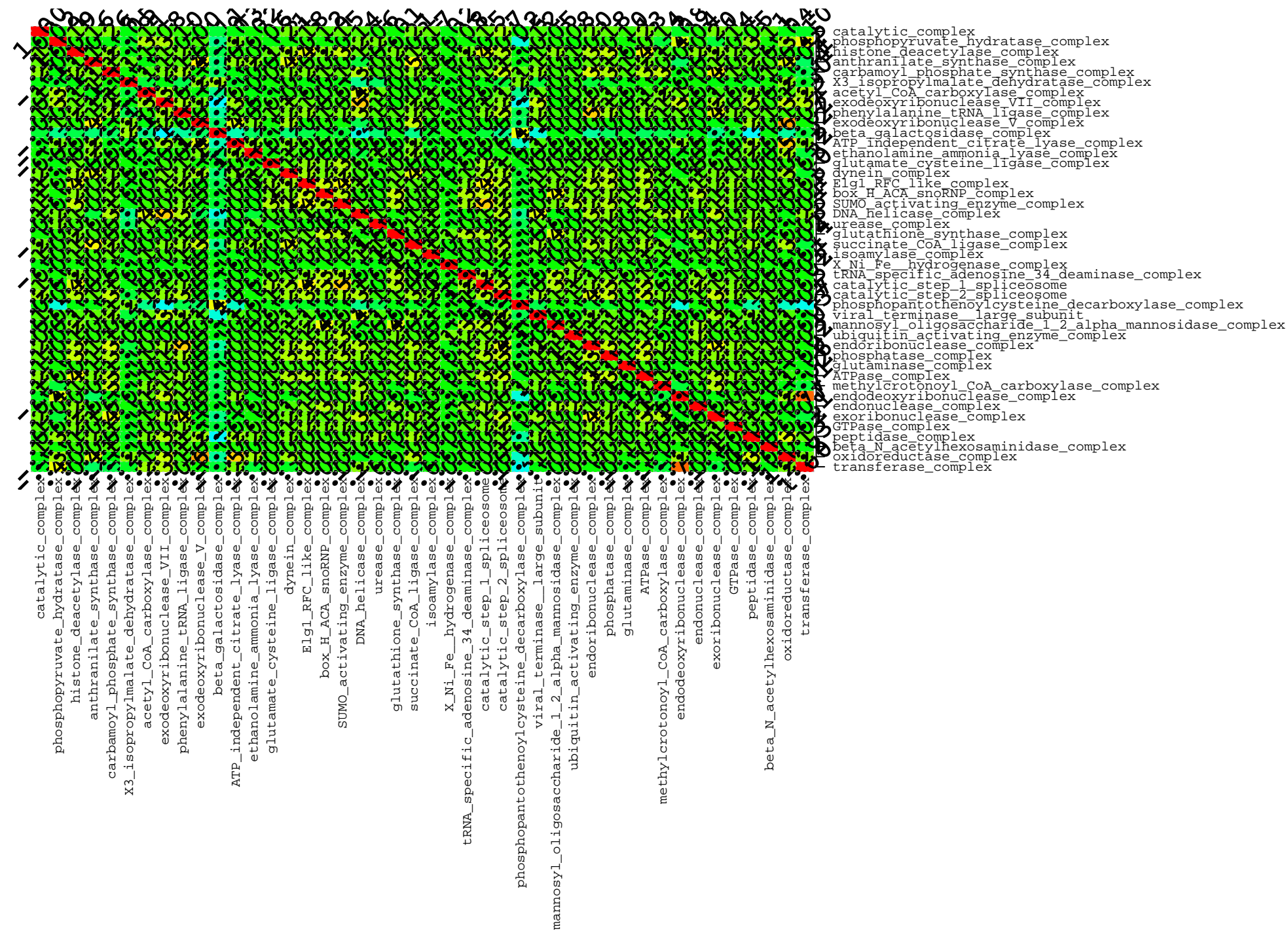
```
Input Summary Table:  GO_1902494.catalytic_complex.tpn100.prof.summary_table.tsv
```

```
Minimum PC Cuml Coverage:
```

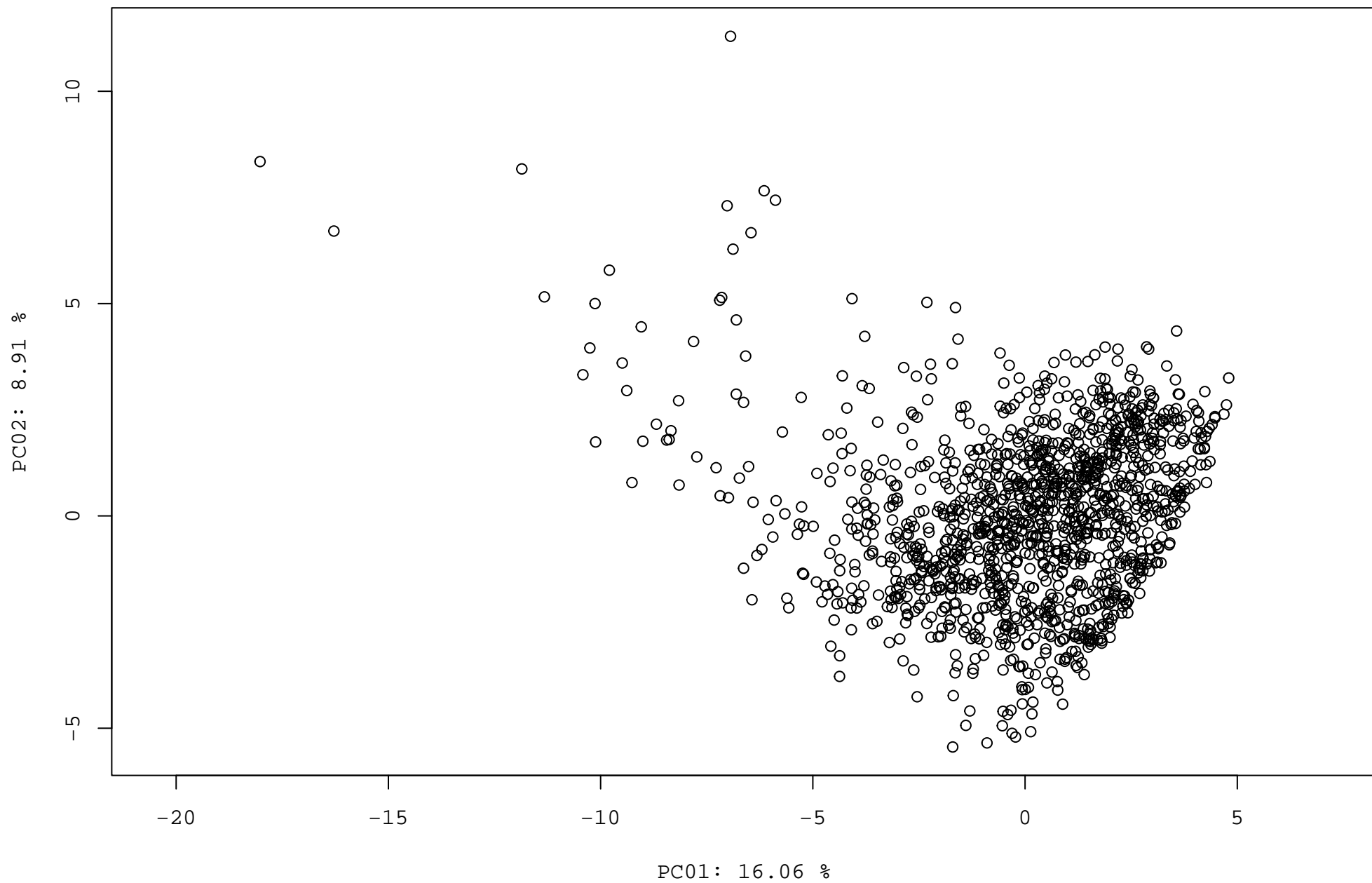
```
Minimum PC Indv Coverage:  0.025
```

```
Output Root:  example
```

