

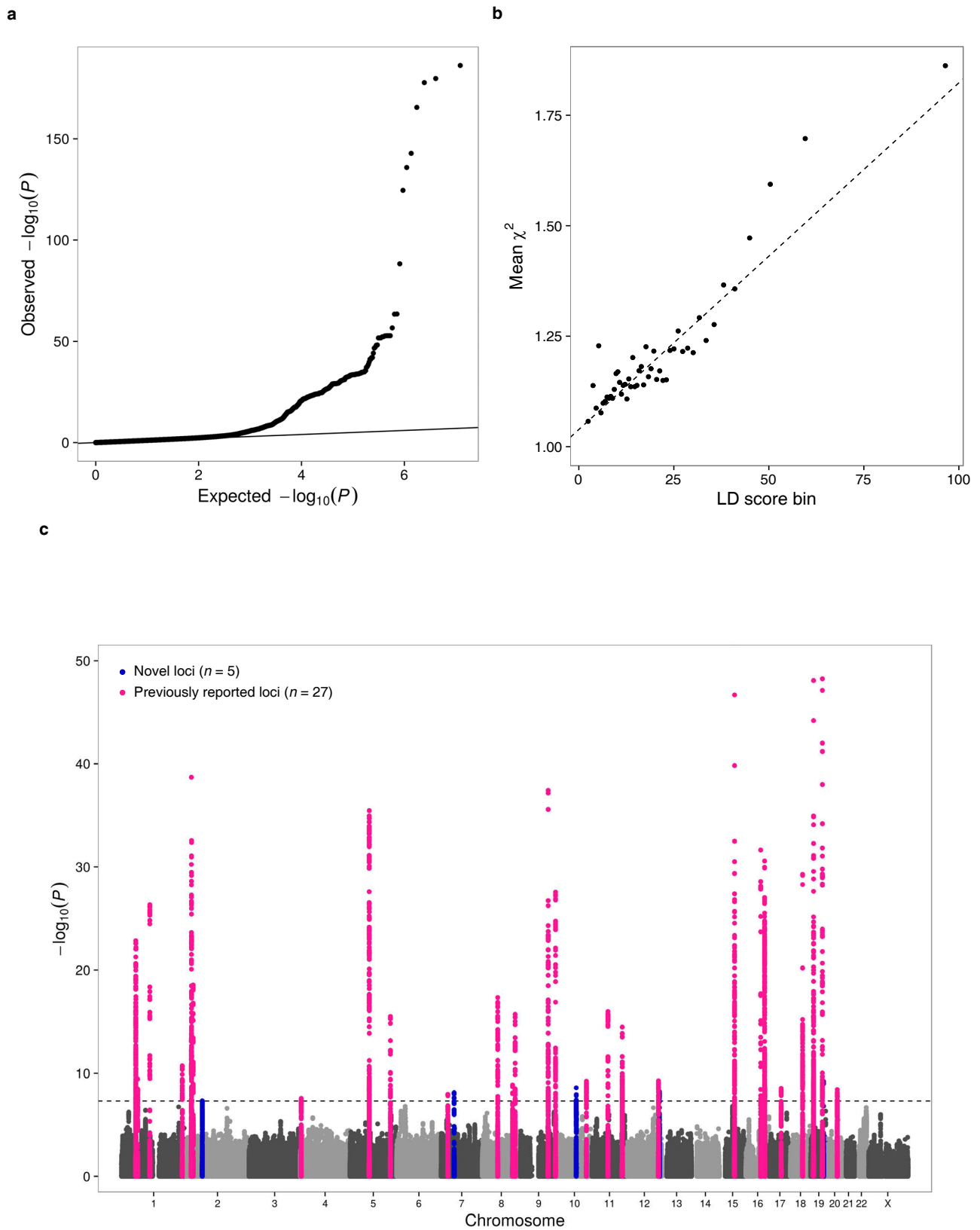
Supplementary Data Set 1 | Manhattan, quantile-quantile, and LD score plots for the 58 quantitative traits.

a, quantile-quantile (QQ) plot. **b**, LD score plot. **c**, Manhattan plot. GWAS was conducted using a linear regression model under the assumption of additive allelic effects of the SNP dosages. Novel loci are colored in blue, whereas known loci are colored in red. The dotted line represents a genome-wide significance threshold ($P = 5.0 \times 10^{-8}$).

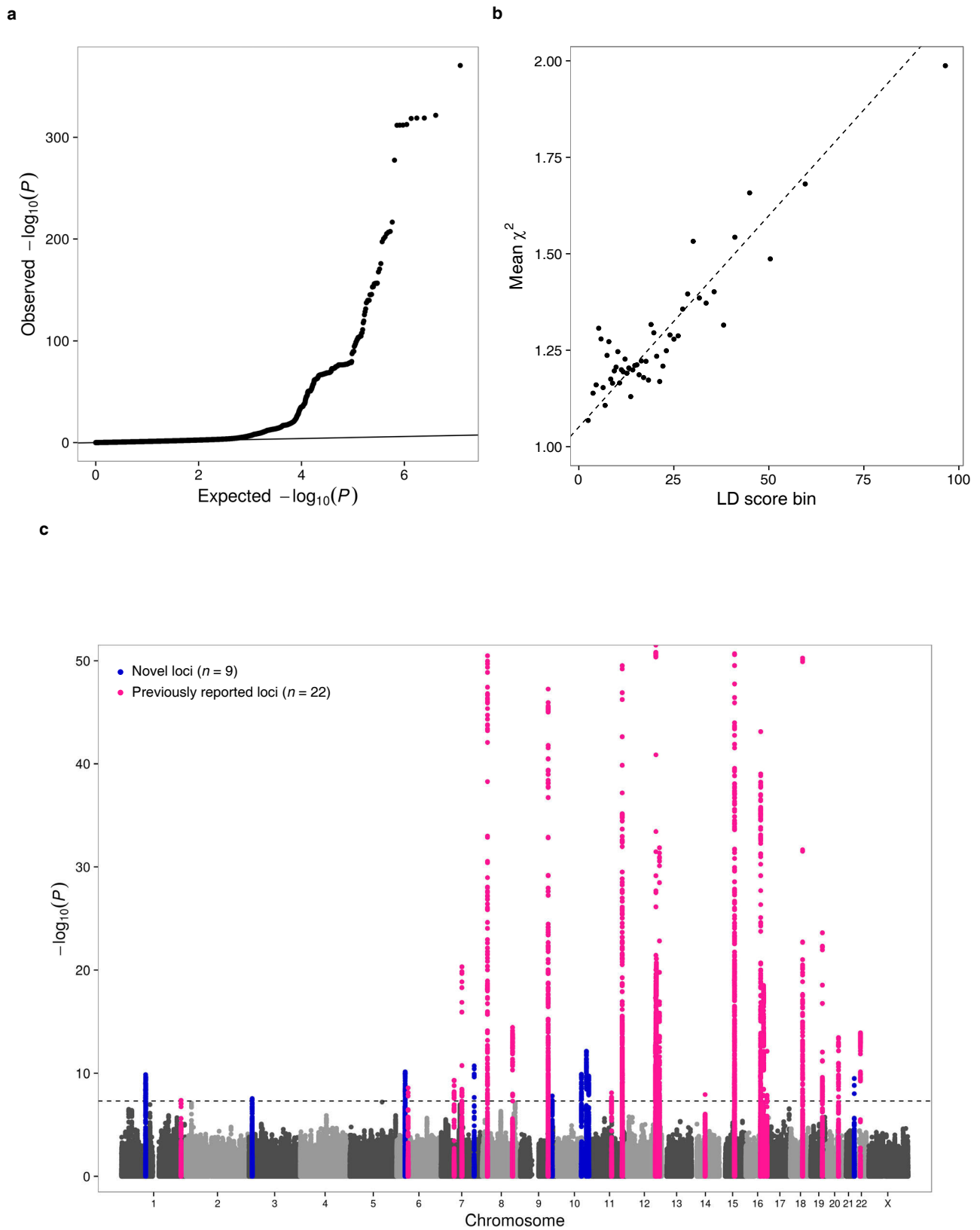
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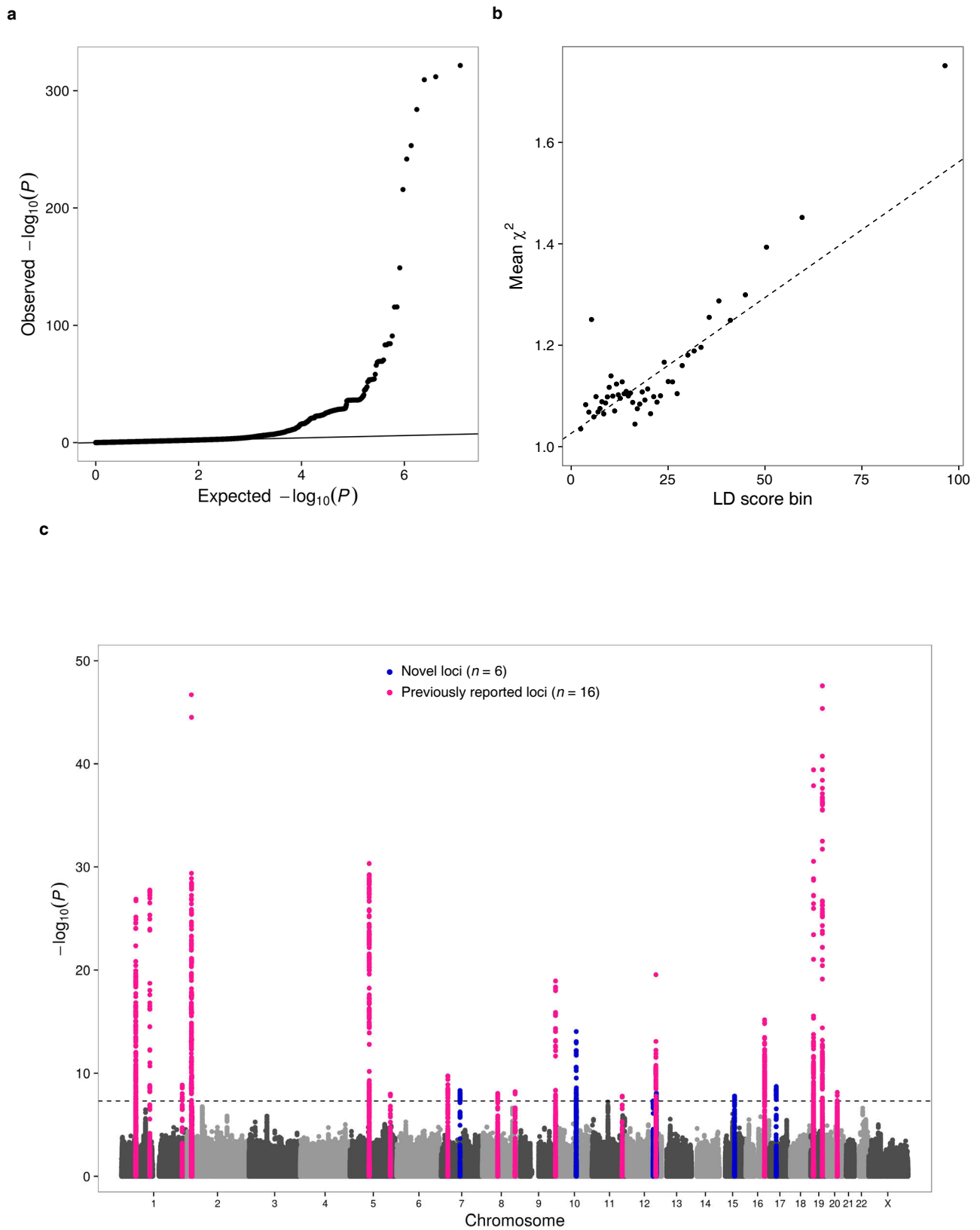
1.1 TC ($n = 128,305$)



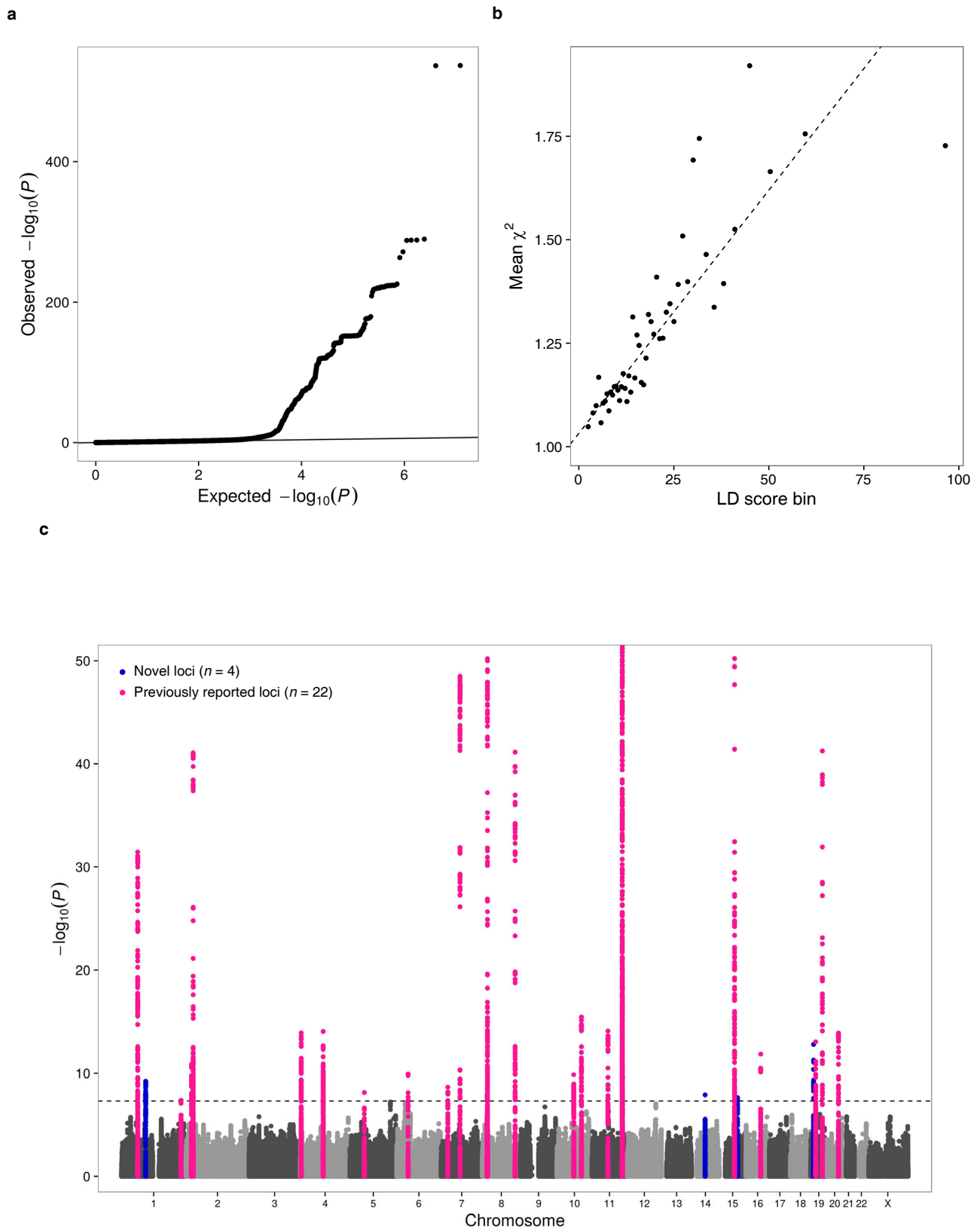
1.2 HDL-C ($n = 70,657$)



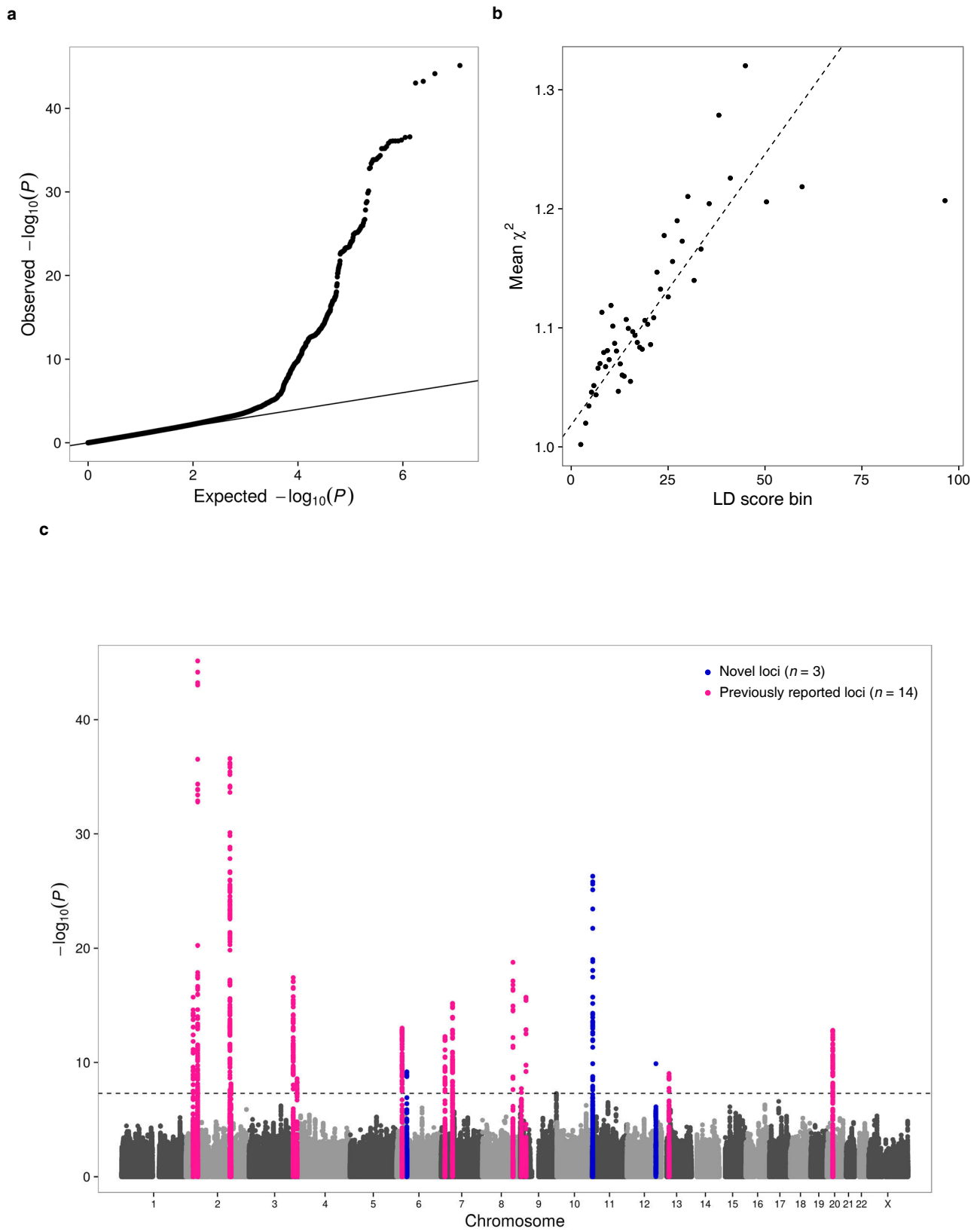
1.3 LDL-C ($n = 72,866$)



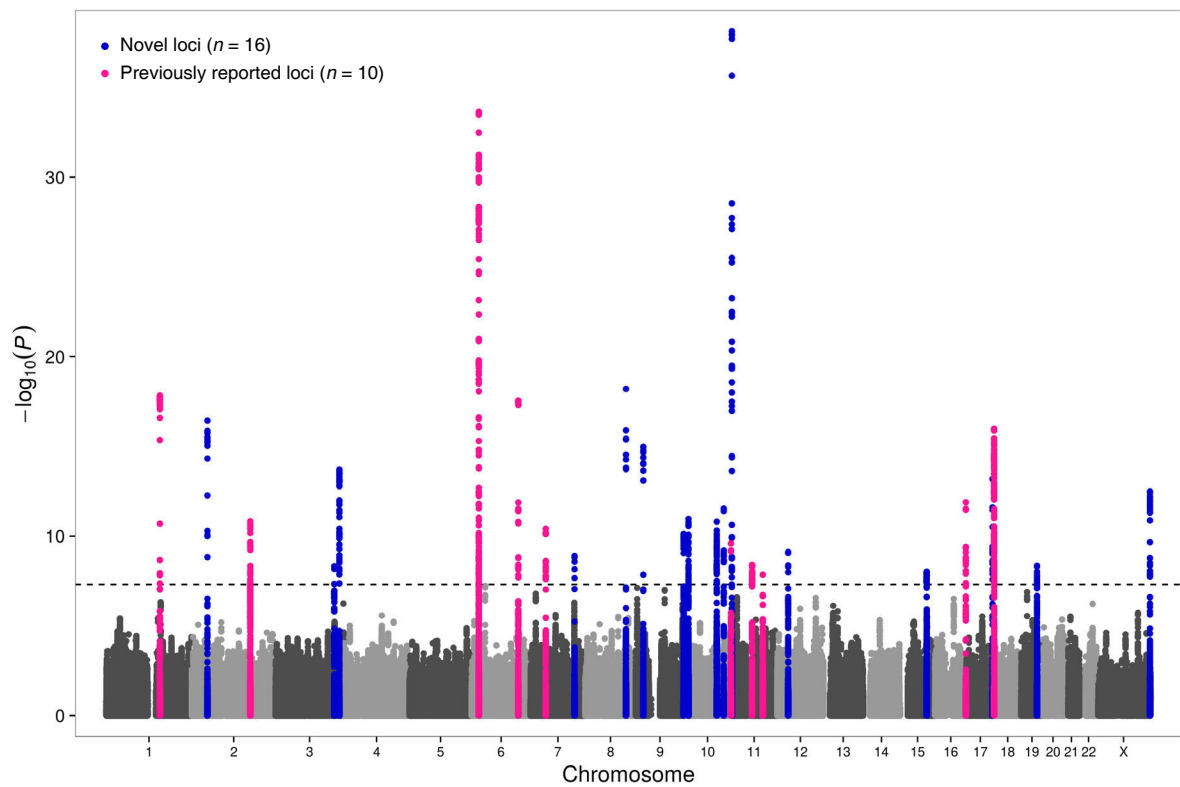
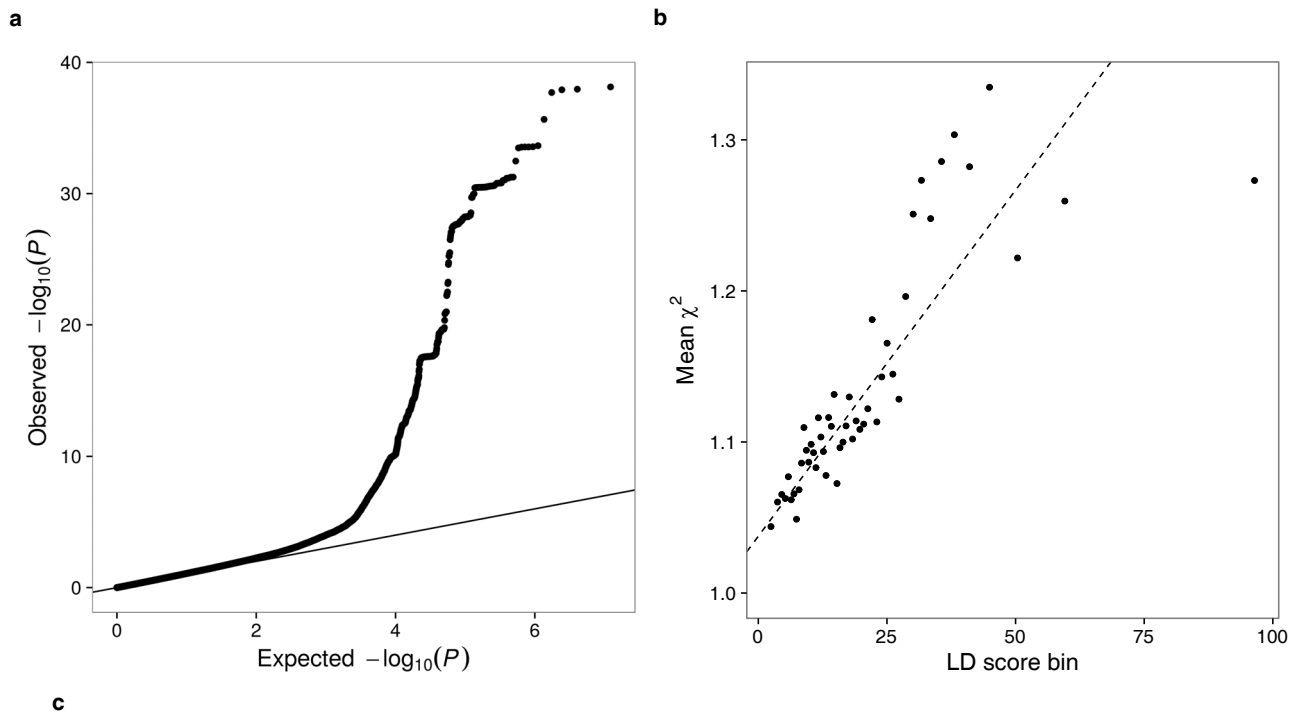
1.4 TG ($n = 105,597$)



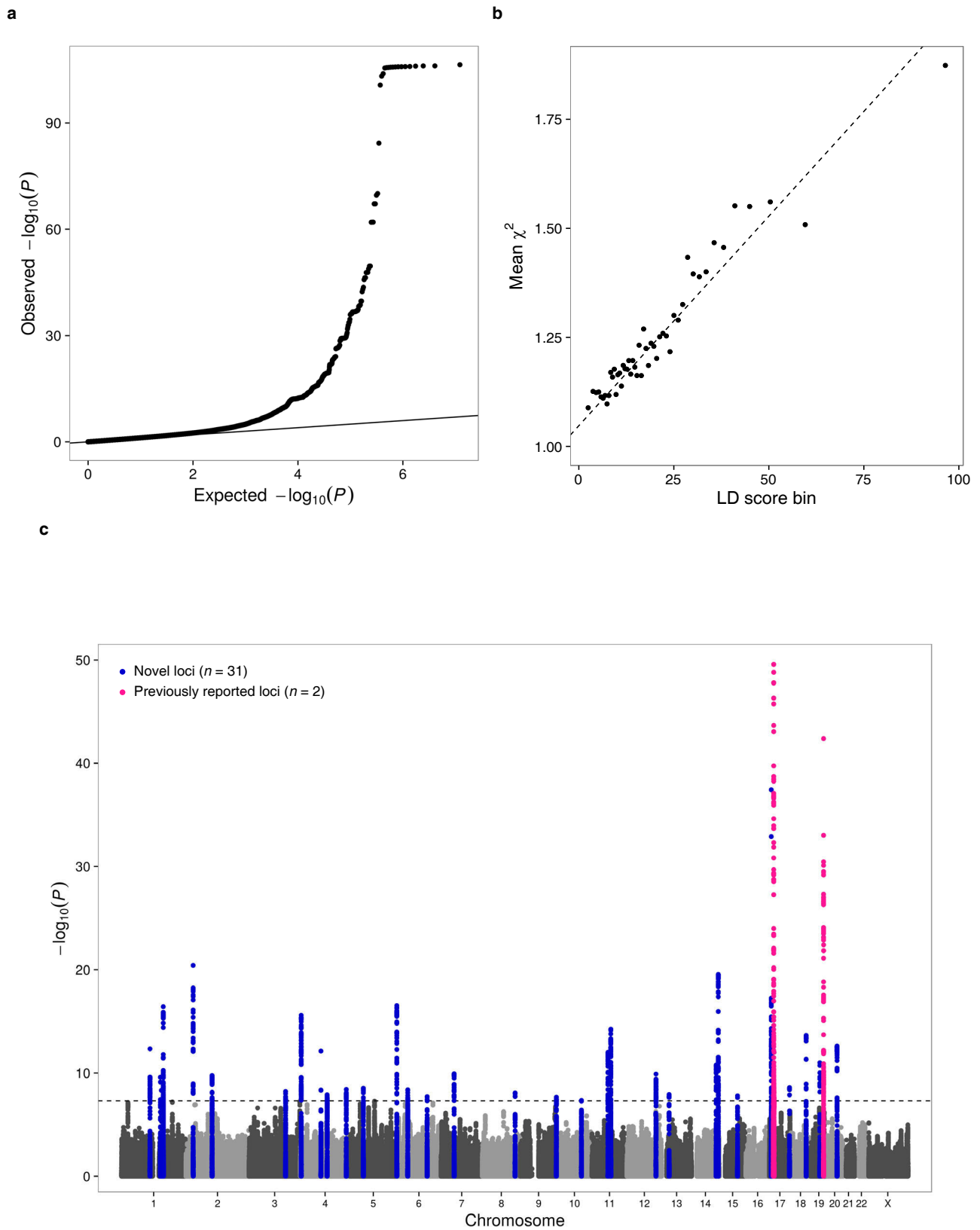
1.5 BS ($n = 93,146$)



