

THE SPECTRUM OF MOLECULAR DEFECTS IN 64 PATIENTS WITH HYPOPHOSPHATEMIC RICKETS IDENTIFIED BY TARGETED NEXT-GENERATION SEQUENCING.

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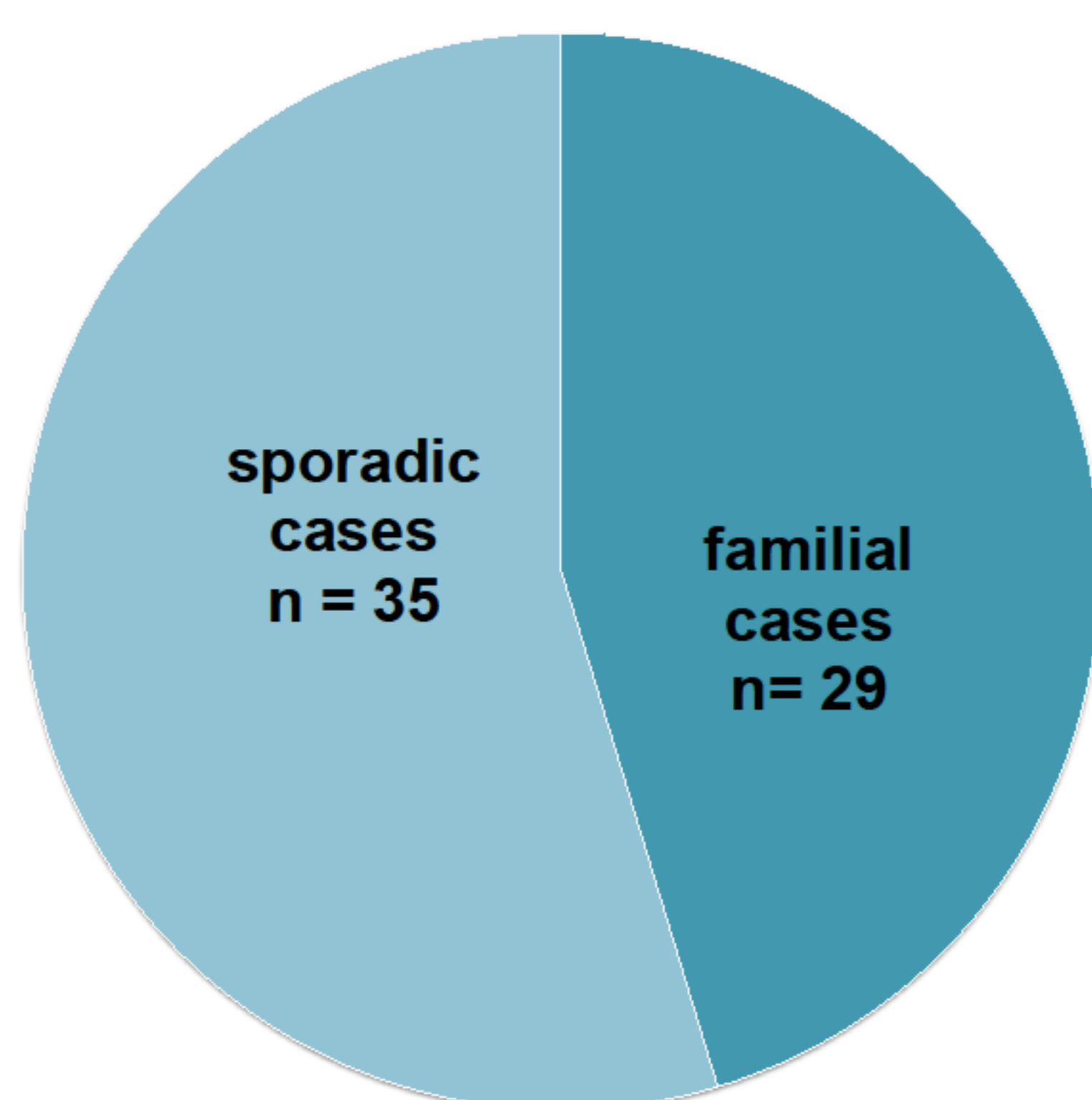
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Introduction and objectives: To assess the value of targeted next-generation sequencing (NGS) used for molecular analysis of candidate genes of Hypophosphatemic rickets (HR).

