Dairy code for fine-mapping chr3 new replicated locus - rs778801698 3 50024027 49524027 50524027

13/05/2024

In place with all the codes to run finemapping with FINEMAP and SuSiE for chr3 new locus. Although I have a credible set with a lot of variants – I am trying to understand why. So I am now re-running the fine mapping.

14/04/1014

I ran again the fine-mapping. The fine-mapping is correct – it is that lots of the variants have PIP < 0.01, so the 95% credible set is made up of lots of variants with small PIP – four variant have PIP >= 0.01. Copied the new results with chromosome 3 region and without MHC region on /data/. Updated the report and uploaded in the PhD webpage script. Moving to variant-to-gene mapping analysis.