## Spearman Correlation Matrix

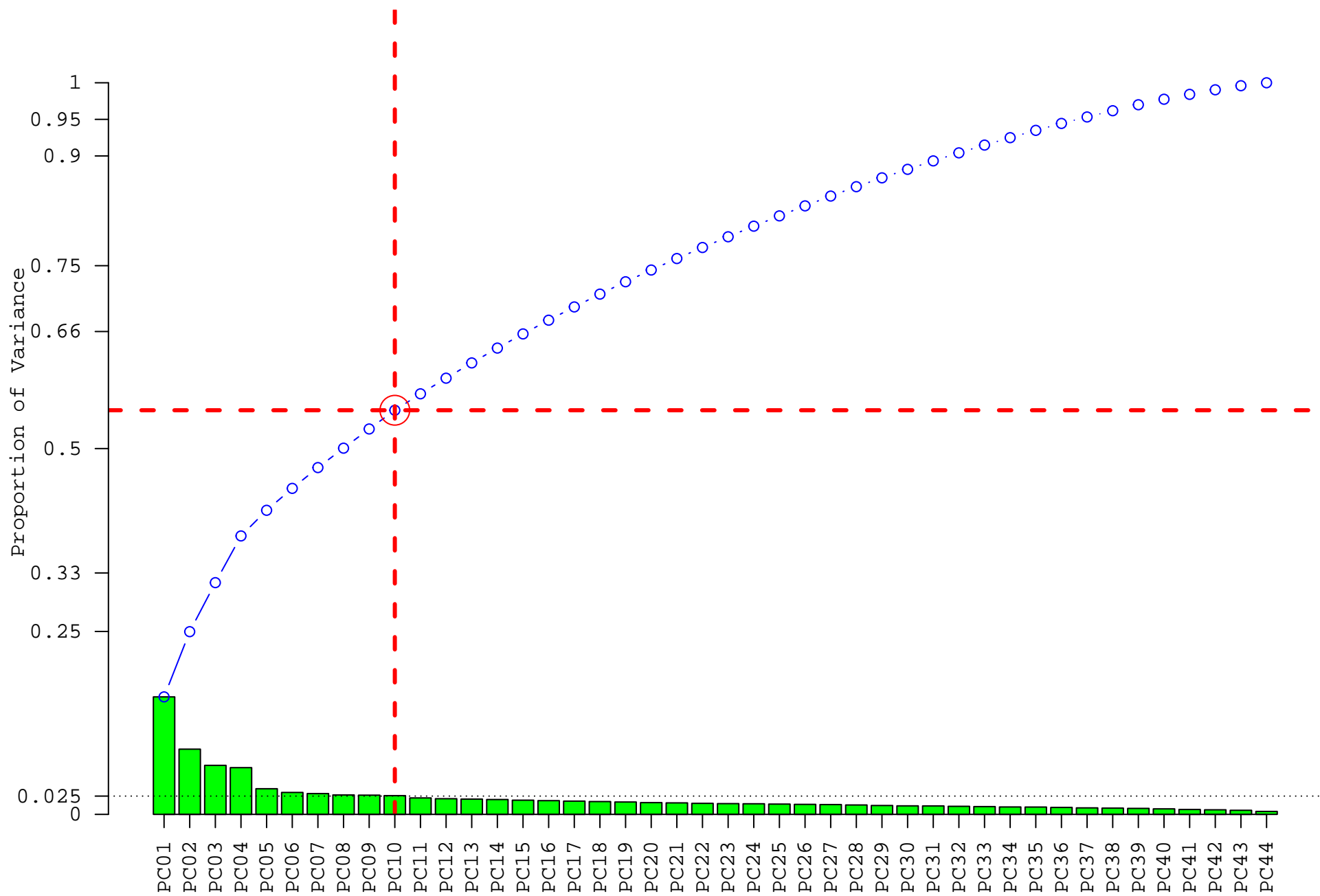


Top 2 PCs



PCA Variance Allocation:

	Prop	Cuml
PC01	0.16059	0.16059
PC02	0.08913	0.24972
PC03	0.06701	0.31673
PC04	0.06387	0.38060
PC05	0.03503	0.41563
PC06	0.02996	0.44559
PC07	0.02842	0.47401
PC08	0.02654	0.50055
PC09	0.02624	0.52679
PC10	0.02559	0.55238
PC11	0.02246	0.57484
PC12	0.02138	0.59622
PC13	0.02085	0.61707
PC14	0.02028	0.63735
PC15	0.01938	0.65673
PC16	0.01876	0.67549
PC17	0.01811	0.69360
PC18	0.01751	0.71111
PC19	0.01690	0.72800
PC20	0.01605	0.74406
PC21	0.01571	0.75977
PC22	0.01506	0.77483
PC23	0.01468	0.78951
PC24	0.01448	0.80400
PC25	0.01406	0.81805
PC26	0.01369	0.83174
PC27	0.01341	0.84515
PC28	0.01281	0.85796
PC29	0.01209	0.87005
PC30	0.01163	0.88168
PC31	0.01155	0.89323
PC32	0.01098	0.90421
PC33	0.01062	0.91484
PC34	0.01012	0.92495
PC35	0.01000	0.93495
PC36	0.00946	0.94441
PC37	0.00886	0.95327
PC38	0.00854	0.96181
PC39	0.00816	0.96997
PC40	0.00753	0.97750
PC41	0.00667	0.98417
PC42	0.00624	0.99041
PC43	0.00556	0.99598
PC44	0.00402	1.00000



