

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).