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](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 – \( D'=1, \text{LOD}<2 \); white – \( D'<1, \text{LOD}<2 \); pink/red – \( \text{LOD} \geq 2 \)).