

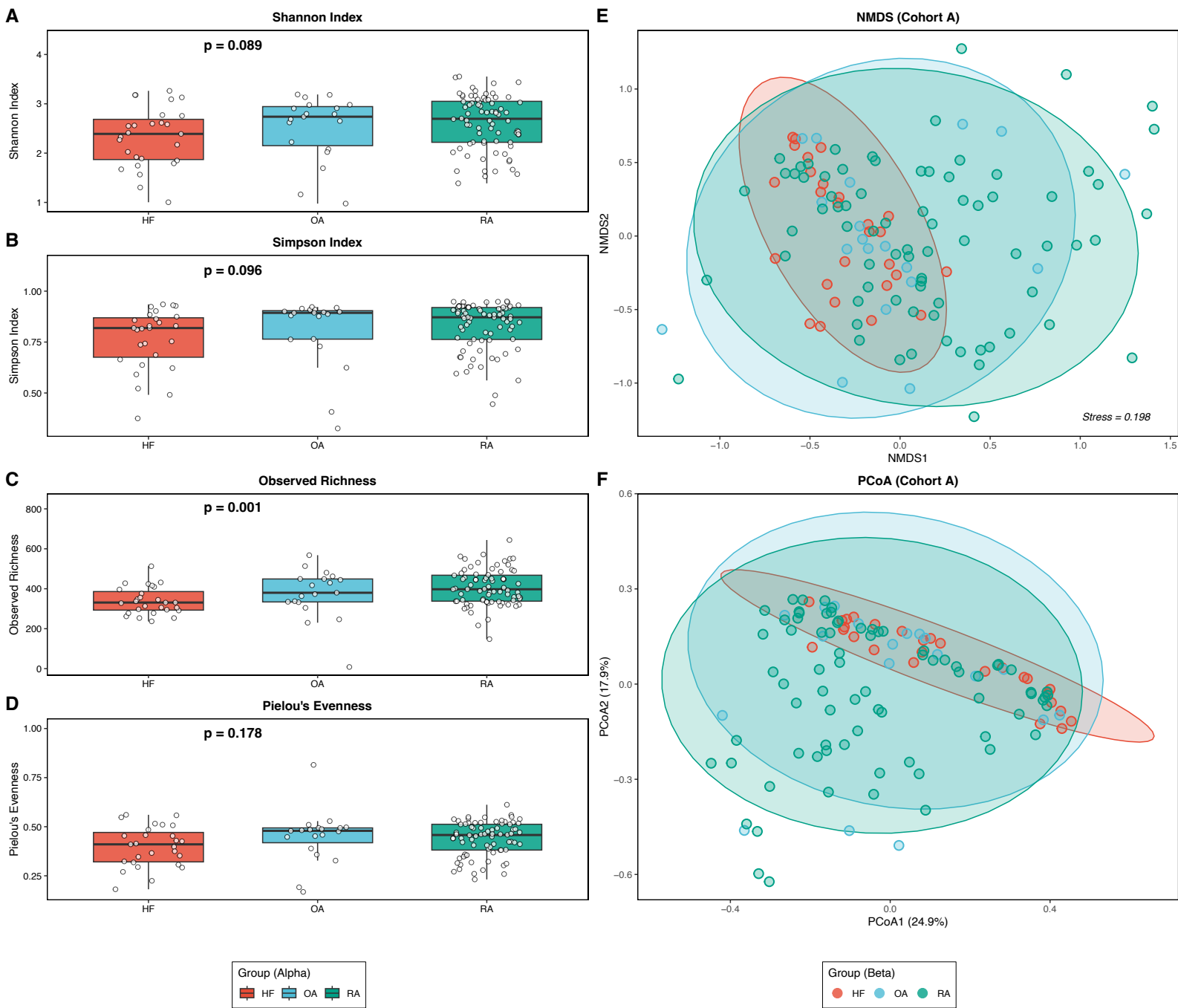


Figure S1

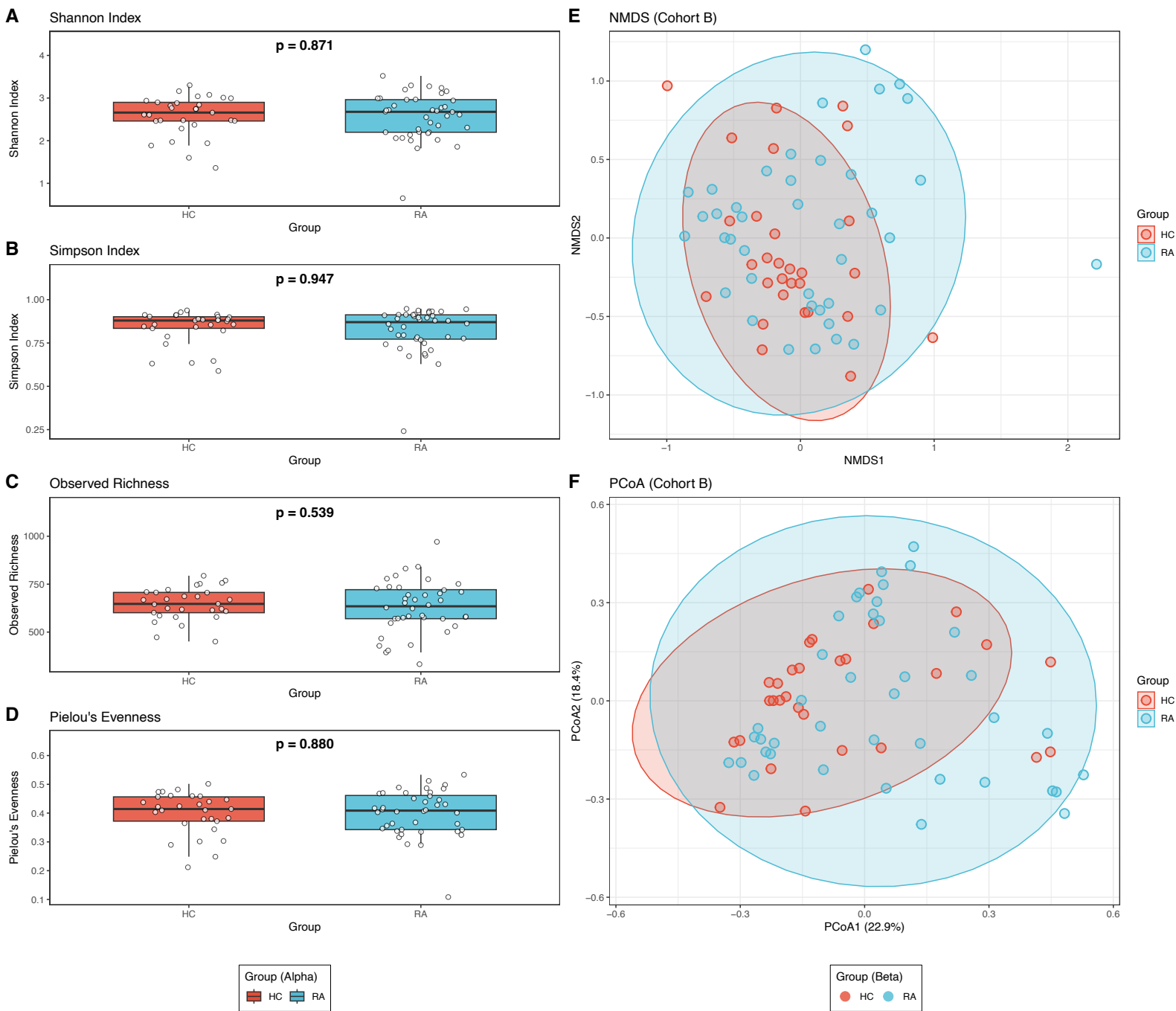


Figure S2

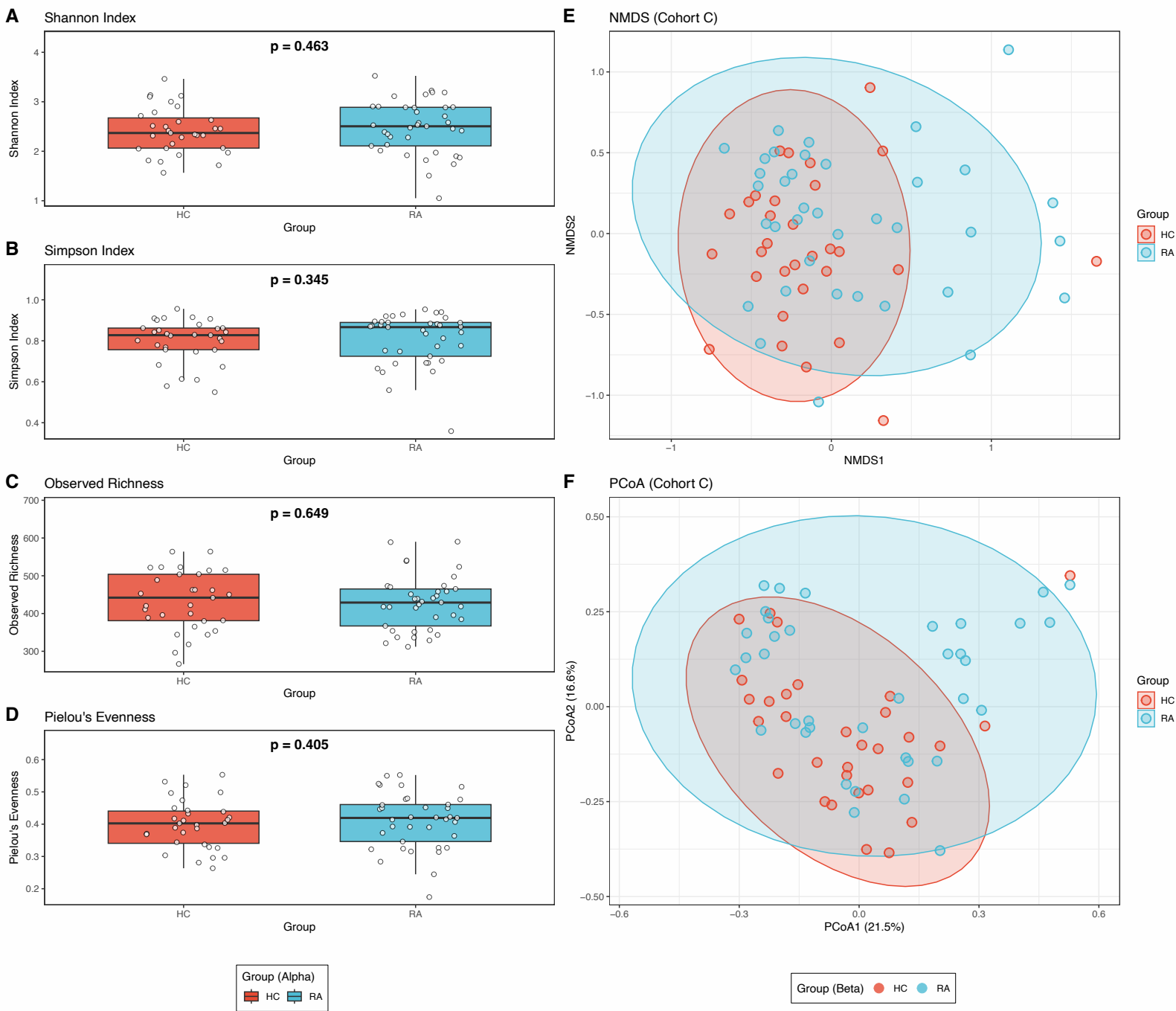


Figure S3

