Appendix S5. All genomic regions with LOD > 1.175 (nominal p-value < 0.01) for the presence of horn size and body mass QTL in the Ram Mountain bighorn sheep population and their estimated parameters (V_{QTL}, phenotypic variance explained by the QTL after having accounted for fixed effects; q^2, proportion of phenotypic variance explained by the QTL after having accounted for fixed effects; h^2, residual heritability after having fitted the QTL effect). Areas with LOD > 1.175 used to test for QTL co-localization between bighorn sheep and domestic sheep are also presented.

trait	LOD	chr.	pos. (cM)[†]	closest marker	1-LOD drop (cM)	LOD > 1.175 (cM)	V_{QTL}	q^2	h^2	domestic sheep QTL
Male trait										
Horn volume	1.59	1	361	BMS2263	310 - 361	352 - 361	0.47 (0.09)	0.56 (0.08)	0.00 (0.00)	
	1.66	10	0	OarSEJ10, 11	0 - 6	0 - 2	0.36 (0.11)	0.39 (0.10)	0.00 (0.00)	[1]
	1.37	23	28	AGLA269	4 - 44	26 - 34	0.47 (0.15)	0.56 (0.13)	0.00 (0.00)	
Horn length	1.91	1	361	BMS2263	346 - 361	352 - 361	0.50 (0.09)	0.60 (0.08)	0.00 (0.00)	
	1.31	18	12	ILSTS52	0 - 28	8 - 14	0.42 (0.16)	0.48 (0.15)	0.11 (0.13)	
	2.82	23	26	AGLA269	16 - 38	6 - 38	0.65 (0.12)	0.73 (0.06)	0.00 (0.00)	
Horn base circ.	1.45	10	0	OarSEJ10, 11	0 - 6	0 - 2	0.32 (0.12)	0.37 (0.12)	0.06 (0.16)	[1]
Body mass	1.35	23	37	RT9	16 - 80	32 - 40	0.25 (0.09)	0.45 (0.13)	0.00 (0.00)	[2-4]
Female trait										
Horn volume	1.74	18	12	ILSTS52	0 - 30	0 - 20	0.36 (0.11)	0.38 (0.10)	0.00 (0.00)	
	1.33	18	108	CSAP28E	78 - 108	104 - 108	0.38 (0.12)	0.41 (0.11)	0.00 (0.00)	
Horn base circ.	1.30	5	55	TGLA303	26 - 84	48 - 62	0.40 (0.11)	0.44 (0.09)	0.00 (0.00)	
	1.58	6	66	JMP36	52 - 80	60 - 72	0.40 (0.10)	0.43 (0.08)	0.00 (0.00)	
	1.59	18	12	ILSTS52	0 - 40	0 - 20	0.26 (0.11)	0.29 (0.12)	0.12 (0.14)	
	1.42	19	49	MCM61A	0 - 72	42 - 56	0.38 (0.10)	0.43 (0.09)	0.00 (0.00)	
Body mass	1.32	2	190	BM81124	166 - 296	180 - 198	0.11 (0.04)	0.22 (0.07)	0.00 (0.00)	[5-7]
	1.44	24	44	BP28	0 - 54	30 - 50	0.12 (0.04)	0.24 (0.07)	0.00 (0.00)	[8-9]
	2.15	26	40	JMP58	30 - 44	32 - 44	0.13 (0.04)	0.26 (0.07)	0.00 (0.00)	[10]
Sexes combined										
Horn volume	1.95	18	9	ILSTS52	0 - 48	0 - 44	0.30 (0.09)	0.33 (0.08)	0.00 (0.00)	
	1.21	18	108	CSAP28E	90 - 108	108	0.26 (0.08)	0.29 (0.08)	0.00 (0.00)	
Horn length	1.29	22	50	MAF92	28 - 58	48 - 52	0.30 (0.09)	0.31 (0.08)	0.00 (0.00)	
Horn base circ.	2.35	18	1	SRCRSP5	0 - 30	0 - 34	0.30 (0.08)	0.33 (0.07)	0.00 (0.00)	
	1.27	19	46	MCM61A	0 - 66	42 - 50	0.27 (0.07)	0.31 (0.07)	0.00 (0.00)	
Body mass	1.47	2	190	BM81124	156 - 242	172 - 198	0.12 (0.04)	0.21 (0.06)	0.00 (0.00)	[5-7]
	1.25	22	10	HEL11	0 - 32	6 - 14	0.13 (0.04)	0.23 (0.06)	0.00 (0.00)	
	1.18	X	124	MCM25	80 - 124	124	0.09 (0.04)	0.15 (0.07)	0.08 (0.08)	

[†]Map distances are based on Haldane's mapping function (see appendix S1) and therefore not directly comparable to distances presented in Poissant et al. (2010) where Kosambi's mapping function was used. [1] Horn morphology, Johnston *et al.* (2010), [2] body weight, Margawati *et al.*, (2006), [3] carcass weight, no 95% CI, Margawati *et al.*, (2009), [4] growth rate, Raadsma *et al.*,

(2009), [5] muscle development, Laville *et al*. (2004), [6] carcass weight, no 95% CI, Margawati *et al*., (2009), [7] weight, suggestive, Walling *et al*. (2004), [8] muscle mass, Campbell *et al*. (2003), [9] body weight and growth rate, Raadsma *et al*. (2009), [10] body weight and growth rate, Raadsma *et al*. (2009).