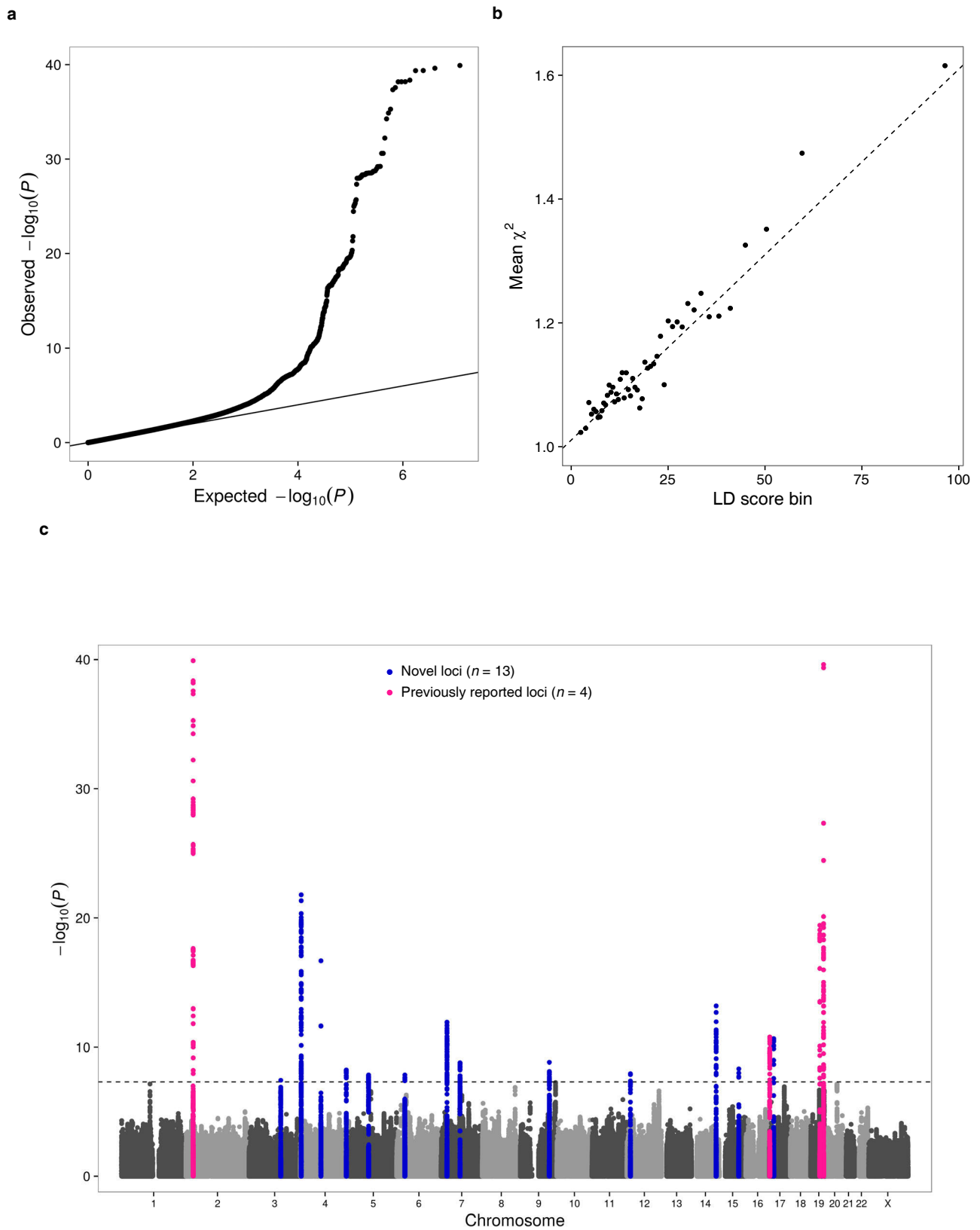
1.6 HbA1c ($n = 42,790$)



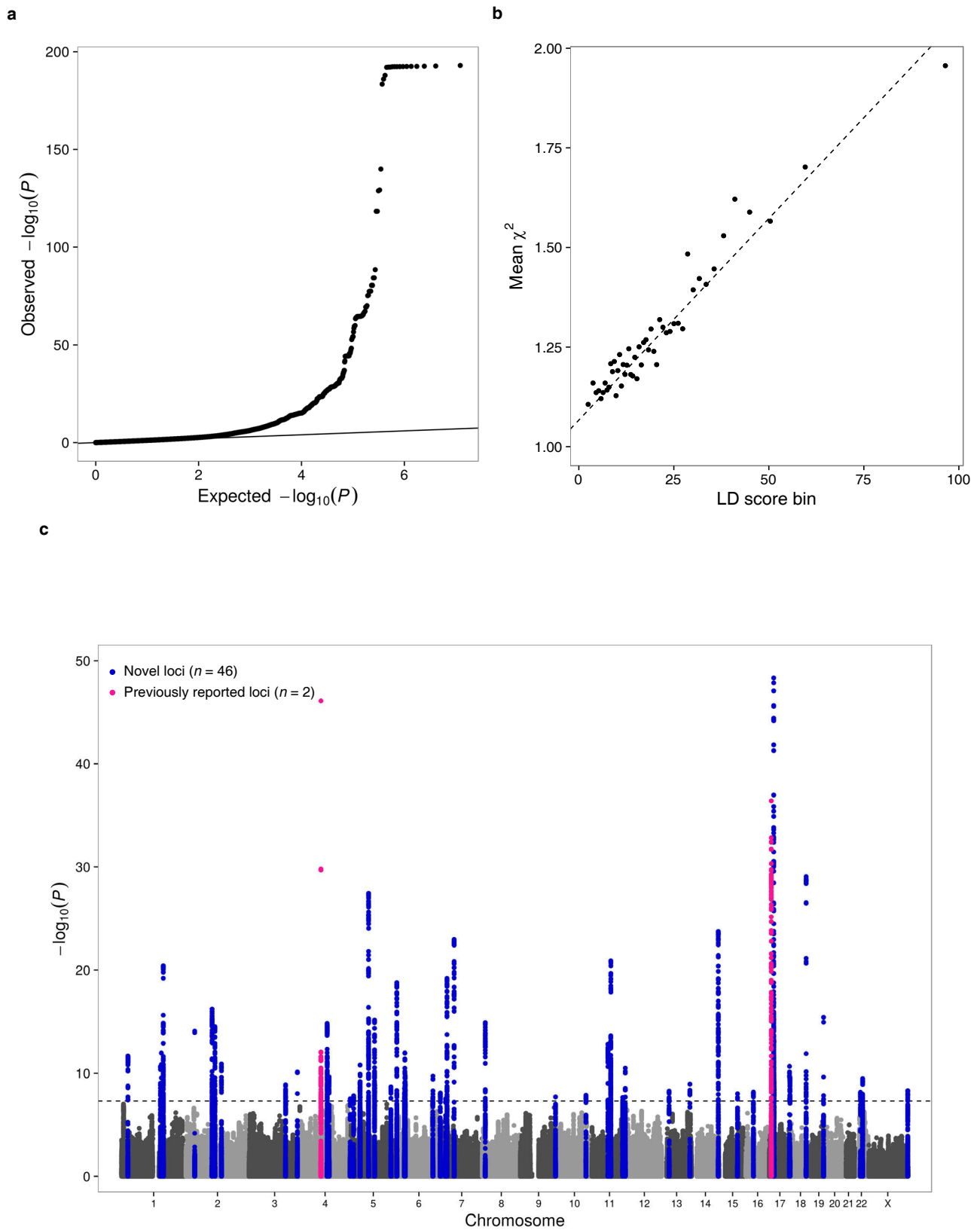
1.7 TP ($n = 113,509$)



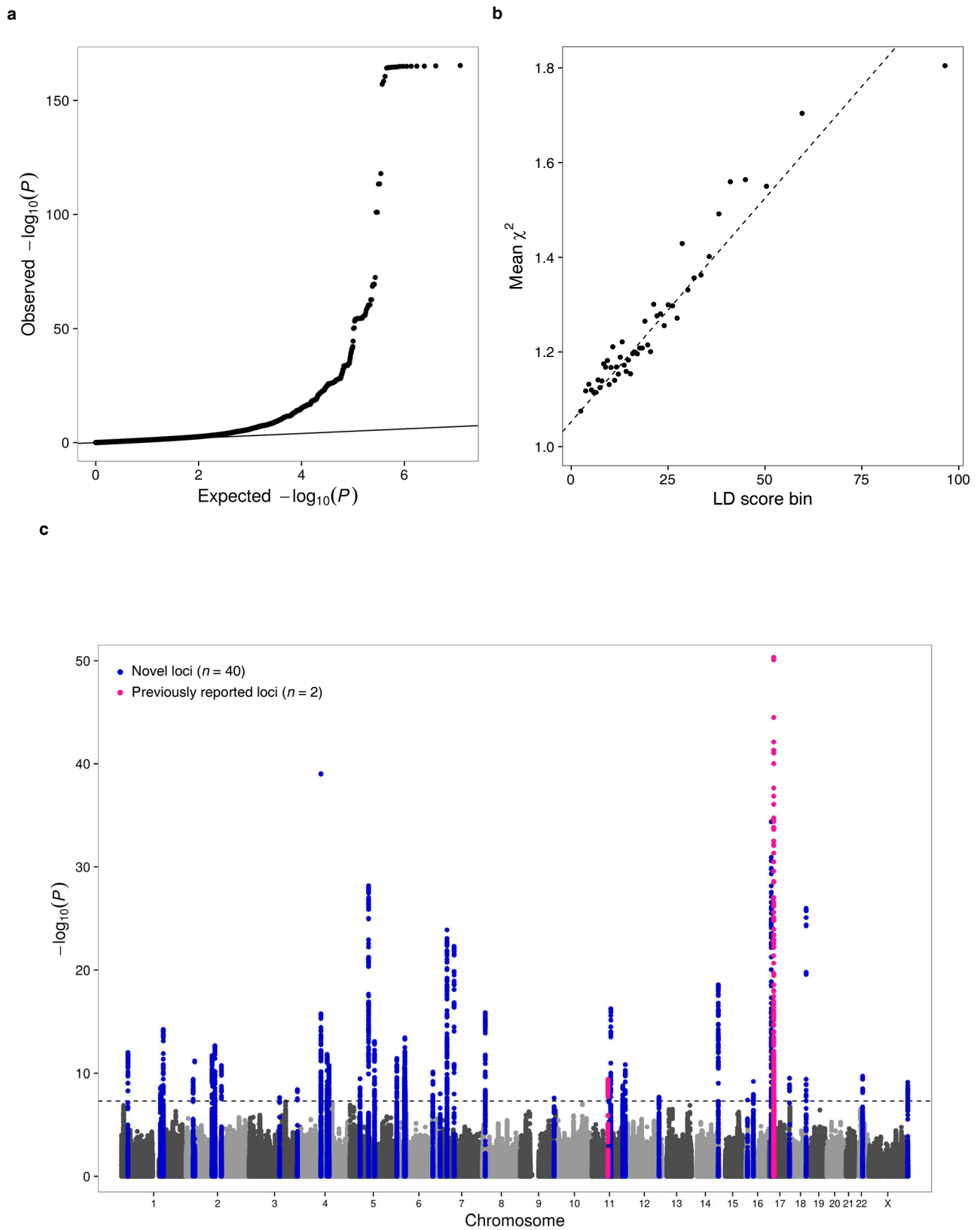
1.8 Alb ($n = 102,223$)



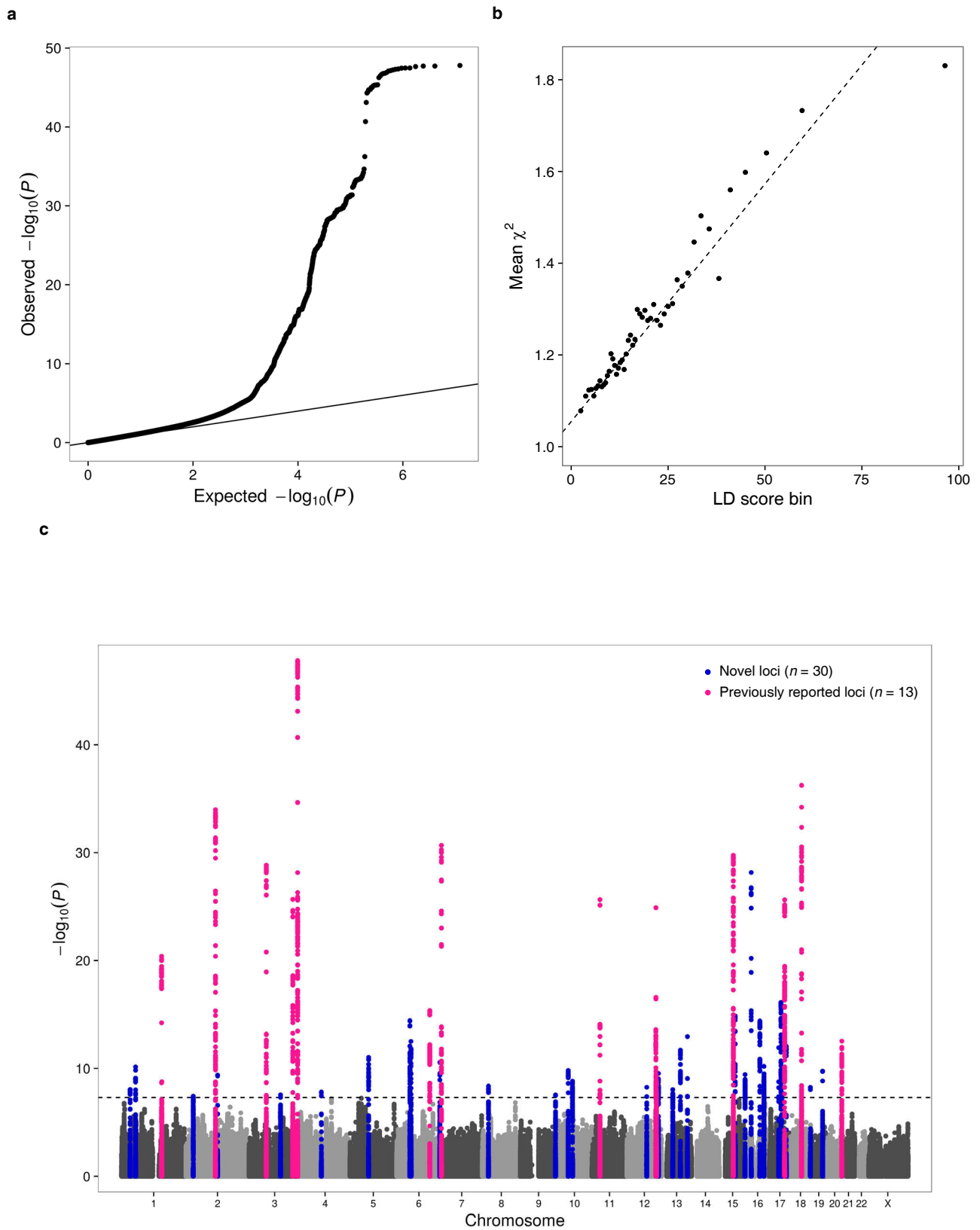
1.9 NAP ($n = 98,538$)



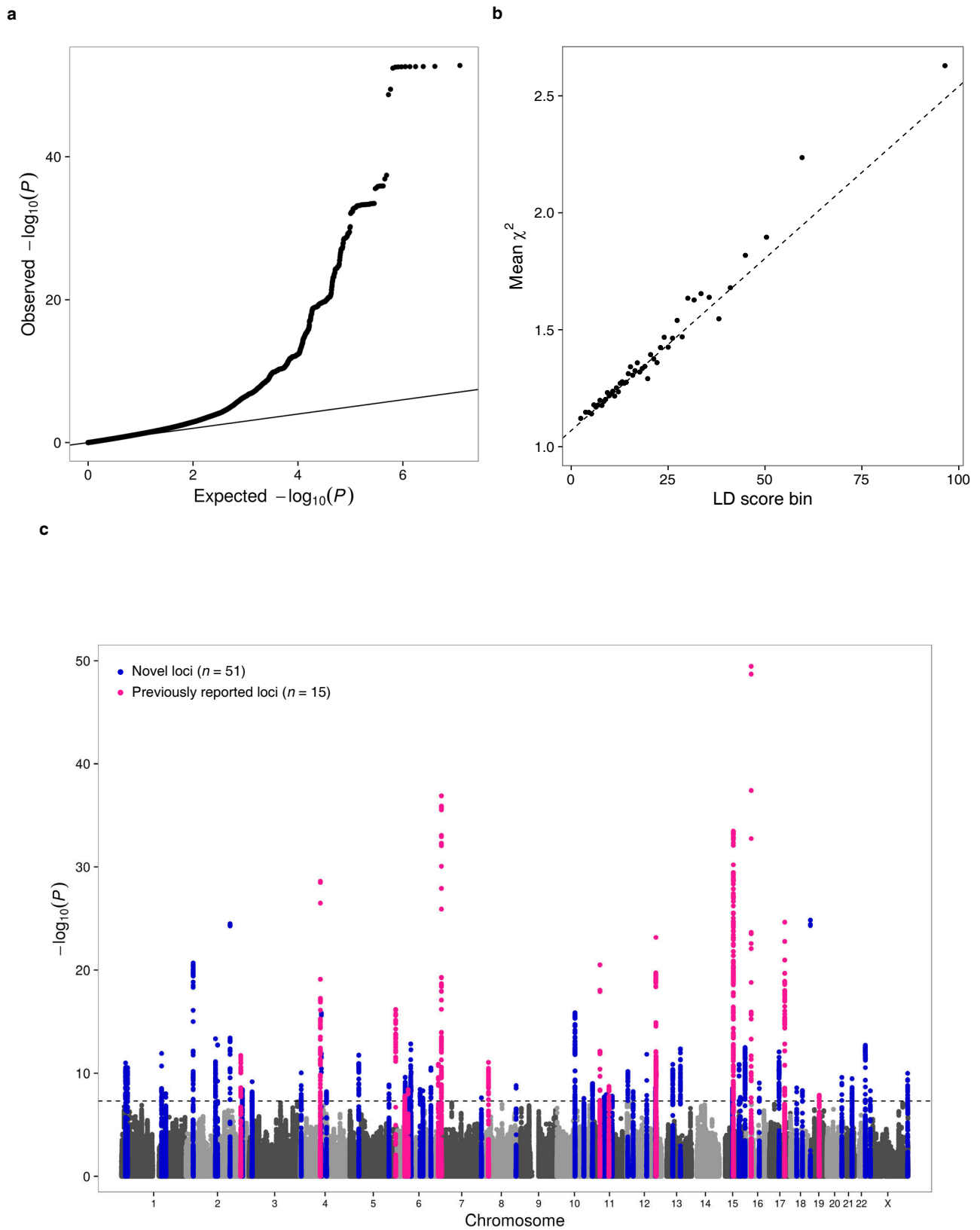
1.10 A/G ($n = 98,626$)



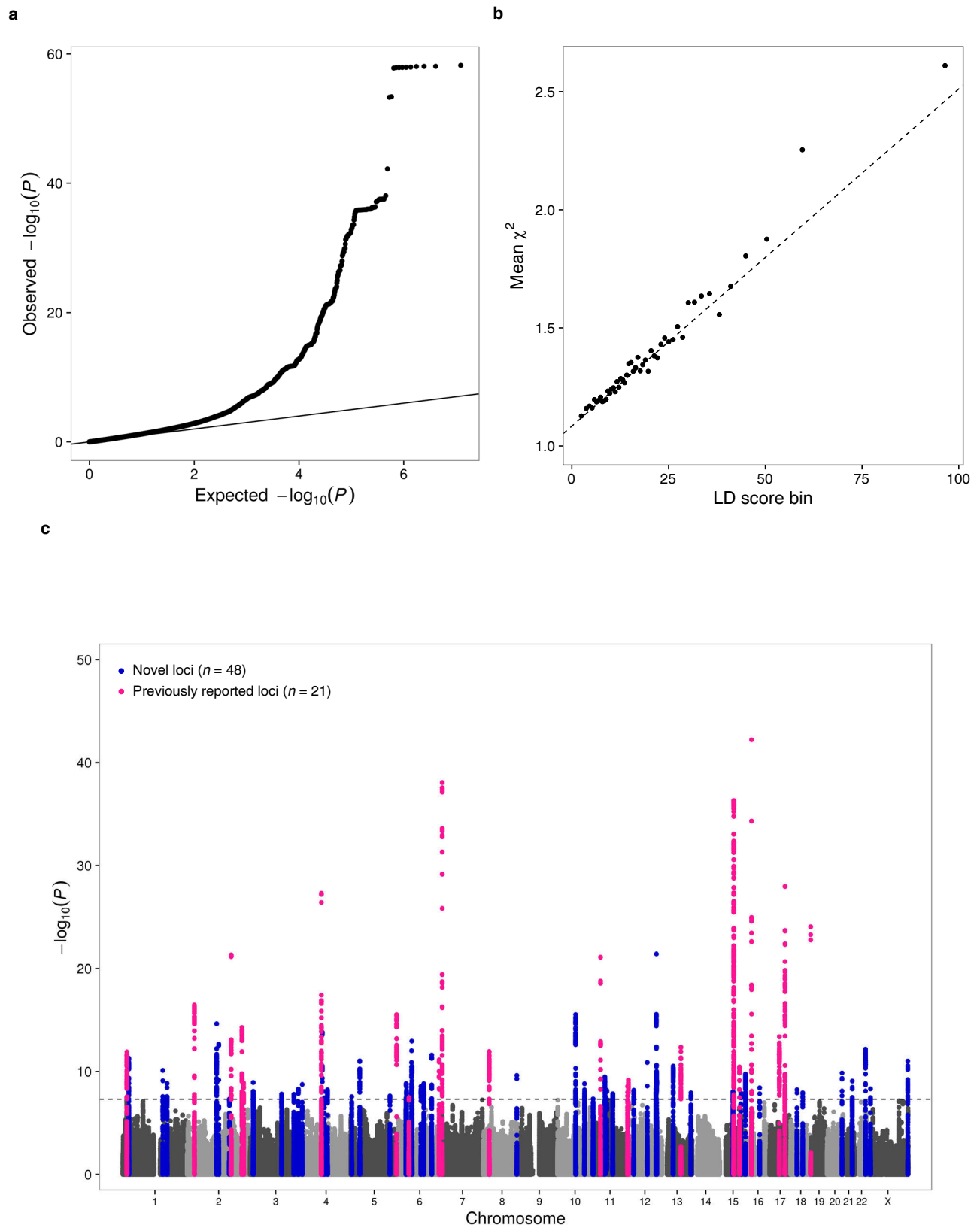
1.11 BUN ($n = 139,818$)



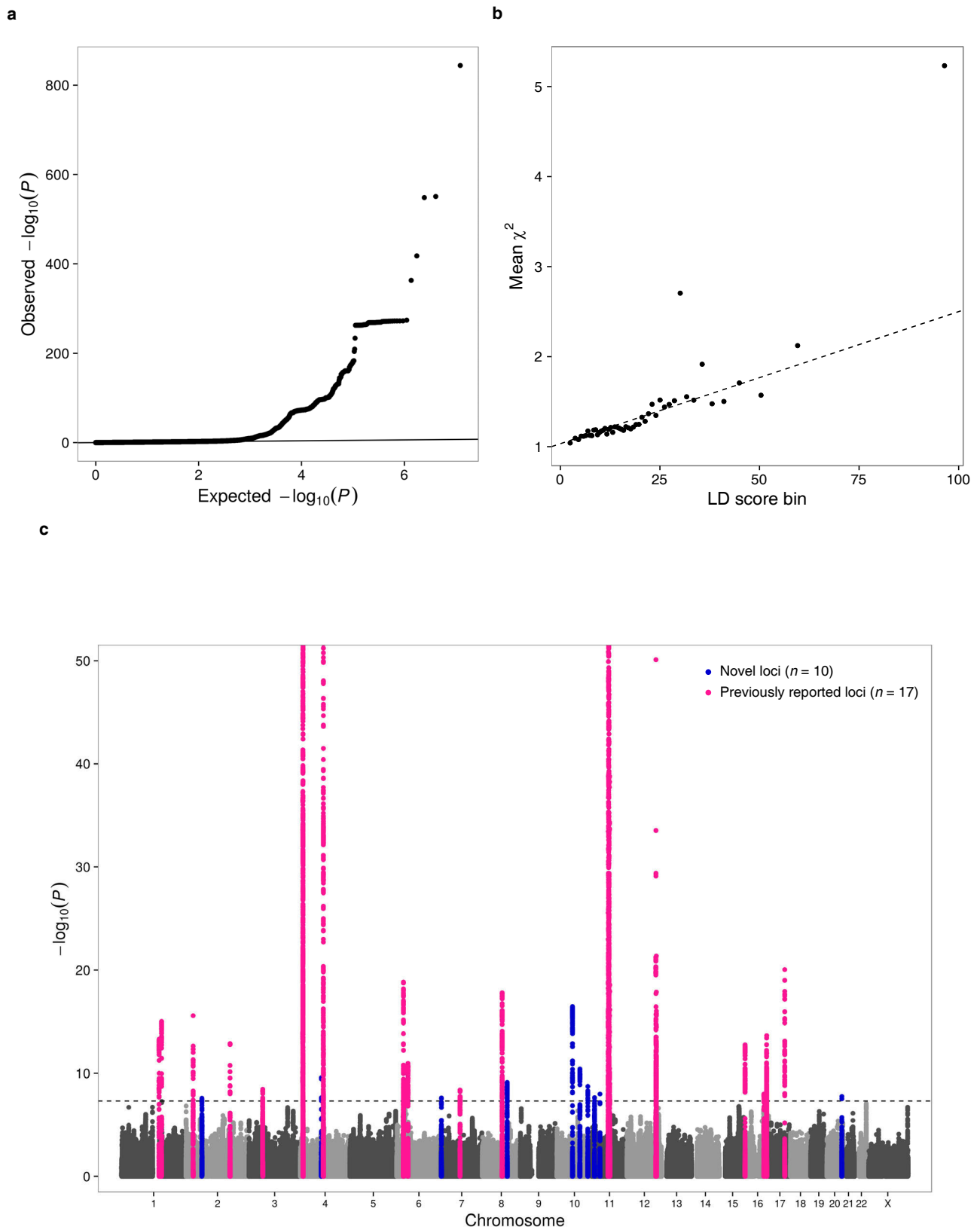
1.12 sCr ($n = 142,097$)



