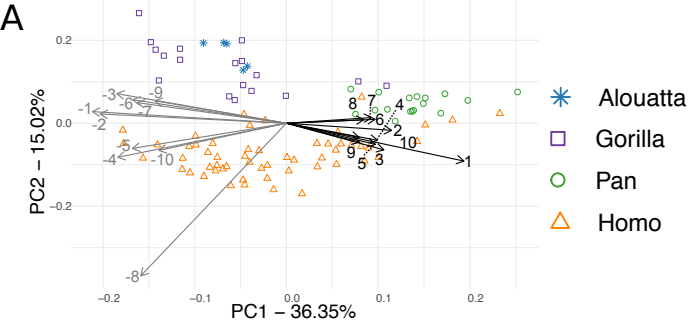
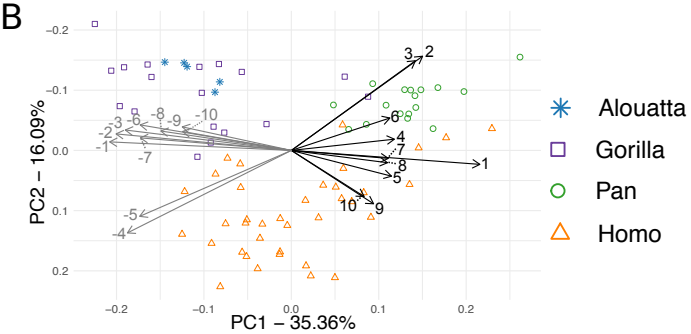
A



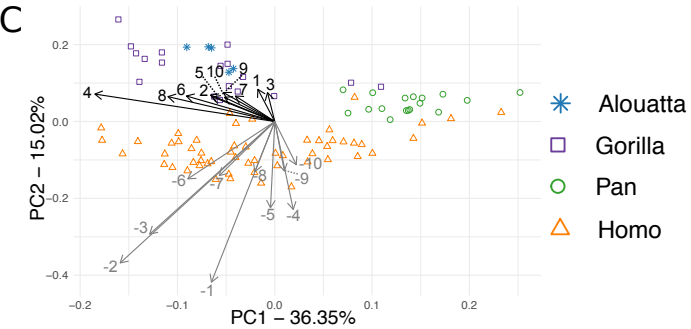

| PC1 negative loadings | | PC1 positive loadings | |
|---|---|---|---|
| -1 | **Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)** | 1 | **Duplicated ATPase component BL0693 of energizing module of predicted ECF transporter** |
| -2 | **Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid** | 2 | **Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)** |
| -3 | **Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)** | 3 | **Pyrophosphate-energized proton pump (EC 3.6.1.1)** |
| -4 | **Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3)** | 4 | **Transport ATP-binding protein CydC** |
| -5 | **Maltodextrin phosphorylase (EC 2.4.1.1)** | 5 | **Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps** |
| -6 | **Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)** | 6 | **DNA topoisomerase III (EC 5.99.1.2)** |
| -7 | **Oligopeptidase A (EC 3.4.24.70)** | 7 | **Putative mobilization protein BF0133** |
| -8 | Serine endopeptidase ScpC (EC 3.4.21.-) | 8 | **Conjugative transposon protein TraG** |
| -9 | **Chaperone protein HscA** | 9 | Pyrophosphate-dependent fructose 6-phosphate-1-kinase (EC 2.7.1.90) |
| -10 | Beta-lactamase (EC 3.5.2.6) | 10 | Pyruvate,phosphate dikinase (EC 2.7.9.1) |

