

Table S1. Mean and standard deviation [SD] of the measured traits in each population.

Population	Sex	Standing Height			Sitting Height			Sitting/Standing Ratio			Subischial Leg Length			BMI			
		N	mean	SD	N	mean	SD	N	mean	SD	N	mean	SD	N	mean	SD	
Pygmies	Central/Eastern Baka	all	35	149.04	5.49	35	78.01	2.77	35	0.5236	0.0110	35	71.03	3.54	34	19.43	1.83
		males	17	152.38	4.60	17	79.63	2.25	17	0.5227	0.0087	17	72.75	3.00	17	19.96	1.58
		females	18	145.88	4.33	18	76.48	2.33	18	0.5244	0.0130	18	69.40	3.29	17	18.90	1.94
	Southeastern Baka	all	9	157.17	7.22	9	82.27	3.87	9	0.5236	0.0139	9	74.90	4.46	9	20.76	1.11
		males	8	157.11	7.72	8	81.90	3.96	8	0.5215	0.0132	8	75.21	4.66	8	20.60	1.08
		females	1	157.60	–	1	85.20	–	1	0.5406	–	1	72.40	–	1	22.02	–
	Koya	all	22	152.48	7.54	22	78.73	3.70	22	0.5167	0.0188	22	73.75	5.57	22	20.85	2.18
		males	14	155.19	7.49	14	80.06	3.71	14	0.5164	0.0210	14	75.12	5.93	14	20.85	1.76
		females	8	147.75	5.13	8	76.39	2.37	8	0.5173	0.0155	8	71.36	4.19	8	20.86	2.91
Southern Bezan	all	8	156.63	7.42	–	–	–	–	–	–	–	–	–	8	20.23	2.47	
	males	6	156.62	6.49	–	–	–	–	–	–	–	–	–	6	19.45	2.07	
	females	2	156.65	13.22	–	–	–	–	–	–	–	–	–	2	22.56	2.65	
Central Bongo	all	4	153.00	4.97	4	81.75	1.26	4	0.5345	0.0099	4	71.25	3.77	4	20.50	1.41	
	males	4	153.00	4.97	4	81.75	1.26	4	0.5345	0.0099	4	71.25	3.77	4	20.50	1.41	
	females	–	–	–	–	–	–	–	–	–	–	–	–	–	–	–	
Southern Bongo	all	14	156.29	5.34	14	80.36	2.06	14	0.5145	0.0157	14	75.93	4.65	14	20.98	2.25	
	males	9	159.44	3.43	9	81.00	1.73	9	0.5082	0.0130	9	78.44	3.40	9	20.68	2.29	
	females	5	150.60	2.51	5	79.20	2.28	5	0.5259	0.0144	5	71.40	2.70	5	21.53	2.30	
Eastern Bongo	all	23	155.70	7.01	23	80.72	2.55	23	0.5189	0.0159	23	74.98	5.45	23	19.60	2.63	
	males	15	157.13	7.68	15	81.03	2.92	15	0.5161	0.0144	15	76.10	5.59	15	19.41	2.57	
	females	8	153.00	4.86	8	80.13	1.66	8	0.5241	0.0184	8	72.88	4.82	8	19.96	2.88	
Non-Pygmies	Bangando	all	5	157.32	5.48	5	82.46	2.72	5	0.5242	0.0045	5	74.86	2.92	5	20.78	2.01
		males	2	163.30	0.99	2	85.35	0.35	2	0.5227	0.0010	2	77.95	0.64	2	22.87	0.07
		females	3	153.33	0.21	3	80.53	0.91	3	0.5252	0.0061	3	72.80	0.95	3	19.38	0.88
	Nzime	all	20	156.55	8.72	20	79.52	4.35	20	0.5081	0.0141	20	77.03	5.33	20	20.44	3.20
		males	2	174.25	5.30	2	86.90	1.56	2	0.4988	0.0062	2	87.35	3.75	2	17.97	1.82
		females	18	154.58	6.51	18	78.69	3.73	18	0.5092	0.0144	18	75.88	4.12	18	20.71	3.23
	Tikar	all	19	162.24	7.90	–	–	–	–	–	–	–	–	–	19	22.99	2.28
		males	12	166.68	3.78	–	–	–	–	–	–	–	–	–	12	22.94	2.28
		females	7	154.61	7.34	–	–	–	–	–	–	–	–	–	7	23.07	2.47
All Pygmies	all	115	153.21	7.06	107	79.54	3.21	107	0.5204	0.0151	107	73.41	4.95	114	20.13	2.18	
	males	73	155.67	6.55	67	80.62	2.92	67	0.5185	0.0152	67	74.97	4.91	73	20.16	1.95	
	females	42	148.95	5.82	40	77.75	2.89	40	0.5235	0.0147	40	70.81	3.84	41	20.06	2.56	
All Non-Pygmies	all	44	159.09	8.39	25	80.10	4.21	25	0.5113	0.0143	25	76.60	4.97	44	21.58	2.94	
	males	16	167.21	4.61	4	86.13	1.28	4	0.5108	0.0143	4	82.65	5.85	16	22.31	2.63	
	females	28	154.45	6.23	21	78.96	3.51	21	0.5115	0.0146	21	75.44	3.97	28	20.16	3.07	

Table S2. Consistency of *VEGAS* genes for P/NP categories with/without village covariates.