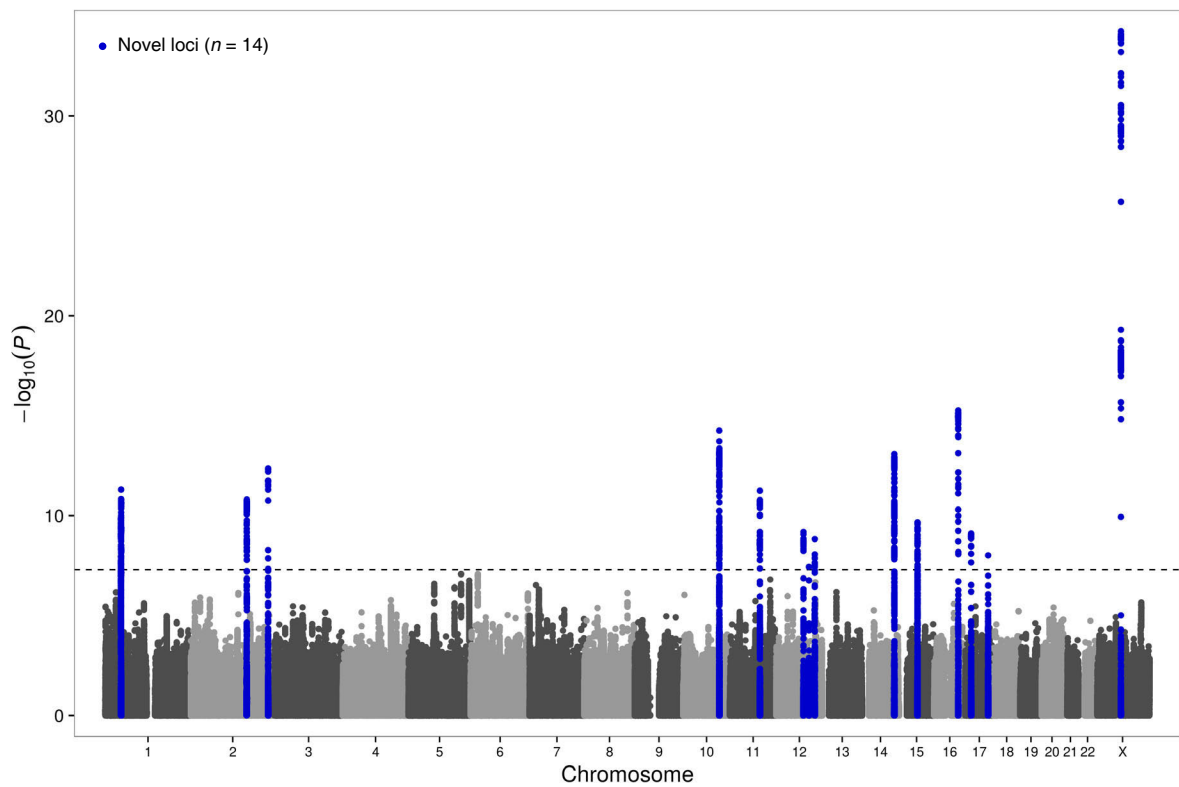
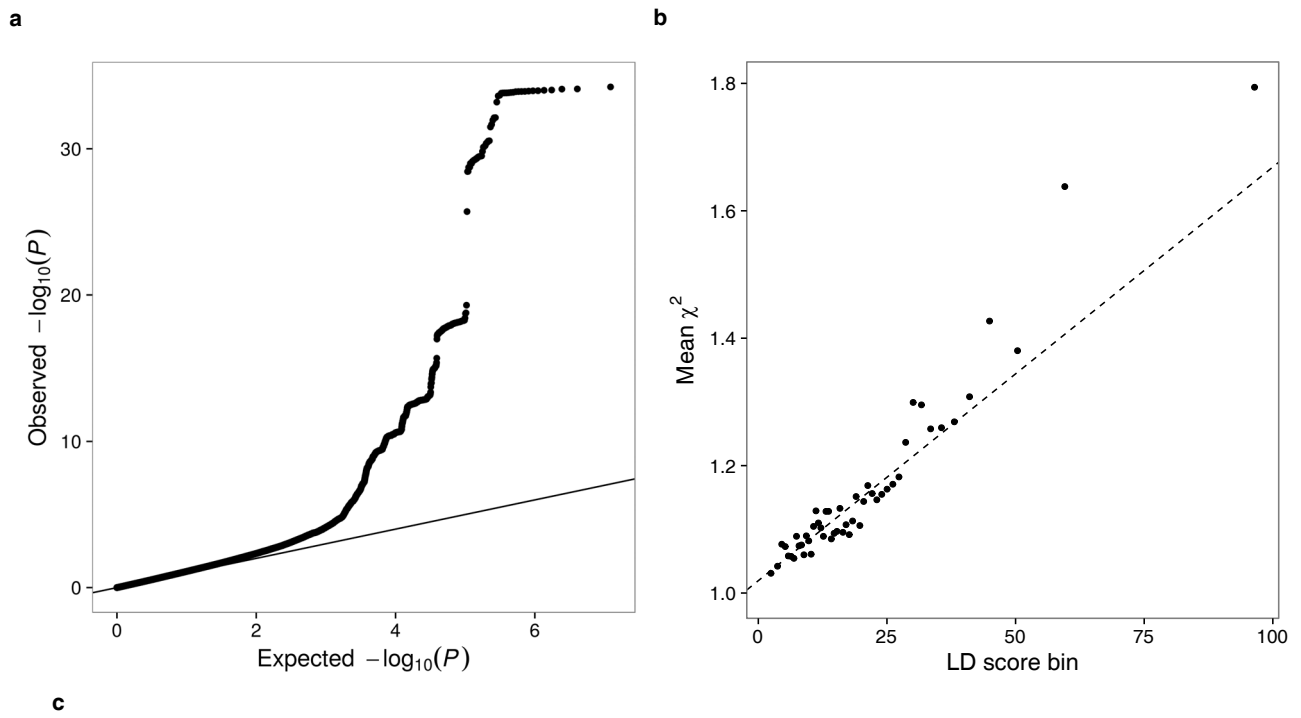
1.13 eGFR ($n = 143,658$)



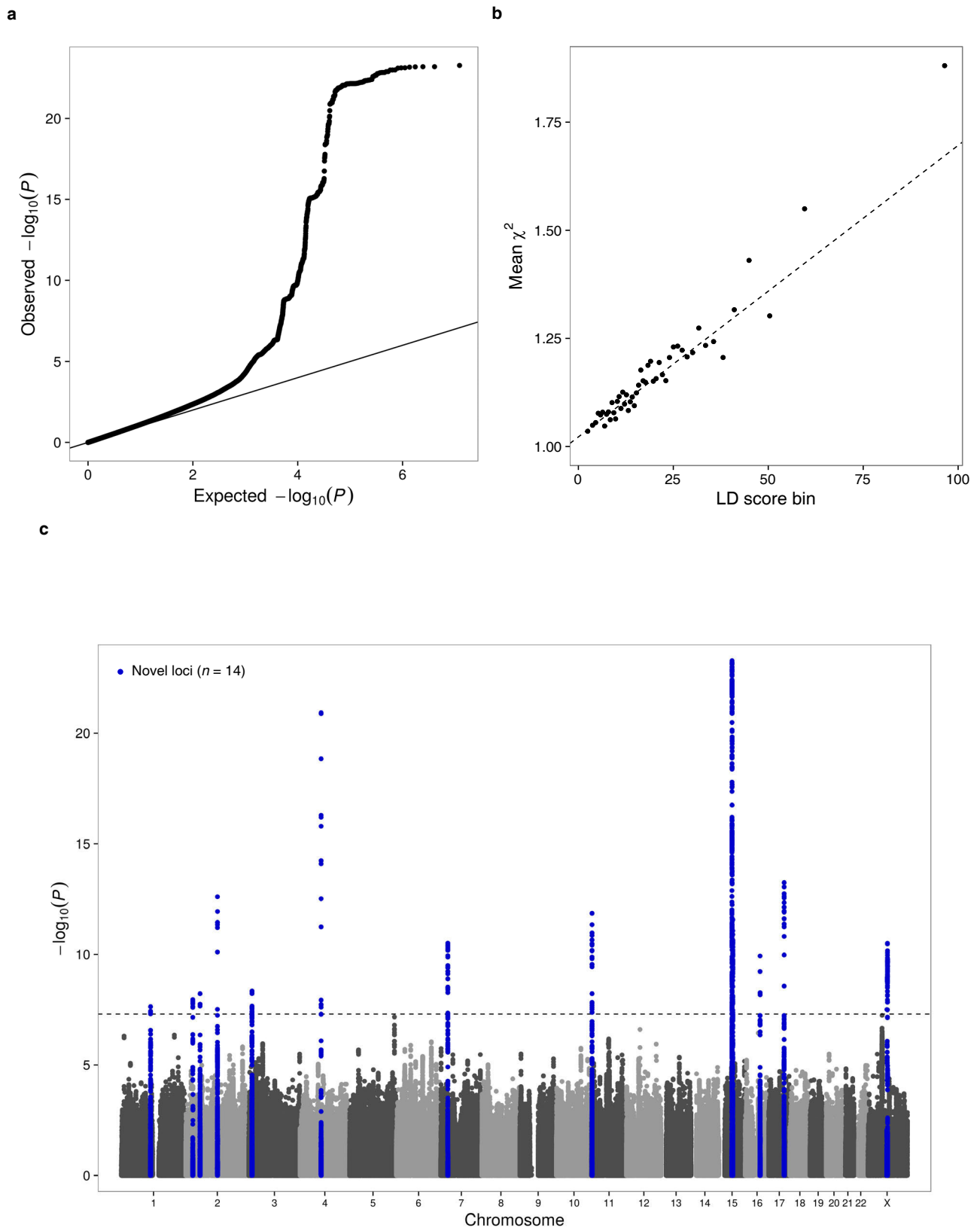
1.14 UA ($n = 109,029$)



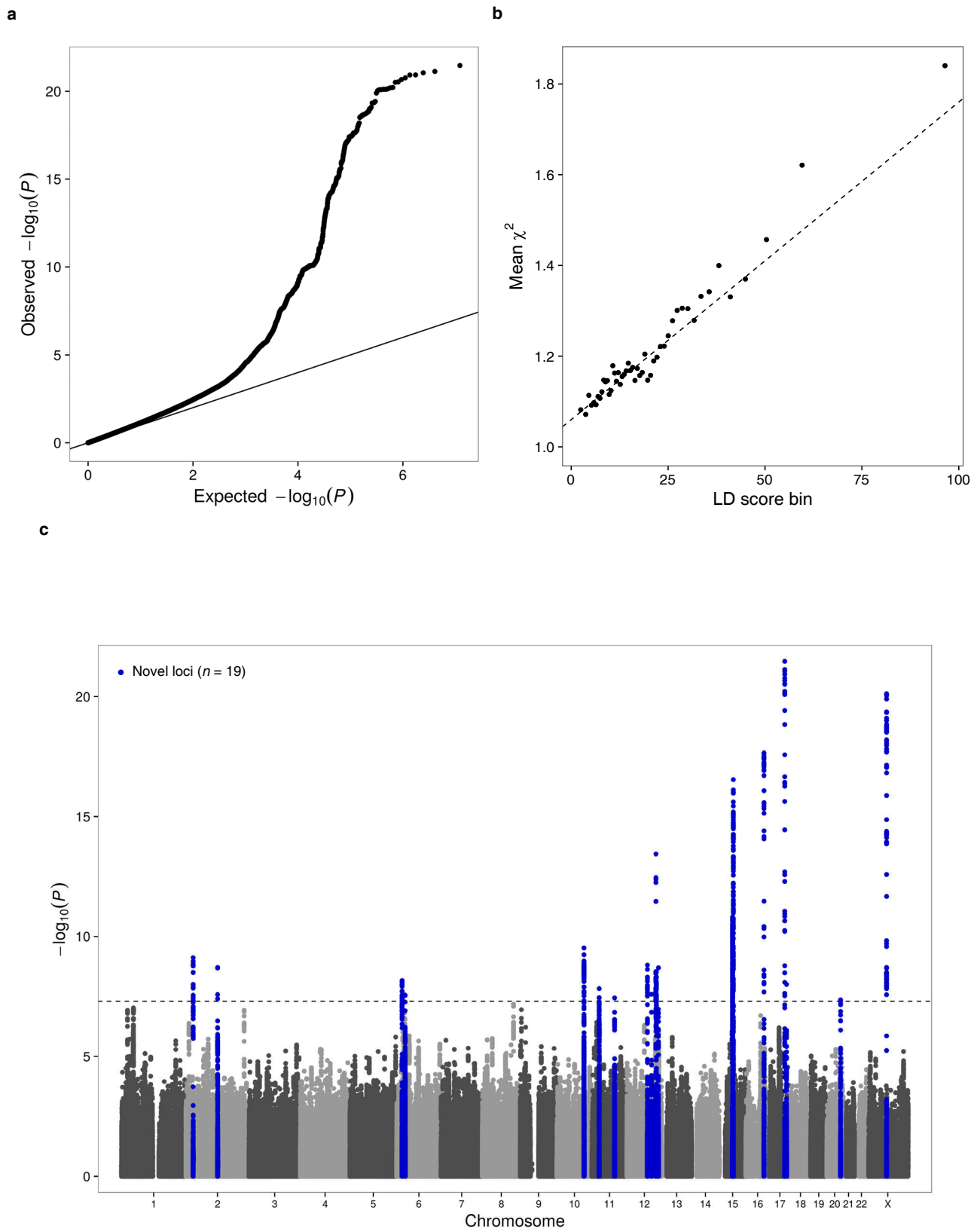
1.15 Na ($n = 127,304$)



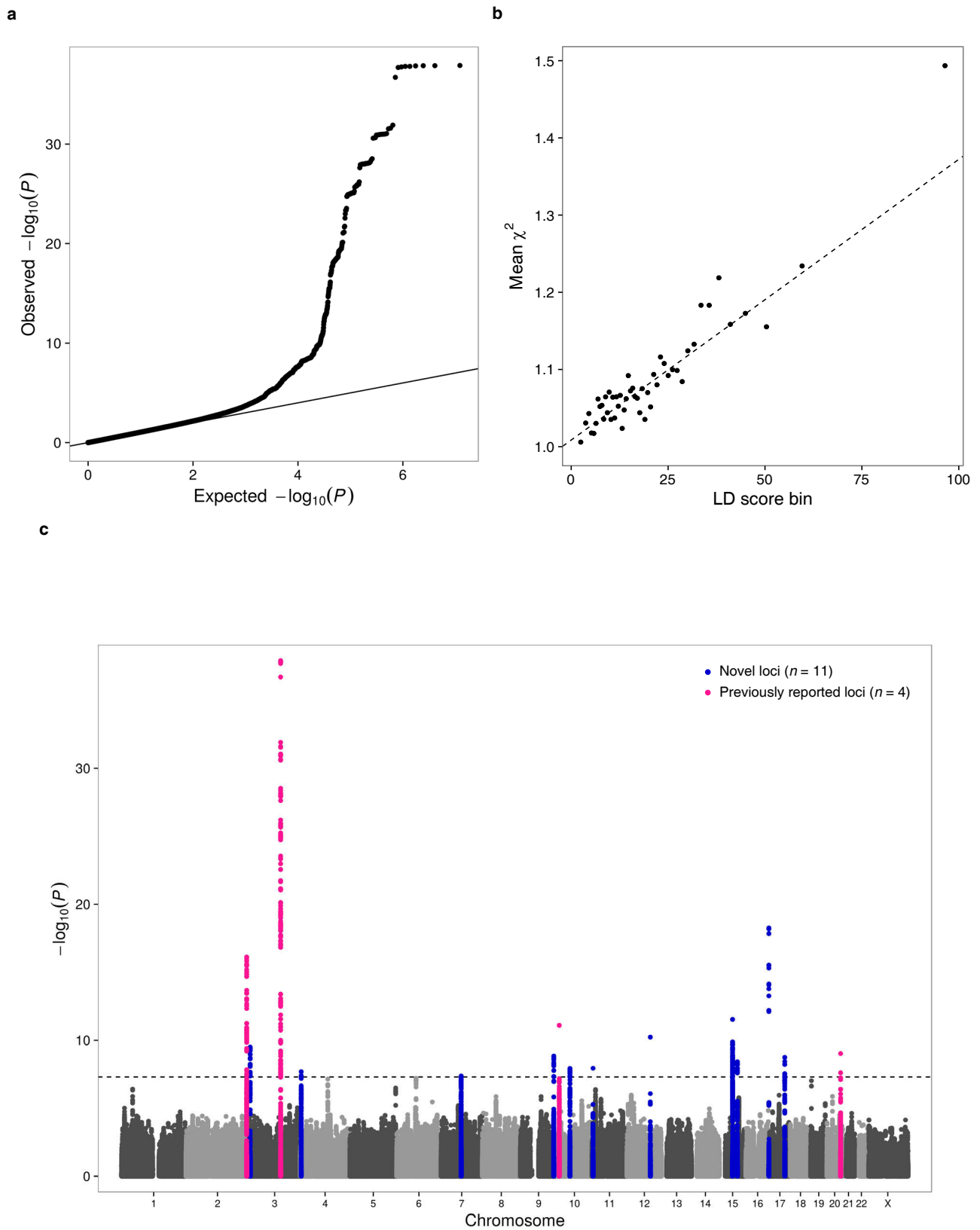
1.16 K ($n = 132,938$)



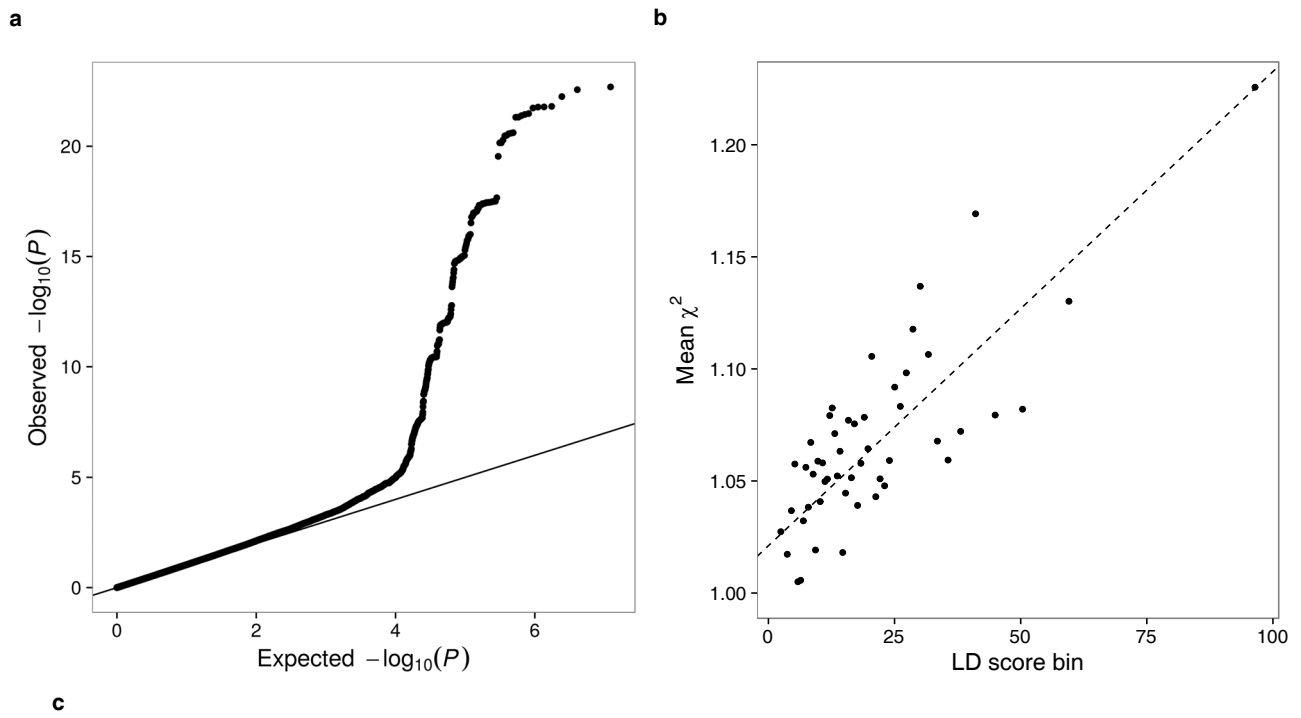
1.17 CI ($n = 126,402$)



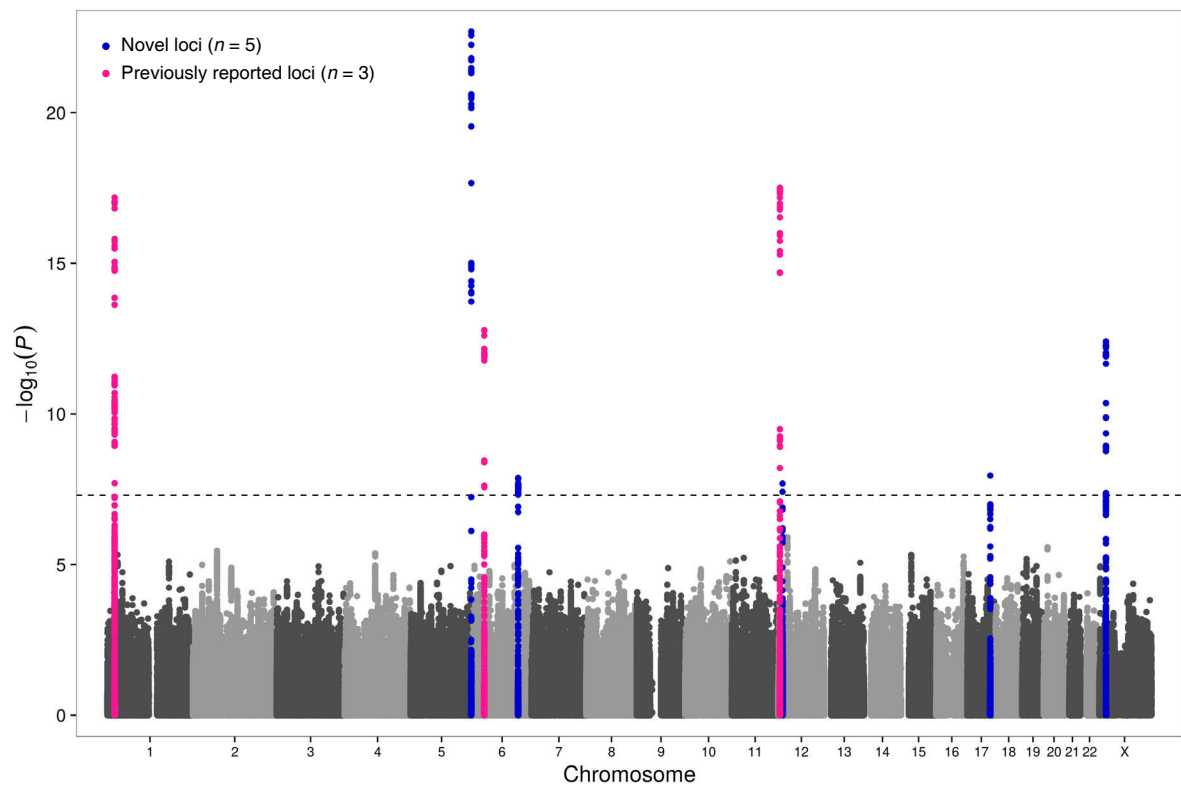
1.18 Ca ($n = 71,701$)



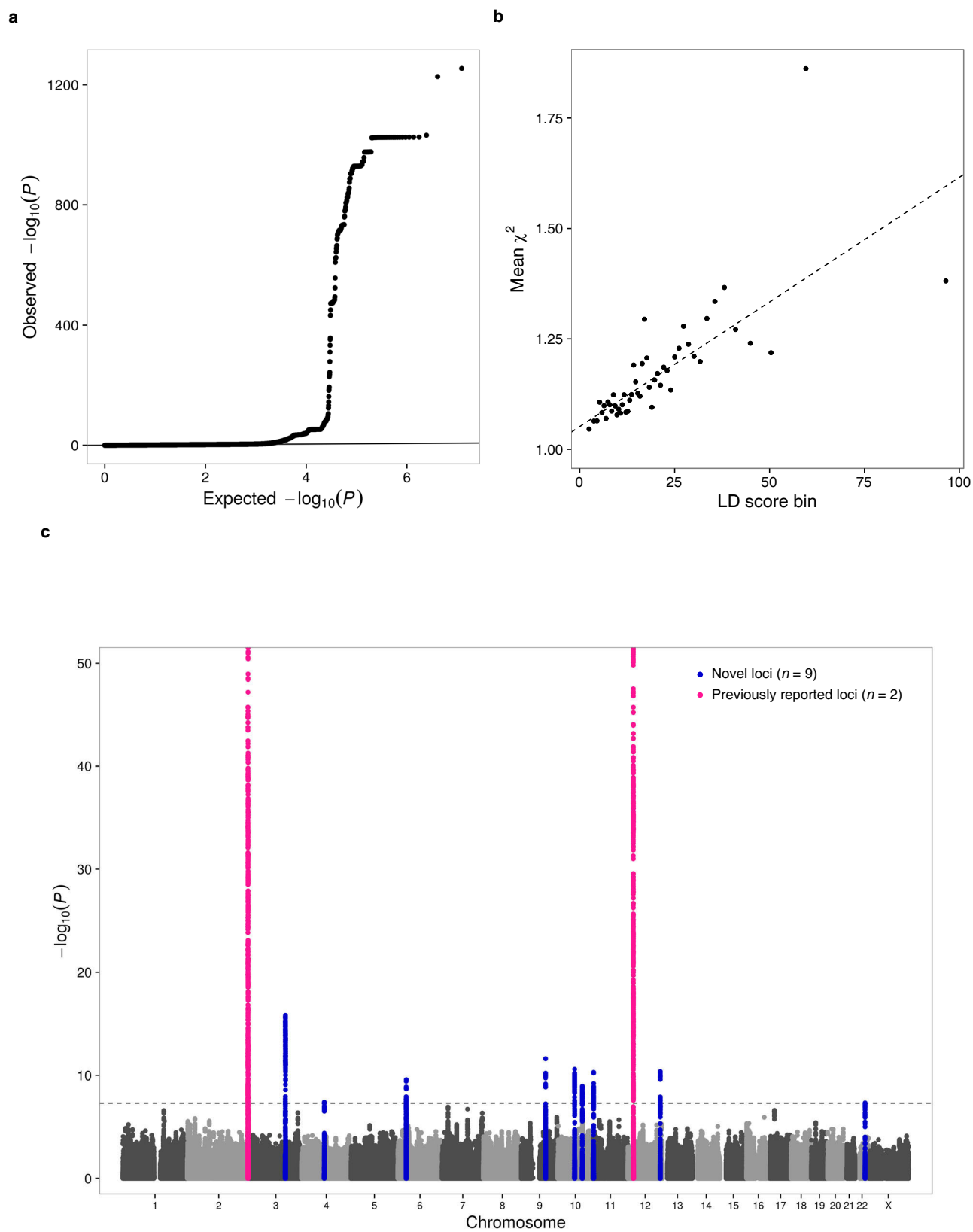
1.19 P ($n = 42,793$)



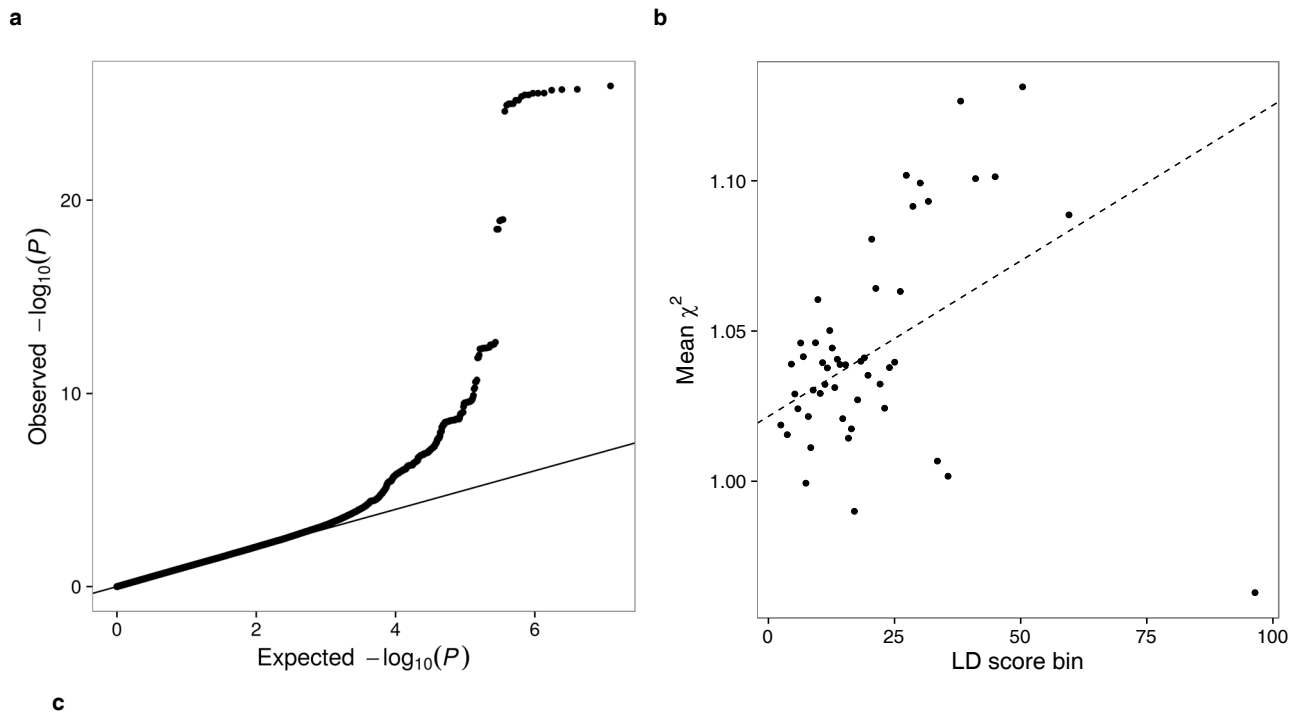
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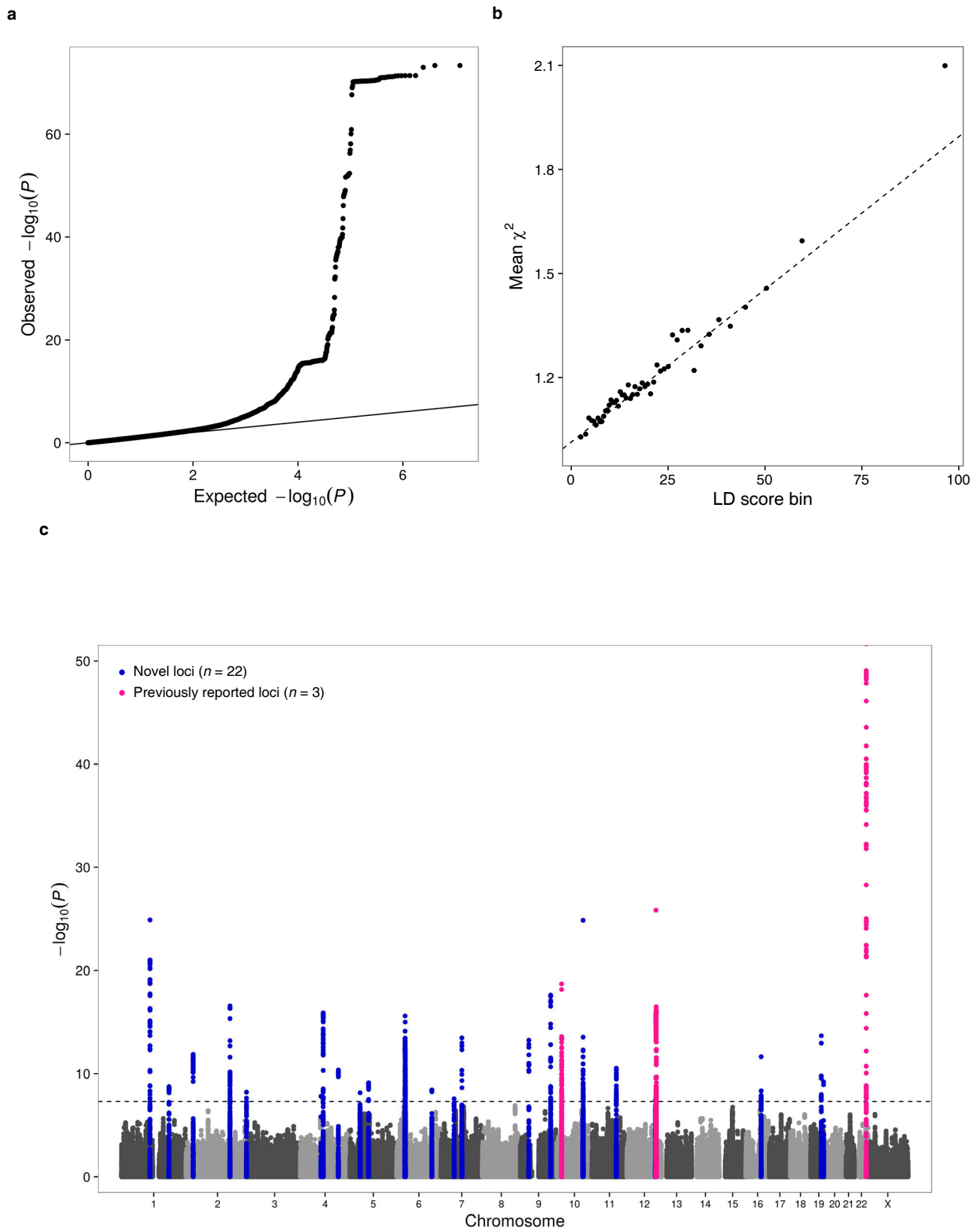
1.20 TBil ($n = 110,207$)