PC:1

	correl_w_ratios	mag_correl
catalytic_complex	-0.33244790	0.33244790
phosphopyruvate_hydratase_complex	-0.28656103	0.28656103
histone_deacetylase_complex	-0.46154907	0.46154907
anthranilate_synthase_complex	-0.41023206	0.41023206
carbamoyl_phosphate_synthase_complex	-0.50194728	0.50194728
X3_isopropylmalate_dehydratase_complex	0.13359699	0.13359699
acetyl_CoA_carboxylase_complex	-0.35988534	0.35988534
exodeoxyribonuclease_VII_complex	-0.60663311	0.60663311
phenylalanine_tRNA_ligase_complex	-0.46854971	0.46854971
exodeoxyribonuclease_V_complex	-0.27470291	0.27470291
beta_galactosidase_complex	0.66741552	0.66741552
ATP_independent_citrate_lyase_complex	-0.32105689	0.32105689
ethanolamine_ammonia_lyase_complex	-0.17306258	0.17306258
glutamate_cysteine_ligase_complex	-0.11948510	0.11948510
dynein_complex	-0.49651808	0.49651808
Elg1_RFC_like_complex	-0.36182713	0.36182713
box_H_ACA_snoRNP_complex	-0.23434270	0.23434270
SUMO_activating_enzyme_complex	-0.29739460	0.29739460
DNA_helicase_complex	-0.53929227	0.53929227
urease_complex	-0.27505745	0.27505745
glutathione_synthase_complex	-0.16469545	0.16469545
succinate_CoA_ligase_complex	-0.53799488	0.53799488
isoamylase_complex	-0.27503291	0.27503291
X_Ni_Fe_hydrogenase_complex	-0.02346682	0.02346682
tRNA_specific_adenosine_34_deaminase_complex	-0.14903030	0.14903030
catalytic_step_1_spliceosome	-0.32239283	0.32239283
catalytic_step_2_spliceosome	-0.59620933	0.59620933
phosphopantothienoylcysteine_decarboxylase_complex	0.35379474	0.35379474
viral_terminase_large_subunit	-0.48962804	0.48962804
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	-0.17316836	0.17316836
ubiquitin_activating_enzyme_complex	-0.14974467	0.14974467
endoribonuclease_complex	-0.60497543	0.60497543
phosphatase_complex	-0.50012716	0.50012716
glutaminase_complex	-0.14000485	0.14000485
ATPase_complex	-0.53457430	0.53457430
methylcrotonoyl_CoA_carboxylase_complex	-0.34887554	0.34887554
endodeoxyribonuclease_complex	-0.19444790	0.19444790
endonuclease_complex	-0.17311077	0.17311077
exoribonuclease_complex	-0.52372475	0.52372475
GTPase_complex	-0.29632038	0.29632038
peptidase_complex	-0.48312595	0.48312595
beta_N_acetylhexosaminidase_complex	-0.15259802	0.15259802
oxidoreductase_complex	-0.38373292	0.38373292
transferase_complex	-0.12182722	0.12182722

Greatest Magnitude of Correlation: 0.667415516544359  
(Index: 11 )  
Best Proxy: beta\_galactosidase\_complex

PC:2

	correl_w_ratios	mag_correl
catalytic_complex	1.889916e-01	1.889916e-01
phosphopyruvate_hydratase_complex	-6.070399e-01	6.070399e-01
histone_deacetylase_complex	2.052716e-01	2.052716e-01
anthranilate_synthase_complex	-1.440849e-02	1.440849e-02
carbamoyl_phosphate_synthase_complex	2.584935e-01	2.584935e-01
X3_isopropylmalate_dehydratase_complex	1.042652e-01	1.042652e-01
acetyl_CoA_carboxylase_complex	-3.384520e-01	3.384520e-01
exodeoxyribonuclease_VII_complex	-5.223516e-01	5.223516e-01
phenylalanine_tRNA_ligase_complex	-3.207590e-02	3.207590e-02
exodeoxyribonuclease_V_complex	-3.369028e-01	3.369028e-01
beta_galactosidase_complex	4.445104e-01	4.445104e-01
ATP_independent_citrate_lyase_complex	-5.138643e-01	5.138643e-01
ethanolamine_ammonia_lyase_complex	-9.421812e-02	9.421812e-02
glutamate_cysteine_ligase_complex	1.143633e-01	1.143633e-01
dynein_complex	6.776266e-02	6.776266e-02
Elg1_RFC_like_complex	1.942327e-01	1.942327e-01
box_H_ACA_snoRNP_complex	1.607113e-01	1.607113e-01
SUMO_activating_enzyme_complex	2.371362e-01	2.371362e-01
DNA_helicase_complex	-2.744566e-01	2.744566e-01
urease_complex	-1.819452e-01	1.819452e-01
glutathione_synthase_complex	1.371910e-01	1.371910e-01
succinate_CoA_ligase_complex	-3.983534e-02	3.983534e-02
isoamylase_complex	6.141576e-02	6.141576e-02
X_Ni_Fe_hydrogenase_complex	-4.895885e-05	4.895885e-05
tRNA_specific_adenosine_34_deaminase_complex	1.351884e-01	1.351884e-01
catalytic_step_1_spliceosome	2.249165e-01	2.249165e-01
catalytic_step_2_spliceosome	1.071890e-01	1.071890e-01
phosphopantothienoylcysteine_decarboxylase_complex	7.046362e-01	7.046362e-01
viral_terminase_large_subunit	-1.579972e-01	1.579972e-01
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	1.433325e-01	1.433325e-01
ubiquitin_activating_enzyme_complex	1.183739e-01	1.183739e-01
endoribonuclease_complex	9.774250e-02	9.774250e-02
phosphatase_complex	1.581491e-01	1.581491e-01
glutaminase_complex	1.001059e-01	1.001059e-01
ATPase_complex	1.750749e-01	1.750749e-01
methylcrotonoyl_CoA_carboxylase_complex	1.145399e-01	1.145399e-01
endodeoxyribonuclease_complex	-5.720832e-01	5.720832e-01
endonuclease_complex	1.433866e-01	1.433866e-01
exoribonuclease_complex	1.766641e-01	1.766641e-01
GTPase_complex	1.305650e-01	1.305650e-01
peptidase_complex	-4.335586e-01	4.335586e-01
beta_N_acetylhexosaminidase_complex	6.169823e-02	6.169823e-02
oxidoreductase_complex	-5.639788e-01	5.639788e-01
transferase_complex	-6.051334e-01	6.051334e-01

Greatest Magnitude of Correlation: 0.704636230872208

(Index: 28 )

Best Proxy: phosphopantothienoylcysteine\_decarboxylase\_complex

PC:3

	correl_w_ratios	mag_correl
catalytic_complex	-0.062894832	0.062894832
phosphopyruvate_hydratase_complex	-0.146161064	0.146161064
histone_deacetylase_complex	-0.051796271	0.051796271
anthranilate_synthase_complex	0.578316152	0.578316152
carbamoyl_phosphate_synthase_complex	-0.154877101	0.154877101
X3_isopropylmalate_dehydratase_complex	0.454310424	0.454310424
acetyl_CoA_carboxylase_complex	-0.323812762	0.323812762
exodeoxyribonuclease_VII_complex	-0.195829577	0.195829577
phenylalanine_tRNA_ligase_complex	-0.173371730	0.173371730
exodeoxyribonuclease_V_complex	0.645143620	0.645143620
beta_galactosidase_complex	0.136292545	0.136292545
ATP_independent_citrate_lyase_complex	0.307253091	0.307253091
ethanolamine_ammonia_lyase_complex	0.395917235	0.395917235
glutamate_cysteine_ligase_complex	-0.038688137	0.038688137
dynein_complex	0.326847912	0.326847912
Elg1_RFC_like_complex	-0.074294396	0.074294396
box_H_ACA_snoRNP_complex	0.089532495	0.089532495
SUMO_activating_enzyme_complex	-0.033912153	0.033912153
DNA_helicase_complex	-0.607474503	0.607474503
urease_complex	-0.138259474	0.138259474
glutathione_synthase_complex	0.111229159	0.111229159
succinate_CoA_ligase_complex	0.343546695	0.343546695
isoamylase_complex	-0.099027223	0.099027223
X_Ni_Fe_hydrogenase_complex	0.060718258	0.060718258
tRNA_specific_adenosine_34_deaminase_complex	0.072658066	0.072658066
catalytic_step_1_spliceosome	-0.050603558	0.050603558
catalytic_step_2_spliceosome	-0.197308044	0.197308044
phosphopantothenoylcysteine_decarboxylase_complex	0.134221635	0.134221635
viral_terminase_large_subunit	-0.192721566	0.192721566
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.142760477	0.142760477
ubiquitin_activating_enzyme_complex	0.066292793	0.066292793
endoribonuclease_complex	-0.140675344	0.140675344
phosphatase_complex	-0.062628835	0.062628835
glutaminase_complex	0.032143206	0.032143206
ATPase_complex	-0.009723904	0.009723904
methylcrotonoyl_CoA_carboxylase_complex	-0.149737449	0.149737449
endodeoxyribonuclease_complex	-0.252755258	0.252755258
endonuclease_complex	0.075161969	0.075161969
exoribonuclease_complex	-0.191902837	0.191902837
GTPase_complex	-0.032819219	0.032819219
peptidase_complex	0.092736204	0.092736204
beta_N_acetylhexosaminidase_complex	-0.003571585	0.003571585
oxidoreductase_complex	0.521711025	0.521711025
transferase_complex	-0.305298923	0.305298923

