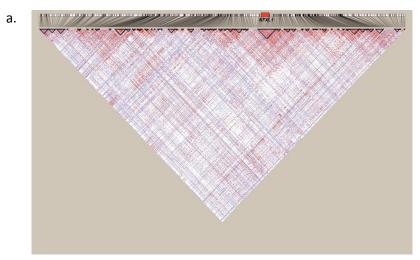
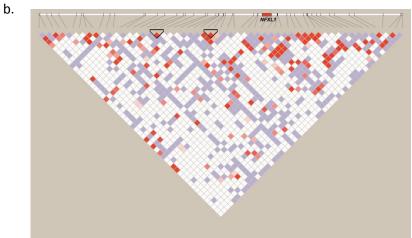
Figure S3 - Linkage disequilibrium between markers across NFXL1 region.





- **a** Linkage disequilibrium between all genotyped markers (n=929) across chr4:46-49Mb (hg19)
- **b** Linkage disequilibrium between all analyzed markers (n=55) across chr4:46-49Mb (hg19), after pruning for $r^2>0.5$

Position of *NFXL1* gene is shown by red box. Plots were generated in haploview (http://www.broadinstitute.org/scientific-community/science/programs/medical-and-population-genetics/haploview/haploview) using linkage pedigrees (as shown in Figure S2). Color scheme is standard haploview colour scheme (blue − D'=1, LOD<2; white - D'<1, LOD<2; pink/red − LOD≥2).