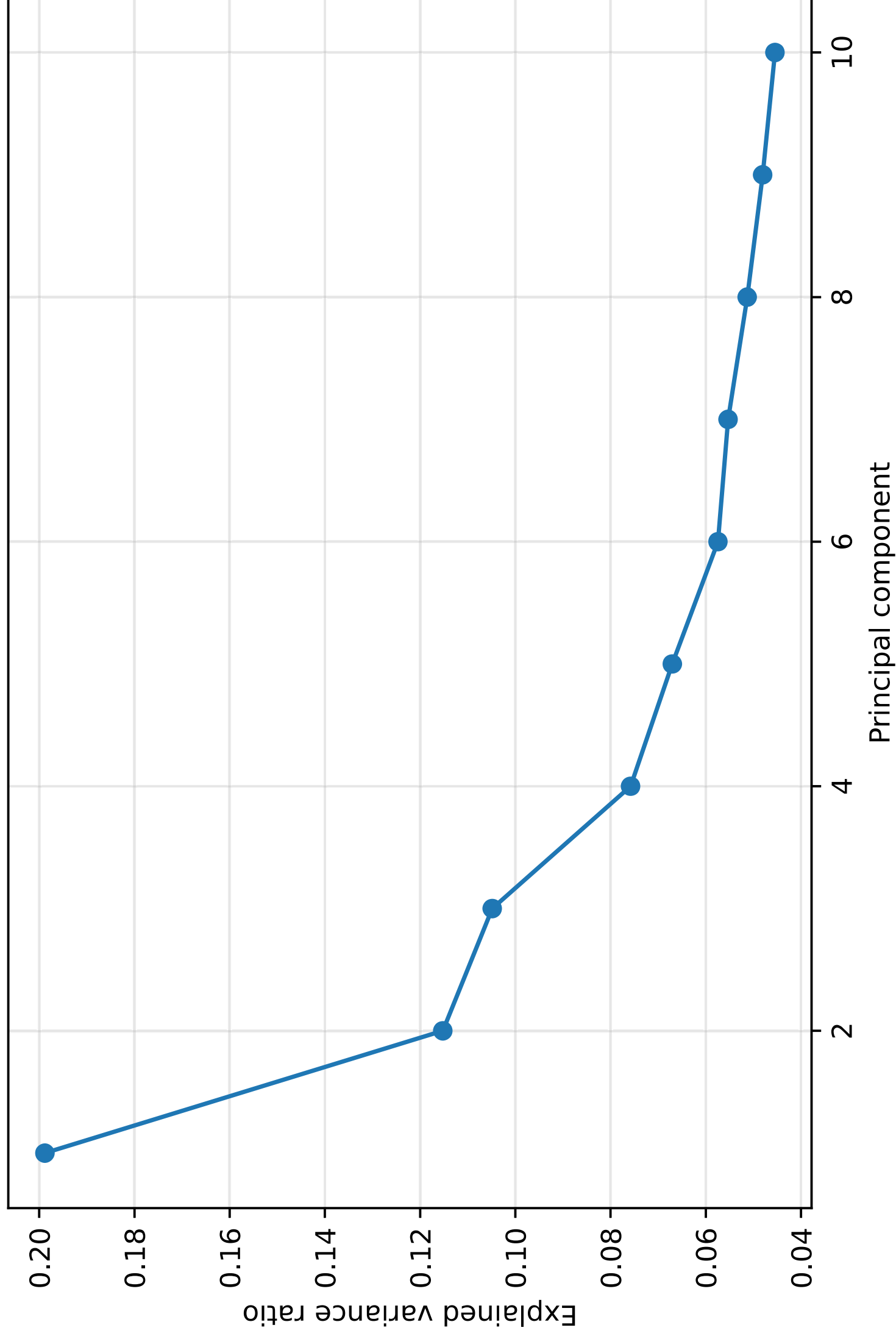
