

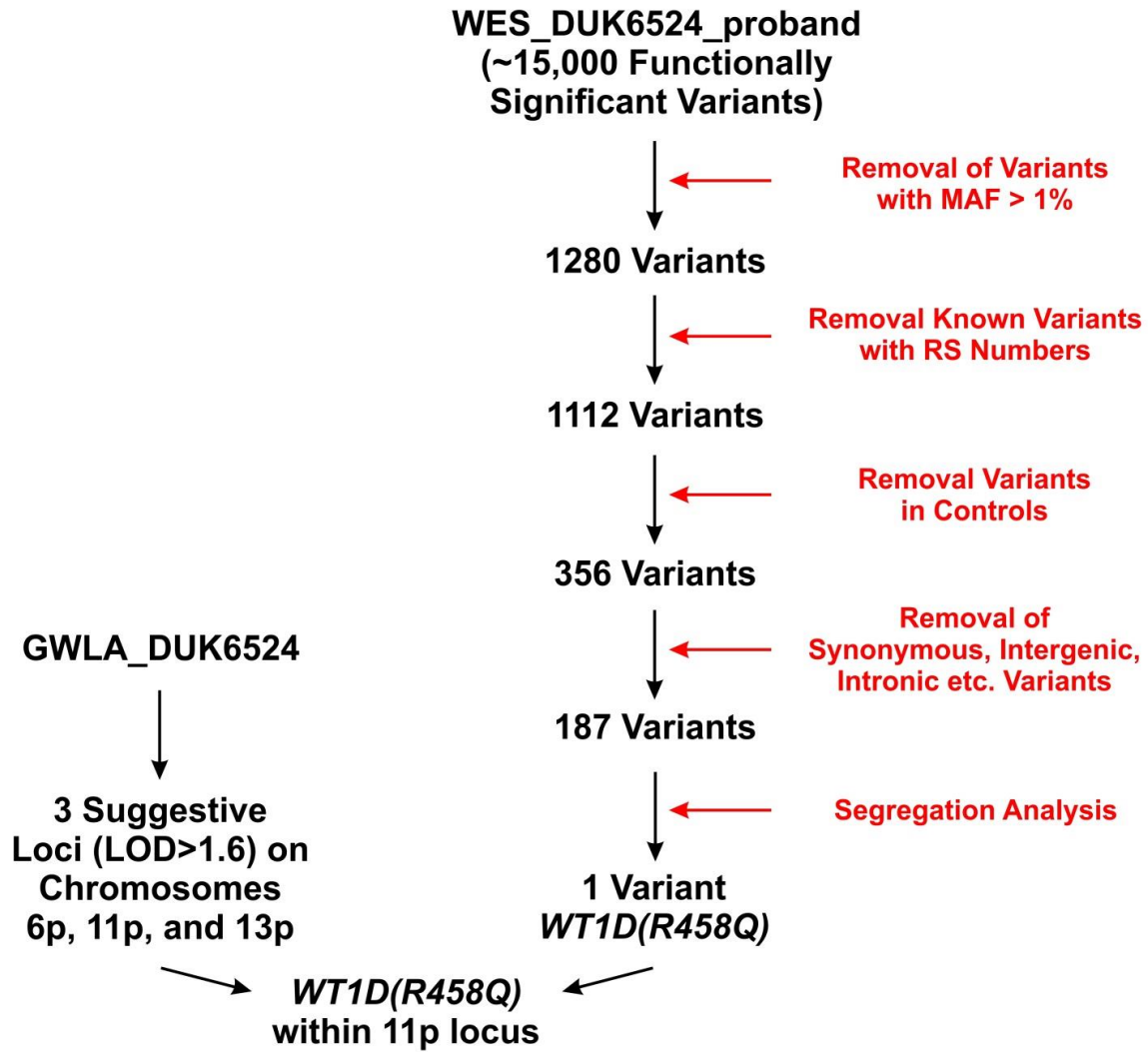
Figure Legends for Supplemental Data

Supplemental Figure 1 – *WT1D* mutation in two kindreds with autosomal dominant FSGS.

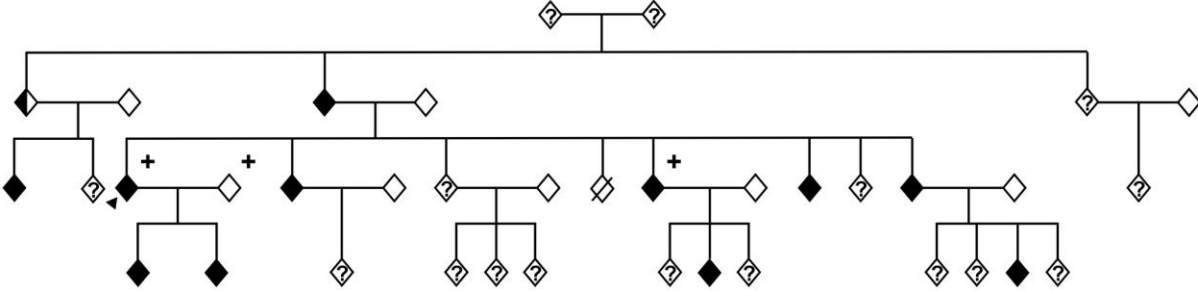
Abbreviated pedigree for family DUK6975 demonstrating male-to-male transmission and at least one affected family member in multiple successive generations consistent with an autosomal dominant inheritance pattern.

Supplemental Figure 2 - *Algorithm for the Identification of the WT1D^{R458Q} Variant in Family DUK6524*. Algorithm for the genomic analysis of family DUK6524. Suggestive peaks with LOD scores of 1.6 identified through GWLA. A heterozygous missense variant in exon 9 of *WT1D* identified through WES. R458Q was the only variant that segregated with disease in the family and was found within the suggestive linkage peak on chromosome 11p.

Supplemental Figure 1: Algorithm for the Identification of the *WT1D*^{R458Q} Variant in Family DUK6524



Supplemental Figure 2: Family DUK6975 Pedigree



◆ Affected ◊ Unaffected ◌ Deceased ◐ Obligate Heterozygote ◑ Unknown