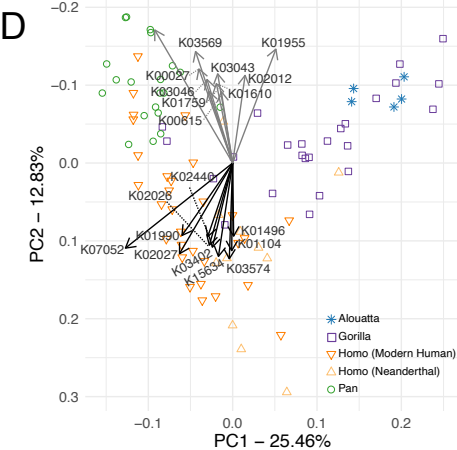
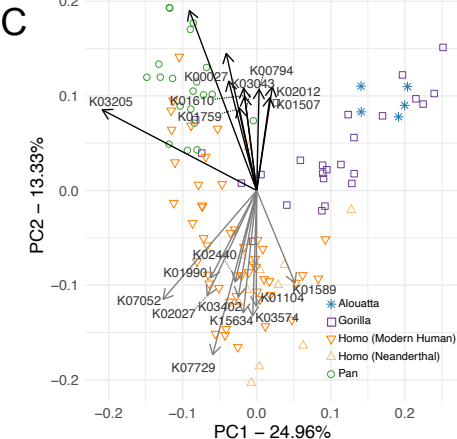
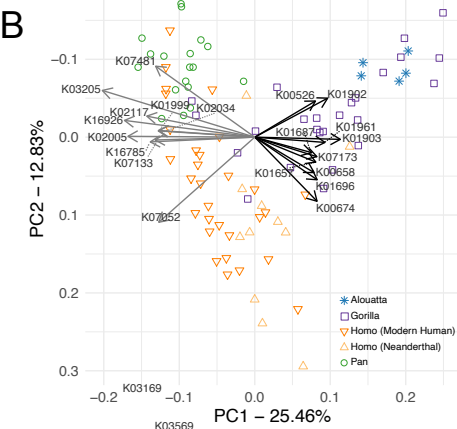


A PCA plot showing the relationship between genetic data (PC1 = 24.96%, PC2 = 13.33%) and various human populations. The plot includes a legend for populations: Alouatta (blue asterisk), Gorilla (purple square), Homo (Modern Human) (orange triangle), Homo (Neanderthal) (orange inverted triangle), and Pan (green circle). Genetic markers are labeled with IDs like K03205, K02117, K02034, K16926, K06147, K02005, K01999, K07133, K16785, K07052, K00526, K01902, K01903, K01961, K01092, K07171, K00658, K01696, K00674, K01657, and K07052. The plot shows that genetic markers are distributed across the PC1-PC2 space, with some markers (e.g., K03205, K02117, K02034, K16926, K06147, K02005, K01999, K07133, K16785, K07052) showing strong negative PC1 values, and others (e.g., K00526, K01902, K01903, K01961, K01092, K07171, K00658, K01696, K00674, K01657) showing strong positive PC1 values. The populations are clustered by species: Alouatta (blue asterisks) and Gorilla (purple squares) are in the upper right; Homo (Modern Human) (orange triangles) and Homo (Neanderthal) (orange inverted triangles) are in the lower right; and Pan (green circles) are in the upper left.