Greatest Magnitude of Correlation: 0.645143620127092

(Index: 10 )

Best Proxy: exodeoxyribonuclease\_V\_complex



PC:4

	correl_w_ratios	mag_correl
catalytic_complex	-0.264381644	0.264381644
phosphopyruvate_hydratase_complex	0.256488145	0.256488145
histone_deacetylase_complex	0.040886383	0.040886383
anthranilate_synthase_complex	-0.395650527	0.395650527
carbamoyl_phosphate_synthase_complex	-0.468746656	0.468746656
X3_isopropylmalate_dehydratase_complex	0.041109171	0.041109171
acetyl_CoA_carboxylase_complex	0.002497154	0.002497154
exodeoxyribonuclease_VII_complex	-0.121184710	0.121184710
phenylalanine_tRNA_ligase_complex	-0.277810520	0.277810520
exodeoxyribonuclease_V_complex	-0.116866118	0.116866118
beta_galactosidase_complex	0.269781896	0.269781896
ATP_independent_citrate_lyase_complex	0.021152600	0.021152600
ethanolamine_ammonia_lyase_complex	-0.158665418	0.158665418
glutamate_cysteine_ligase_complex	0.105999378	0.105999378
dynein_complex	-0.211222189	0.211222189
Elg1_RFC_like_complex	0.133581225	0.133581225
box_H_ACA_snoRNP_complex	0.209055097	0.209055097
SUMO_activating_enzyme_complex	0.201819144	0.201819144
DNA_helicase_complex	-0.205634053	0.205634053
urease_complex	-0.132204196	0.132204196
glutathione_synthase_complex	0.169220840	0.169220840
succinate_CoA_ligase_complex	-0.478895040	0.478895040
isoamylase_complex	-0.145881069	0.145881069
X_Ni_Fe_hydrogenase_complex	0.059951896	0.059951896
tRNA_specific_adenosine_34_deaminase_complex	0.147477477	0.147477477
catalytic_step_1_spliceosome	0.226676689	0.226676689
catalytic_step_2_spliceosome	-0.263808739	0.263808739
phosphopantothienoylcysteine_decarboxylase_complex	-0.261540172	0.261540172
viral_terminase_large_subunit	-0.388829806	0.388829806
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.172073827	0.172073827
ubiquitin_activating_enzyme_complex	0.134461333	0.134461333
endoribonuclease_complex	-0.348863512	0.348863512
phosphatase_complex	-0.063996873	0.063996873
glutaminase_complex	-0.076547524	0.076547524
ATPase_complex	-0.132349124	0.132349124
methylcrotonoyl_CoA_carboxylase_complex	-0.437980137	0.437980137
endodeoxyribonuclease_complex	0.444603542	0.444603542
endonuclease_complex	0.173973988	0.173973988
exoribonuclease_complex	-0.487439619	0.487439619
GTPase_complex	-0.011960477	0.011960477
peptidase_complex	-0.108968725	0.108968725
beta_N_acetylhexosaminidase_complex	-0.130099024	0.130099024
oxidoreductase_complex	0.058562199	0.058562199
transferase_complex	0.521797748	0.521797748

Greatest Magnitude of Correlation: 0.521797747857637

(Index: 44 )

Best Proxy: transferase\_complex

PC:5

	correl_w_ratios	mag_correl
catalytic_complex	0.0046703170	0.0046703170
phosphopyruvate_hydratase_complex	0.1587361107	0.1587361107
histone_deacetylase_complex	-0.0694057778	0.0694057778
anthranilate_synthase_complex	0.0101165994	0.0101165994
carbamoyl_phosphate_synthase_complex	-0.0743145497	0.0743145497
X3_isopropylmalate_dehydratase_complex	-0.4790863111	0.4790863111
acetyl_CoA_carboxylase_complex	0.2441804166	0.2441804166
exodeoxyribonuclease_VII_complex	-0.1440757957	0.1440757957
phenylalanine_tRNA_ligase_complex	-0.1593963353	0.1593963353
exodeoxyribonuclease_V_complex	-0.1615920778	0.1615920778
beta_galactosidase_complex	-0.2926932820	0.2926932820
ATP_independent_citrate_lyase_complex	-0.0766502898	0.0766502898
ethanolamine_ammonia_lyase_complex	0.2540393466	0.2540393466
glutamate_cysteine_ligase_complex	-0.0894432016	0.0894432016
dynein_complex	-0.1308713472	0.1308713472
Elg1_RFC_like_complex	-0.1841649999	0.1841649999
box_H_ACA_snoRNP_complex	0.0603190081	0.0603190081
SUMO_activating_enzyme_complex	-0.0885036840	0.0885036840
DNA_helicase_complex	0.0159019674	0.0159019674
urease_complex	0.5624089780	0.5624089780
glutathione_synthase_complex	0.1614484909	0.1614484909
succinate_CoA_ligase_complex	-0.0006405421	0.0006405421
isoamylase_complex	0.1243608368	0.1243608368
X_Ni_Fe_hydrogenase_complex	0.0670900652	0.0670900652
tRNA_specific_adenosine_34_deaminase_complex	0.1143113062	0.1143113062
catalytic_step_1_spliceosome	-0.1086906453	0.1086906453
catalytic_step_2_spliceosome	-0.0421605873	0.0421605873
phosphopantothienoylcysteine_decarboxylase_complex	-0.0448257562	0.0448257562
viral_terminase_large_subunit	0.0695104702	0.0695104702
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.1470424441	0.1470424441
ubiquitin_activating_enzyme_complex	0.1175497443	0.1175497443
endoribonuclease_complex	-0.0690331980	0.0690331980
phosphatase_complex	0.0026579087	0.0026579087
glutaminase_complex	0.1762215848	0.1762215848
ATPase_complex	-0.0868098706	0.0868098706
methylcrotonoyl_CoA_carboxylase_complex	0.0160185054	0.0160185054
endodeoxyribonuclease_complex	-0.3430106362	0.3430106362
endonuclease_complex	0.1809835987	0.1809835987
exoribonuclease_complex	-0.1035964018	0.1035964018
GTPase_complex	0.0541656783	0.0541656783
peptidase_complex	0.2888765753	0.2888765753
beta_N_acetylhexosaminidase_complex	-0.0809868937	0.0809868937
oxidoreductase_complex	-0.1999927611	0.1999927611
transferase_complex	-0.2004202216	0.2004202216

