Table S3: The location of the top 5 most significant QTLs associated with each of the skeletal traits in the meta-analysis.

Trait	Chr	Start	End	No of suggestive and significant SNPs	Most significant SNP	P-Value	Candidate genes within this QTL
Wither Height	5	105280734	106302598	28	105783088[a]	$4.00x10^{-7}$	KCNA1, NDUFA9, FGF6, FGF23, TIGAR
	6	32458499	35344463	590	33574963[a]	$1.60x10^{-8}$	CCSER1
	6	36934944	40367479	233	38692833[a]	$1.39x10^{-10}$	PPM1K, ABCG2, PKD2, SPP1, MEPE, LAP3, NCAPG, LCORL
	15	16857667	17866073	3	17357667[a]	$5.08x10^{-7}$	ALKBH8, RAB39A
	22	1921471	3018467	32	2517667[a]	$4.87x10^{-7}$	CMC1
Chest Width	1	78722748	79819964	9	79281613[b]	$1.78x10^{-7}$	TPRG1, LPP
	2	84546041	85547642	17	85047257[a]	$6.63x10^{-7}$	SLC39A10, DNAH7, STK17B, HECW2
	8	111704513	112713771	5	112207970[b]	$1.49x10^{-6}$	CDK5RAP2, FBXW2, TRAF1
	16	34222491	35399155	7	34722616[b]	$1.01x10^{-6}$	AKT3, SDCCAG8, CEP170
	19	60882962	61882988	3	61382974[a]	$3.64x10^{-7}$	KCNJ2, KCNJ16, MAP2K6, ABCA5
Chest Depth	1	116367840	117409053	15	116884742[c]	$7.63x10^{-7}$	MBNL1, AADAC
	5	3711874	4919423	75	4314400[a]	$1.44x10^{-7}$	CAPS2
	5	80773564	81859095	13	81273564[a]	$1.29x10^{-9}$	CCDC91
	11	77828096	78855720	2	78355720[a]	$5.74x10^{-7}$	GDF7, RHOB, SDC1
	13	67722025	68774518	3	68222752[b]	$8.81x10^{-9}$	KIAA1755, ADIG, DHX35
Back Length	2	1	9238659	969	5535691[a]	$1.69x10^{-19}$	ASNSD1,ARHGEF4,MYO7B,NABI,MFSD6,MSTN,PMS1,ORMDL1,COL3A1,COL5A2,ANKAR,SLC40A1
	6	32966339	34249299	192	33471768[d]	$1.66x10^{-8}$	
	6	36399608	40835172	107	38672441[c]	$4.04x10^{-10}$	PPM1K, ABCG2, PKD2, SPP1, MEPE, LAP3, NCAPG, LCORL
	12	41360854	42774040	8	41860854[a]	$3.67x10^{-7}$	
	13	75166652	76244228	3	75166652[b]	$4.86x10^{-7}$	DNTTIP1, TNNC2, PLTP, NCOA5, CDH22, OCSTAMP
Hip Width	6	37042897	40544352	36	38648218[b]	$2.58x10^{-7}$	PPM1K, ABCG2, PKD2, SPP1, MEPE, LAP3, NCAPG, LCORL
	11	74549091	75686706	7	75078608[b]	$3.54x10^{-7}$	NCOA1, ITSN1, FKBP1B, ATAD2B, KLHL29
	15	7741333	8881109	3	8381102[a]	$2.76x10^{-7}$	ARHGAP42
	18	9307588	10781382	4	10281382[a]	$3.42x10^{-7}$	CDH13, HSBP1, MBTPS1, DNAAF1, TAF1C, ATP2C2, COTL1
	23	6956952	7970369	3	7456952[a]	$5.27x10^{-7}$	GCLC, DSB, TAP2, PSMB8, TAP1, PSMB9, COL11A2, HSD17B8, RING1, RPS18, DAXX, BAK1

Superscript denotes SNP classification: [a]intergenic, [b]intron, [c]upstream gene variant, [d]downstream gene varianT