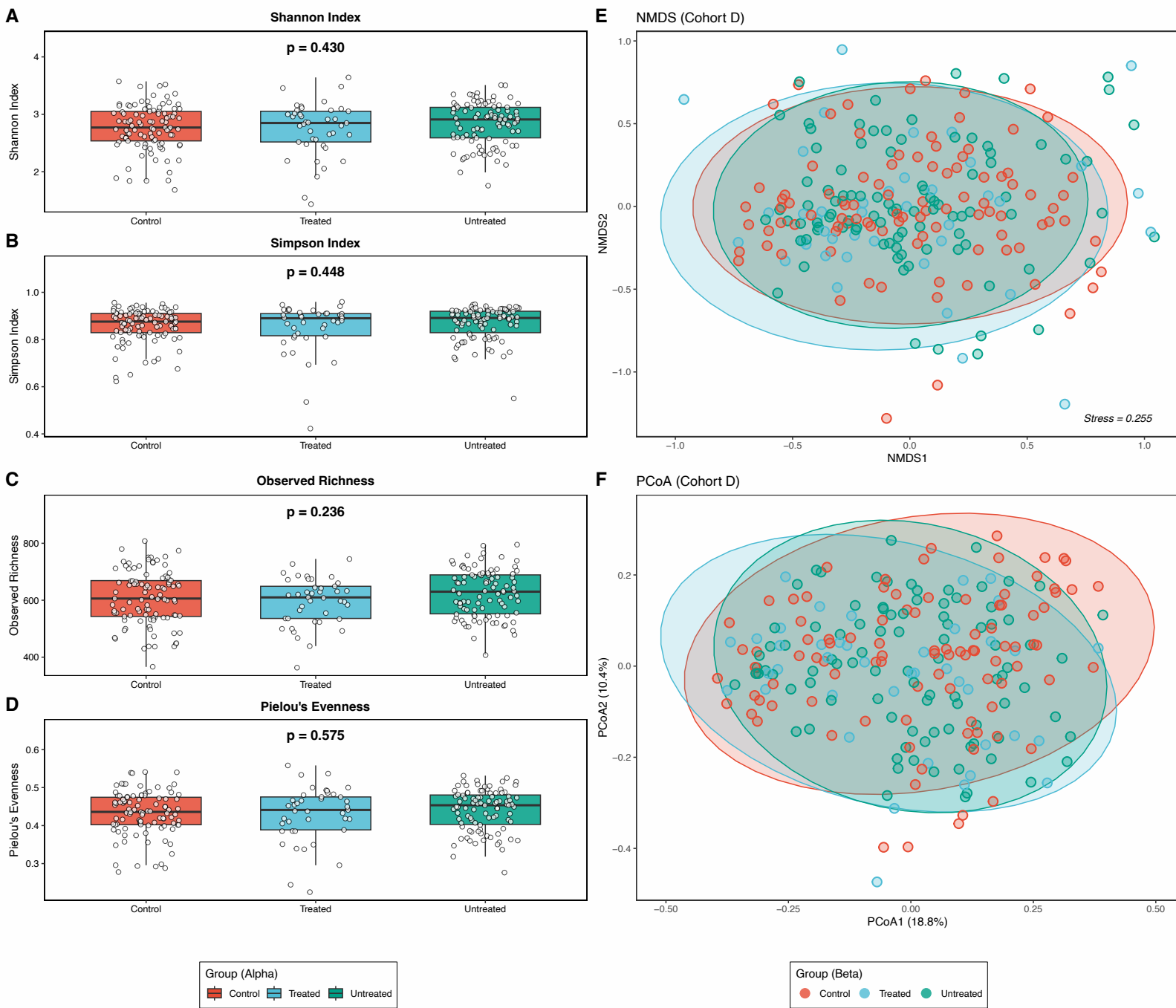


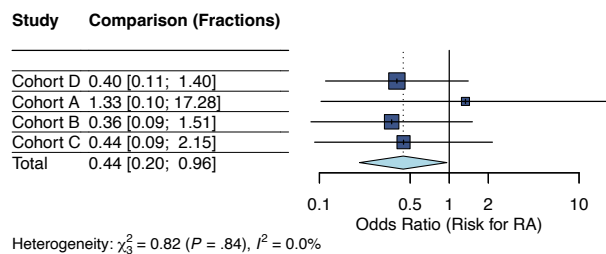
Figure S4

Cross-Cohort Validation of Quantile-Scaled SHAP Summaries (Union Set)