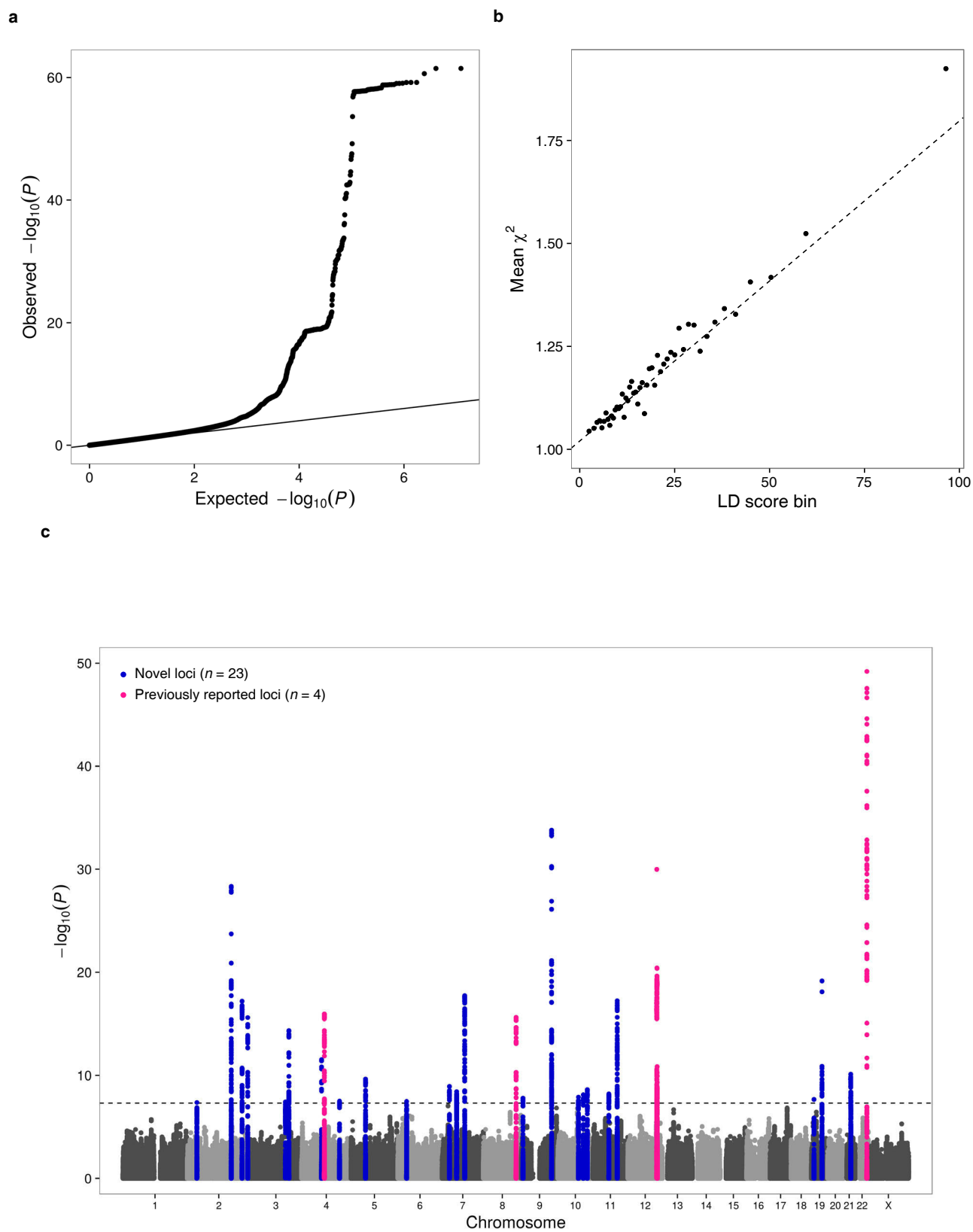
1.21 ZTT ($n = 12,303$)



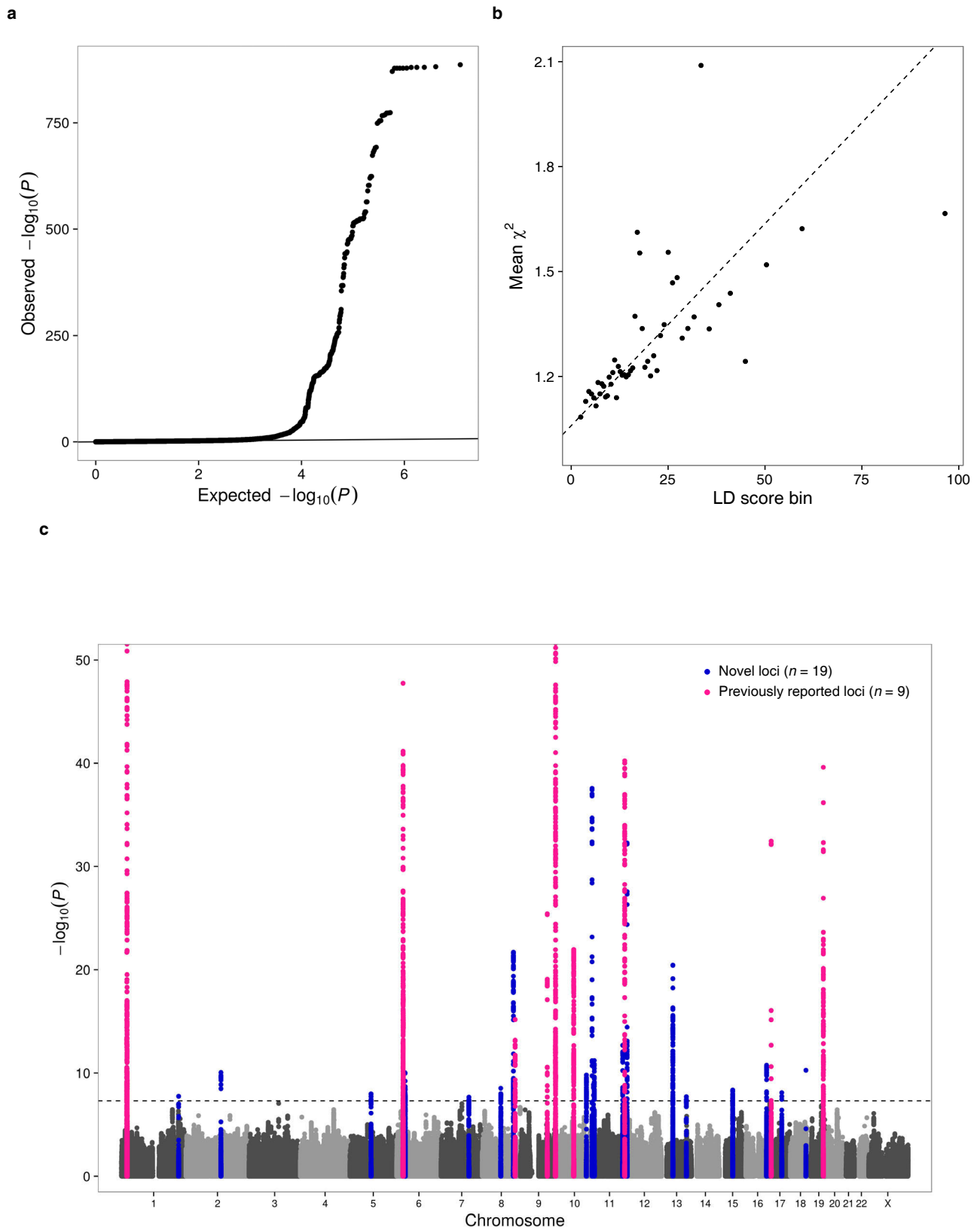
1.22 AST ($n = 134,154$)



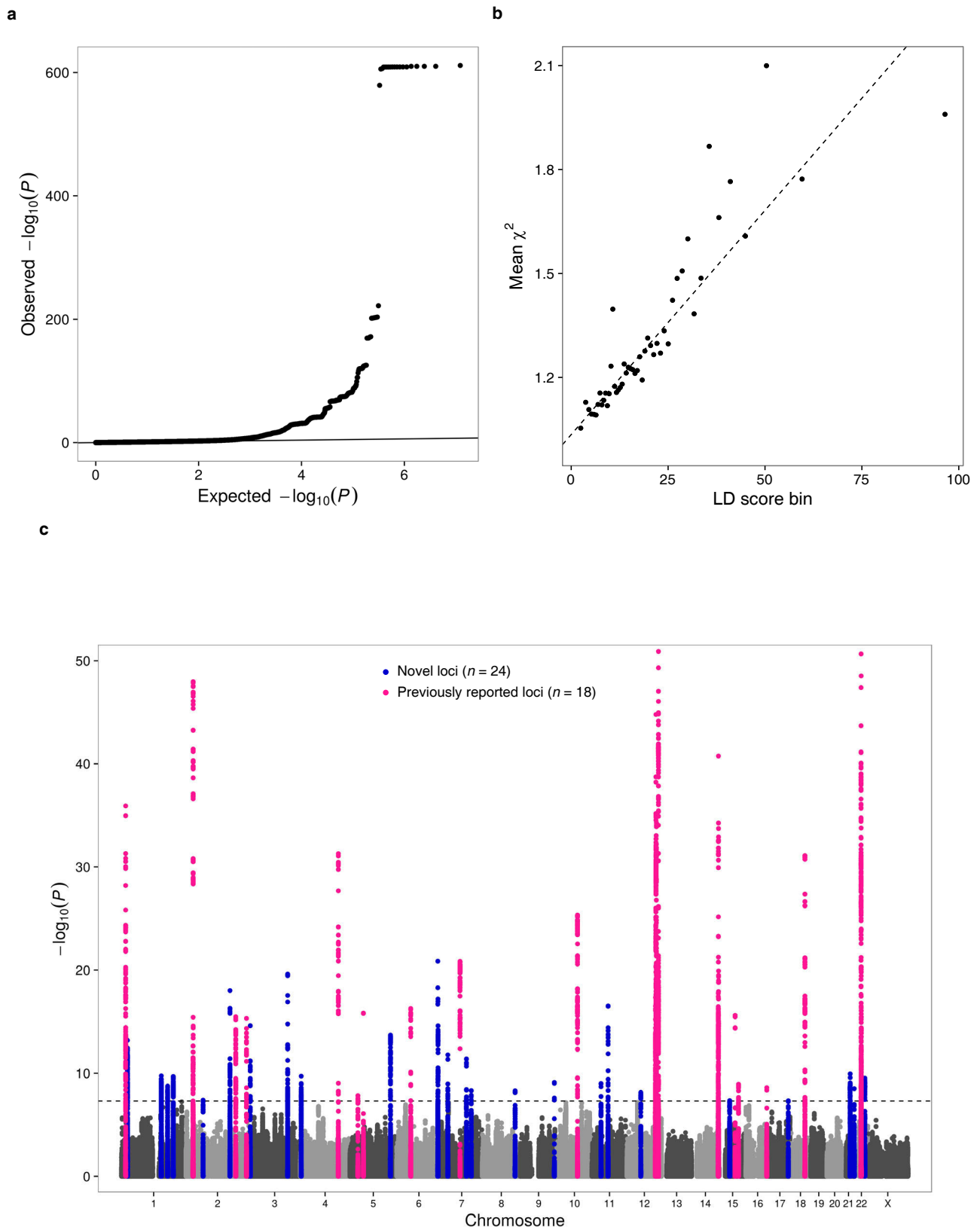
1.23 ALT ($n = 134,182$)



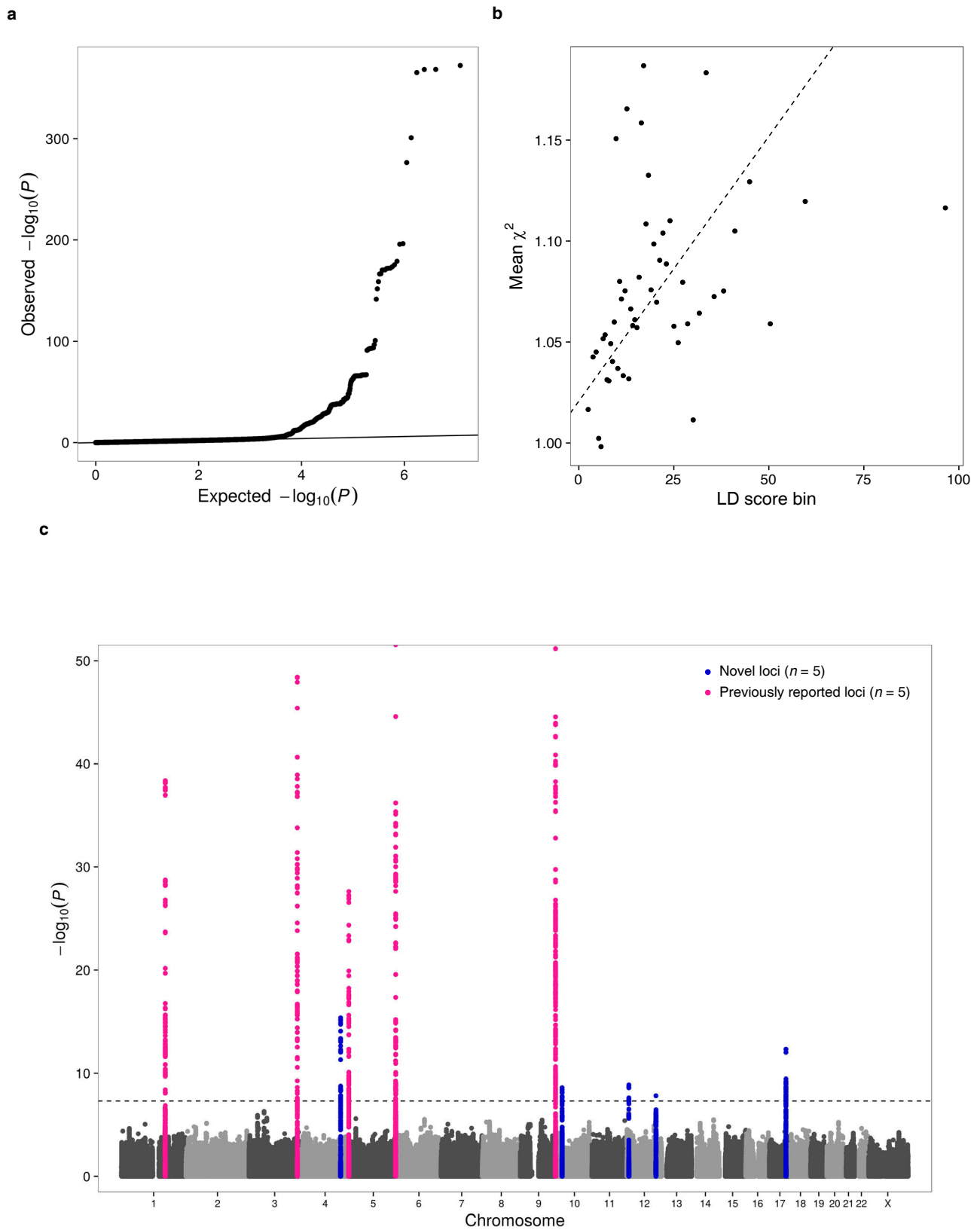
1.24 ALP ($n = 105,030$)



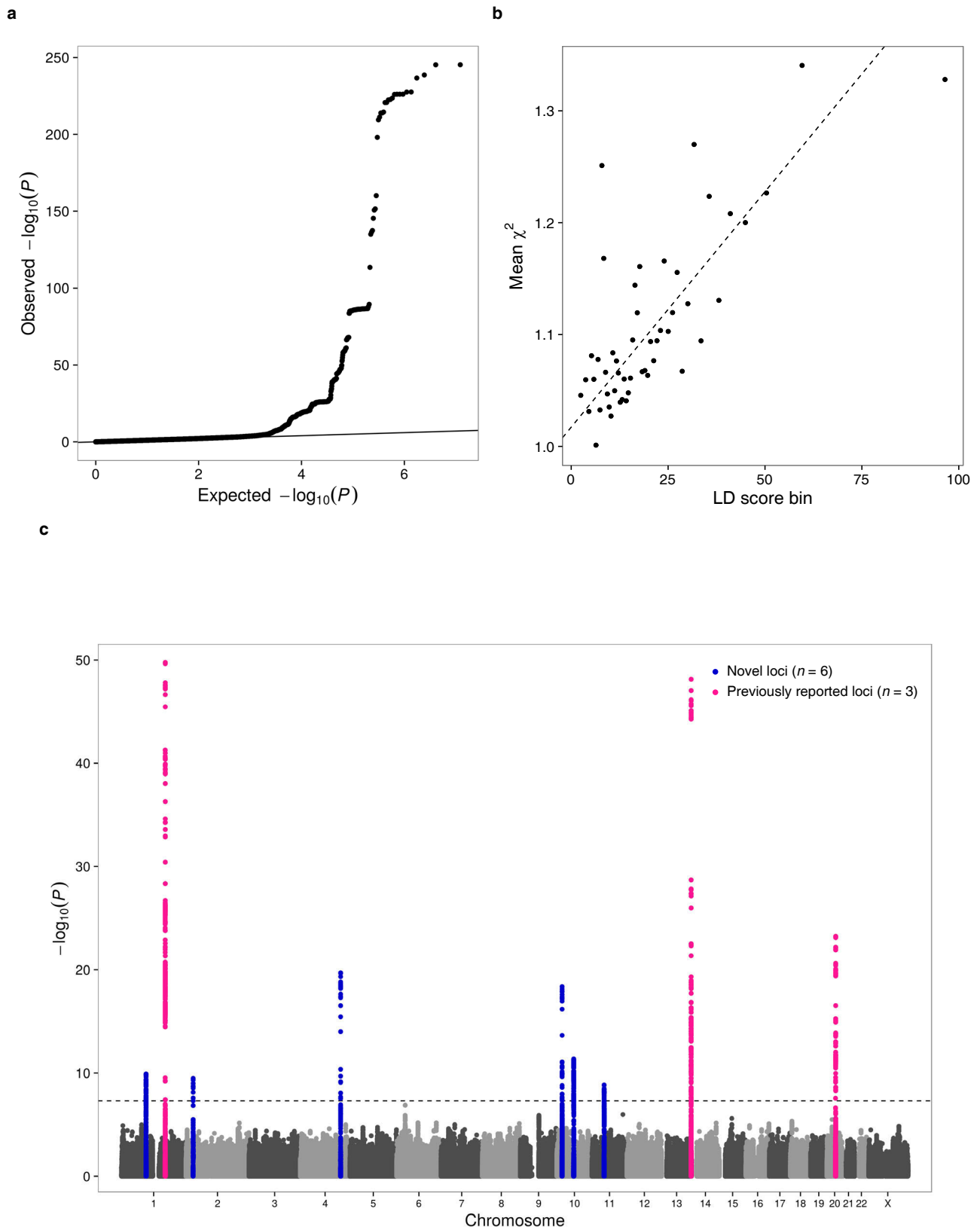
1.25 GGT ($n = 118,309$)



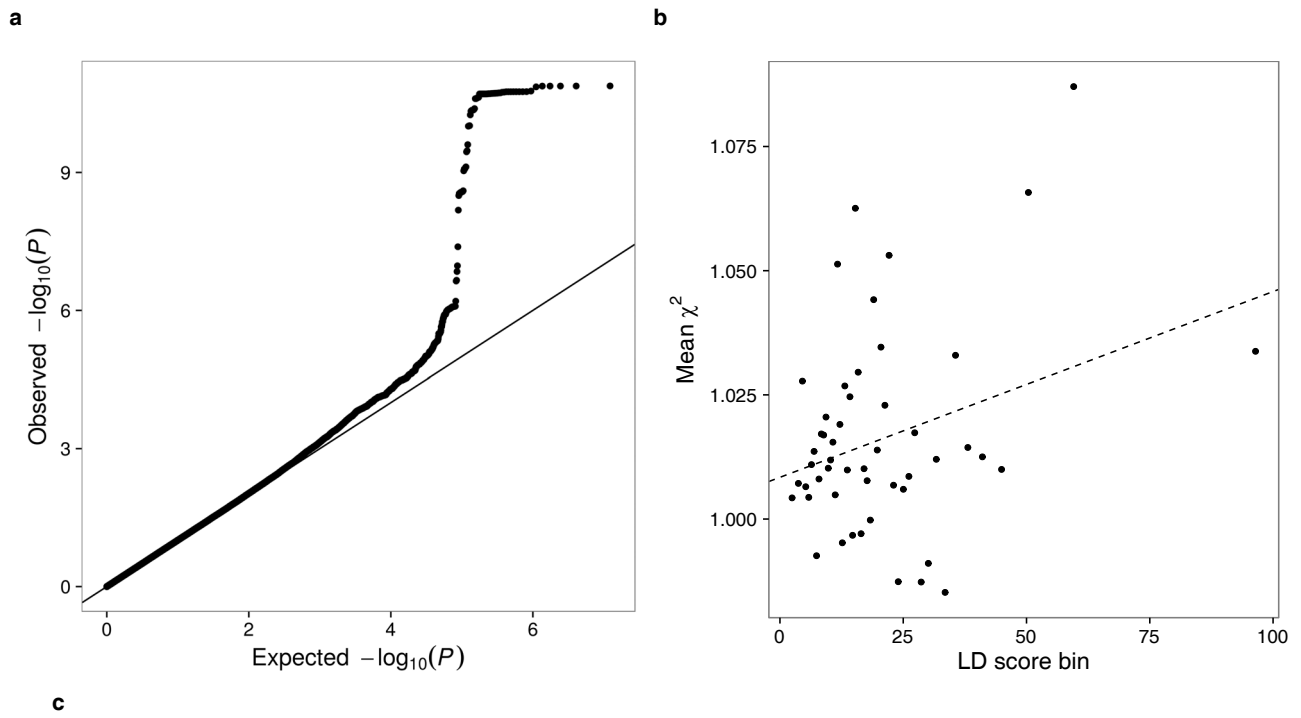
1.26 APTT ($n = 37,767$)



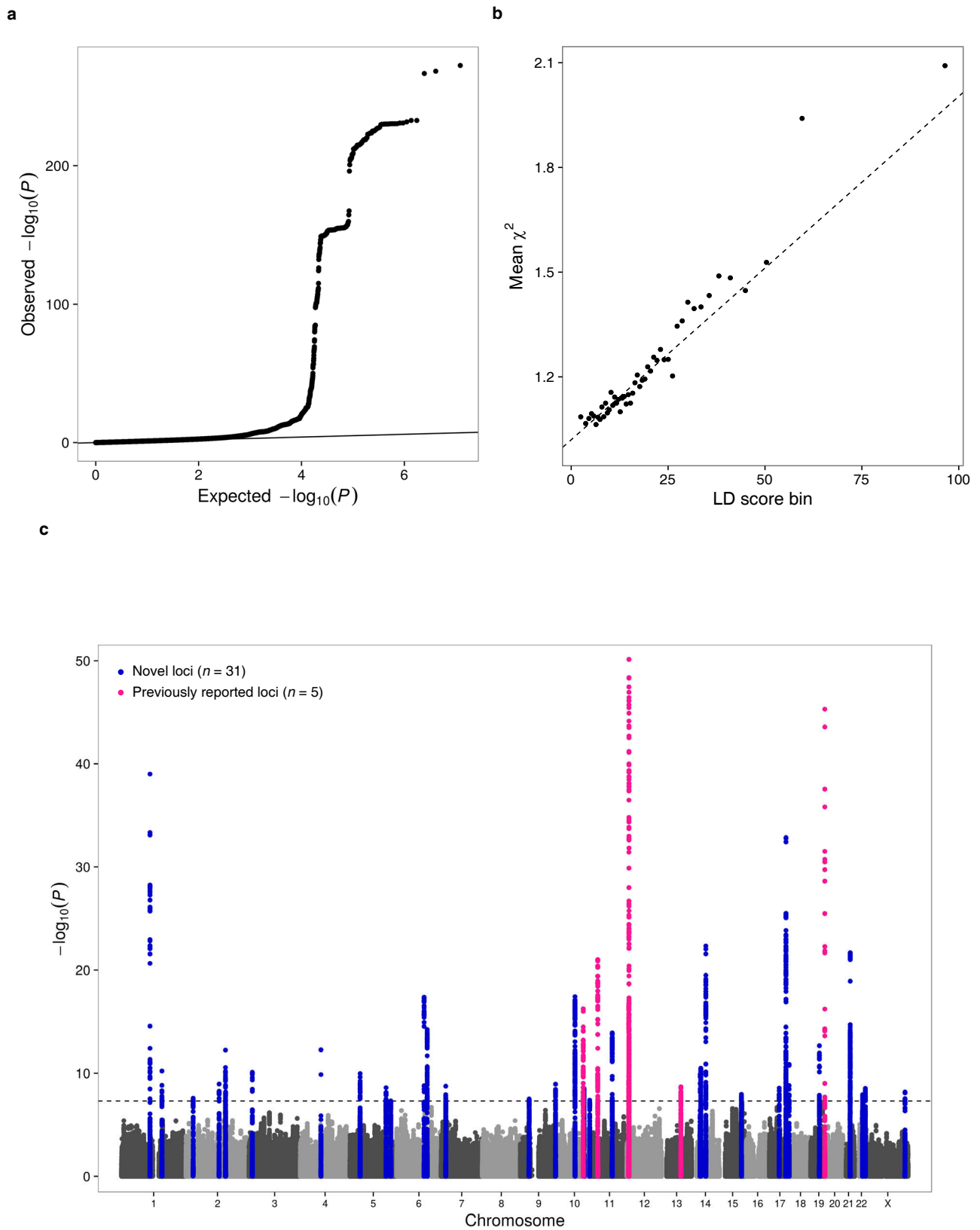
1.27 PT ($n = 58,110$)