B



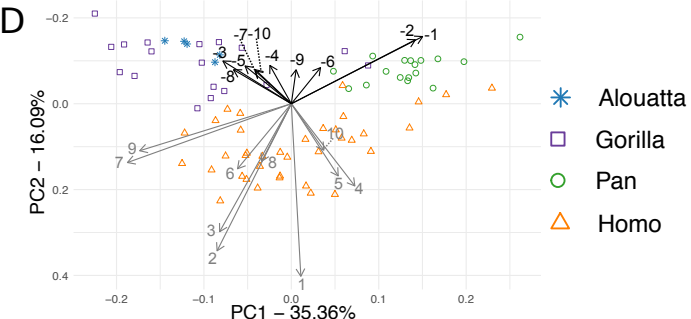

| PC1 negative loadings – no modern humans | | PC1 positive loadings – no modern humans | |
|---|---|---|---|
| -1 | **Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)** | 1 | **Duplicated ATPase component BL0693 of energizing module of predicted ECF transporter** |
| -2 | **Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)** | 2 | **Putative mobilization protein BF0133** |
| -3 | **Outer membrane receptor for ferric coprogen and ferric-rhodotorulic acid** | 3 | **Conjugative transposon protein TraG** |
| -4 | **Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3)** | 4 | **Pyruvate-flavodoxin oxidoreductase (EC 1.2.7.-)** |
| -5 | **Maltodextrin phosphorylase (EC 2.4.1.1)** | 5 | **Pyrophosphate-energized proton pump (EC 3.6.1.1)** |
| -6 | **Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)** | 6 | **DNA topoisomerase III (EC 5.99.1.2)** |
| -7 | **Oligopeptidase A (EC 3.4.24.70)** | 7 | **Transport ATP-binding protein CydC** |
| -8 | **Chaperone protein HscA** | 8 | **Multi antimicrobial extrusion protein (Na(+)/drug antiporter), MATE family of MDR efflux pumps** |
| -9 | Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) | 9 | V-type ATP synthase subunit A (EC 3.6.3.14) |
| -10 | Exodeoxyribonuclease V beta chain (EC 3.1.11.5) | 10 | V-type ATP synthase subunit B (EC 3.6.3.14) |

C




| PC2 negative loadings | | PC2 positive loadings | |
|---|---|---|---|
| -1 | **Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase** | 1 | **Acriflavin resistance protein** |
| -2 | **Serine endopeptidase ScpC (EC 3.4.21.-)** | 2 | **Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)** |
| -3 | **Pullulanase (EC 3.2.1.41)** | 3 | Glutathione-regulated potassium-efflux system ATP-binding protein |
| -4 | **Choline binding protein A** | 4 | Exodeoxyribonuclease V gamma chain (EC 3.1.11.5) |
| -5 | **Sialidase (EC 3.2.1.18)** | 5 | **3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41)** |
| -6 | **FtsK/SpoIIIE family protein, putative EssC component of Type VII secretion system** | 6 | **Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)** |
| -7 | **ATP-dependent nuclease, subunit B** | 7 | **GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II** |
| -8 | Beta-hexosaminidase (EC 3.2.1.52) | 8 | ATP-dependent DNA helicase Rep |
| -9 | **Alpha-galactosidase (EC 3.2.1.22)** | 9 | Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1) |
| -10 | Alpha-1,2-mannosidase | 10 | Catalase (EC 1.11.1.6) |

D




| PC2 negative loadings – no modern humans | | PC2 positive loadings – no modern humans | |
|---|---|---|---|
| -1 | Putative mobilization protein BF0133 | 1 | **Pyruvate-utilizing enzyme, similar to phosphoenolpyruvate synthase** |
| -2 | Conjugative transposon protein TraG | 2 | **Serine endopeptidase ScpC (EC 3.4.21.-)** |
| -3 | **Na(+)-translocating NADH-quinone reductase subunit F (EC 1.6.5.-)** | 3 | **Pullulanase (EC 3.2.1.41)** |
| -4 | **Acriflavin resistance protein** | 4 | **Choline binding protein A** |
| -5 | **Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)** | 5 | **Sialidase (EC 3.2.1.18)** |
| -6 | Ferric iron ABC transporter, permease protein | 6 | **FtsK/SpoIIIE family protein, putative EssC component of Type VII secretion system** |
| -7 | **GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II** | 7 | Glutathione biosynthesis bifunctional protein gshF (EC 6.3.2.2)(EC 6.3.2.3) |
| -8 | **3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41)** | 8 | **ATP-dependent nuclease, subunit B** |
| -9 | Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49) | 9 | Maltodextrin phosphorylase (EC 2.4.1.1) |
| -10 | Lipid-A-disaccharide synthase (EC 2.4.1.182) | 10 | **Alpha-galactosidase (EC 3.2.1.22)** |