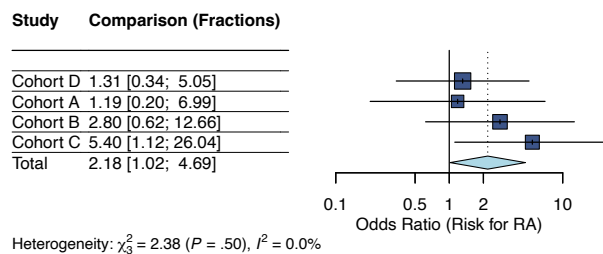


Figure S5

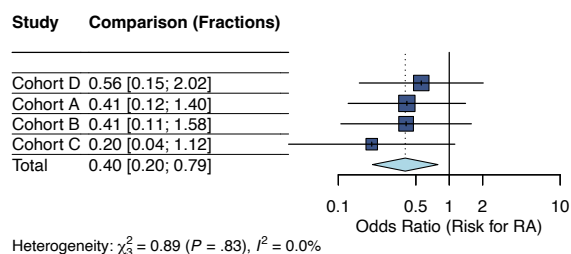
A. *Oscillibacter* sp.: 557_558;1131_1132



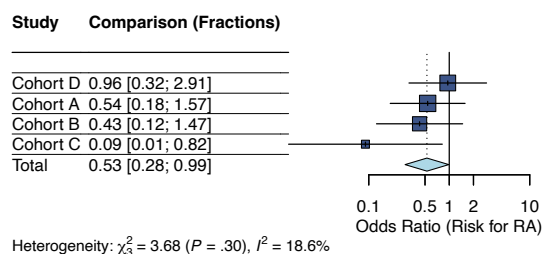
B. *Bacteroides xylanisolvens*: 5601_5602



C. *Agathobacter rectalis*: 662_663



D. *Faecalibacterium prausnitzii*:537_538



E. *Faecalibacterium prausnitzii*: 781_783

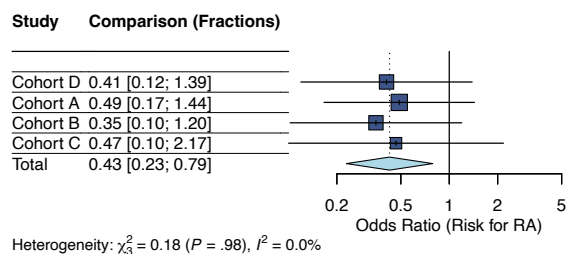
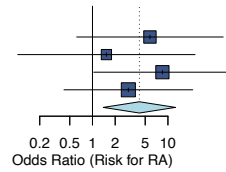


Figure S6

Study Comparison (OR Scale fractions)

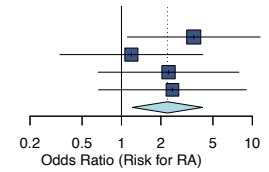
Cohort D	5.78 [0.62; 54.02]
Cohort A	1.53 [0.10; 22.89]
Cohort B	8.45 [1.04; 68.68]
Cohort C	2.99 [0.42; 21.34]
Total	4.18 [1.39; 12.60]



Heterogeneity: $\chi^2_3 = 1.16$ ($P = .76$), $I^2 = 0.0\%$

Study Comparison (OR Scale fractions)

Cohort D	3.57 [1.11; 11.46]
Cohort A	1.19 [0.34; 4.19]
Cohort B	2.29 [0.66; 7.90]
Cohort C	2.45 [0.67; 9.00]
Total	2.25 [1.21; 4.18]

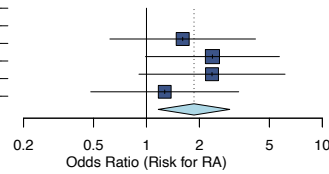


Heterogeneity: $\chi^2_3 = 1.60$ ($P = .66$), $I^2 = 0.0\%$

C. *Bacteroides uniformis*: 3880_3883

Study Comparison (OR Scale fractions)

Cohort D	1.61 [0.62; 4.17]
Cohort A	2.37 [0.99; 5.70]
Cohort B	2.36 [0.91; 6.14]
Cohort C	1.27 [0.48; 3.35]
Total	1.86 [1.17; 2.98]

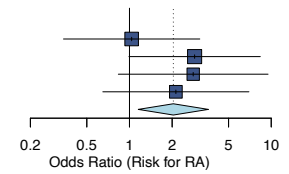


Heterogeneity: $\chi^2_3 = 1.22$ ($P = .75$), $I^2 = 0.0\%$

D. *Agathobacter rectalis*: 3036_3037

Study Comparison (OR Scale fractions)

Cohort D	1.04 [0.34; 3.13]
Cohort A	2.88 [0.99; 8.37]
Cohort B	2.82 [0.83; 9.50]
Cohort C	2.13 [0.65; 6.96]
Total	2.04 [1.15; 3.60]

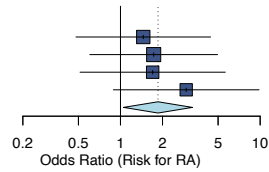


Heterogeneity: $\chi^2_3 = 2.12$ ($P = .55$), $I^2 = 0.0\%$

E. *Agathobacter rectalis*: 3102_3105;3105_3106

Study Comparison (OR Scale fractions)

Cohort D	1.46 [0.48; 4.42]
Cohort A	1.73 [0.60; 4.96]
Cohort B	1.70 [0.51; 5.63]
Cohort C	2.95 [0.89; 9.82]
Total	1.86 [1.05; 3.27]

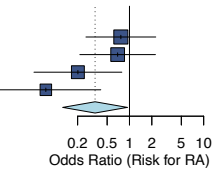


Heterogeneity: $\chi^2_3 = 0.80$ ($P = .85$), $I^2 = 0.0\%$

F. *Ruminococcus bromii*: 97_103

Study Comparison (OR Scale fractions)

Cohort D	0.77 [0.26; 2.26]
Cohort A	0.69 [0.21; 2.24]
Cohort B	0.20 [0.05; 0.79]
Cohort C	0.07 [0.01; 0.41]
Total	0.34 [0.13; 0.94]

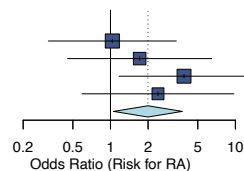


Heterogeneity: $\chi^2_3 = 6.91$ ($P = .07$), $I^2 = 56.6\%$

G. *Alistipes shahii*: 2252_2255;2255_2257;2257_2259;2259_2262;2262_2264;2265_2266

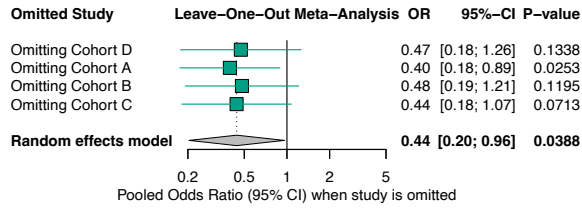
Study Comparison (OR Scale fractions)