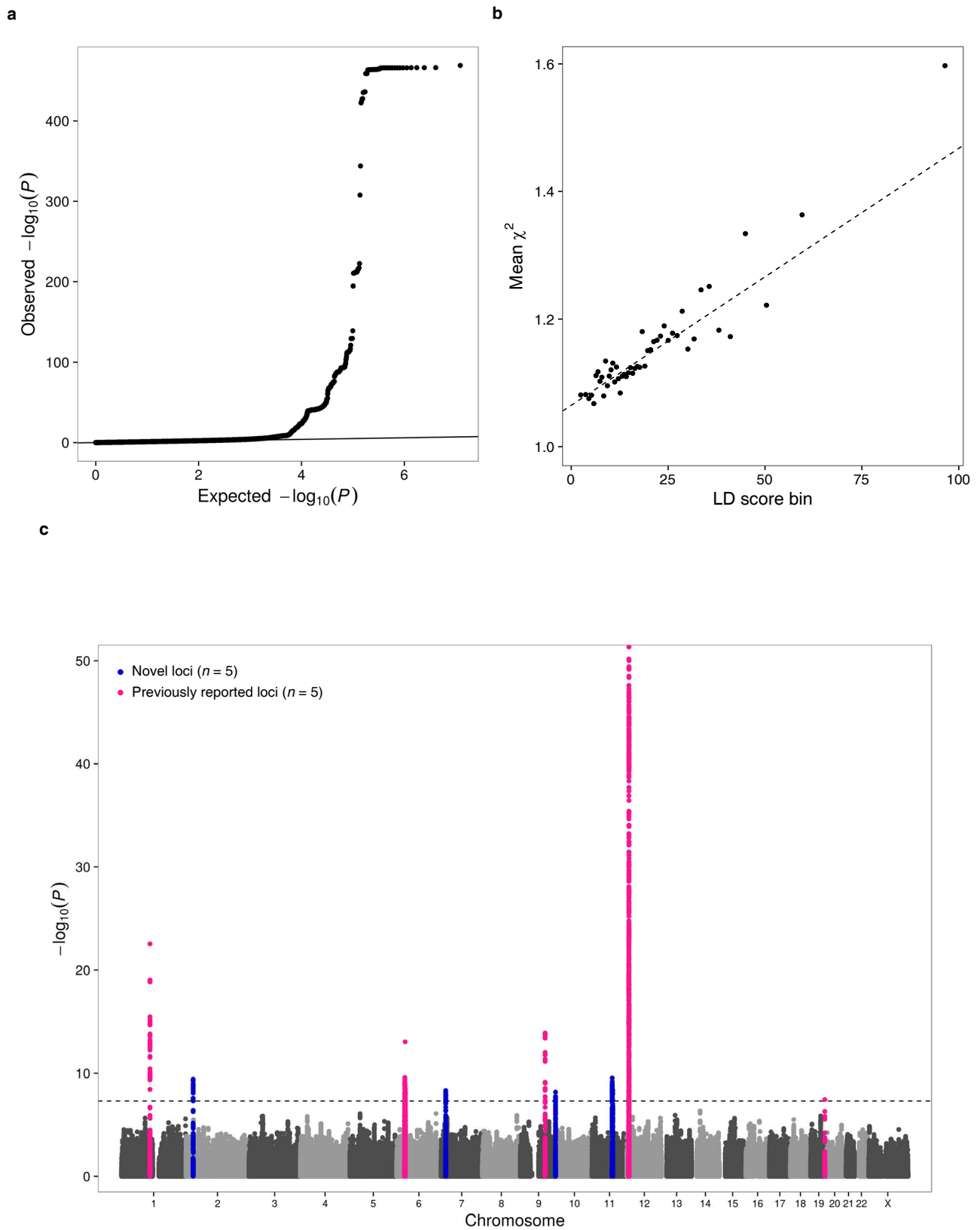
1.28 Fbg ($n = 18,348$)



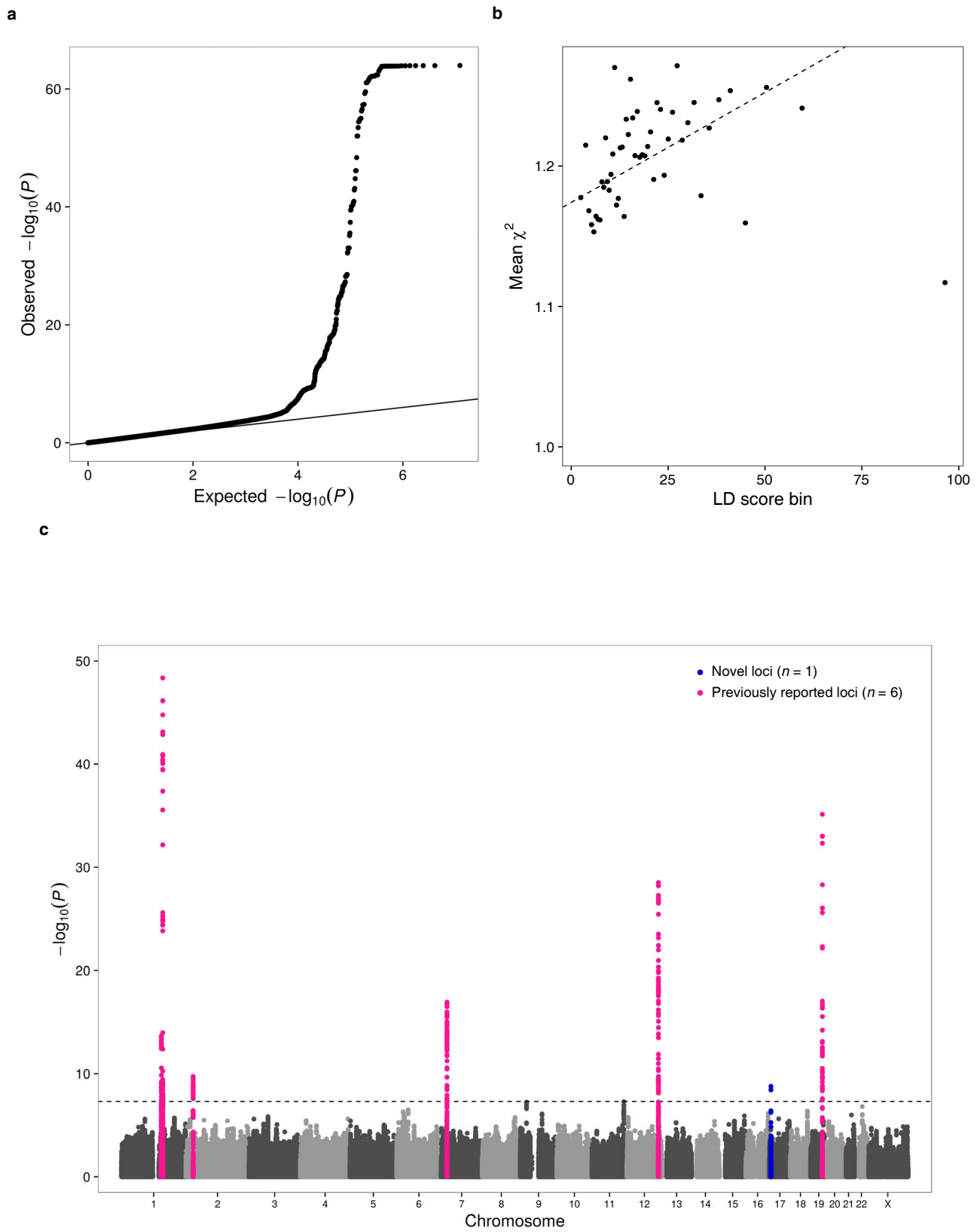
1.29 CK ($n = 106,080$)



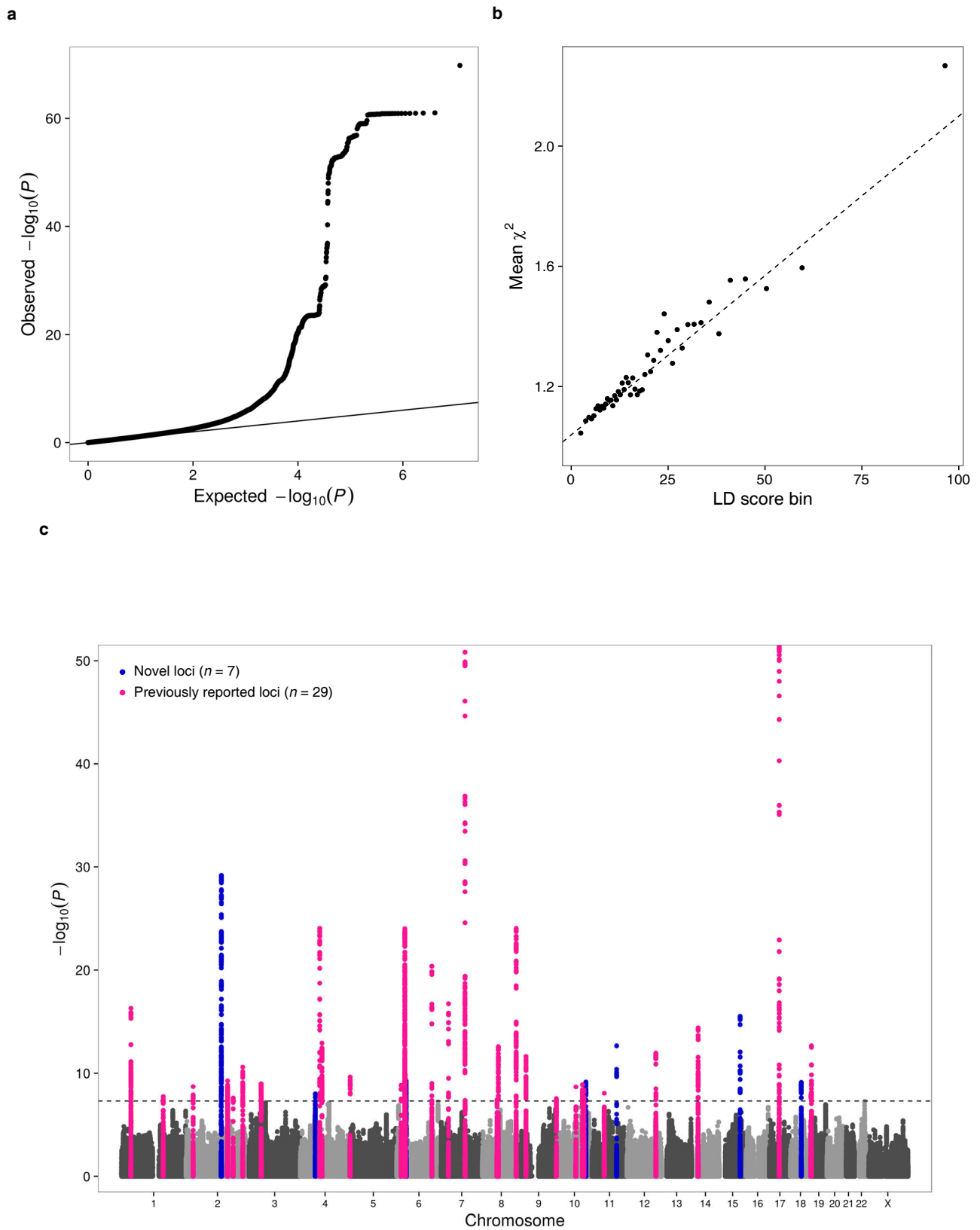
1.30 LDH ($n = 126,319$)



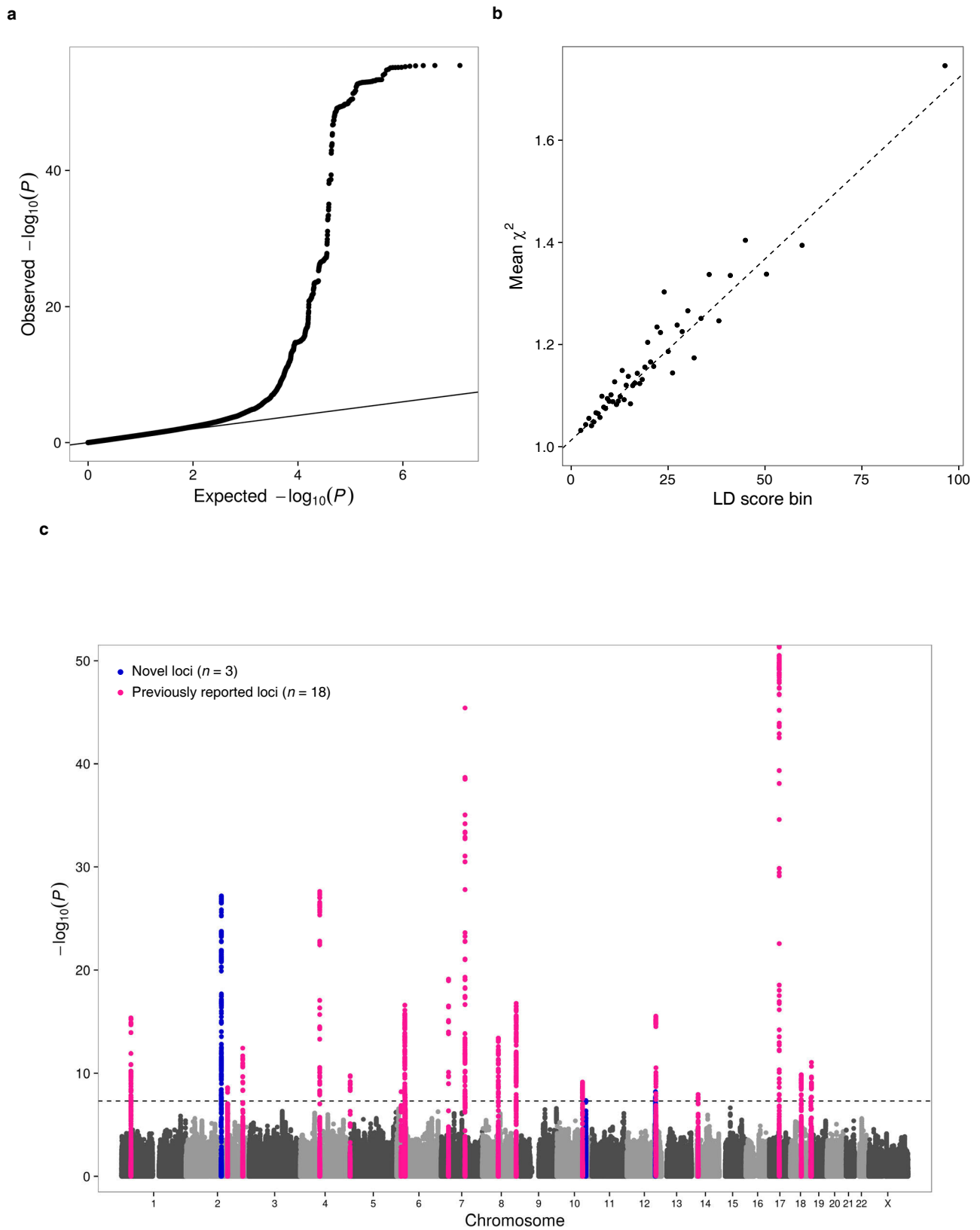
1.31 CRP ($n = 75,391$)



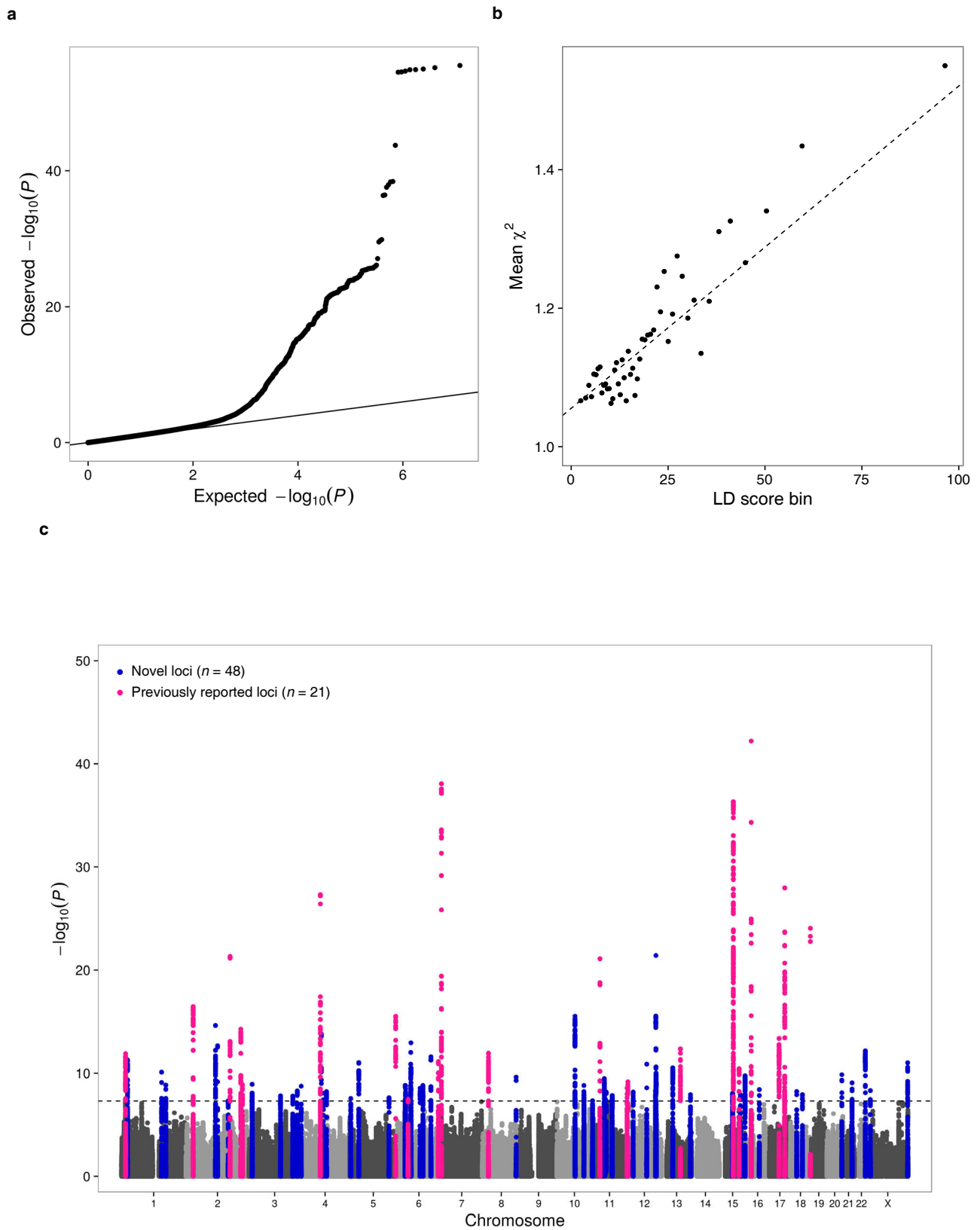
1.32 WBC ($n = 107,964$)



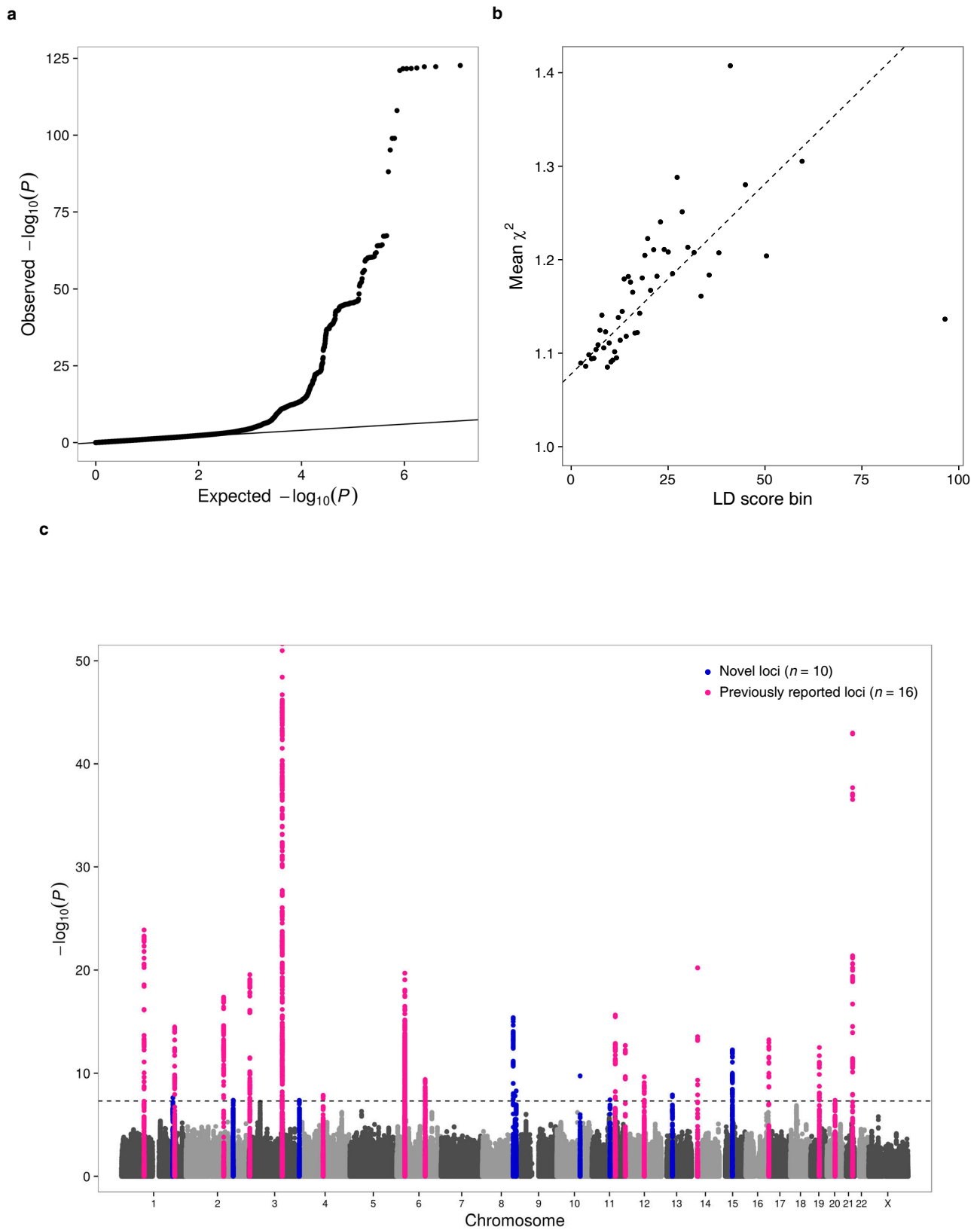
1.33 Neutro ($n = 62,076$)



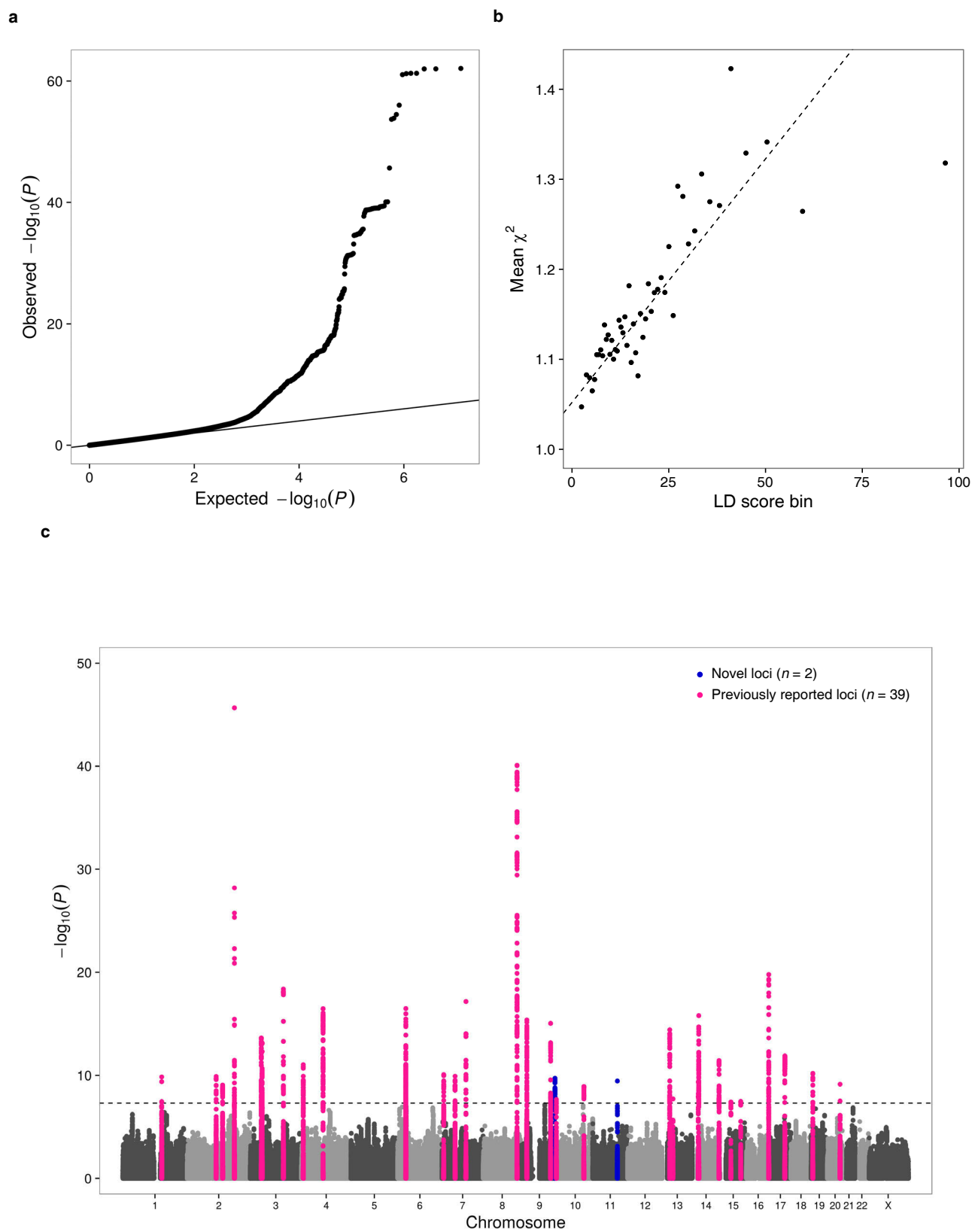
1.34 Eosino ($n = 62,076$)



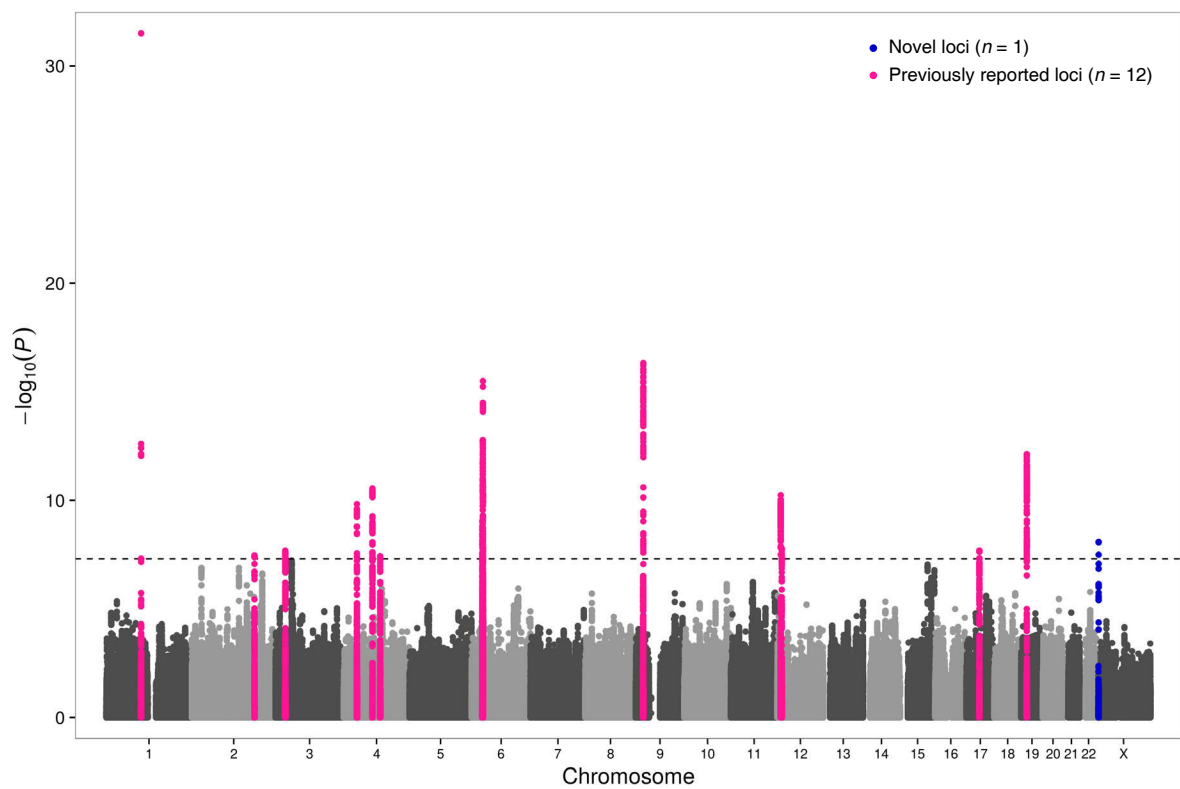
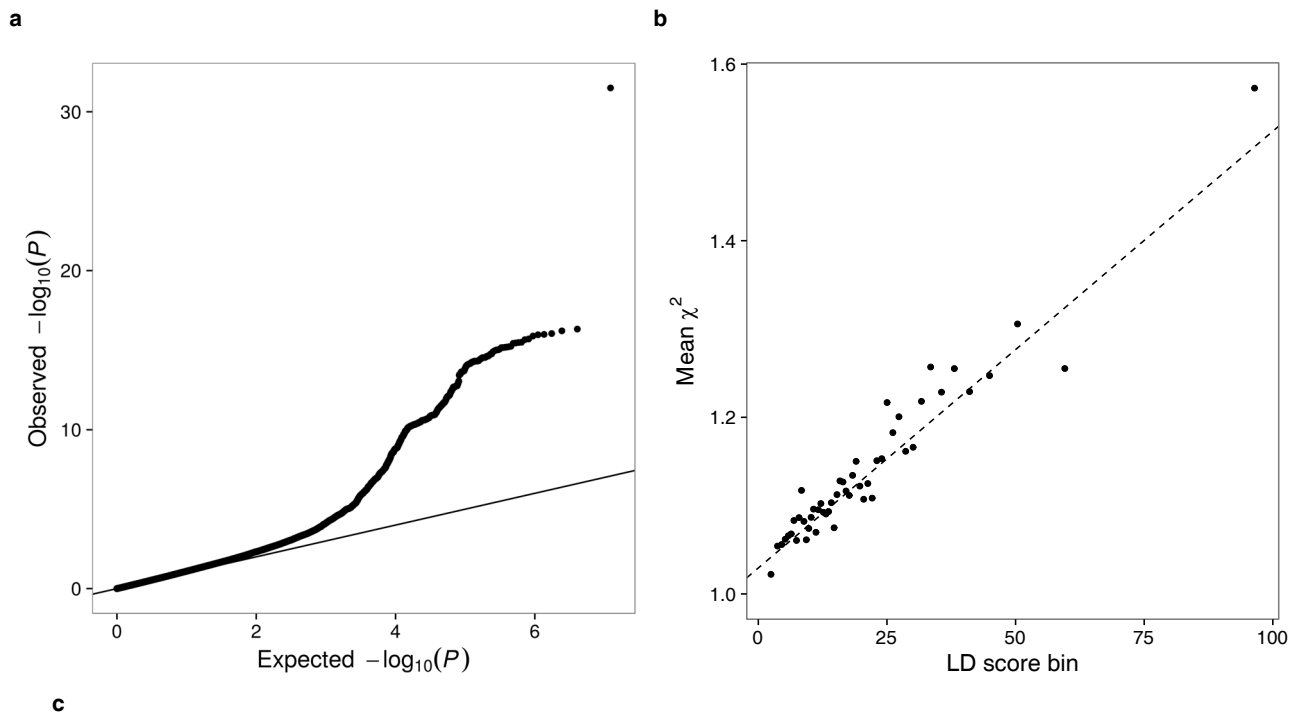
1.35 Baso ($n = 62,076$)