Gene	Genomic position		Number of SNPs	P/NP Categories		
	Chr	Begin (bp)		End (bp)	None	Village
<i>DLGAP1</i>	18	3,496,029	4,455,266	165	Yes	Yes
<i>GPC6</i>	13	93,879,077	95,060,273	111	Yes	Yes
<i>MACROD2</i>	20	13,976,145	16,033,841	183	Yes	Yes
<i>CACNA1C</i>	12	2,162,415	2,807,115	76	Yes	Yes
<i>PPP2R2B</i>	5	145,969,066	146,461,083	24		Yes
<i>GP1BB</i>	22	19,704,742	19,712,297	6	Yes	Yes
<i>CLDN10</i>	13	96,085,852	96,232,010	10		Yes
<i>IPO9</i>	1	201,657,383	201,798,687	16	Yes	
<i>ANKHD1</i>	5	139,781,398	139,919,441	2	Yes	
<i>EIF4EBP3</i>	5	139,781,398	139,929,163	2	Yes	
<i>RPS6KA2</i>	6	166,822,853	167,275,771	51	Yes	
<i>PSMG3</i>	7	1,606,969	1,609,668	10	Yes	
<i>ST7</i>	7	116,592,500	116,594,388	10	Yes	
<i>ZNF32</i>	10	44,124,264	44,170,147	24	Yes	
<i>KIRREL3</i>	11	126,293,395	126,870,766	357	Yes	

EMMAX analyses considered either no covariate (“None”) or village affiliation as a covariate (“Village”). “Yes” indicates comparisons in which the gene’s P_{perm} is significant. Genes present in **Table 3** are shown in **bold** and the comparisons in which their P_{perm} was significant are highlighted in grey.

Table S3. Consistency of significant *VEGAS* genes for height-associated traits with population-based covariates in addition to sex.

Gene	Genomic position		Number of SNPs	Standing Height			Sitting Height			Standing/Sitting Ratio			Subischial Leg Length			
	Chr	Begin (bp)		End (bp)	None	P/NP	Village	None	P/NP	Village	None	P/NP	Village	None	P/NP	Village
<i>GPC6</i>	13	93,879,077	95,060,273	111	Yes	Yes	Yes	Yes	Yes		Yes	Yes	Yes	Yes	Yes	Yes
<i>DLGAP1</i>	18	3,496,029	4,455,266	165	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes
<i>MACROD2</i>	20	13,976,145	16,033,841	183	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	Yes	
<i>CACNA1C</i>	12	2,162,415	2,807,115	76	Yes			Yes	Yes		Yes	Yes		Yes	Yes	
<i>DSCAM</i>	21	41,384,342	42,219,039	75	Yes	Yes	Yes				Yes	Yes	Yes	Yes	Yes	Yes
<i>DPYD</i>	1	97,543,299	98,386,615	30							Yes	Yes	Yes	Yes	Yes	Yes
<i>ERC2</i>	3	55,542,335	56,502,391	36								Yes		Yes	Yes	Yes
<i>XXYLT1</i>	3	194,789,012	194,991,895	18	Yes	Yes			Yes							
<i>MAGI2</i>	7	77,646,373	79,082,890	132	Yes	Yes	Yes	Yes	Yes	Yes						
<i>NRG1</i>	8	31,497,267	32,622,558	87	Yes			Yes		Yes	Yes	Yes	Yes	Yes	Yes	Yes
<i>FOXP3</i>	14	89,622,515	90,085,494	63	Yes	Yes		Yes	Yes	Yes						
<i>RDH14</i>	2	18,735,988	18,770,846	10		Yes	Yes									
<i>NT5C1B</i>	2	18,735,988	18,770,846	10		Yes	Yes									
<i>NPPA</i>	1	11,900,375	11,907,673	618				Yes	Yes	Yes						
<i>PACRG</i>	6	163,148,163	163,736,524	48				Yes	Yes	Yes			Yes			
<i>TNFRSF6B</i>	20	62,289,162	62,330,051	24				Yes	Yes							
<i>ZNF32</i>	10	44,124,264	44,170,147	24							Yes	Yes				
<i>SHANK2</i>	11	70,313,960	70,935,808	27											Yes	
<i>CCDC169</i>	13	36,742,344	36,871,992	8										Yes	Yes	
<i>EGFLAM</i>	5	38,258,510	38,465,582	27	Yes		Yes									
<i>DISC1</i>	1	231,664,398	232,177,019	26	Yes											
<i>ADIPOQ</i>	3	186,560,462	186,576,252	32	Yes											
<i>LNX1</i>	4	54,326,436	54,457,753	33	Yes											
<i>RPS6KA2</i>	6	166,822,853	167,275,771	51	Yes											
<i>LMCD1</i>	3	8,262,833	8,543,344	26				Yes		Yes						
<i>IL12A</i>	3	159,631,189	159,924,879	16				Yes								
<i>COL18A1</i>	21	46,825,096	46,933,634	12				Yes								
<i>GDNF</i>	5	37,812,778	37,839,782	12						Yes						
<i>INHBA</i>	7	41,728,600	41,742,706	4						Yes						
<i>ARHGAP5</i>	14	32,544,624	32,545,905	4							Yes					
<i>CNTN4</i>	3	2,140,549	3,099,645	58									Yes			
<i>LHFPL3</i>	7	103,969,103	104,549,003	60									Yes			
<i>PDX1</i>	13	28,403,895	28,495,541	22										Yes		
<i>OSBPL10</i>	3	31,702,316	32,023,342	10												Yes
<i>RAD51</i>	15	40,985,952	40,987,303	2												Yes

Sex was included as a covariate either on its own (“None”) or in combination with Pygmy/non-Pygmy categorization (“P/NP”) or village affiliation (“Village”). “Yes” indicates comparisons in which the gene’s P_{perm} is significant. Genes present in **Table 4** are shown in **bold** and the comparisons in which their P_{perm} was significant are highlighted in grey.