Cohort D	1.03 [0.32; 3.37]
Cohort A	1.71 [0.45; 6.47]
Cohort B	3.88 [1.17; 12.87]
Cohort C	2.40 [0.59; 9.73]
Total	1.99 [1.06; 3.76]

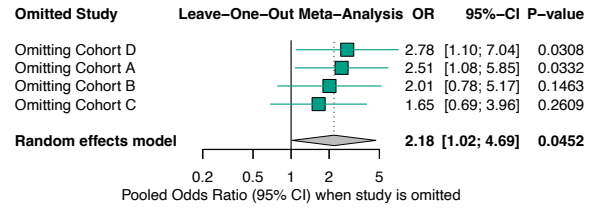


Heterogeneity: $\chi^2_3 = 2.49$ ($P = .48$), $I^2 = 0.0\%$

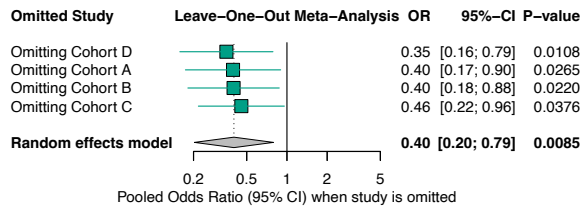
A. LOO Sensitivity: *Oscillibacter* sp.: 557_558;1131_1132



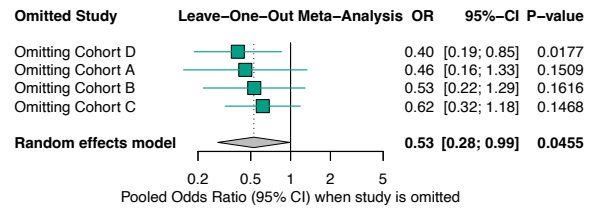
B. LOO Sensitivity: *Bacteroides xylanisolvens*: 5601_5602



C. LOO Sensitivity: *Agathobacter rectalis*: 662_663



D. LOO Sensitivity: *Faecalibacterium prausnitzii*: 537_538



E. LOO Sensitivity: *Faecalibacterium prausnitzii*: 781_783

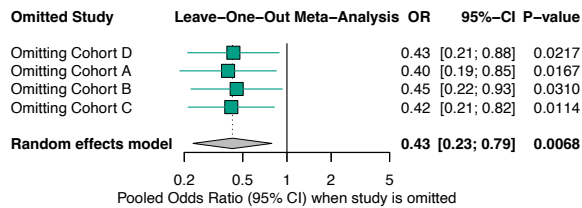


Figure S8

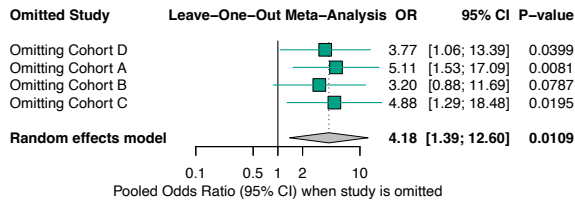
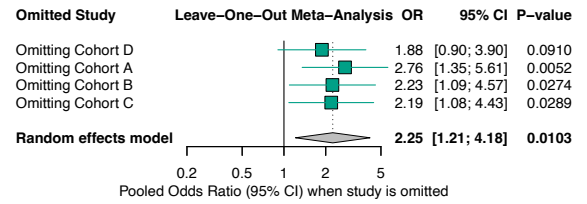
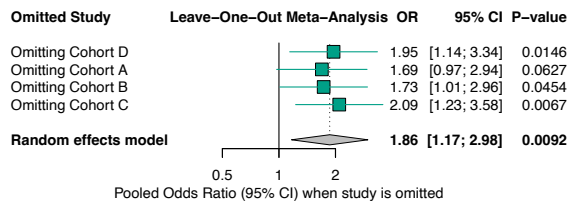
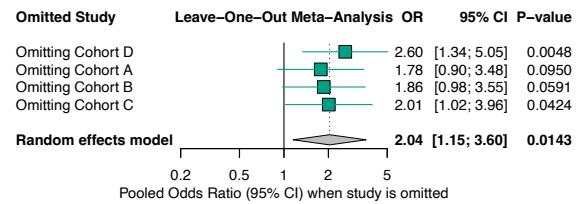
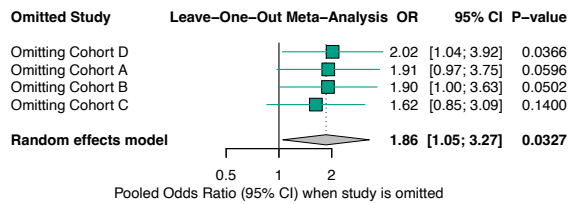
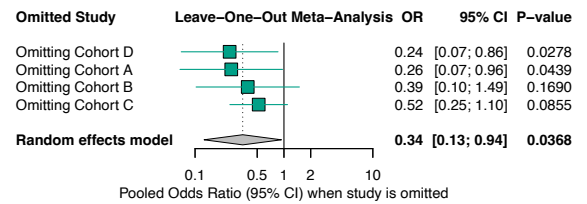
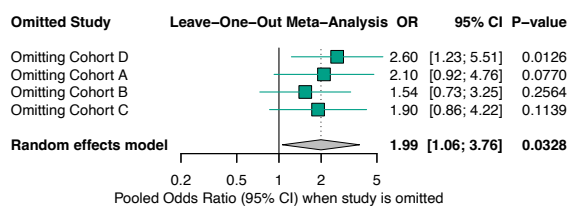
A. LOO Sensitivity: *Bacteroides fragilis*: 4781_4788B. LOO Sensitivity: *Parabacteroides merdae*: 782_783;2923_2924C. LOO Sensitivity: *Bacteroides uniformis*: 3880_3883D. LOO Sensitivity: *Agathobacter rectalis*: 3036_3037E. LOO Sensitivity: *Agathobacter rectalis*: 3102_3105;3105_3106F. LOO Sensitivity: *Ruminococcus bromii*: 97_103G. LOO Sensitivity: *Alistipes shahii*: 2252_2255;2255_2257;2257_2259;2259_2262;2262_2264;2265_2266