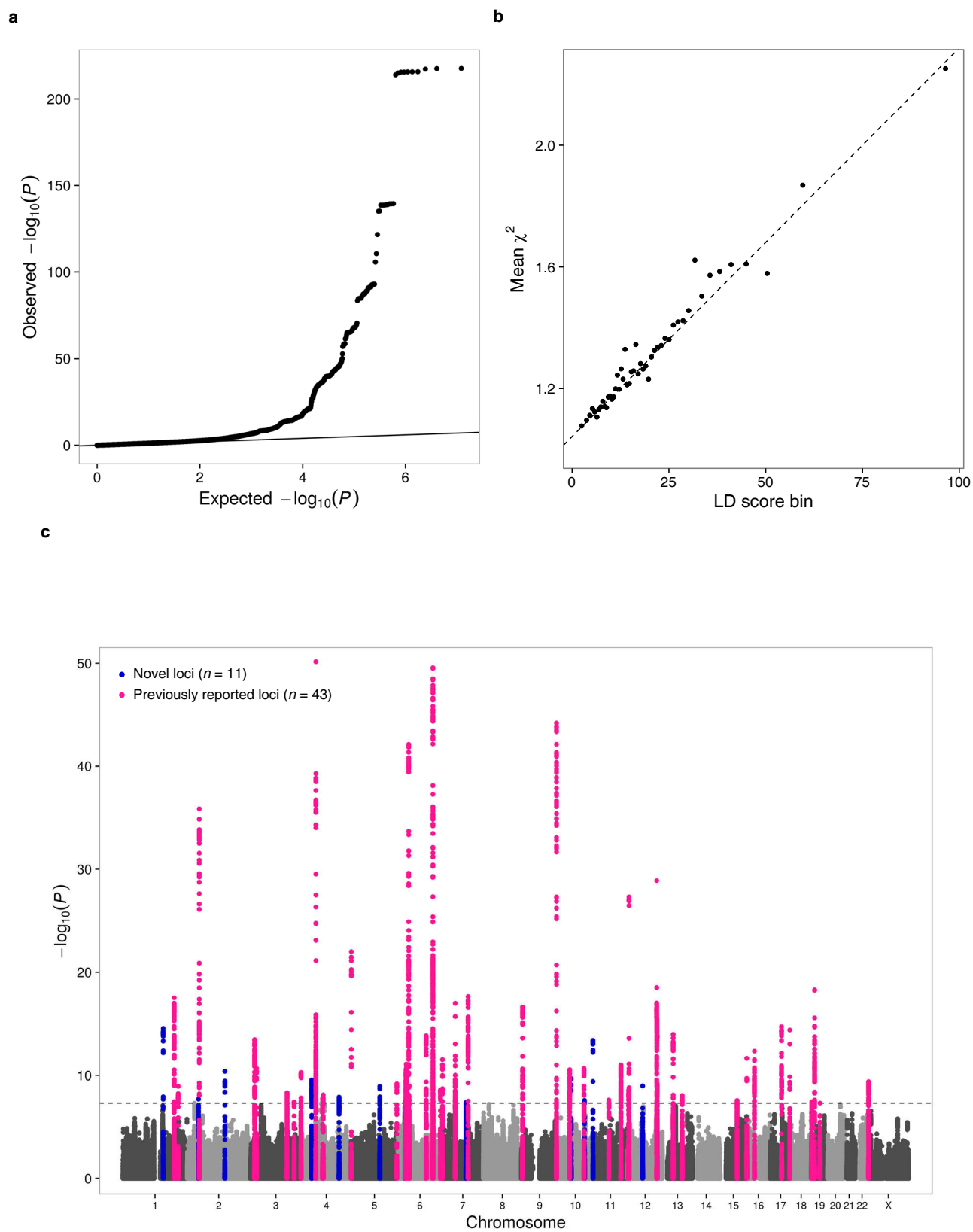
1.36 Mono ($n = 62,076$)



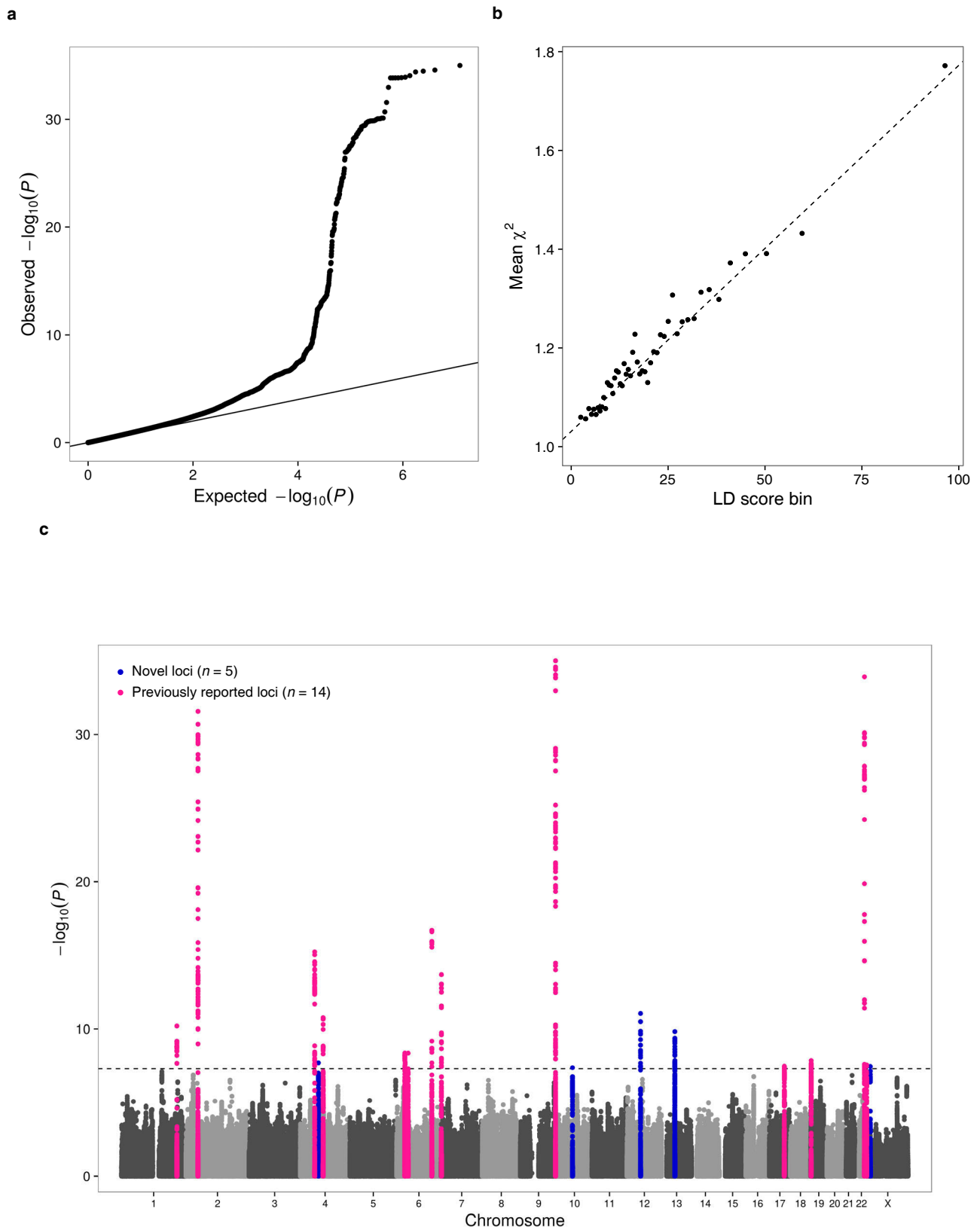
1.37 Lym ($n = 62,076$)



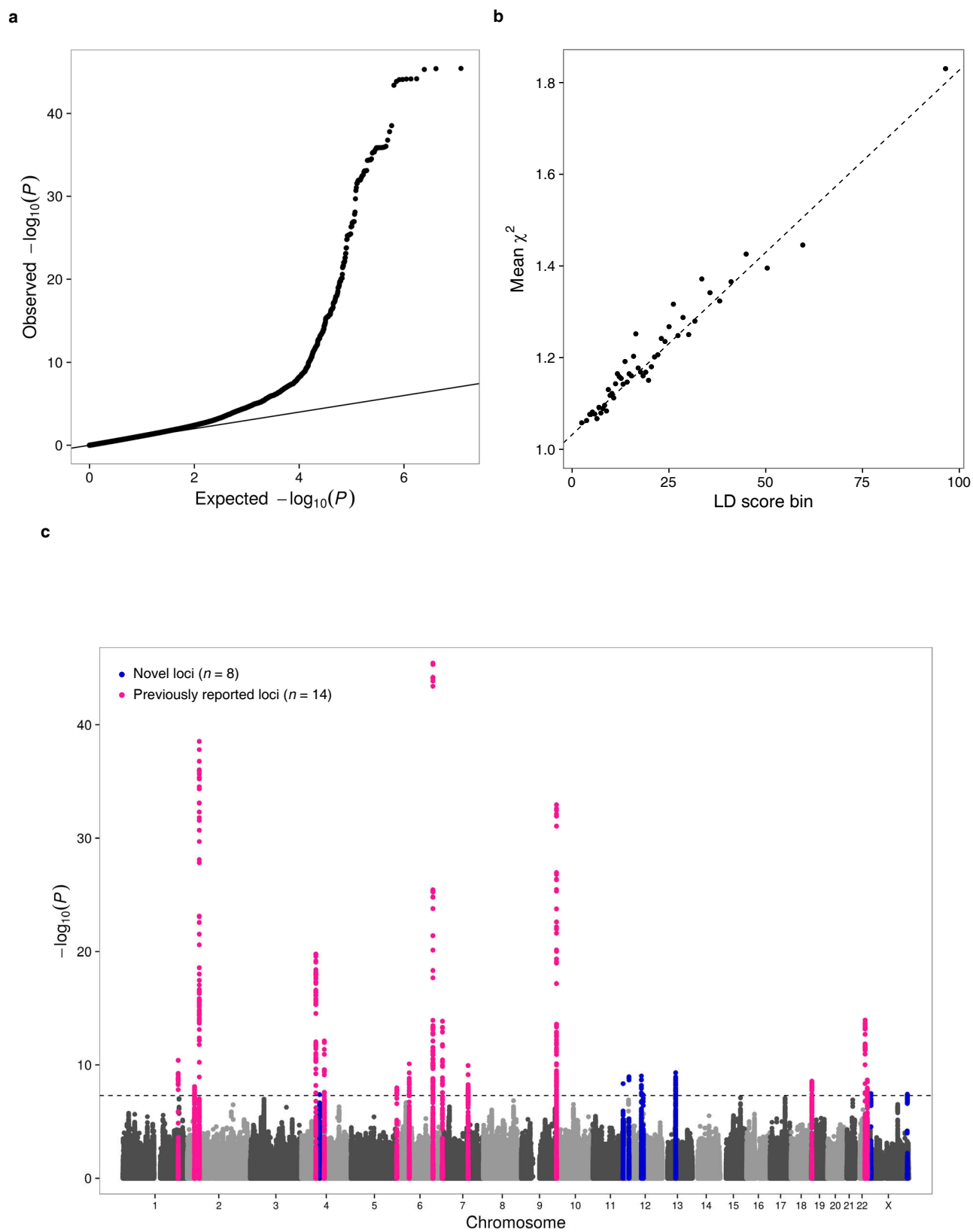
1.38 RBC ($n = 108,794$)



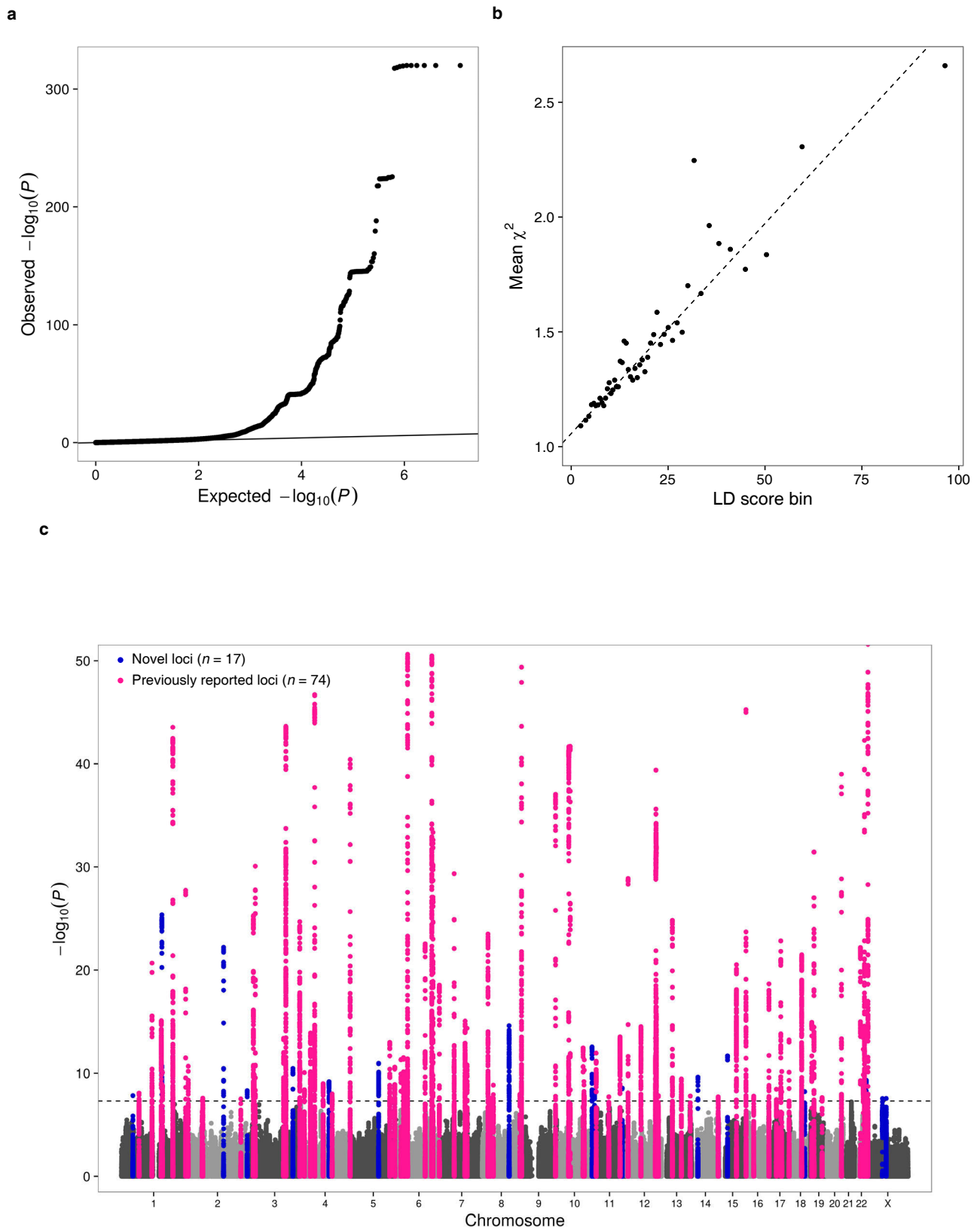
1.39 Hb ($n = 108,769$)



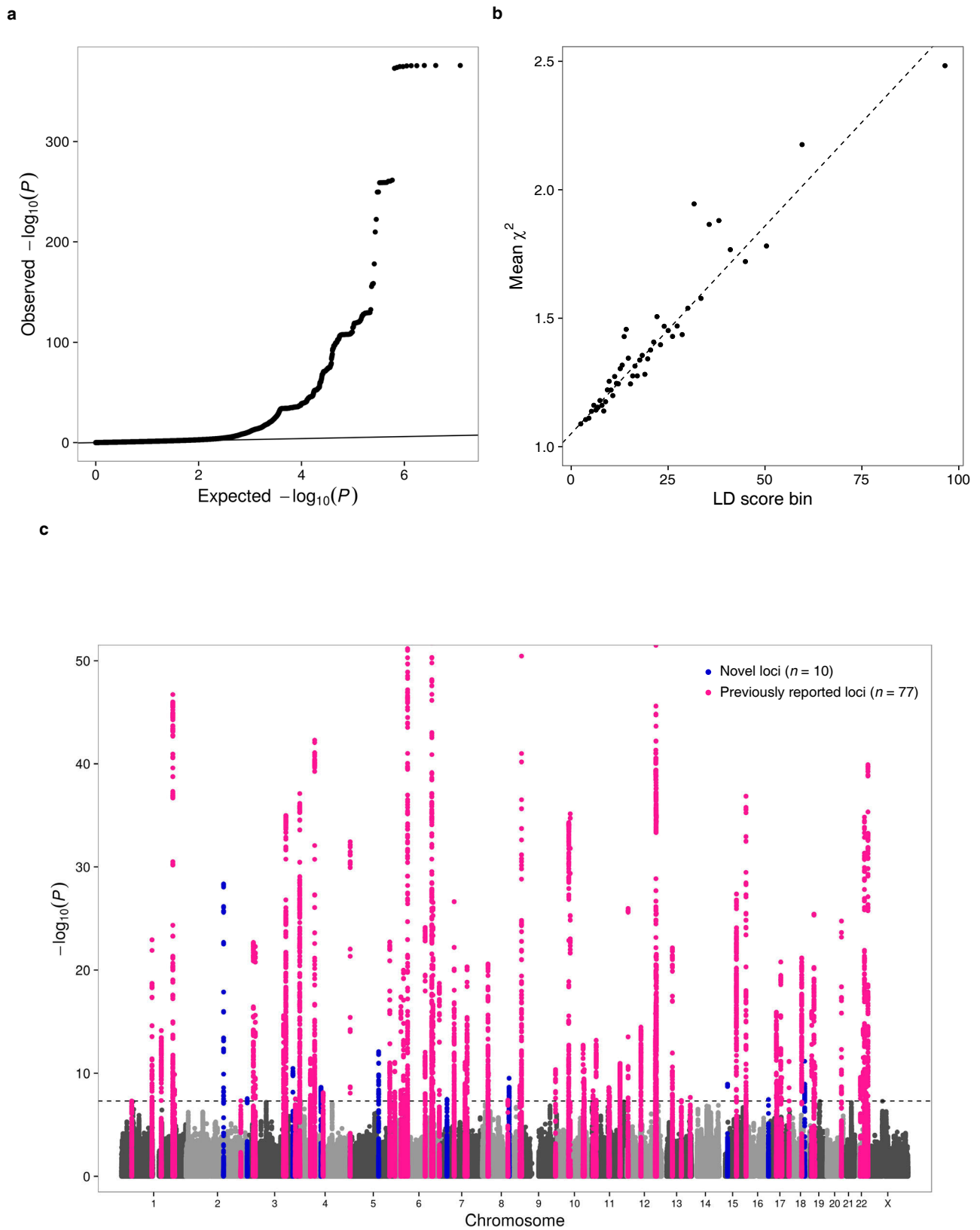
1.40 Ht ($n = 108,757$)



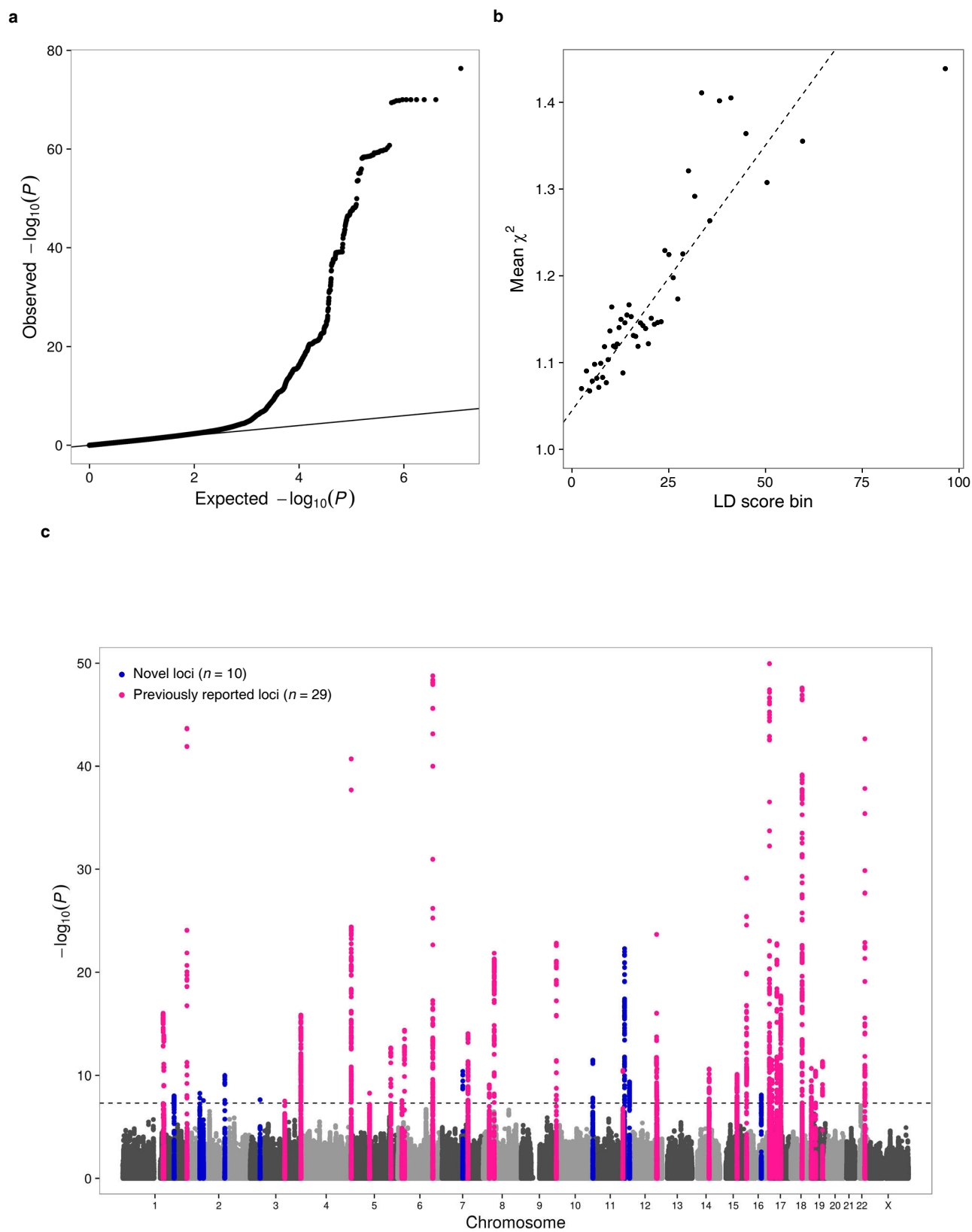
1.41 MCV ($n = 108,256$)



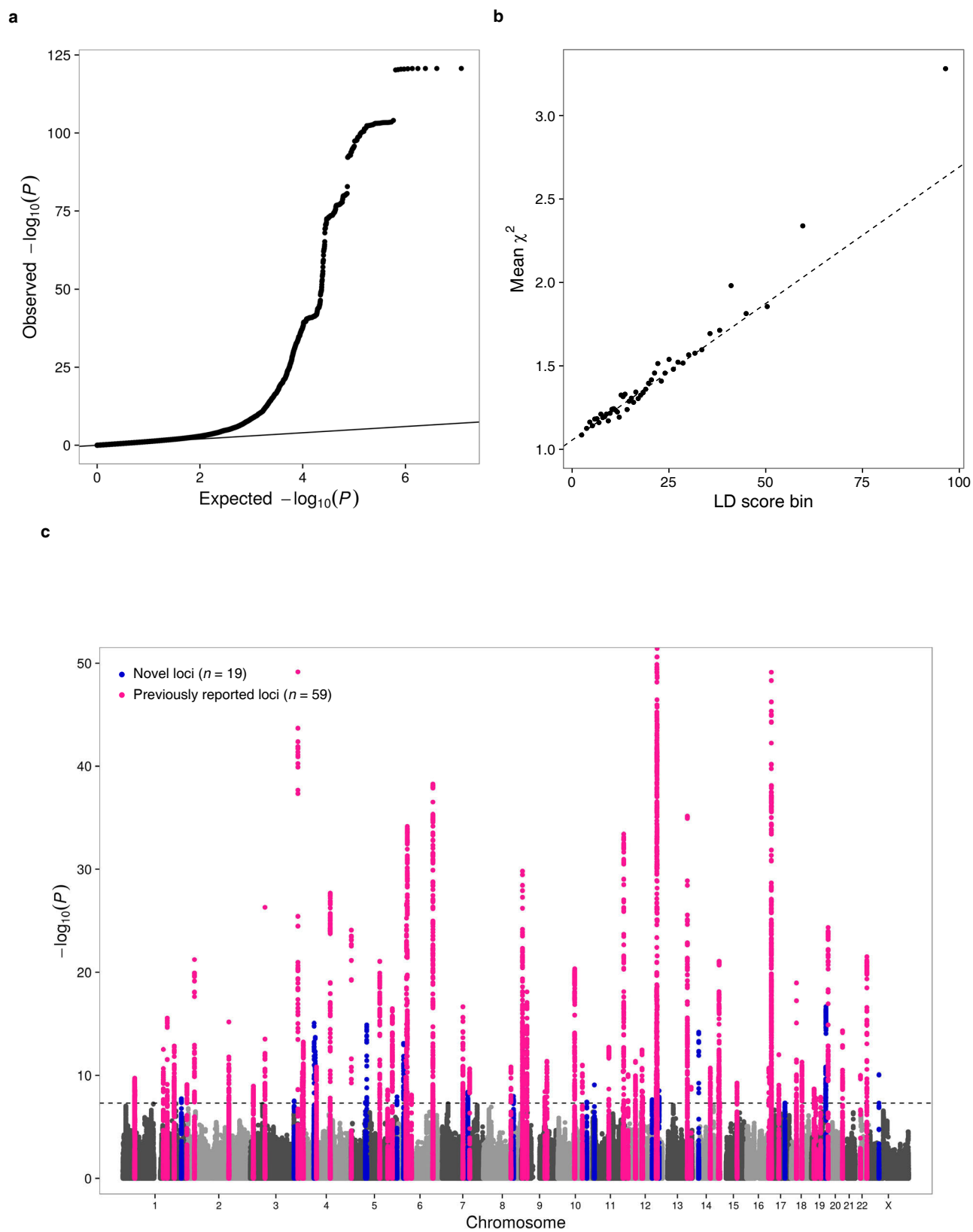
1.42 MCH ($n = 108,054$)