Greatest Magnitude of Correlation: 0.562408978047498

(Index: 20 )

Best Proxy: urease\_complex

PC:6

	correl_w_ratios	mag_correl
catalytic_complex	-0.22561782	0.22561782
phosphopyruvate_hydratase_complex	-0.08038182	0.08038182
histone_deacetylase_complex	0.03261356	0.03261356
anthranilate_synthase_complex	-0.10213592	0.10213592
carbamoyl_phosphate_synthase_complex	-0.29529447	0.29529447
X3_isopropylmalate_dehydratase_complex	-0.47194963	0.47194963
acetyl_CoA_carboxylase_complex	-0.37455770	0.37455770
exodeoxyribonuclease_VII_complex	-0.21075259	0.21075259
phenylalanine_tRNA_ligase_complex	0.27941803	0.27941803
exodeoxyribonuclease_V_complex	-0.11830424	0.11830424
beta_galactosidase_complex	-0.15653274	0.15653274
ATP_independent_citrate_lyase_complex	0.13234105	0.13234105
ethanolamine_ammonia_lyase_complex	0.30430253	0.30430253
glutamate_cysteine_ligase_complex	0.09662870	0.09662870
dynein_complex	-0.01638514	0.01638514
Elg1_RFC_like_complex	0.15069405	0.15069405
box_H_ACA_snoRNP_complex	-0.07532123	0.07532123
SUMO_activating_enzyme_complex	0.07080068	0.07080068
DNA_helicase_complex	-0.17765318	0.17765318
urease_complex	0.19614863	0.19614863
glutathione_synthase_complex	-0.06467130	0.06467130
succinate_CoA_ligase_complex	-0.04778849	0.04778849
isoamylase_complex	-0.21191720	0.21191720
X_Ni_Fe_hydrogenase_complex	-0.05640645	0.05640645
tRNA_specific_adenosine_34_deaminase_complex	-0.08983525	0.08983525
catalytic_step_1_spliceosome	0.08407750	0.08407750
catalytic_step_2_spliceosome	-0.08049519	0.08049519
phosphopantothienoylcysteine_decarboxylase_complex	-0.11982066	0.11982066
viral_terminase_large_subunit	-0.04164918	0.04164918
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	-0.07450353	0.07450353
ubiquitin_activating_enzyme_complex	-0.14834060	0.14834060
endoribonuclease_complex	0.15901447	0.15901447
phosphatase_complex	0.04683179	0.04683179
glutaminase_complex	-0.11293020	0.11293020
ATPase_complex	-0.07811403	0.07811403
methylcrotonoyl_CoA_carboxylase_complex	-0.29436547	0.29436547
endodeoxyribonuclease_complex	-0.11148819	0.11148819
endonuclease_complex	-0.13916220	0.13916220
exoribonuclease_complex	-0.10624886	0.10624886
GTPase_complex	0.05862717	0.05862717
peptidase_complex	0.12246263	0.12246263
beta_N_acetylhexosaminidase_complex	-0.05506888	0.05506888
oxidoreductase_complex	-0.09698671	0.09698671
transferase_complex	-0.09256731	0.09256731

Greatest Magnitude of Correlation: 0.471949632289619

(Index: 6 )

Best Proxy: X3\_isopropylmalate\_dehydratase\_complex

PC:7

	correl_w_ratios	mag_correl
catalytic_complex	-0.383218982	0.383218982
phosphopyruvate_hydratase_complex	-0.306754779	0.306754779
histone_deacetylase_complex	-0.181443306	0.181443306
anthranilate_synthase_complex	-0.096314567	0.096314567
carbamoyl_phosphate_synthase_complex	0.046123368	0.046123368
X3_isopropylmalate_dehydratase_complex	-0.001789849	0.001789849
acetyl_CoA_carboxylase_complex	-0.071288963	0.071288963
exodeoxyribonuclease_VII_complex	0.229137598	0.229137598
phenylalanine_tRNA_ligase_complex	0.119848839	0.119848839
exodeoxyribonuclease_V_complex	0.007486512	0.007486512
beta_galactosidase_complex	-0.202091507	0.202091507
ATP_independent_citrate_lyase_complex	0.178080031	0.178080031
ethanolamine_ammonia_lyase_complex	-0.035294044	0.035294044
glutamate_cysteine_ligase_complex	0.079238654	0.079238654
dynein_complex	-0.139242200	0.139242200
Elg1_RFC_like_complex	-0.089380603	0.089380603
box_H_ACA_snoRNP_complex	0.080909731	0.080909731
SUMO_activating_enzyme_complex	-0.012429824	0.012429824
DNA_helicase_complex	0.197349742	0.197349742
urease_complex	-0.290153054	0.290153054
glutathione_synthase_complex	0.112391628	0.112391628
succinate_CoA_ligase_complex	-0.130969617	0.130969617
isoamylase_complex	-0.332261614	0.332261614
X_Ni_Fe_hydrogenase_complex	0.067090065	0.067090065
tRNA_specific_adenosine_34_deaminase_complex	0.073914929	0.073914929
catalytic_step_1_spliceosome	-0.039520945	0.039520945
catalytic_step_2_spliceosome	-0.121786539	0.121786539
phosphopantothenoylcysteine_decarboxylase_complex	0.031131269	0.031131269
viral_terminase_large_subunit	0.304082861	0.304082861
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.100060703	0.100060703
ubiquitin_activating_enzyme_complex	0.089290095	0.089290095
endoribonuclease_complex	0.019232562	0.019232562
phosphatase_complex	-0.189646361	0.189646361
glutaminase_complex	-0.048319249	0.048319249
ATPase_complex	-0.299841307	0.299841307
methylcrotonoyl_CoA_carboxylase_complex	0.294113708	0.294113708
endodeoxyribonuclease_complex	-0.109340381	0.109340381
endonuclease_complex	0.038842136	0.038842136
exoribonuclease_complex	0.236917447	0.236917447
GTPase_complex	-0.103384554	0.103384554
peptidase_complex	0.003711330	0.003711330
beta_N_acetylhexosaminidase_complex	-0.046242842	0.046242842
oxidoreductase_complex	0.032948645	0.032948645
transferase_complex	-0.143380252	0.143380252

Greatest Magnitude of Correlation: 0.383218982266698

(Index: 1 )