Figure S9

Comparative Analysis of Significant dSVs

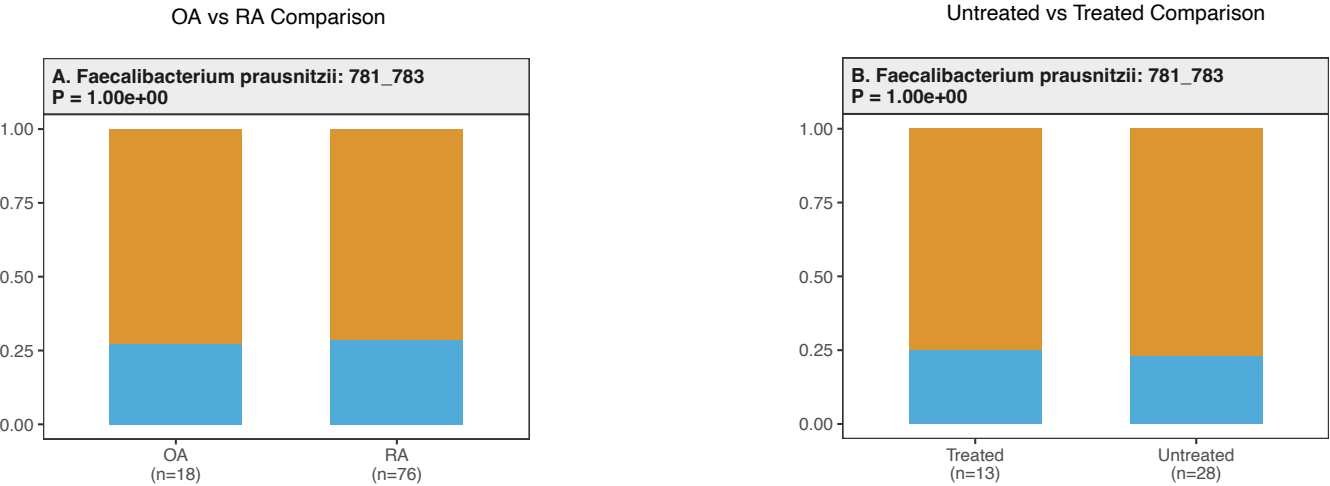
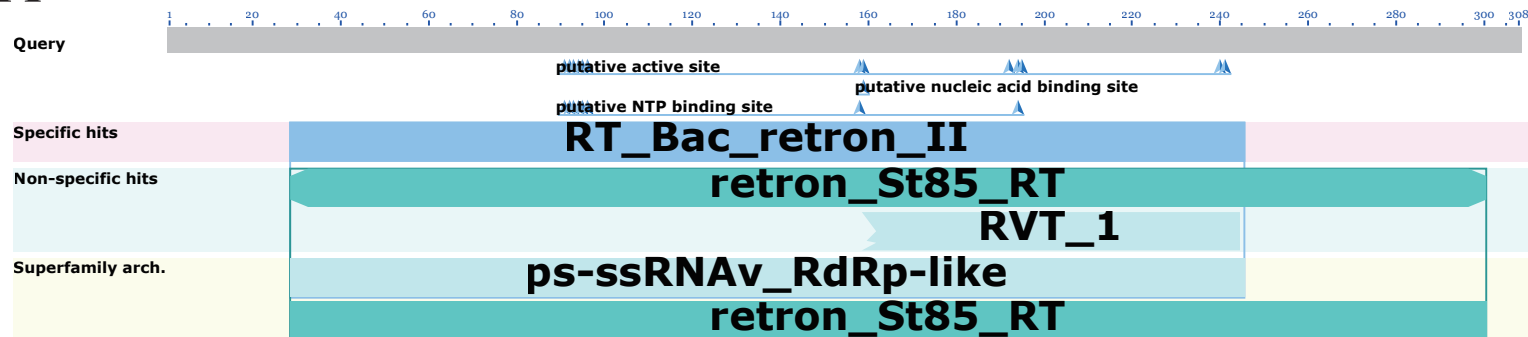


Figure S10

A



B

Domain ID: Name

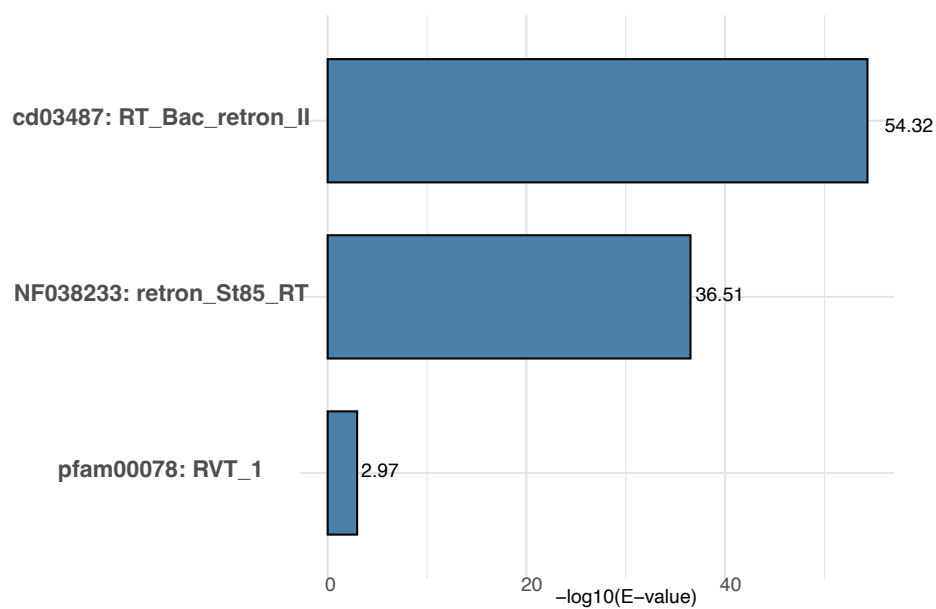


Figure S11

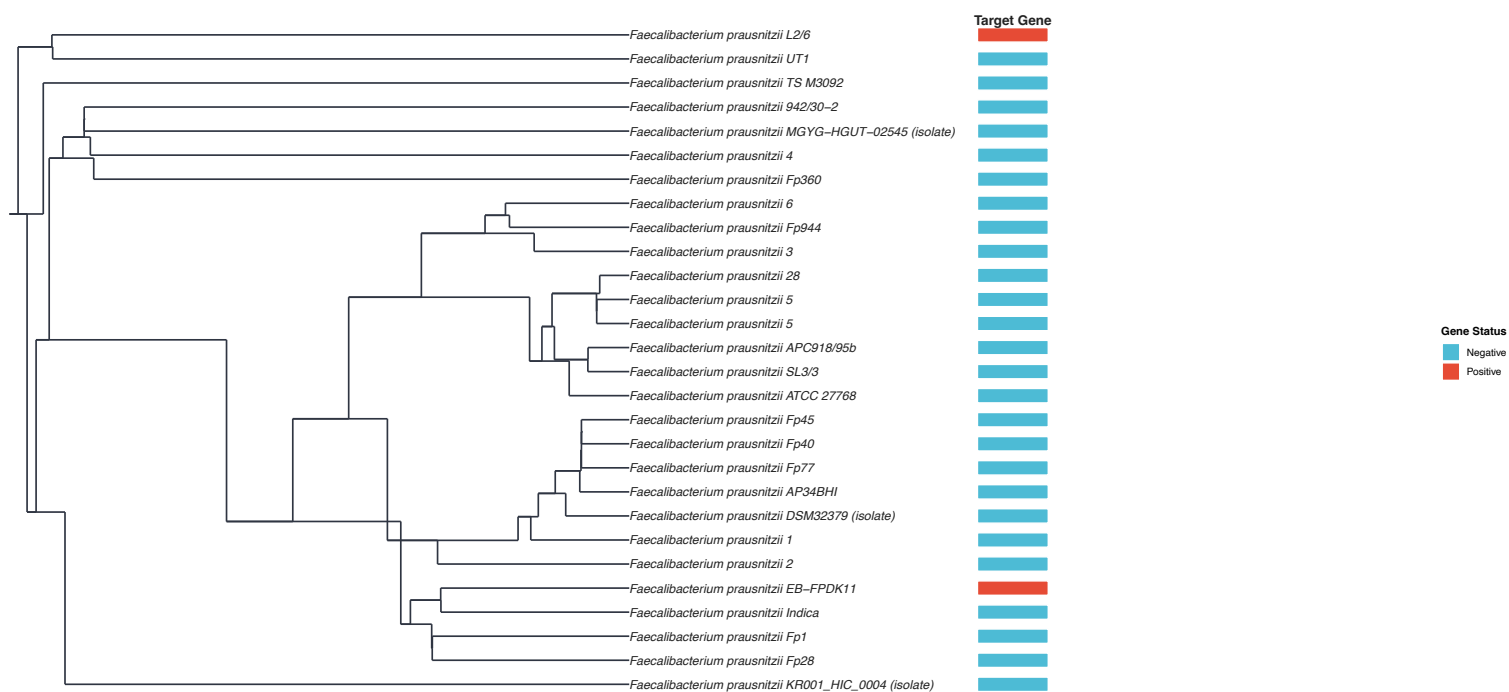


Figure S12

No.	E-value	Sites	Width
1	7.20E-88	22	20
2	4.60E-65	18	20
3	5.90E-49	22	20
4	5.40E-22	13	16
5	1.90E-08	18	12

