

GWAS identifies three loci, implicating the planar cell polarity pathway and the MYCN-DDX1 2p24.3 amplicon region in Wilms tumor susceptibility

Lizzie Perdeaux Childhood Cancer 2012

Wilms tumor

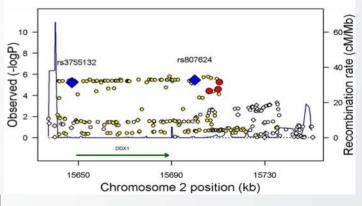
- Childhood kidney tumor that affects 1 in 10,000 children
- Median age of diagnosis is 3 4 years
- Evidence for a genetic basis for Wilms
 - Incidence rates in migrant populations match that of their parent population rather than their host population
 - 2% of cases have a family history of Wilms
 - Several known genetic causes of Wilms WT1 & 11p15
- Underlying cause unknown in 95% unselected cases

GWAS

- GWAS is used to identify common, low risk genetic variants that cause disease
- Scanned ~600,000 common variants distributed across the whole genome
- Compared variant genotypes between cases and controls
- Variants showing significant differences were verified in a second series of cases and controls
- 4 variants within 3 regions were found to be more common in Wilms tumor patients than controls

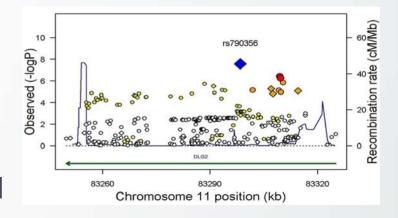
rs3755132 & rs807624 - DDX1

- $P = 1.03x10^{-14}$ and $1.32x10^{-14}$
- 109 kB linkage region on 2p24.3
- Both variants associate with the region independently
- MYCN is 250 kB from DDX1 and both genes are often amplified in childhood tumors



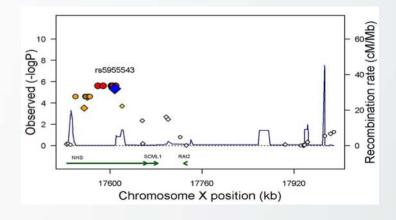
rs790356 - DLG2

- $P = 4.35 \times 10^{-15}$
- 68 kB linkage region on 11q14.1
- Drosophila homolog, dlg, interacts with Scribble and Lgl
- Scribble and Lgl are both Planar Cell Polarity Pathway genes
- SCRIB expression is activated by WT1



rs5955543 - NHS, SCML1 & RAI2

- P=1.04x10⁻⁹
- 403 kB linkage region on Xp22.13
- NHS homologous to gukh, which in Drosophila facilitates interaction between Dlg and Scribble
- SCML1 and RAI2 control developmental processes and cell fate determination



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