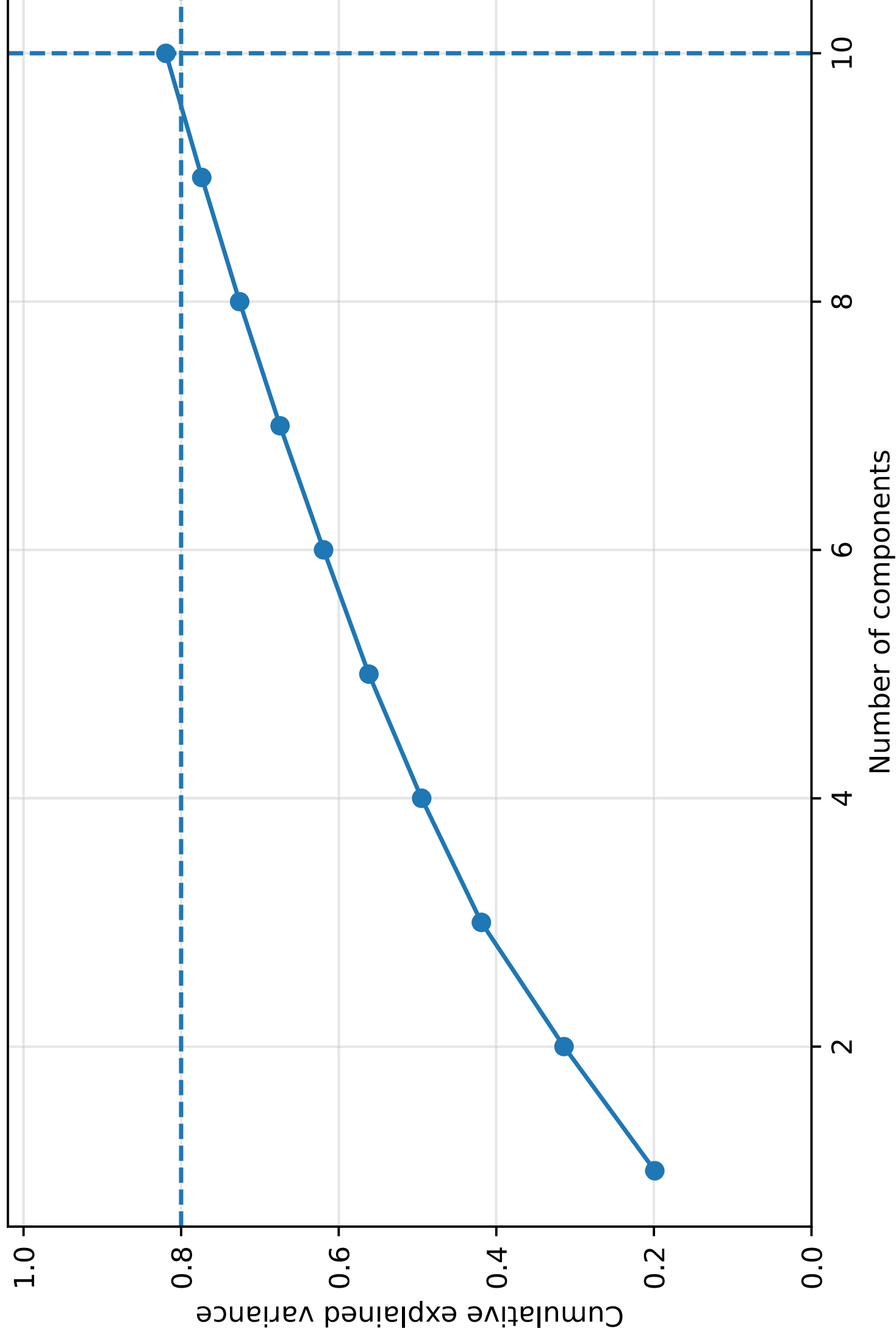