Best Proxy: catalytic\_complex

PC:8

	correl_w_ratios	mag_correl
catalytic_complex	0.100314350	0.100314350
phosphopyruvate_hydratase_complex	0.002911895	0.002911895
histone_deacetylase_complex	0.213621988	0.213621988
anthranilate_synthase_complex	0.070392443	0.070392443
carbamoyl_phosphate_synthase_complex	-0.001392411	0.001392411
X3_isopropylmalate_dehydratase_complex	-0.078314255	0.078314255
acetyl_CoA_carboxylase_complex	0.279319050	0.279319050
exodeoxyribonuclease_VII_complex	0.097025910	0.097025910
phenylalanine_tRNA_ligase_complex	-0.387370481	0.387370481
exodeoxyribonuclease_V_complex	0.058268929	0.058268929
beta_galactosidase_complex	-0.211788939	0.211788939
ATP_independent_citrate_lyase_complex	0.048140143	0.048140143
ethanolamine_ammonia_lyase_complex	-0.057471470	0.057471470
glutamate_cysteine_ligase_complex	0.023653434	0.023653434
dynein_complex	0.133163327	0.133163327
Elg1_RFC_like_complex	0.103321272	0.103321272
box_H_ACA_snoRNP_complex	0.089059014	0.089059014
SUMO_activating_enzyme_complex	0.025338879	0.025338879
DNA_helicase_complex	0.132040144	0.132040144
urease_complex	0.022933436	0.022933436
glutathione_synthase_complex	-0.013343164	0.013343164
succinate_CoA_ligase_complex	-0.031396715	0.031396715
isoamylase_complex	-0.146584853	0.146584853
X_Ni_Fe_hydrogenase_complex	-0.067140699	0.067140699
tRNA_specific_adenosine_34_deaminase_complex	0.116111395	0.116111395
catalytic_step_1_spliceosome	0.152108811	0.152108811
catalytic_step_2_spliceosome	0.078747988	0.078747988
phosphopantothienoylcysteine_decarboxylase_complex	-0.052308003	0.052308003
viral_terminase_large_subunit	0.206248628	0.206248628
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.121799233	0.121799233
ubiquitin_activating_enzyme_complex	-0.140668443	0.140668443
endoribonuclease_complex	-0.294643926	0.294643926
phosphatase_complex	-0.007639391	0.007639391
glutaminase_complex	-0.258470514	0.258470514
ATPase_complex	0.074753980	0.074753980
methylcrotonoyl_CoA_carboxylase_complex	0.361992622	0.361992622
endodeoxyribonuclease_complex	-0.300657013	0.300657013
endonuclease_complex	0.049807532	0.049807532
exoribonuclease_complex	-0.071735233	0.071735233
GTPase_complex	-0.137718992	0.137718992
peptidase_complex	0.165871924	0.165871924
beta_N_acetylhexosaminidase_complex	-0.247523234	0.247523234
oxidoreductase_complex	0.009086520	0.009086520
transferase_complex	-0.206834628	0.206834628

Greatest Magnitude of Correlation: 0.38737048064994  
(Index: 9 )  
Best Proxy: phenylalanine\_tRNA\_ligase\_complex

PC:9

	correl_w_ratios	mag_correl
catalytic_complex	-0.247879930	0.247879930
phosphopyruvate_hydratase_complex	-0.005370537	0.005370537
histone_deacetylase_complex	0.034329091	0.034329091
anthranilate_synthase_complex	0.001355512	0.001355512
carbamoyl_phosphate_synthase_complex	0.155422190	0.155422190
X3_isopropylmalate_dehydratase_complex	0.216993451	0.216993451
acetyl_CoA_carboxylase_complex	-0.260569365	0.260569365
exodeoxyribonuclease_VII_complex	0.004816332	0.004816332
phenylalanine_tRNA_ligase_complex	0.335445035	0.335445035
exodeoxyribonuclease_V_complex	-0.014889543	0.014889543
beta_galactosidase_complex	0.149618324	0.149618324
ATP_independent_citrate_lyase_complex	-0.126609671	0.126609671
ethanolamine_ammonia_lyase_complex	0.099345809	0.099345809
glutamate_cysteine_ligase_complex	-0.124910181	0.124910181
dynein_complex	-0.124460519	0.124460519
Elg1_RFC_like_complex	-0.062650452	0.062650452
box_H_ACA_snoRNP_complex	0.095418829	0.095418829
SUMO_activating_enzyme_complex	-0.195780662	0.195780662
DNA_helicase_complex	-0.048412432	0.048412432
urease_complex	0.186576752	0.186576752
glutathione_synthase_complex	0.118947301	0.118947301
succinate_CoA_ligase_complex	0.070512814	0.070512814
isoamylase_complex	0.007393181	0.007393181
X_Ni_Fe_hydrogenase_complex	-0.066482915	0.066482915
tRNA_specific_adenosine_34_deaminase_complex	0.082458776	0.082458776
catalytic_step_1_spliceosome	-0.123554621	0.123554621
catalytic_step_2_spliceosome	0.070525987	0.070525987
phosphopantothienoylcysteine_decarboxylase_complex	0.120381880	0.120381880
viral_terminase_large_subunit	-0.119798442	0.119798442
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	0.159946524	0.159946524
ubiquitin_activating_enzyme_complex	-0.144194822	0.144194822
endoribonuclease_complex	0.330239263	0.330239263
phosphatase_complex	0.040820234	0.040820234
glutaminase_complex	-0.190352143	0.190352143
ATPase_complex	0.123189082	0.123189082
methylcrotonoyl_CoA_carboxylase_complex	-0.091315171	0.091315171
endodeoxyribonuclease_complex	0.289667252	0.289667252
endonuclease_complex	0.009378698	0.009378698
exoribonuclease_complex	0.268370254	0.268370254
GTPase_complex	0.233899964	0.233899964
peptidase_complex	-0.057623756	0.057623756
beta_N_acetylhexosaminidase_complex	-0.151662188	0.151662188
oxidoreductase_complex	0.006001132	0.006001132
transferase_complex	0.150251356	0.150251356

Greatest Magnitude of Correlation: 0.335445034780866

(Index: 9 )

Best Proxy: phenylalanine\_tRNA\_ligase\_complex

PC:10

	correl_w_ratios	mag_correl
catalytic_complex	0.055530738	0.055530738
phosphopyruvate_hydratase_complex	0.007405692	0.007405692
histone_deacetylase_complex	0.344240585	0.344240585
anthranilate_synthase_complex	0.092308679	0.092308679
carbamoyl_phosphate_synthase_complex	0.223088520	0.223088520
X3_isopropylmalate_dehydratase_complex	0.054921128	0.054921128
acetyl_CoA_carboxylase_complex	0.134710968	0.134710968
exodeoxyribonuclease_VII_complex	-0.031351240	0.031351240
phenylalanine_tRNA_ligase_complex	-0.075026729	0.075026729
exodeoxyribonuclease_V_complex	-0.098863510	0.098863510
beta_galactosidase_complex	0.008590725	0.008590725
ATP_independent_citrate_lyase_complex	-0.143135803	0.143135803
ethanolamine_ammonia_lyase_complex	0.199523752	0.199523752
glutamate_cysteine_ligase_complex	0.011919543	0.011919543
dynein_complex	0.242350549	0.242350549
Elg1_RFC_like_complex	0.112443016	0.112443016
box_H_ACA_snoRNP_complex	-0.175822629	0.175822629
SUMO_activating_enzyme_complex	0.108258220	0.108258220
DNA_helicase_complex	0.079174718	0.079174718
urease_complex	-0.106704561	0.106704561
glutathione_synthase_complex	-0.001241681	0.001241681
succinate_CoA_ligase_complex	0.196758125	0.196758125
isoamylase_complex	-0.042437843	0.042437843
X_Ni_Fe_hydrogenase_complex	0.067140699	0.067140699
tRNA_specific_adenosine_34_deaminase_complex	-0.107599239	0.107599239
catalytic_step_1_spliceosome	0.114926917	0.114926917
catalytic_step_2_spliceosome	0.230412701	0.230412701
phosphopantothienoylcysteine_decarboxylase_complex	0.147231191	0.147231191
viral_terminase_large_subunit	0.018516760	0.018516760
mannosyl_oligosaccharide_1_2_alpha_mannosidase_complex	-0.133688143	0.133688143
ubiquitin_activating_enzyme_complex	0.062334765	0.062334765
endoribonuclease_complex	-0.007180733	0.007180733
phosphatase_complex	0.281027782	0.281027782
glutaminase_complex	-0.267757932	0.267757932
ATPase_complex	0.424403870	0.424403870
methylcrotonoyl_CoA_carboxylase_complex	0.314032118	0.314032118
endodeoxyribonuclease_complex	-0.066826859	0.066826859
endonuclease_complex	-0.074291037	0.074291037
exoribonuclease_complex	0.086457907	0.086457907
GTPase_complex	0.287169011	0.287169011
peptidase_complex	0.051439928	0.051439928
beta_N_acetylhexosaminidase_complex	-0.253094218	0.253094218
oxidoreductase_complex	-0.053252740	0.053252740
transferase_complex	-0.052034358	0.052034358