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)-monophosphate [EC:3.1.3.15]
-3	K02005	HlyD family translocation protein V/A-type H ⁺ /Na ⁺ -secreting ATPase subunit A [EC:7.1.2.2 7.2.2.1]	3	K01902	succinyl-CoA synthetase alpha subunit [EC:6.2.1.5]
-4	K02117	uncharacterized protein	4	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
-5	K07133	energy-coupling factor transport system permease protein	5	K00526	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]
-6	K16785	peptide/nickel transport system permease protein	6	K01696	tryptophan synthase beta chain [EC:4.2.1.20]
-7	K02034	uncharacterized protein	7	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
-8	K07052	uncharacterized protein	8	K00674	2,3,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase [EC:2.3.1.117]
-9	K01999	branched-chain amino acid transport system substrate-binding protein	9	K00658	2-oxoglutarate dehydrogenase E2 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 V1A-type H ⁺ /Na ⁺ -transporting ATPase subunit A [EC:7.1.2.2 7.2.2.1]	3	K01961	acetyl-CoA carboxylase, biotin carboxylase subunit [EC:6.4.1.2 6.3.4.14]
-4	K02117	energy-coupling factor transport system permease protein	4	K01696	tryptophan synthase beta chain [EC:4.2.1.20]
-5	K16785	uncharacterized protein	5	K00674	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate L-succinyltransferase [EC:2.3.1.117]
-6	K07133	transposase, ISS family branched-chain amino acid transport system substrate-binding protein	6	K07173	S-ribosylhomocysteine lyase [EC:4.4.1.21]
-7	K07481	peptide/nickel transport system permease protein	7	K00658	2-oxoglutarate dehydrogenase E2 component (dihydrolipoamide succinyltransferase) [EC:2.3.1.61]
-8	K01999	uncharacterized protein	8	K00526	ribonucleoside-diphosphate reductase beta chain [EC:1.17.4.1]
-9	K02034	uncharacterized 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 8-oxo-dGTP diphosphatase [EC:3.6.1.55]	1	K03169	DNA topoisomerase III [EC:5.6.2.1] rod shape-determining protein MreB and related proteins
-2	K03574	probable phosphoglycerate mutase [EC:5.4.2.12]	2	K03569	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]
-3	K15634	protein-tyrosine phosphatase [EC:3.1.3.48]	3	K00027	iron(III) transport system substrate-binding protein
-4	K01104	uncharacterized protein transcriptional regulator of arginine metabolism	4	K02012	DNA-directed RNA polymerase subunit beta [EC:7.7.7.6]
-5	K07052	multiple sugar transport system substrate-binding protein	5	K03043	6,7-dimethyl-8-ribityllumazine synthase [EC:2.5.1.78]
-6	K03402	5-(carboxyamino)imidazole ribonucleotide synthase [EC:6.3.4.18]	6	K00794	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]
-7	K02027	glycerol uptake facilitator protein ABC-2 type transport system ATP-binding protein	7	K01610	inorganic pyrophosphatase [EC:3.6.1.1] lactylglutathione lyase [EC:4.4.1.5]
-8	K01589		8	K01507	type IV secretion system protein VirD4 [EC:7.4.2.8]
-9	K02440		9	K01759	
-10	K01990		10	K03205	

PC2 negative loadings – no modern humans			PC2 positive loadings – no modern humans		
-1	K03169	DNA topoisomerase III [EC:5.6.2.1] carbamoyl-phosphate synthase large subunit [EC:6.3.5.3]	1	K03574	8-oxo-dGTP diphosphatase [EC:3.6.1.55] probable phosphoglycerate mutase [EC:5.4.2.12]
-2	K01955	rod shape-determining protein MreB and related proteins	2	K15634	multiple sugar transport system substrate-binding protein
-3	K03569	malate dehydrogenase (oxaloacetate-decarboxylating) [EC:1.1.1.38]	3	K02027	protein-tyrosine phosphatase [EC:3.1.3.48]
-4	K00027	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6] (rpoB)	4	K01104	uncharacterized protein
-5	K03043	iron (III) transport system substrate-binding protein	5	K07052	transcriptional regulator of arginine metabolism
-6	K02012	DNA-directed RNA polymerase subunit beta [EC:2.7.7.6] (rpoC)	6	K03402	multiple sugar transport system permease protein
-7	K03046	phosphoenolpyruvate carboxykinase (ATP) [EC:4.1.1.49]	7	K02026	
-8	K01610	lactoylglutathione lyase [EC:4.4.1.5]	8	K02440	glycerol uptake facilitator protein phosphoribosyl-AMP cyclohydrolase [EC:3.5.4.19]
-9	K01759	transketolase [EC:2.2.1.1]	9	K01496	ABC-2 type transport system ATP-binding protein
10	K00615		10	K01990	