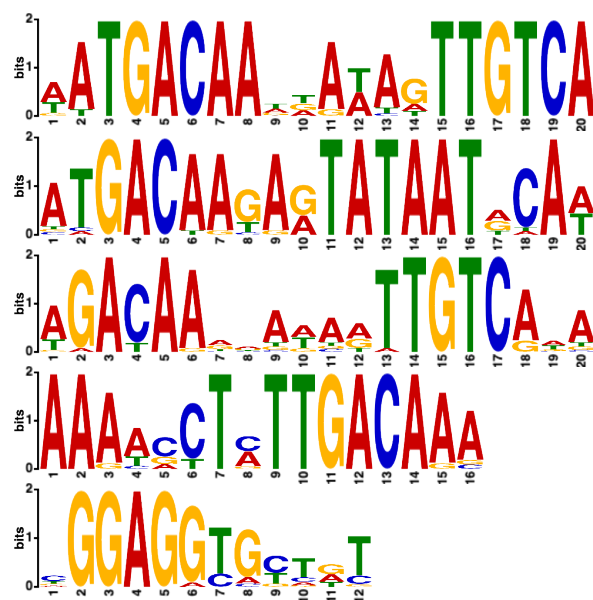


Figure S13

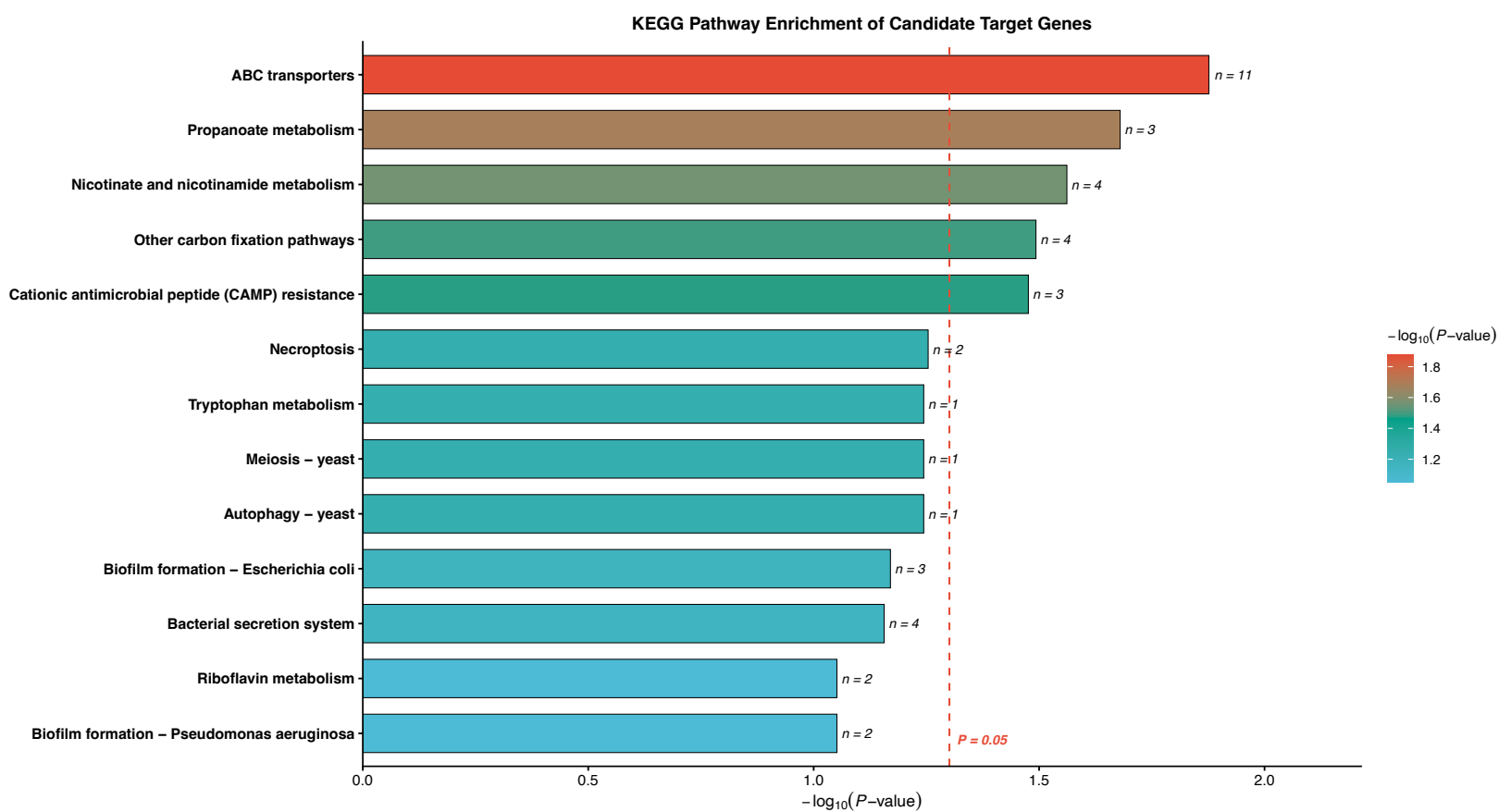
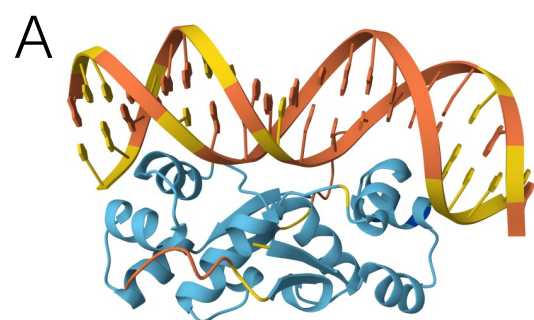
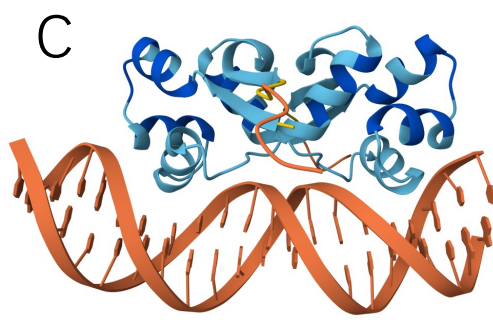


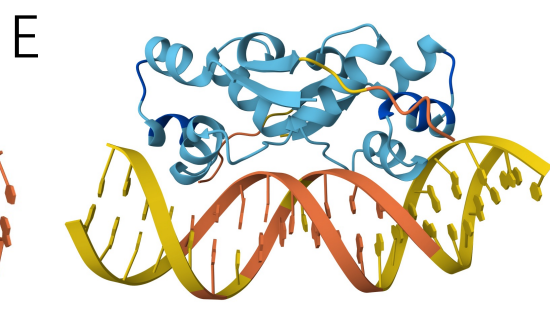
Figure S14



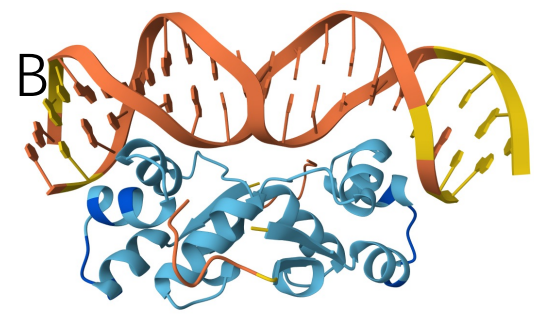
XK27_07105 dimer-XK27_07105_WT:
ipTM = 0.61; pTM = 0.69



