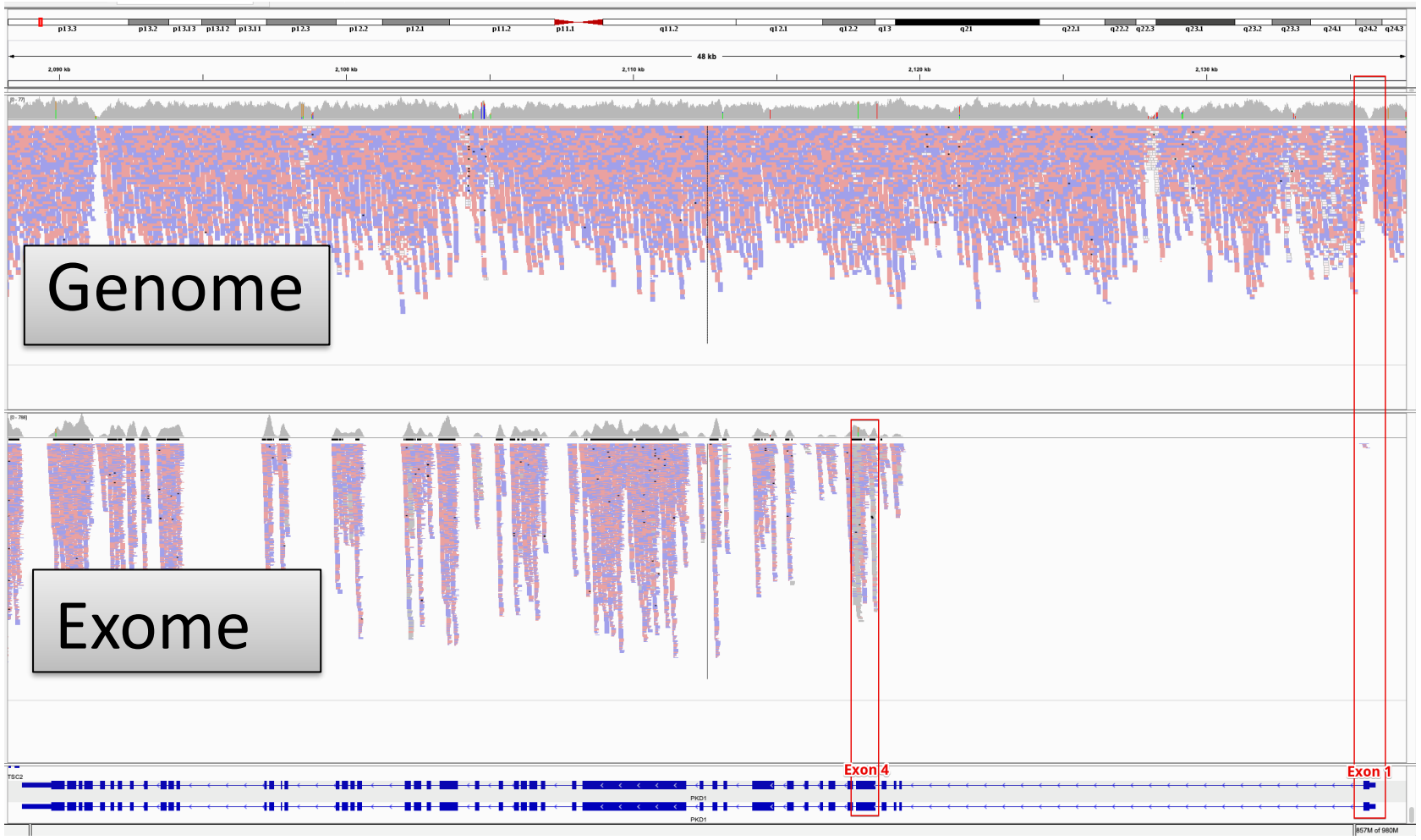
PKD1 trackable with both exome and WGS sequencing



- 150bp paired-end reads enough to distinguish *PKD1* from pseudogene
  - Applies to both Exome and Genome sequencing
- Exome coverage of *PKD1* coding region almost identical to Genome

Integrative Genomics Viewer. Nature Biotechnology 29, 24–26 (2011)

Exome for cystic kidney disease diagnosis

At VCGS the diagnostic yield for cystic kidney diseases is comparable between Exome sequencing and Whole Genome Sequencing (WGS):

2019-2021*	Exome	WGS
Diagnostic Yield	62%	52%

*Audit of cases with clinical indication of "Cystic kidney"
N=50 cases each for exome and WGS from 2019-2021
(VCGS ClinGen laboratory data)
Note: there is no non-coding region coverage or CNV analysis via exome