Greatest Magnitude of Correlation: 0.42440386975562  
(Index: 35 )  
Best Proxy: ATPase\_complex

# Selected Proxies for each PC

	Prop	Cuml	ClosestProxy	Correl
PC01	0.16059	0.16059	beta_galactosidase_complex	0.6674
PC02	0.08913	0.24972	phosphopantothencysteine_decarboxylase_complex	0.7046
PC03	0.06701	0.31673	exodeoxyribonuclease_V_complex	0.6451
PC04	0.06387	0.38060	transferase_complex	0.5218
PC05	0.03503	0.41563	urease_complex	0.5624
PC06	0.02996	0.44559	X3_isopropylmalate_dehydratase_complex	-0.4719
PC07	0.02842	0.47401	catalytic_complex	-0.3832
PC08	0.02654	0.50055	phenylalanine_tRNA_ligase_complex	-0.3874
PC09	0.02624	0.52679	phenylalanine_tRNA_ligase_complex	0.3354
PC10	0.02559	0.55238	ATPase_complex	0.4244

## Non-Redundant Selected Variables:

1. beta\_galactosidase\_complex
2. phosphopantothencysteine\_decarboxylase\_complex
3. exodeoxyribonuclease\_V\_complex
4. transferase\_complex
5. urease\_complex
6. X3\_isopropylmalate\_dehydratase\_complex
7. catalytic\_complex
8. phenylalanine\_tRNA\_ligase\_complex
9. ATPase\_complex

Num Available Variables: 44

9 of 44 kept.

0.20455 proportion retained.

