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# Effects of polymorphism in the bovine *PTPRQ* gene on the expression of *MYF6* and *MYF5* genes in skeletal muscle and on meat production traits in beef bulls

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## Supplementary Online Material (SOM)

Table S1. Primers used in the experiment and conditions for PCR reaction

| Symbol | Purpose | Primer sequence (5'→3') | PCR product size (bp) | Gene region (sequence spanning) | Annealing temperature (°C) |
|---|---|---|---|---|---|
| MYF6rt-F<br>MYF6rt-R | expression | TGGACCCCTTCAGCTACAGA<br>ATGCTTGTCCCTCCTTCCTT | 180 | exons 1–3 (pos. 625–2030; GenBank Acc. No. NW_001494990.2) | 60 |
| MYF5rt-F<br>MYF5rt-R | expression | ACCAGCCCACCTCAAGTTG<br>GCAATCCAAGCTGGATAAGG | 150 | exons 1–3 (pos. 665–2050; GenBank Acc. No. NW_001494990.2) | 60 |
| PTPRQ1F<br>PTPRQ1R | sequencing and RFLP | TAGTAAGCCACAGTCTTCCATCT<br>CAGCTCTTGAGTTCTGGATT | 740 | partial intron 35 | 55 |
| PTPRQ2F<br>PTPRQ2R | sequencing and RFLP | CCAATGTAATGCCCCAAATG<br>TCAAAACCACACAGCCCTTTA | 835 | exon 36,<br>partial intron 36 | 55 |
| TBPrt-F<br>TBPrt-R | expression | ACAACAGCCTCCCACCCTATGC<br>GTGGAGTCCTGTGCCGTAA | 120 | 3'UTR | 60 |

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tagtaag ccacagtctt ccatctattt tttcatttgt cctttacttc aaaatccaca
tcctcttaca tttgtcactt aagaaatctg gtaagattat ccctgatatt taaaattata
aactttgata aaggtgtatg ttcattttat ttcatacttt gtgccttttg tgttttttta
cagtgctaat ttgttgcgca tgacaaatgt gttattaaag atacacccat ctctgaattt
gggcattgca cagtctattt agctgtttaa aattatttca atttttagag tataaataac
tggactaatg aactgtcaca aaaatgtata aagtaactga aatgactgtc attttttatg
gttatatatt cacaaagact caggaaacaa gatttagtca atttgatgtc atttttcaat
caccttcctt tattcagcat tcttcatgga caaataaaaa agtttcactc acatttacat
ttttagggca ataaatacta tgcaatatat taaaaagtga cctgtaccaa tgtaatgccc
caaatgccca gcaatataaa acattacctt cttagcttga gagaaaagcc aaattattat
ttggccatat ttgggtccaa ataatataat ttcaaaaatg atgtagaatt taaaataatg

**g.200,451A→G** **g.200,467T→C** **g.200,480C→T**

atcac**A**tatc agttaaaggt a**T**agcatgtt ataa**C**tgctg gtttaccatg tttttctaat

AR

CHOP-cEBP

HNF-3BETA

tttaatccag aactcaagag ctgtatcctc aactcataat gcgtttaaca caa**TCTCTGT**
**TGCAG*GTTAC TTAGTTATAG AAAATCCATC AA*GTAAGTTT GTTAAGTATC TTTTCTTCTT**
**TTTGAATACC AACTCTAGAT TCCCTGATTC AATGAATCTT AATGTGTGGT TCCTTTTTTG**
**TATGTTTGGT AGAAAAACCT CCAAGCTGGA TATAAATCAT AAAAGCATGA CTAATTGCAT**
**GGTAACTGGA GAAATGCTTT CTCTCTCTCT GGGGTGAAGC CTGCATGTCT GTATTTTAGC**
**TTGGGAAGTA ATACAGGGAT ATCTAAACTC CTTAGGGTTT AGAAACCATG TCATTATGAG**
**AATGAGGTCA CTGCAATATT TTATATCTTC TAAAACCTTG TAATGTATAA AATGTTCTCT**
**GTATGACAAA GAGGTATTAT ATGCATTAGG ATTCAATGAT AACTTTATGC CCTTACATTT**
**ACTTGAAAAA CTT**tcttcat taaaatgtgc aatcattcat ttaaagtcac ttaaaatttg
aaggatttct gtaccatgaa atacagggaa agtgaactca aagagggaaa gctaattttg
taaatatgac agggtgactt taaagggctg tgtggttttg a

Figure S1. Location of SNPs found in the bovine *PTPRQ* gene close to H1 enhancer. The 1,358 bp sequence study of the bovine *PTPRQ*, resequenced in this gene is shown, amplified from nt 199,788 to nt 201,146 (GenBank Acc. No. NW_001494990.2). Positions of SNPs are given relative to the transcription start site of the *PTPRQ* gene (GenBank Acc. No. NW_001494990.2). H1 enhancer (Maak et al. 2006) is shown in capital letters, exon 35 is doubly underlined and the 145-bp regulatory element (Giordani et al. 2007) is underlined with single line. The putative AR, CHOP-cEBP, and HNF-3β binding sites are shown