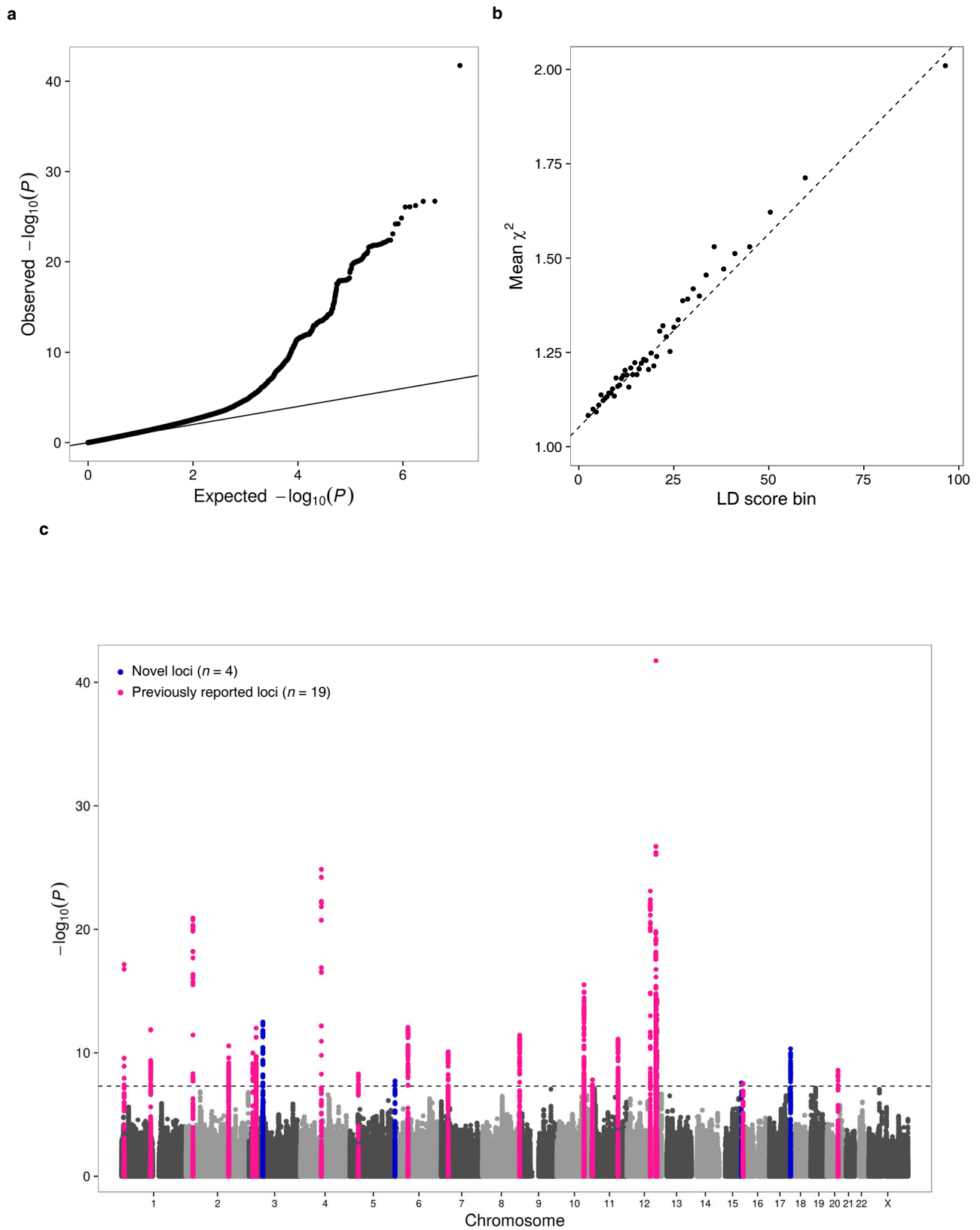
1.43 MCHC ($n = 108,728$)



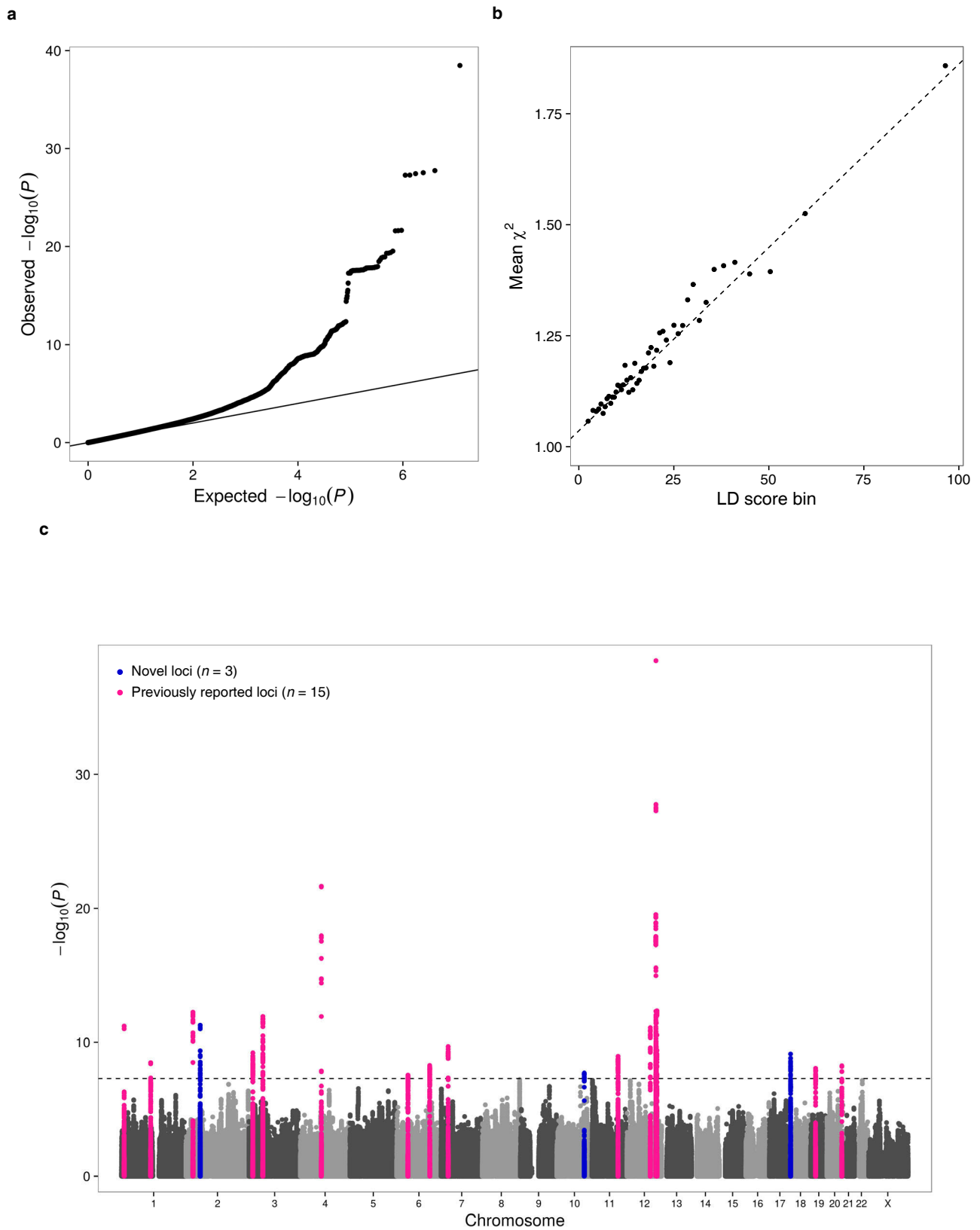
1.44 Plt ($n = 108,208$)



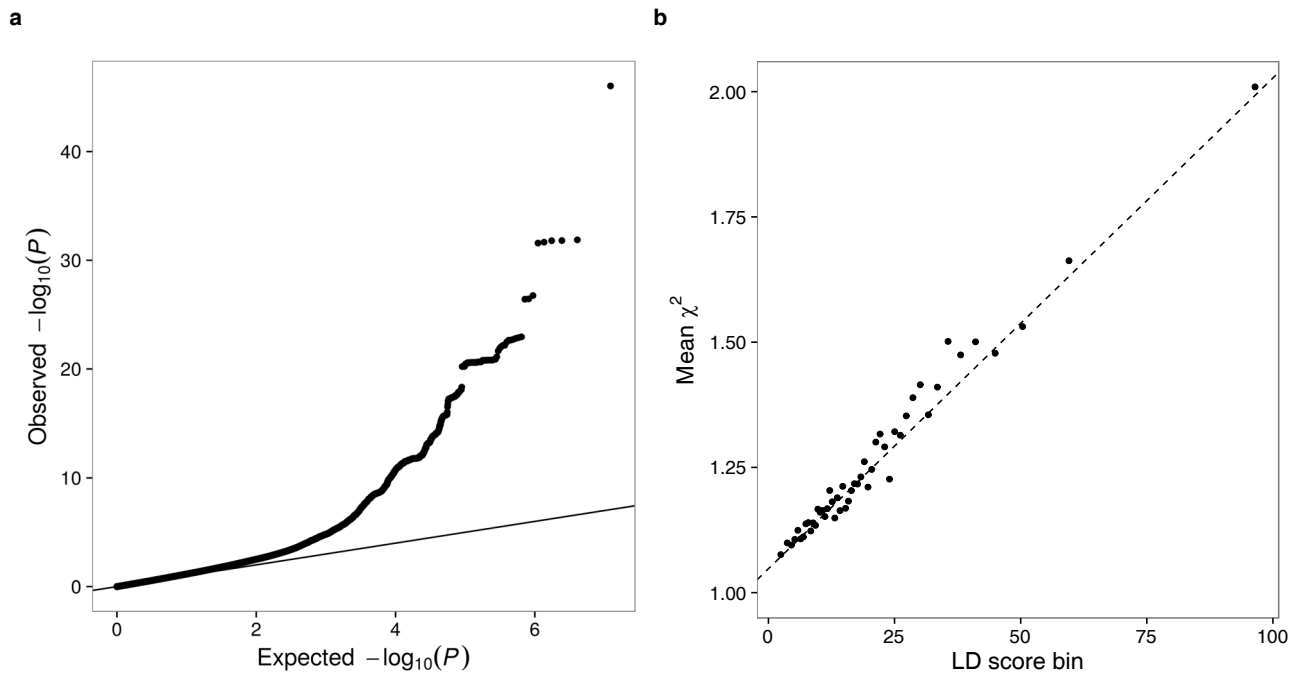
1.45 SBP ($n = 136,597$)



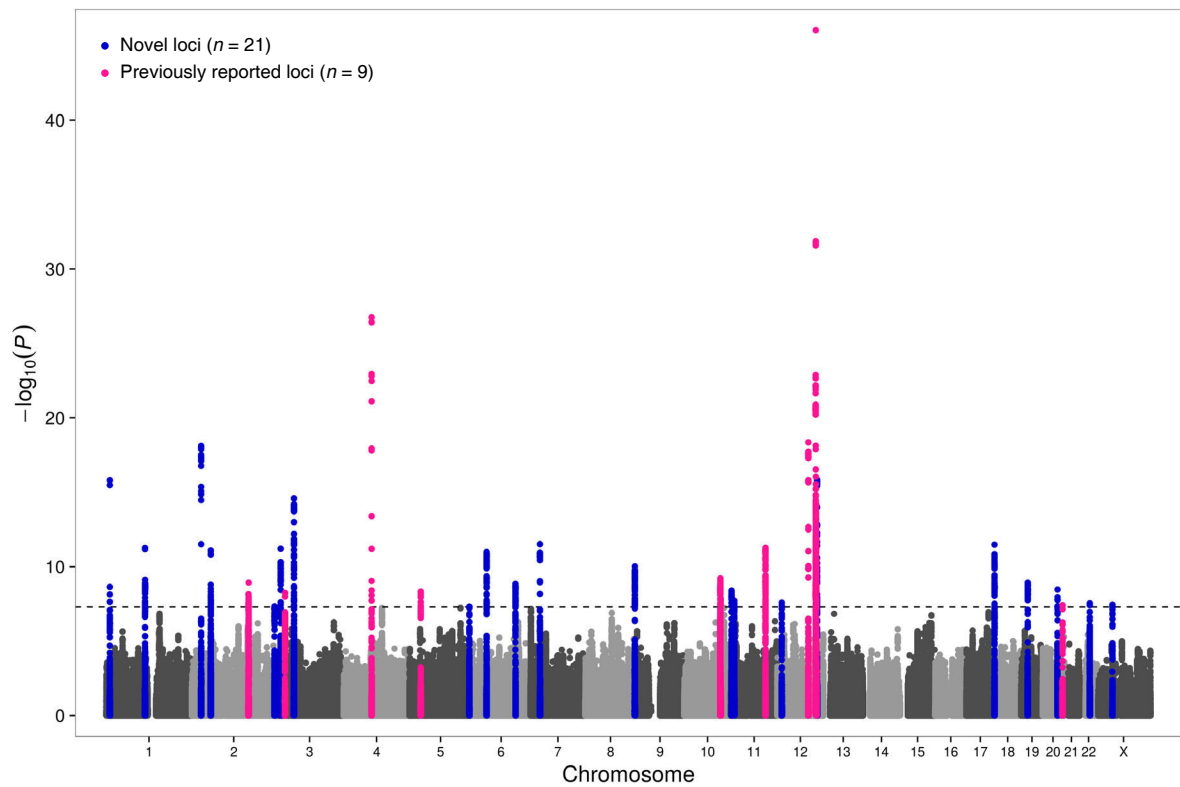
1.46 DBP ($n = 136,615$)



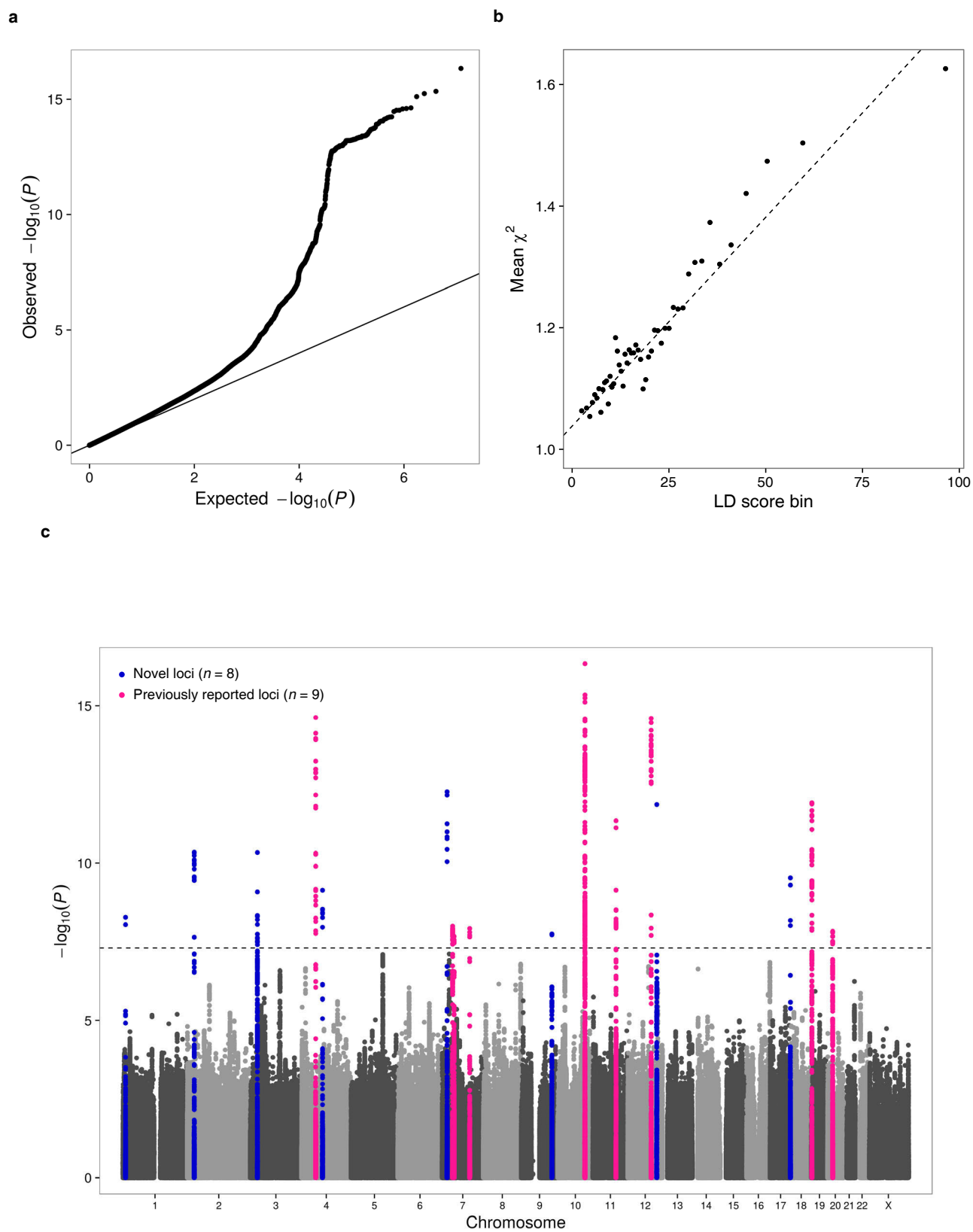
1.47 MAP ($n = 136,482$)



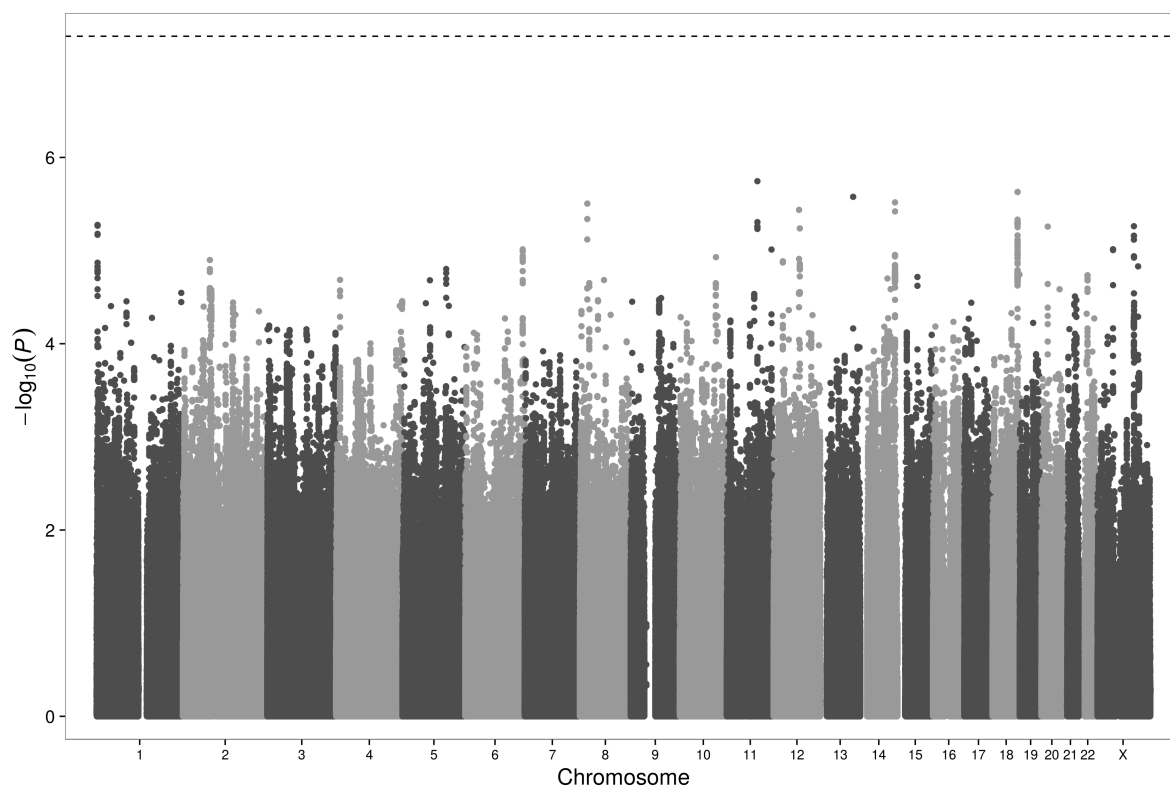
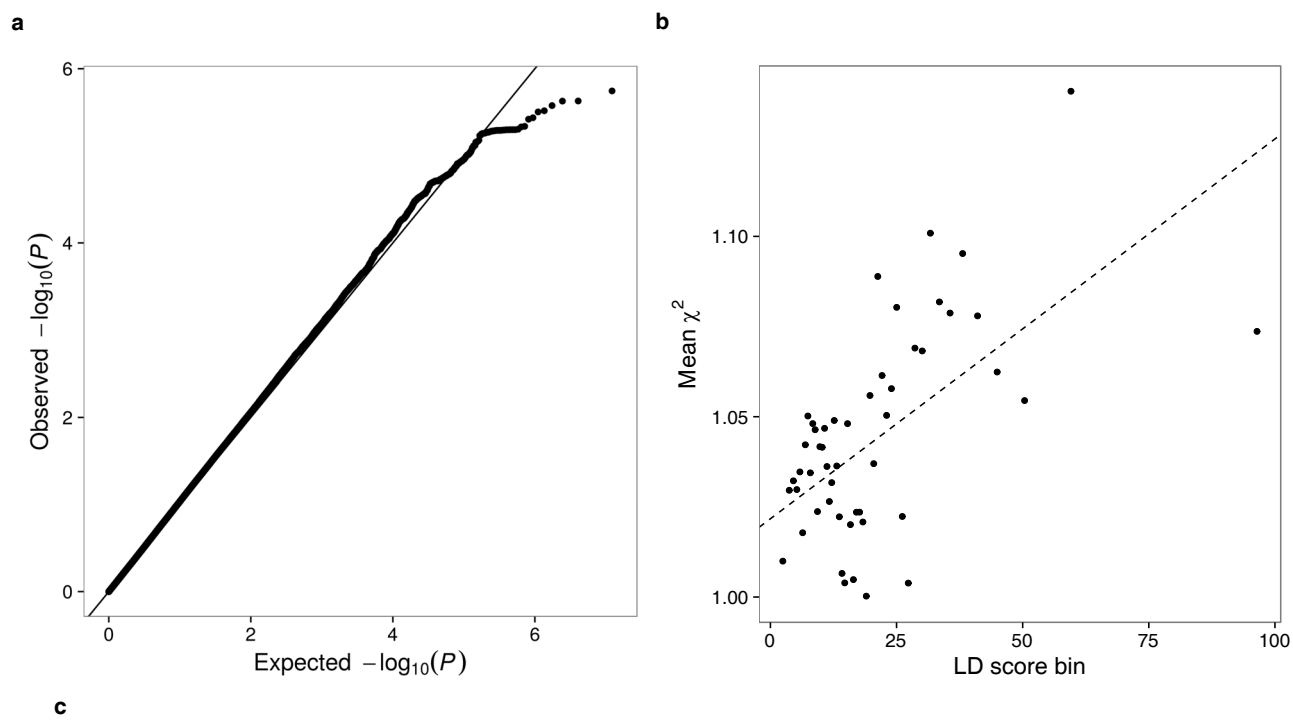
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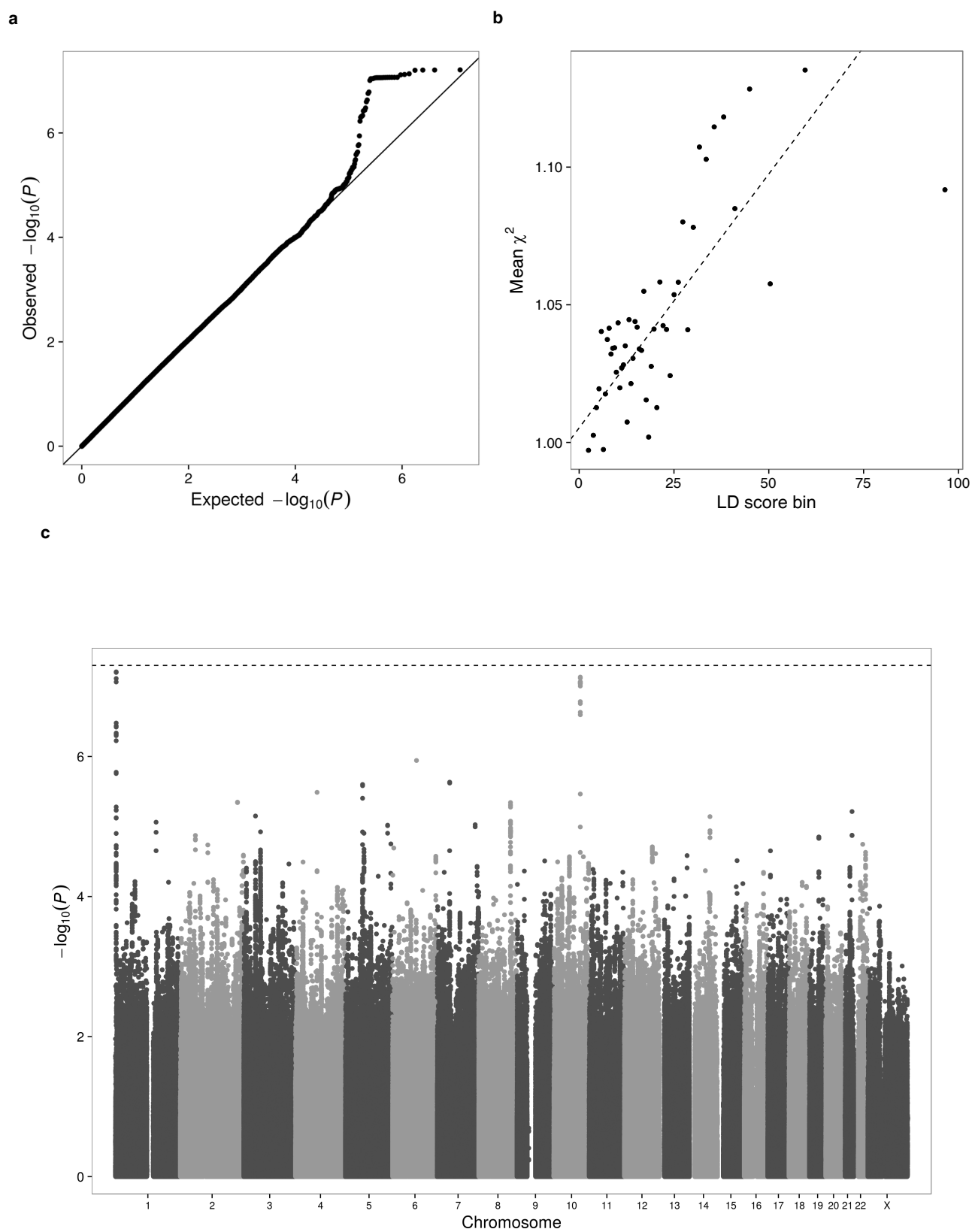
1.48 PP ($n = 136,249$)



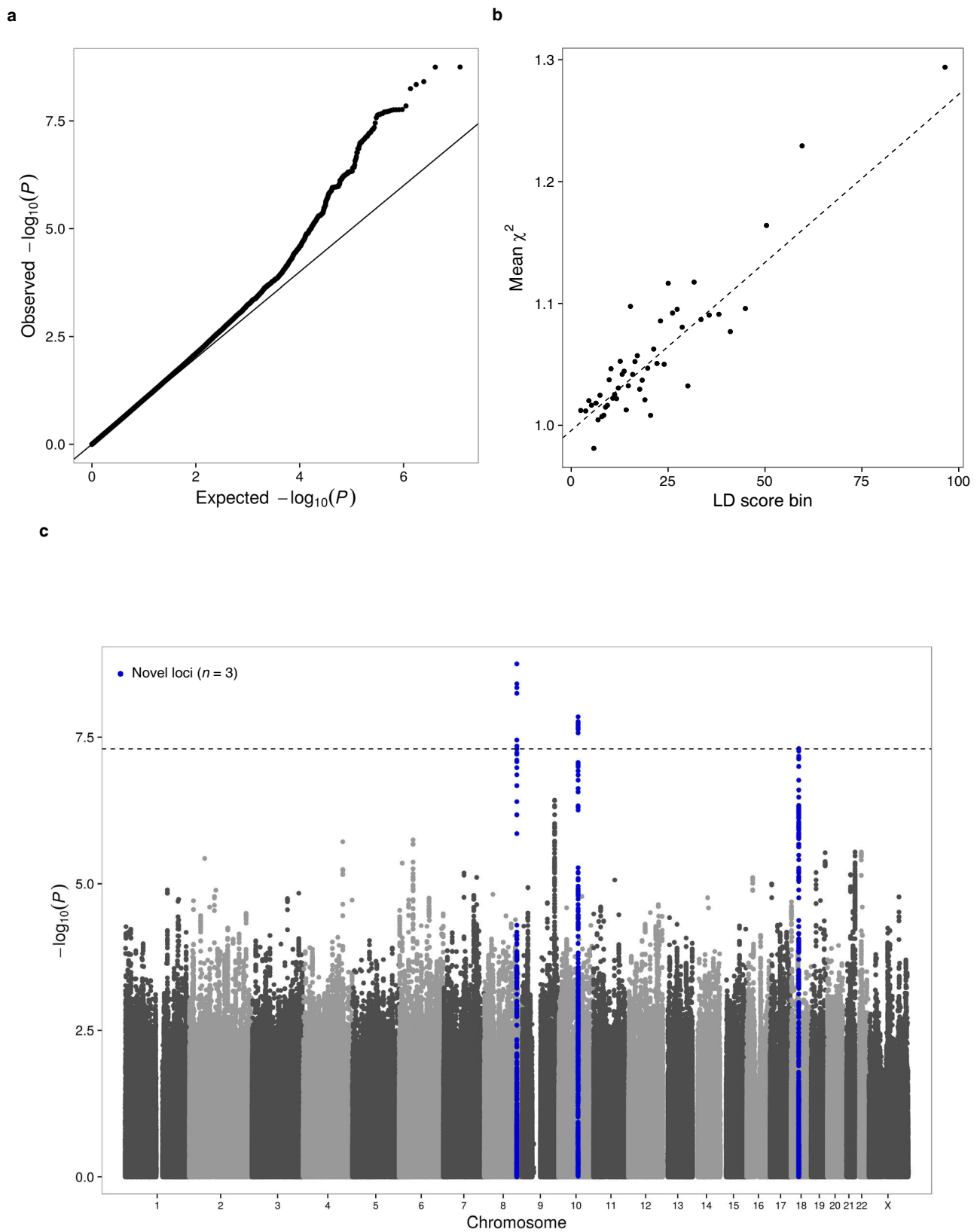
1.49 IVS ($n = 19,318$)