Exome remains the recommended first tier assay for ADPKD

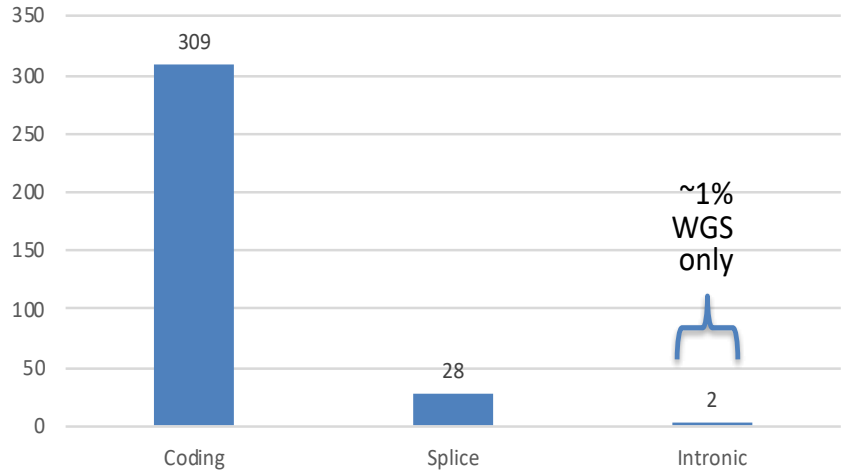
PKD1 gene considerations:

- There is no difference with *PKD1* pseudogene resolution between exome or WGS.
- Recognised lower coverage in exons 1 and 4 via exome, however the vast majority of *PKD1* coding region coverage is comparable between exome and WGS.
  >98% of known pathogenic variants from PKD-DB, ClinVar and the literature are covered by exome
  (audit of databases and literature conducted in 2020 by VCGS- refer below)

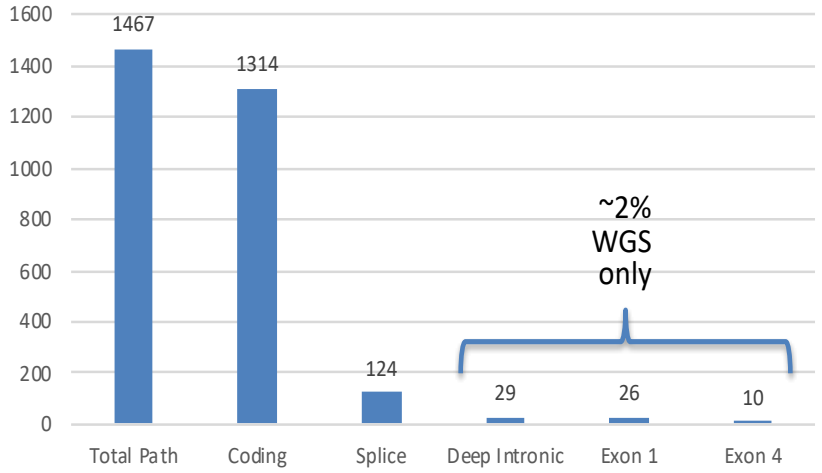
PKD1 Variant location distribution (audit of databases and literature conducted in 2020 by VCGS)

>98% of known variants trackable by exome

Pathogenic *PKD1* Variants in ClinVar



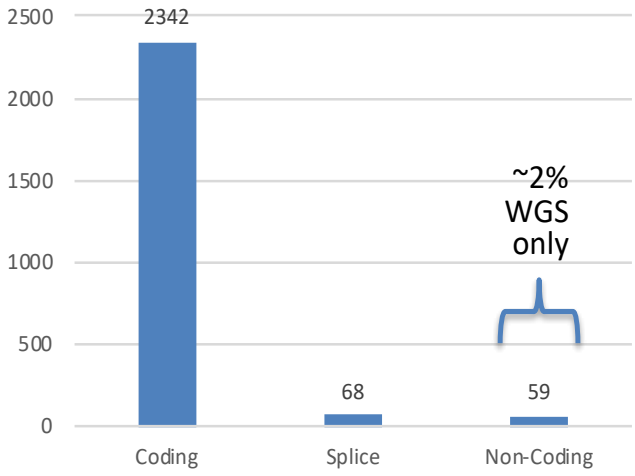
Pathogenic *PKD1* Variants in PKDB



Source: https://pkdb.mayo.edu/

WARNING:
Ascertainment bias
(more data available for exome compared with WGS)

All *PKD1* Variants in Literature



Source: https://mastermind.genomenon.com/