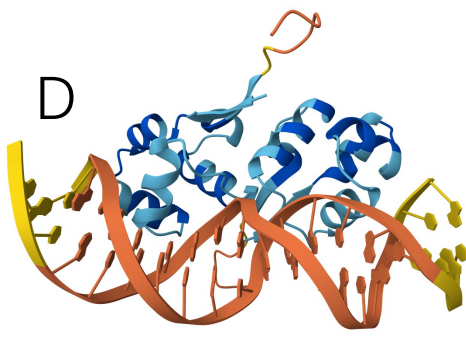
XK27_07105 dimer-*phbA*_WT:
ipTM = 0.55; pTM = 0.65



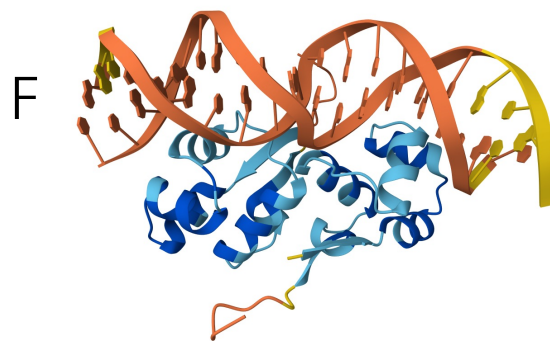
XK27_07105 dimer- *xsa* _WT:
ipTM = 0.62; pTM = 0.69



XK27_07105 dimer-XK27_07105_Mutant:
ipTM = 0.61; pTM = 0.69



XK27_07105 dimer-*phbA*_Mutant:
ipTM = 0.6; pTM = 0.69



XK27_07105 dimer- *xsa* _Mutant:
ipTM = 0.6; pTM = 0.69

Figure S15

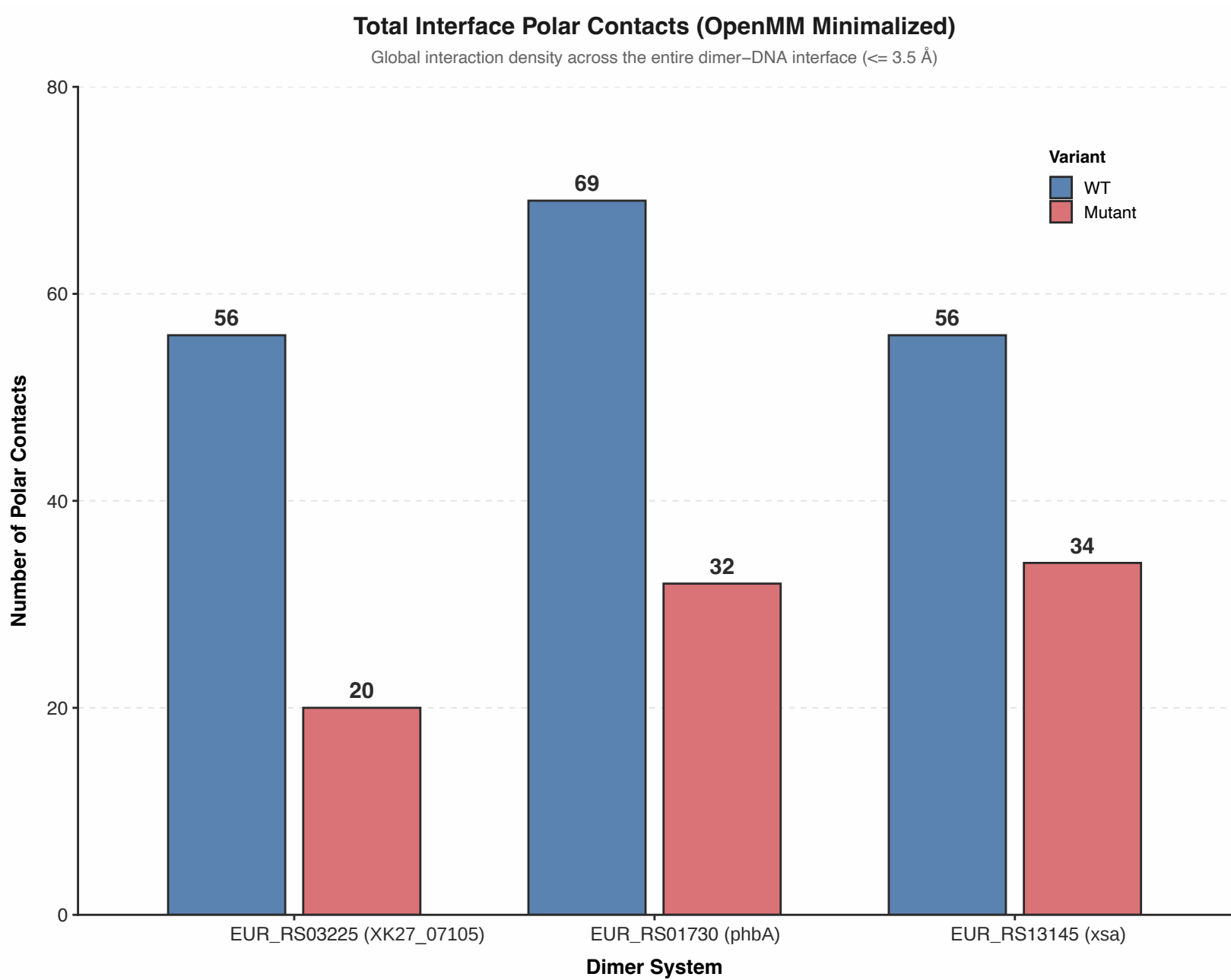
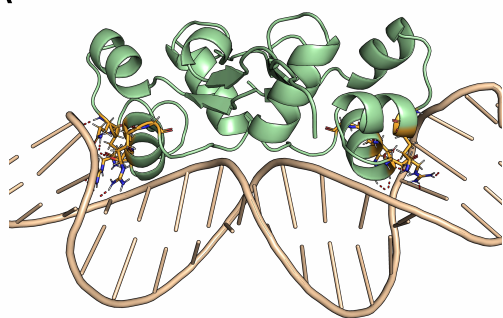