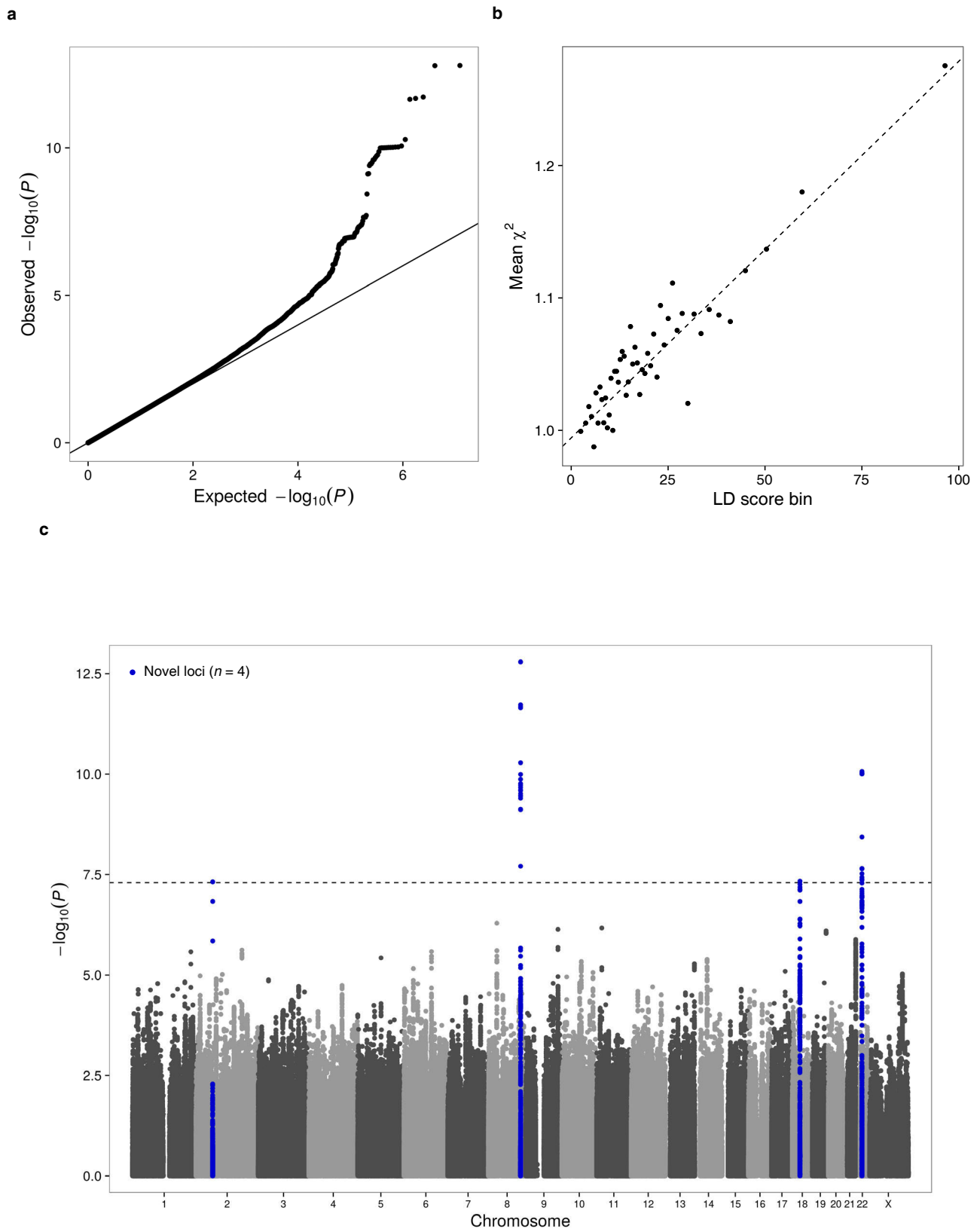
1.50 PW ($n = 19,373$)



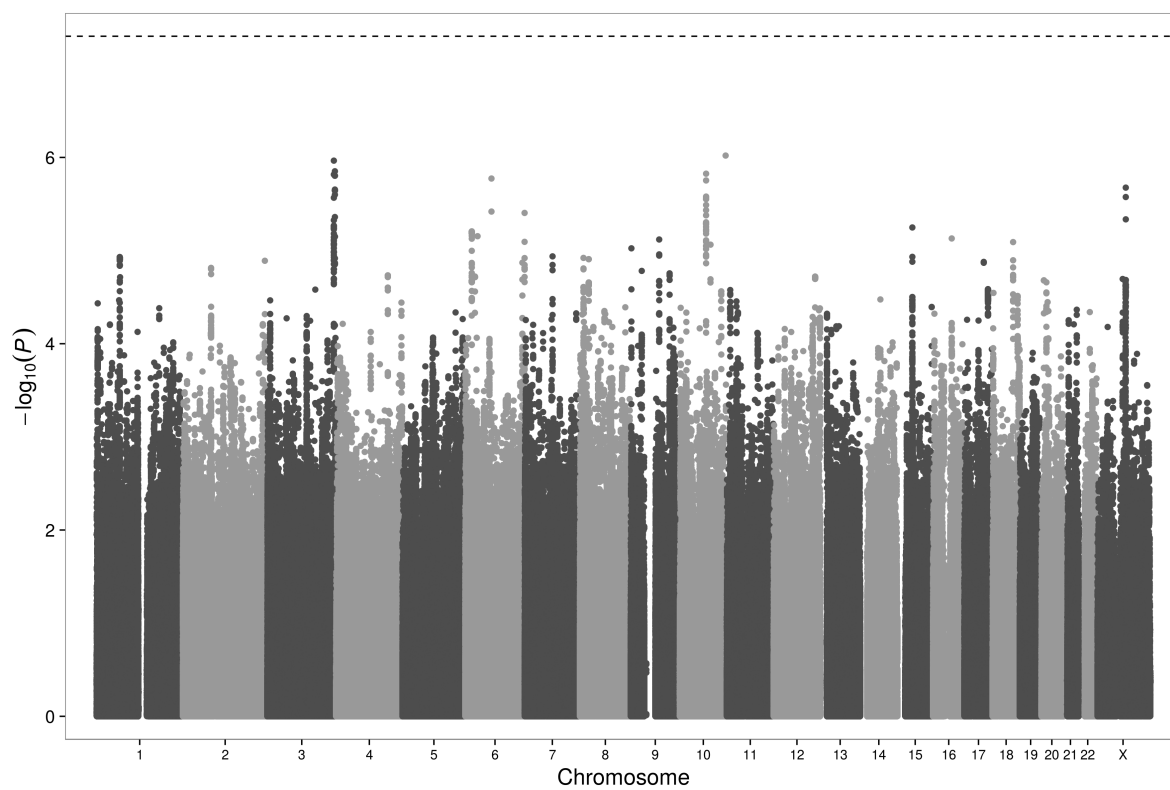
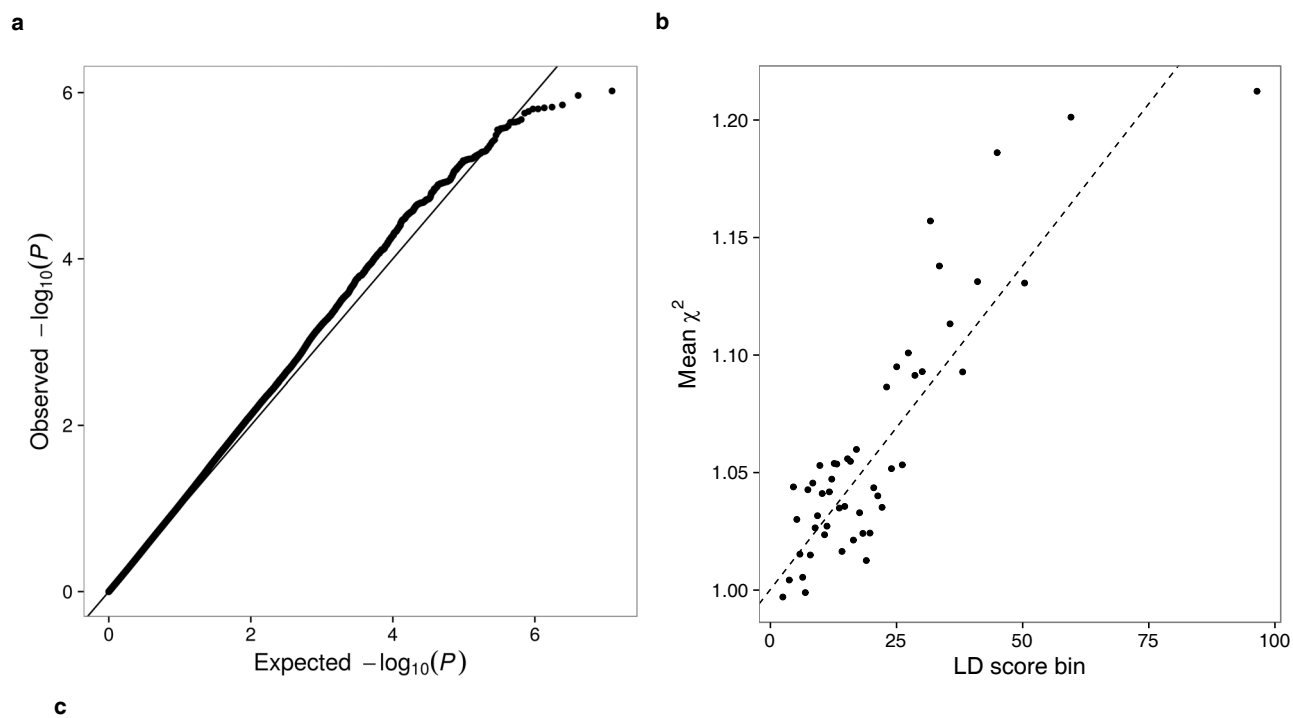
1.51 LVDd ($n = 19,676$)



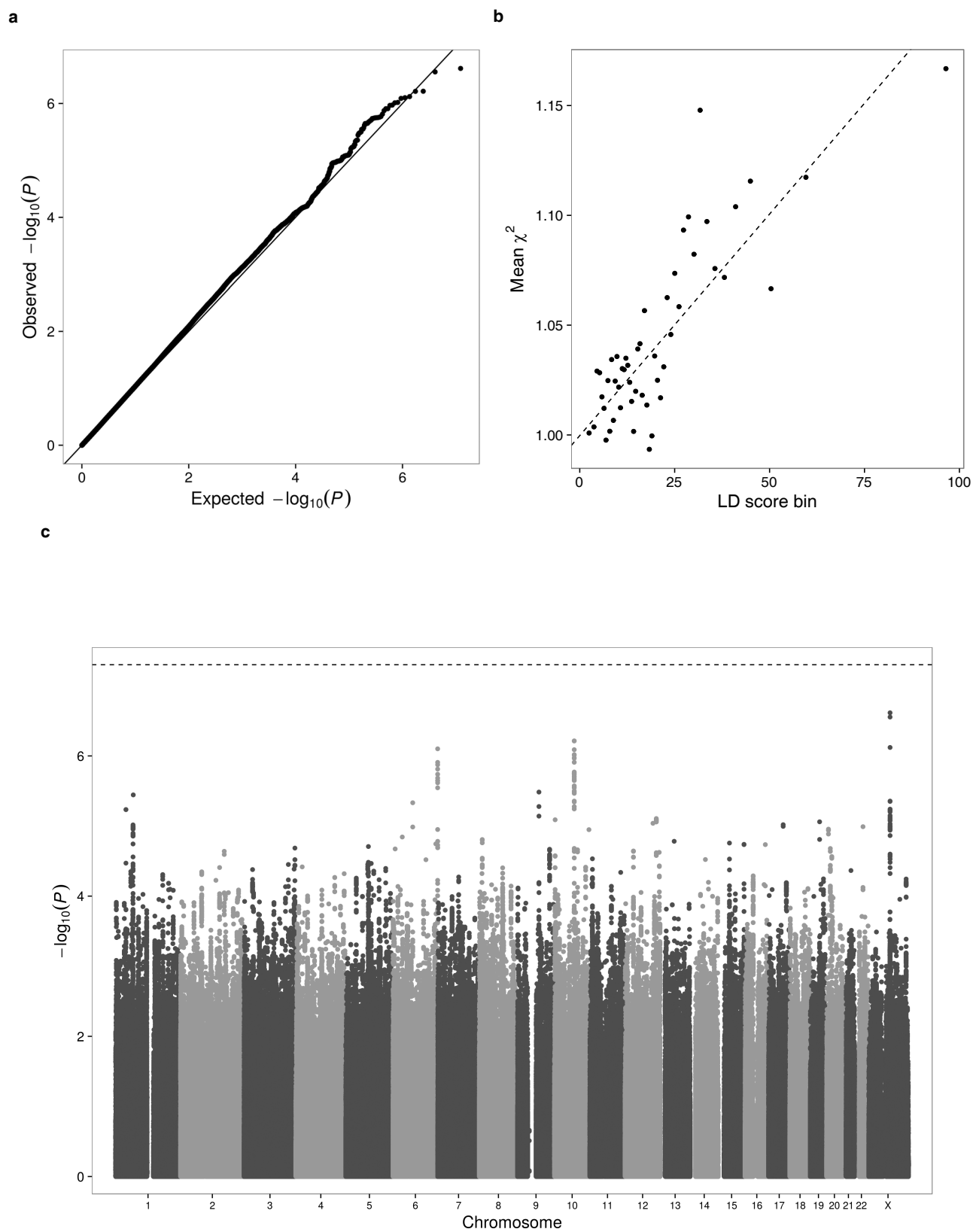
1.52 LVDs ($n = 19,586$)



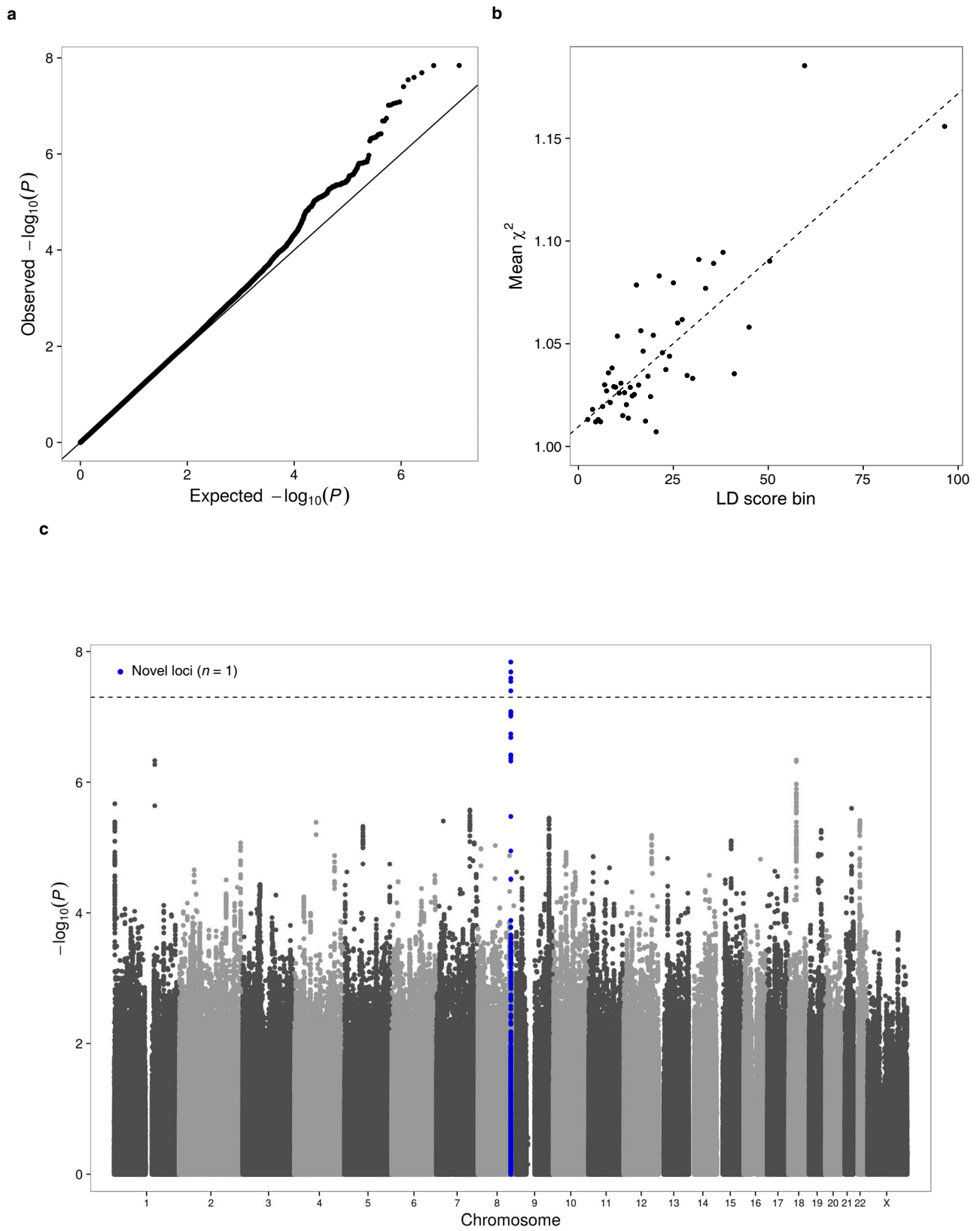
1.53 LVM ($n = 19,076$)



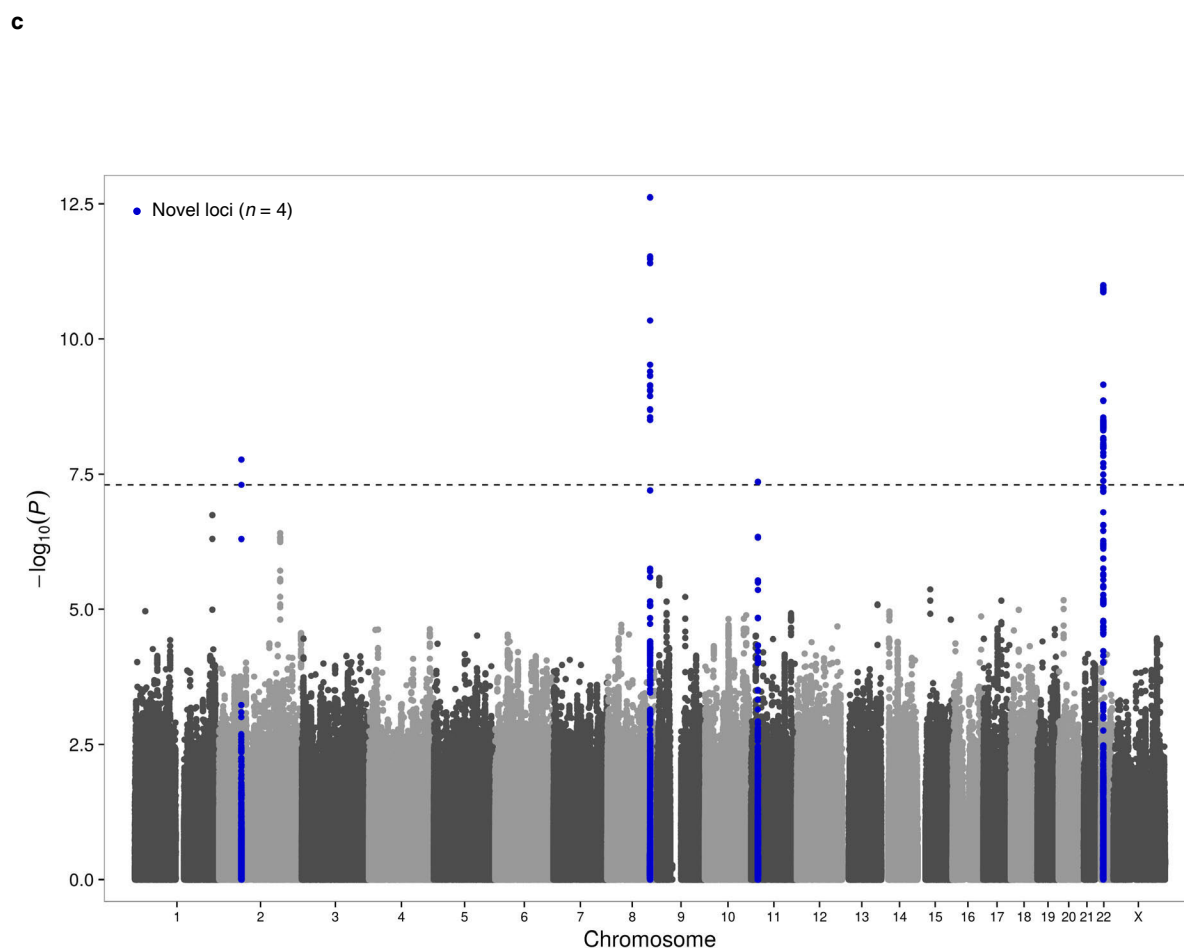
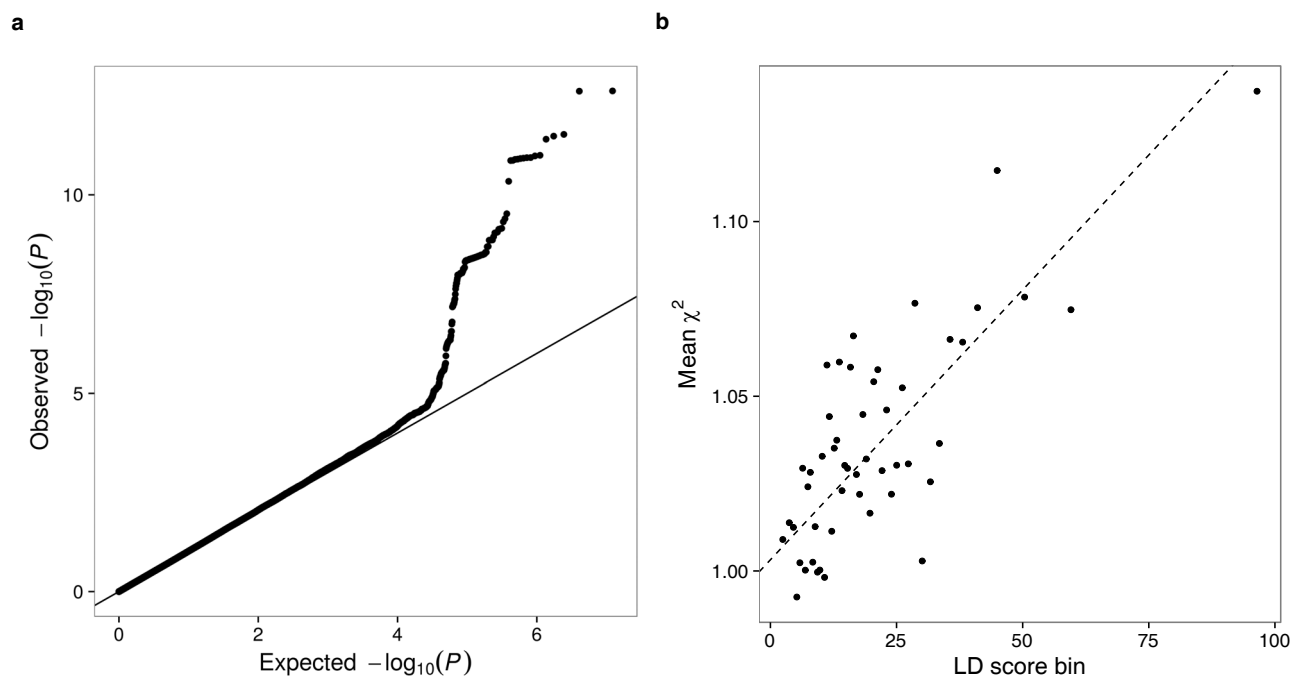
1.54 LVMI ($n = 17,837$)



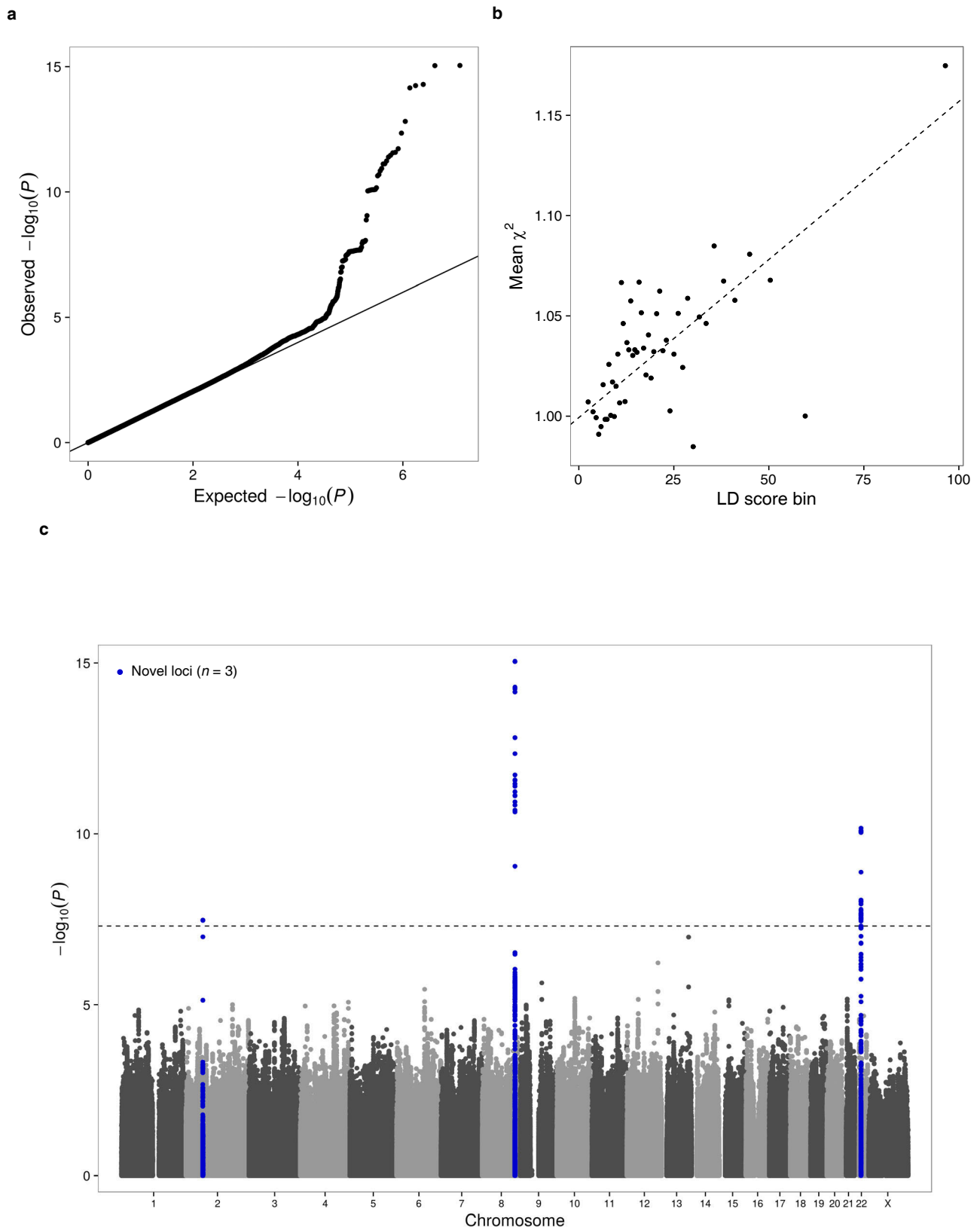
1.55 RWT ($n = 19,311$)



1.56 FS ($n = 19,580$)



1.57 EF ($n = 19,516$)



1.58 E/A ($n = 8,600$)

