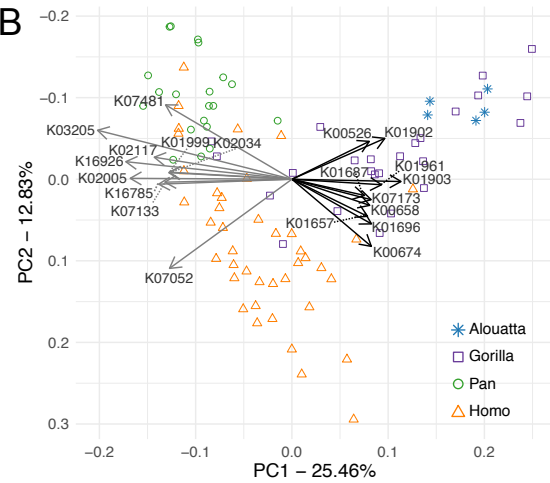
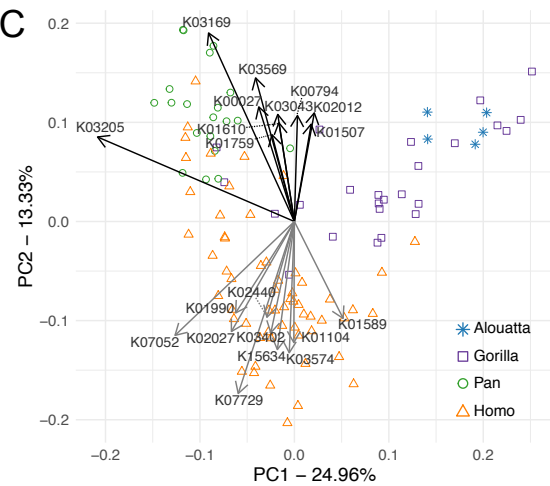


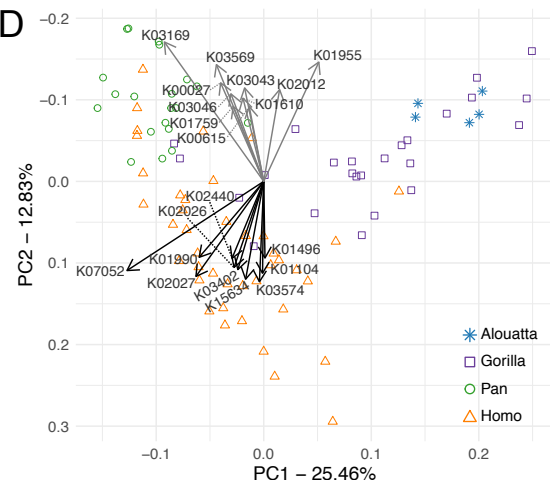
PC1 negative loadings			PC1 positive loadings		
-1	K03205	type IV secretion system protein VirD4 [EC:7.4.2.8]	1	K01903	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
-2	K16926	energy-coupling factor transport system substrate-specific component	2	K01092	myo-inositol-1(or 4)-monophosphatase [EC:3.1.3.25]
-3	K02005	HlyD family secretion protein	3	K01902	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
-4	K02117	V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit A [EC:7.1.2.2 7.2.2.1]	4	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
-5	K07133	uncharacterized protein	5	K00526	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]
-6	K16785	energy-coupling factor transport system permease protein	6	K01696	tryptophan synthase beta chain [EC:4.2.1.20]
-7	K02034	peptide/nickel transport system permease protein	7	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
-8	K07052	uncharacterized protein	8	K00674	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [EC:2.3.1.117]
-9	K01999	branched-chain amino acid transport system substrate-binding protein	9	K00658	component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
-10	K06147	ATP-binding cassette, subfamily B, bacterial	10	K01657	anthranilate synthase component I [EC:4.1.3.27]



PC1 negative loadings – no modern humans			PC1 positive loadings – no modern humans		
-1	K03205	type IV secretion system protein VirD4 [EC:7.4.2.8]	1	K01903	succinyl-CoA synthetase beta subunit [EC:6.2.1.5]
-2	K16926	energy-coupling factor transport system substrate-specific component	2	K01902	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
-3	K02005	HlyD family secretion protein	3	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
-4	K02117	V/A-type H ⁺ /Na ⁺ -transporting ATPase subunit A [EC:7.1.2.2 7.2.2.1]	4	K01696	tryptophan synthase beta chain [EC:4.2.1.20]
-5	K16785	energy-coupling factor transport system permease protein	5	K00674	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [EC:2.3.1.117]
-6	K07133	uncharacterized protein	6	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
-7	K07481	transposase, IS5 family	7	K00658	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
-8	K01999	branched-chain amino acid transport system substrate-binding protein	8	K00526	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]
-9	K02034	peptide/nickel transport system permease protein	9	K01657	anthranilate synthase component I [EC:4.1.3.27]
-10	K07052	uncharacterized protein	10	K01687	dihydroxy-acid dehydratase [EC:4.2.1.9]



PC2 negative loadings			PC2 positive loadings		
-1	K07729	putative transcriptional regulator	1	K03169	DNA topoisomerase III [EC:5.6.2.1]
-2	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.55]	2	K03569	rod shape-determining protein MreB and related proteins
-3	K15634	probable phosphoglycerate mutase [EC:5.4.2.12]	3	K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
-4	K01104	protein-tyrosine phosphatase [EC:3.1.3.48]	4	K02012	iron(III) transport system substrate-binding protein
-5	K07052	uncharacterized protein	5	K03043	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6]
-6	K03402	transcriptional regulator of arginine metabolism	6	K00794	6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]
-7	K02027	multiple sugar transport system substrate-binding protein	7	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]
-8	K01589	5-(carboxyamino)imidazole	8	K01507	inorganic pyrophosphatase [EC:3.6.1.1]
-9	K02440	glycerol uptake facilitator protein	9	K01759	lactoylglutathione lyase [EC:4.4.1.5]
-10	K01990	ABC-2 type transport system ATP-binding protein	10	K03205	type IV secretion system protein VirD4 [EC:7.4.2.8]



PC2 negative loadings – no modern humans			PC2 positive loadings – no modern humans		
-1	K03169	DNA topoisomerase III [EC:5.6.2.1]	1	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.55]
-2	K01955	carbamoyl-phosphate synthase large subunit [EC:6.3.5.5]	2	K15634	probable phosphoglycerate mutase [EC:5.4.2.12]
-3	K03569	rod shape-determining protein MreB and related proteins	3	K02027	multiple sugar transport system substrate-binding protein
-4	K00027	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	4	K01104	protein-tyrosine phosphatase [EC:3.1.3.48]
-5	K03043	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6] (rpoB)	5	K07052	uncharacterized protein
-6	K02012	DNA-directed RNA polymerase subunit binding protein	6	K03402	transcriptional regulator of arginine metabolism
-7	K03046	DNA-directed RNA polymerase subunit beta' [EC:2.7.7.6] (rpoC)	7	K02026	multiple sugar transport system permease protein
-8	K01610	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	8	K02440	glycerol uptake facilitator protein
-9	K01759	lactoylglutathione lyase [EC:4.4.1.5]	9	K01496	phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
-10	K00615	transketolase [EC:2.2.1.1]	10	K01990	ABC-2 type transport system ATP-binding protein