Original Non-Remaining Abundance (Mean): 0.021202

Selected Non-Remaining Abundance (Mean): 0.0017039

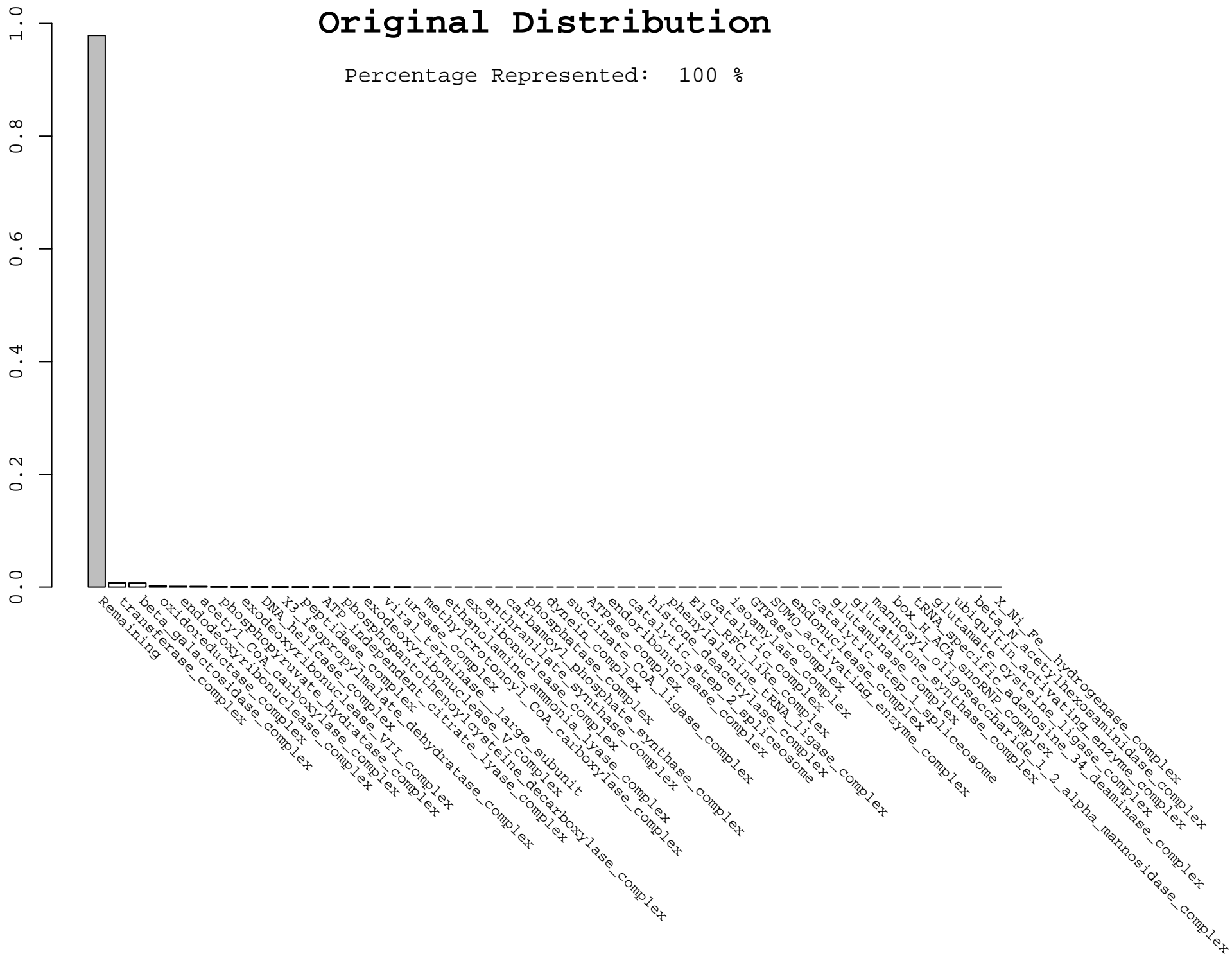
Excluded Abundance (Mean): 0.019498

Proportion Retained: 0.080368



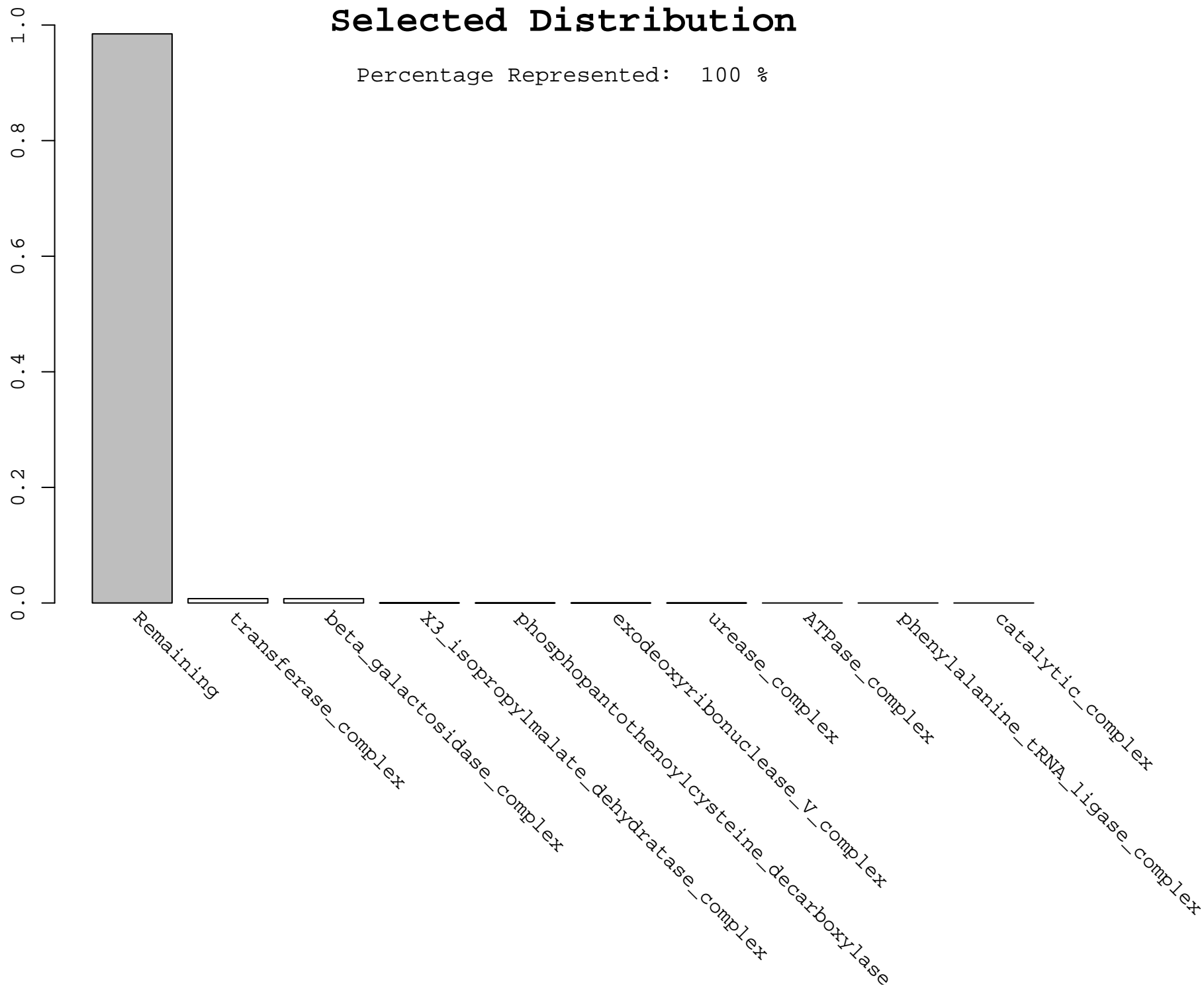
# Original Distribution

Percentage Represented: 100 %

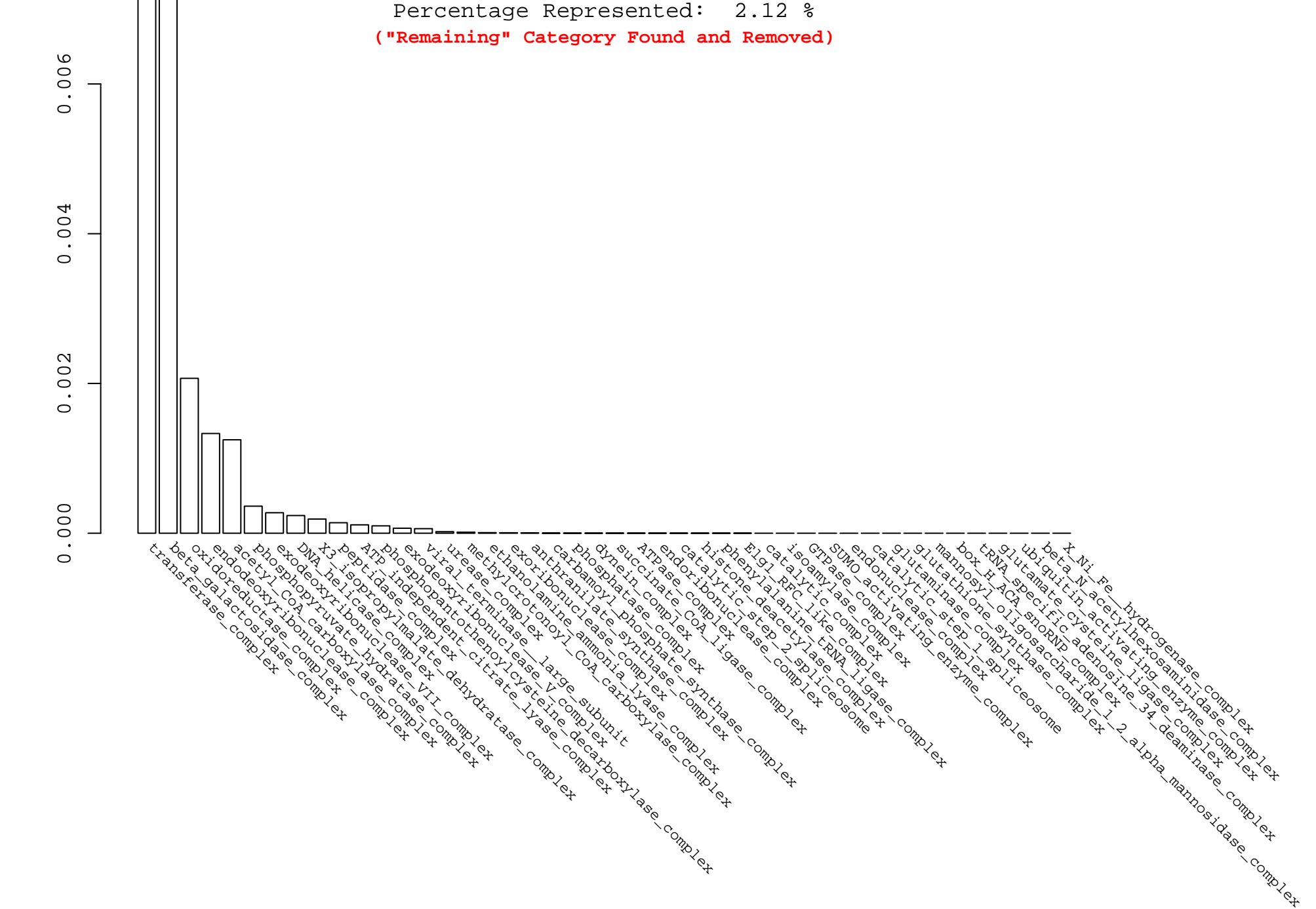


# Selected Distribution

Percentage Represented: 100 %



Percentage Represented: 2.12 %  
 ("Remaining" Category Found and Removed)



## Selected Distribution

Percentage Represented: 1.53 %

("Remaining" Category Found and Removed)

