



Conclusions

- Variation tended to be lowest in coding regions, but this was not significantly different from the distant upstream (5 - 50 kb), upstream, introns, or downstream regions for either species.
- The *FCN* genes of both cattle and horses had a significantly higher variant density as compared to the remaining gene targets. Whether this represents increased evolutionary need for variation in the FCN proteins is unknown.
- A coding mutation similar to a known deleterious mutation in humans and pigs was found in equine *MBL1*.

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- Variants in the bovine and equine collagenous lectins are associated with infectious diseases, suggesting that these genes play a role in infectious disease resistance in these species.

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