

Additional File 9 The chromosomal regions associated with the limb bone lengths under the assumption of the linkage phases being same in the four populations

Trait	Chr ¹	Top SNP	Position, Mb	Effect ± SE	P Value ²	N _{SNP} ³
Scapula	1	ss131149408	282.04	-0.164±0.039	2.43×10 ⁰⁵	1
Scapula	2	ss131211507	3.61	-0.139±0.033	2.70×10 ⁰⁵	1
Ulna	4	ss131269439	81.71	0.195±0.041	1.93×10 ^{06*}	1
Femur	4	ss131270306	84.98	0.163±0.040	4.72×10 ⁰⁵	1
Humerus	4	ss131270306	84.98	0.164±0.038	1.41×10 ⁰⁵	1
Femur	7	ss131342596	33.18	-0.232±0.037	5.46×10 ^{10**}	3
Scapula	7	ss131342596	33.18	-0.194±0.040	9.93×10 ^{07*}	1
Humerus	7	ss131347175	40.85	-0.190±0.034	2.40×10 ^{08**}	4
Tibia	7	ss131347175	40.85	-0.224±0.034	7.51×10 ^{11**}	6
Ulna	7	ss131347175	40.85	-0.233±0.038	6.90×10 ^{10**}	8
Humerus	8	ss131065181	145.99	-0.131±0.032	3.86×10 ⁰⁵	1
Ulna	17	ss131546319	37.50	0.180±0.045	6.46×10 ⁰⁵	1
Tibia	18	ss107862415	52.79	0.143±0.035	3.39×10 ⁰⁵	1
Humerus	X	ss478943984	45.12	0.083±0.019	7.59×10 ⁰⁶	4
Femur	X	ss23131102	63.65	-0.133±0.022	8.67×10 ^{10**}	3
Tibia	X	ss23131102	63.65	-0.140±0.020	4.67×10 ^{12**}	2
Ulna	X	ss23131102	63.65	-0.129±0.022	3.55×10 ^{09**}	2
Scapula	X	ss131070541	106.48	0.123±0.026	2.72×10 ^{06*}	2

Notes: 1. Chromosome; 2. The P value was corrected by genomic control. **: 1% genome-wide significant; *: 5% genome-wide significant; without *: suggestive significant; 3. number of SNPs that surpass the suggestive significance level.