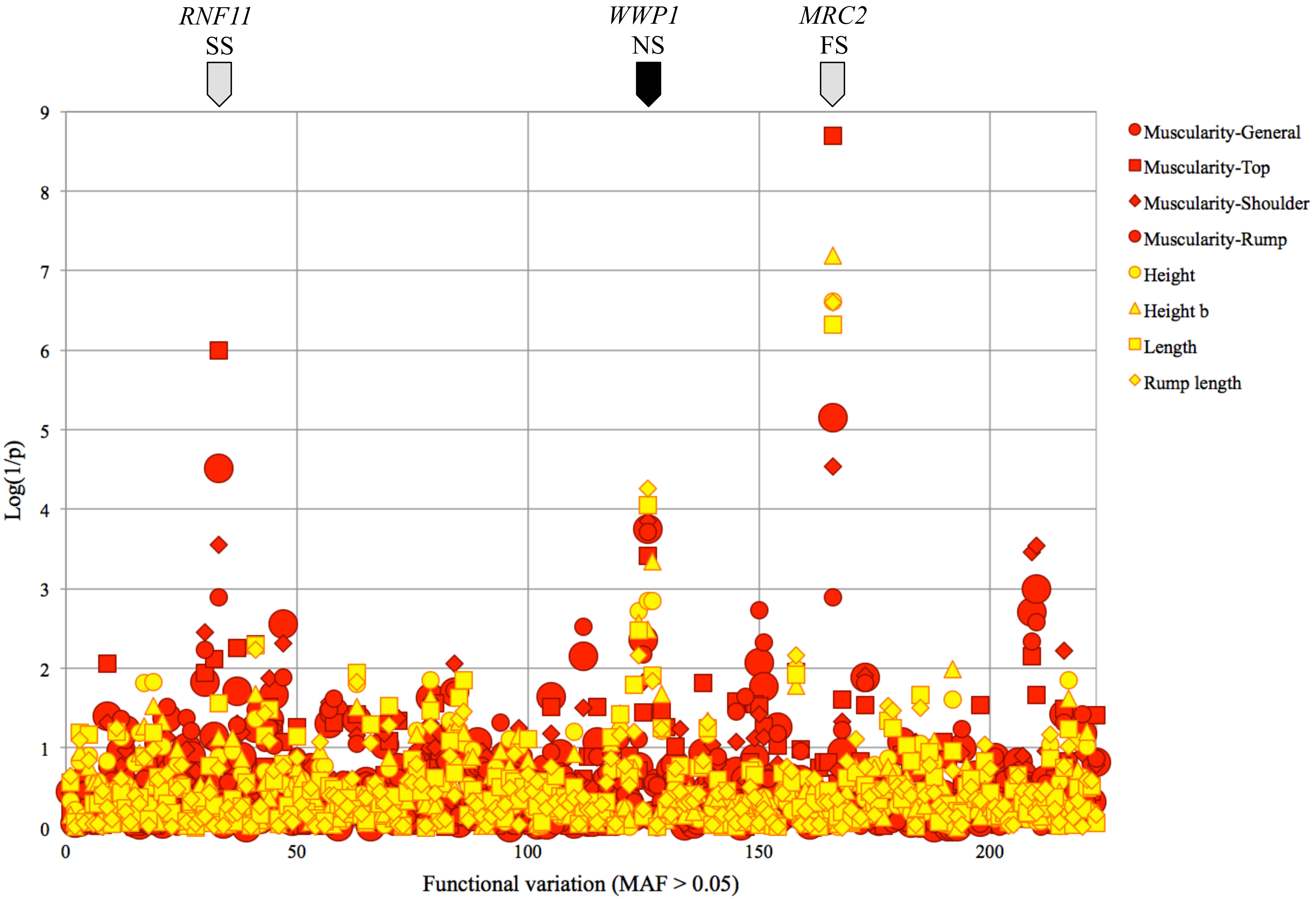
RNF11
SS
WWP1
NS
MRC2
FS
9
8
7
6
5
4
3
2
1
0
Log(1/p)
0
50
100
150
200
Functional variation (MAF > 0.05)
Musculary-General
Muscularity-Top
Muscularity-Shoulder
Muscularity-Rump
Height
Height b
Length
Rump length

Supplemental Figure S2: GWAS conducted in 580 BBC bulls using breeding values for eight trait pertaining to muscularity and stature and genotypes for 223 LoF and missense variants (MAF>5%) sorted according to their genomic position. The two strongest signals correspond to the previously identified frame-shift (FS) *MRC2*[1] and splice-site (SS) *RNF11*[2] mutations, causing Crooked tail Syndrome and Growth Stunting, respectively. The third signal corresponds to the newly identified R844Q non-synonymous (NS) mutation in the *WWP1* gene. The statistical model used was as in Druet et al.[3].

1. Fasquelle et al. Balancing selection of a frame-shift mutation in the MRC2 gene accounts for the outbreak of the Crooked Tail Syndrome in Belgian Blue Cattle. *PLoSGenetics* 5: e1000666 (2009).
2. Sartelet et al. A splice site variant in the bovine RNF11 gene compromises growth and regulation of the inflammatory response. *PLoSGenetics* 8: e1002581 (2012).
3. Druet et al. Selection in action: dissecting the molecular underpinnings of the increasing muscle mass of Belgian Blue Cattle. *BMC Genomics* 15: 796 (2014).