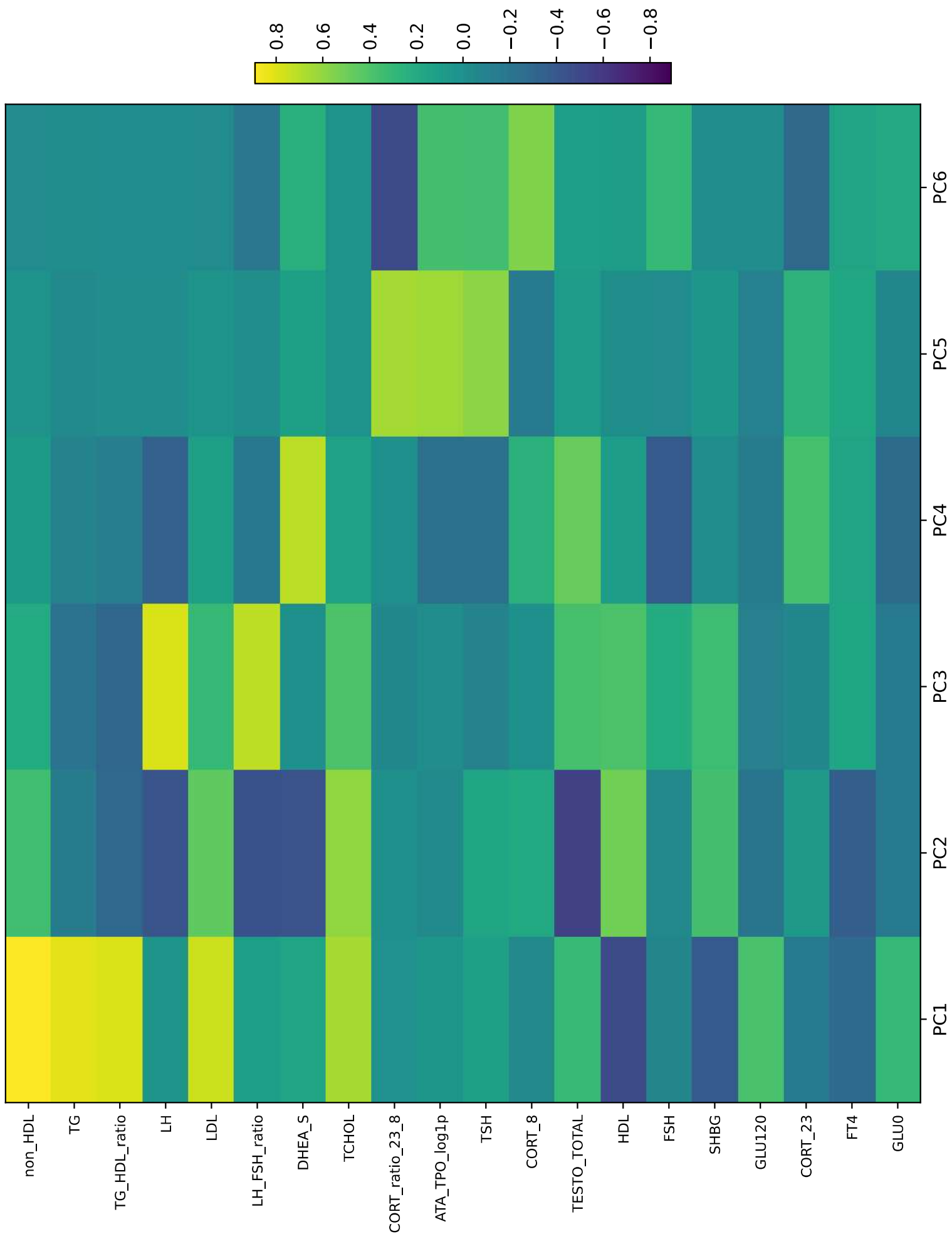
Scree plot: explained variance ratio



Cumulative explained variance (k=10, cumvar=0.819)



Loadings heatmap (top 30 features, first PCs)



PC1 – top feature loadings

Positive loadings:

- + non_HDL: 0.890
- + TG: 0.818
- + TG_HDL_ratio: 0.796
- + LDL: 0.757
- + TCHOL: 0.660
- + GLU120: 0.380
- + TESTO_TOTAL: 0.307
- + GLU0: 0.301
- + DHEA_S: 0.149
- + TSH: 0.127

Negative loadings:

- LH_FSH_ratio: 0.111
- ATA_TPO_loglp: 0.050
- LH: 0.032
- CORT_ratio_23_8: 0.011
- CORT_8: -0.055
- FSH: -0.079
- CORT_23: -0.161
- FT4: -0.271
- SHBG: -0.383
- HDL: -0.486

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC2 – top feature loadings

Positive loadings:

- + TCHOL: 0.600
- + HDL: 0.512
- + LDL: 0.456
- + SHBG: 0.368
- + non_HDL: 0.353
- + CORT_8: 0.193
- + TSH: 0.160
- + CORT_23: 0.074
- + CORT_ratio_23_8: 0.003
- + ATA_TPO_loglp: -0.041

Negative loadings:

- FSH: -0.051
- TG: -0.144
- GLU0: -0.162
- GLU120: -0.201
- TG_HDL_ratio: -0.278
- FT4: -0.348
- LH: -0.420
- DHEA_S: -0.432
- LH_FSH_ratio: -0.442
- TESTO_TOTAL: -0.547

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC3 – top feature loadings

Positive loadings:

- + LH: 0.793
- + LH_FSH_ratio: 0.717
- + HDL: 0.396
- + TCHOL: 0.394
- + TESTO_TOTAL: 0.371
- + SHBG: 0.337
- + LDL: 0.306
- + FSH: 0.211
- + non_HDL: 0.203
- + FT4: 0.160

Negative loadings:

- CORT_8: 0.003
- DHEA_S: 0.002
- ATA_TPO_log1p: -0.013
- CORT_23: -0.059
- CORT_ratio_23_8: -0.060
- TSH: -0.091
- GLU120: -0.112
- GLU0: -0.160
- TG: -0.213
- TG_HDL_ratio: -0.301

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC4 – top feature loadings

Positive loadings:

- + DHEA_S: 0.710
- + TESTO_TOTAL: 0.478
- + CORT_23: 0.372
- + CORT_8: 0.252
- + FT4: 0.148
- + TCHOL: 0.135
- + LDL: 0.125
- + HDL: 0.111
- + non_HDL: 0.081
- + CORT_ratio_23_8: 0.006

Negative loadings:

- SHBG: -0.015
- TG: -0.091
- TG_HDL_ratio: -0.126
- GLU120: -0.144
- LH_FSH_ratio: -0.169
- TSH: -0.223
- ATA_TPO_log1p: -0.240
- GLU0: -0.258
- LH: -0.331
- FSH: -0.389

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC5 – top feature loadings

Positive loadings:

- + CORT_ratio_23_8: 0.653
- + ATA_TPO_log1p: 0.639
- + TSH: 0.578
- + CORT_23: 0.264
- + FT4: 0.175
- + DHEA_S: 0.122
- + TESTO_TOTAL: 0.090
- + SHBG: 0.062
- + LDL: 0.033
- + non_HDL: 0.017

Negative loadings:

- TCHOL: 0.016
- HDL: -0.002
- LH_FSH_ratio: -0.004
- LH: -0.017
- TG_HDL_ratio: -0.020
- FSH: -0.034
- TG: -0.039
- GLU0: -0.071
- GLU120: -0.102
- CORT_8: -0.161

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC6 – top feature loadings

Positive loadings:

- + CORT_8: 0.554
- + ATA_TPO_log1p: 0.362
- + TSH: 0.359
- + FSH: 0.303
- + DHEA_S: 0.237
- + GLU0: 0.187
- + FT4: 0.153
- + TESTO_TOTAL: 0.114
- + HDL: 0.105
- + TCHOL: 0.021

Negative loadings:

- TG: -0.005
- GLU120: -0.017
- SHBG: -0.018
- LH: -0.024
- TG_HDL_ratio: -0.025
- non_HDL: -0.030
- LDL: -0.032
- LH_FSH_ratio: -0.182
- CORT_23: -0.272
- CORT_ratio_23_8: -0.491

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC7 – top feature loadings

Positive loadings:

- + CORT_23: 0.645
- + CORT_8: 0.483
- + FSH: 0.417
- + GLU120: 0.252
- + CORT_ratio_23_8: 0.233
- + LH: 0.189
- + GLU0: 0.135
- + HDL: 0.022
- + TG: 0.020
- + LH_FSH_ratio: 0.015

Negative loadings:

- TG_HDL_ratio: 0.013
- TCHOL: -0.017
- non_HDL: -0.028
- DHEA_S: -0.039
- LDL: -0.039
- TSH: -0.052
- TESTO_TOTAL: -0.108
- ATA_TPO_log1p: -0.158
- SHBG: -0.183
- FT4: -0.186

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC8 – top feature loadings

Positive loadings:

- + FSH: 0.608
- + GLU0: 0.250
- + DHEA_S: 0.237
- + CORT_ratio_23_8: 0.185
- + FT4: 0.166
- + LDL: 0.164
- + non_HDL: 0.094
- + TCHOL: 0.059
- + TESTO_TOTAL: 0.053
- + SHBG: 0.043

Negative loadings:

- LH: -0.044
- GLU120: -0.045
- ATA_TPO_log1p: -0.065
- HDL: -0.074
- CORT_23: -0.127
- TG_HDL_ratio: -0.134
- TG: -0.166
- TSH: -0.270
- CORT_8: -0.367
- LH_FSH_ratio: -0.388

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC9 – top feature loadings

Positive loadings:

- + GLU0: 0.625
- + GLU120: 0.530
- + FT4: 0.171
- + HDL: 0.133
- + SHBG: 0.113
- + CORT_ratio_23_8: 0.059
- + LH_FSH_ratio: 0.056
- + LDL: 0.047
- + TCHOL: 0.046
- + TESTO_TOTAL: 0.043

Negative loadings:

- TSH: 0.041
- CORT_23: -0.009
- CORT_8: -0.015
- non_HDL: -0.017
- DHEA_S: -0.037
- ATA_TPO_log1p: -0.042
- LH: -0.089
- TG: -0.202
- TG_HDL_ratio: -0.208
- FSH: -0.348

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).

PC10 – top feature loadings

Positive loadings:

- + FT4: 0.652
- + SHBG: 0.254
- + CORT_23: 0.238
- + CORT_8: 0.171
- + TG_HDL_ratio: 0.164
- + GLU0: 0.126
- + TG: 0.121
- + non_HDL: 0.103
- + LDL: 0.079
- + ATA_TPO_log1p: 0.044

Negative loadings:

- LH_FSH_ratio: 0.002
- LH: -0.004
- TCHOL: -0.008
- FSH: -0.067
- CORT_ratio_23_8: -0.072
- TESTO_TOTAL: -0.178
- TSH: -0.205
- DHEA_S: -0.232
- HDL: -0.234
- GLU120: -0.257

Notes: PCA fitted on z-scored core features (complete-case cohort);
loadings = components * sqrt(eigenvalue).