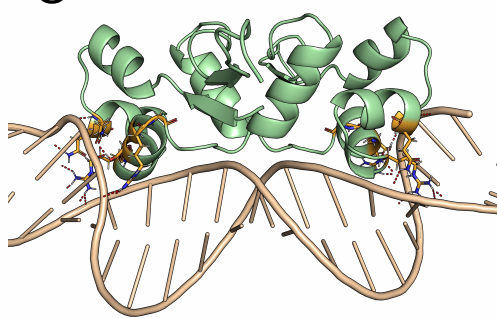
Figure S16

A

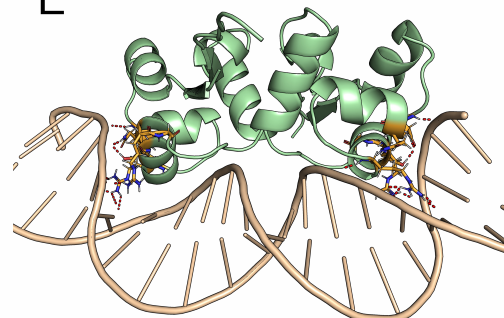


XK27_07105 dimer-XK27_07105_WT

C

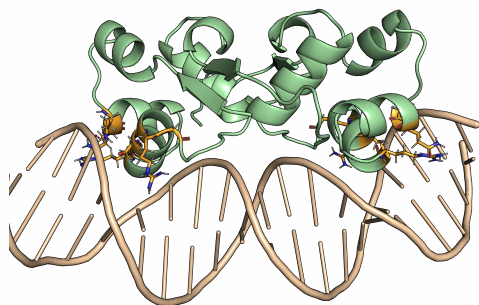
XK27_07105 dimer-*phbA*_WT

E



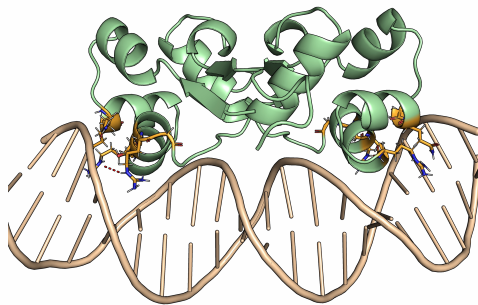
XK27_07105 dimer-xsa_WT

B

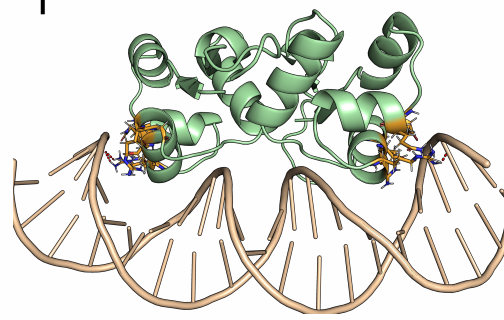


XK27_07105 XK27_07105_Mutant

D

XK27_07105 dimer-*phbA*_Mutant

F



XK27_07105 dimer-xsa_Mutant

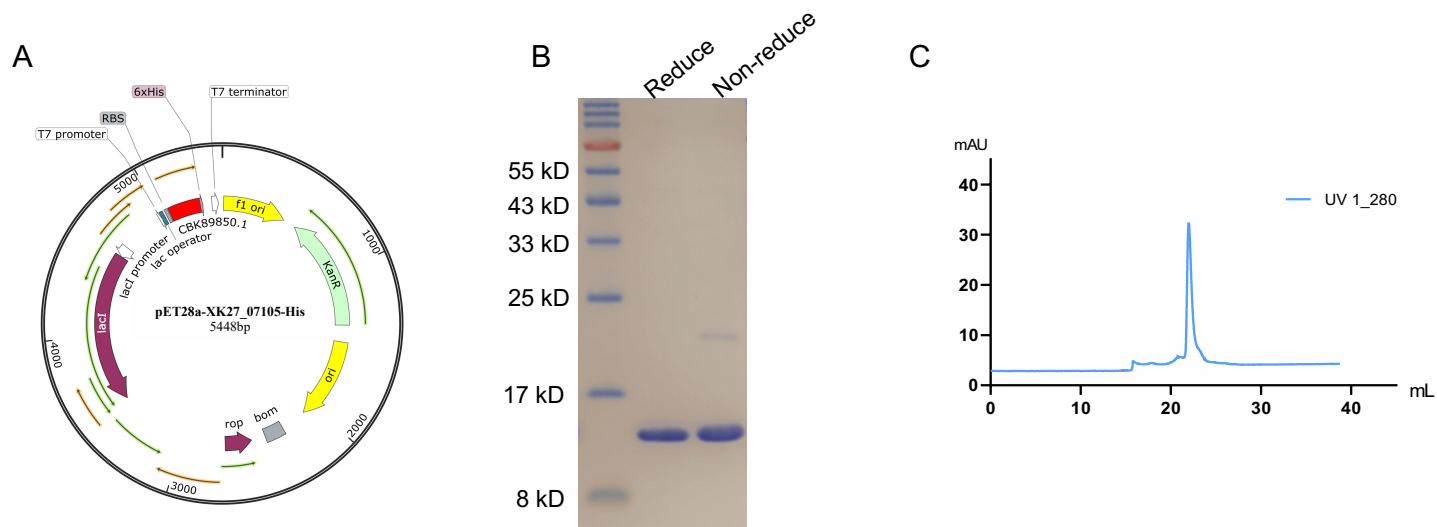


Figure S18

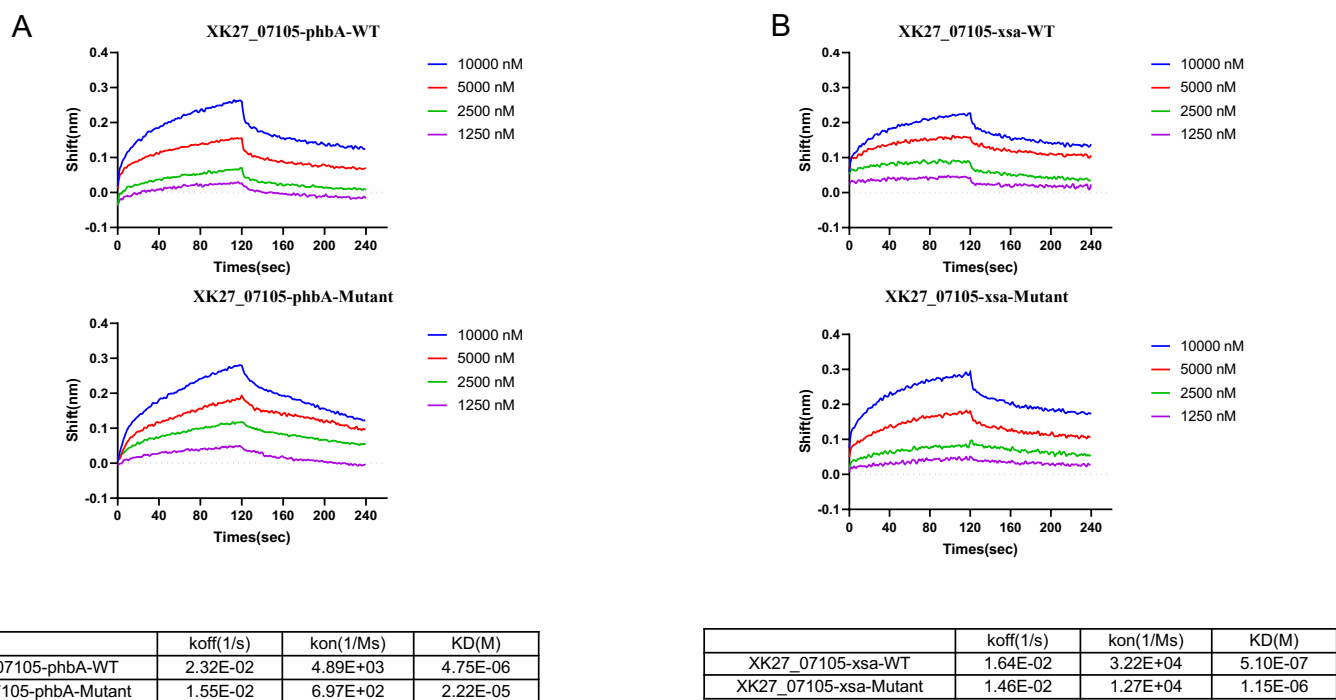


Figure S19