

Supplementary material 2. Impact of detected polymorphic sites on consensus sequences for transcription factors

<b>Polymorphism</b>	<b>Predicted TF binding sites*</b>	
<b>CSN1S1</b>		
c.-1665C>T	<b>Allele C</b> -	<b>Allele T</b> FOS, JUN, JDP2
c.-1732A>G	<b>Allele A</b> RHOXF1	<b>Allele G</b> RHOXF1, ETS1, NFATC1, NFATC2, NFATC3
c.-1917G>T	<b>Allele G</b> NFIC, GATA1, GATA2	<b>Allele T</b> NFIC, PRRX2, DLX3, DLX4, DLX2
c.-1922C>G	<b>Allele C</b> GATA2, RHOXF1, NFIC, NFIX, NFYB	<b>Allele G</b> GATA2, CEBPB, JUN, CEBPA, FOS::JUN
c.-2168G>C	<b>Allele G</b> GATA1, GATA2, MZF1, NFKB1	<b>Allele C</b> GATA1, GATA2, HIC2
<b>CSN1S2</b>		
c.-2047_2048insAT	<b>Allele + (ins)</b> NOTO, Nkx2-5, Arid3a, Barhl1, NKX6-2	<b>Allele - (del)</b> NOTO, Nkx2-5, Pdx1
c.-2543G>A	<b>Allele G</b> NR4A2, Mafb	<b>Allele A</b> NR4A2, SOX10
<b>CSN2</b>		
c.-2105C>G	<b>Allele C</b> RUNX3, RUNX1, RUNX2, ZNF354C, LIN54	<b>Allele G</b> MEIS1
c.-2429C>T	<b>Allele C</b> -	<b>Allele T</b> Rxra, NR4A2
c.-2817T>C	<b>Allele T</b> FOXC1, MEIS1	<b>Allele C</b> FOXC1
c.-2973C>G	<b>Allele C</b> Bhlha15, HLTF, FOXL1	<b>Allele G</b> Bhlha15, HLTF, FOXL1, MEIS1
<b>CSN3</b>		
c.-2925C>G	<b>Allele C</b> MZF1, ETS1	<b>Allele G</b> -
c.-2970C>T	<b>Allele C</b> Ahr::Arnt	<b>Allele T</b> TBX21, MGA, TBX1, TBR1, EOMES
c.-3012G>C	<b>Allele G</b> GATA2, GATA3, FOXL1, HOXA5	<b>Allele C</b> GATA2, GATA3, FOXL1
c.-3515G>A	<b>Allele G</b> RHOXF1	<b>Allele A</b> -
c.-3669G>C	<b>Allele G</b> -	<b>Allele C</b> BARHL2
c.-3711T>C	<b>Allele T</b> FOXC1, SPIB, ETS1, ARID3A,	<b>Allele C</b> FOXC1, NR2E1

TF – transcription factors, \*only 1-5 consensus sites with the highest relative scores are shown (according to JASPAR database)

Cieslak et. al. (2018) 5'-flanking variants of equine casein genes (CSN1S1, CSN1S2, CSN2, CSN3) and their relationship with gene expression and milk composition. *Journal of Applied Genetics.*