Patients: n= 64 patients with HR aged 3 months to 45 years

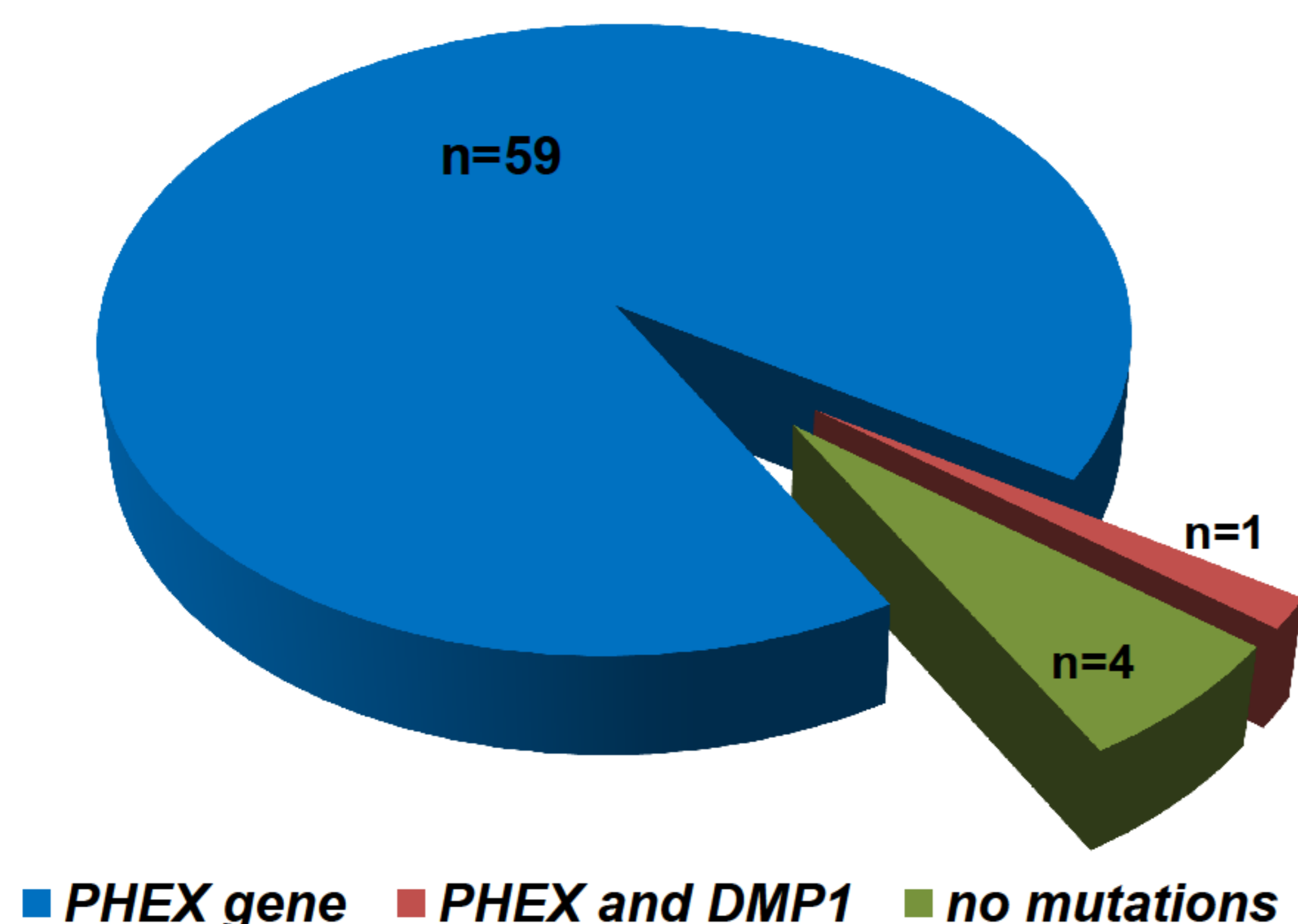


Methods:

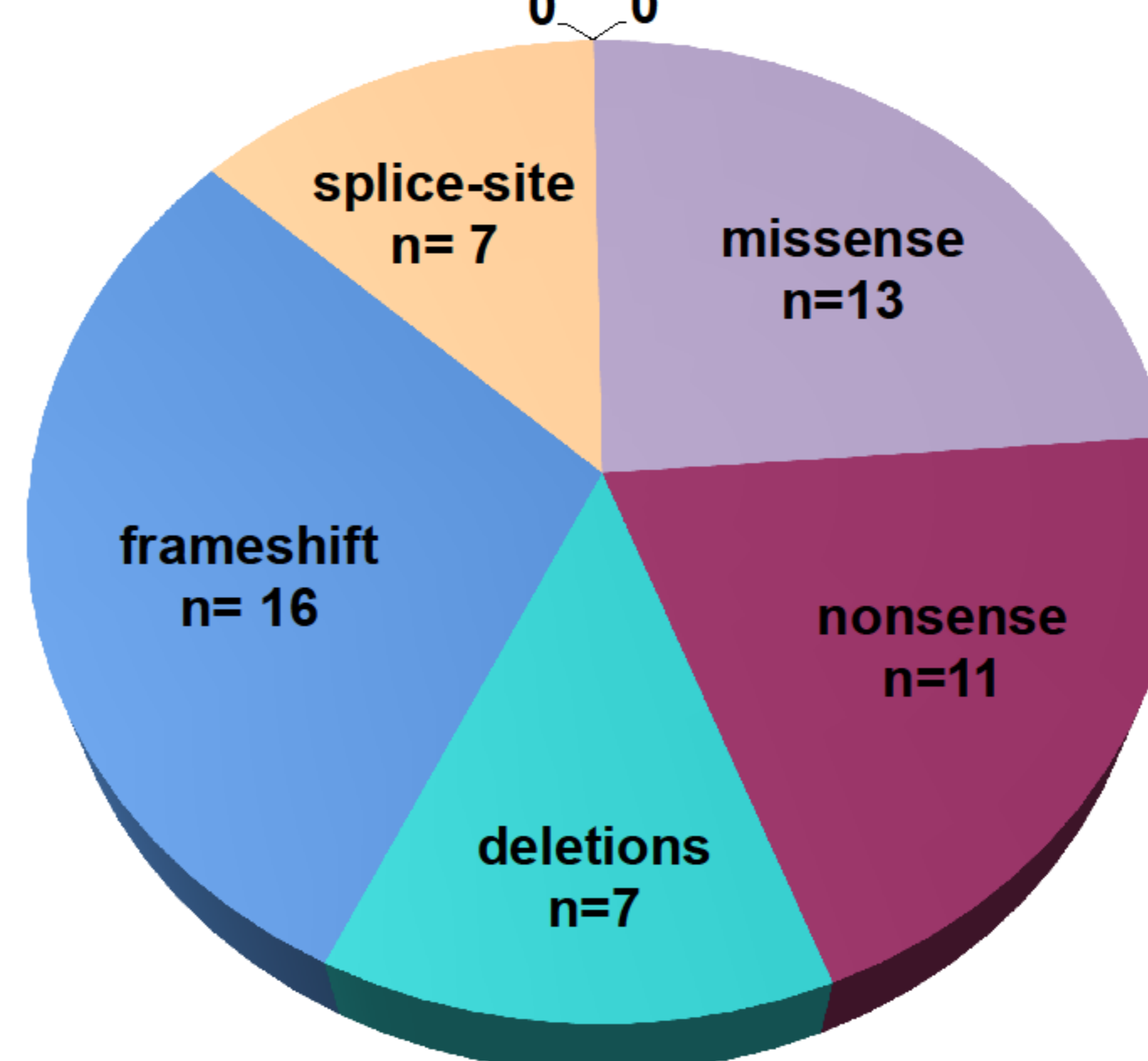
1. Custom Ion AmpliSeq™ "Calcium Disorders" gene panel:
 - 22 genes (*ALPL*, *ATP6V0A4*, *ATP6V1B1*, *CASR*, *CLCN5*, *CLCNKB*, *CYP24A1*, *CYP27B1*, *CYP2R1*, *DMP1*, *ENPP1*, *FGF23*, *GALNT3*, *KL*, *LRP5*, *PHEX*, *PTH1R*, *SLC2A2*, *SLC34A1*, *SLC34A3*, *SLC9A3R1*, *VDR*);
 - ~83 kb, 409 amplicons, coverage 98.5%.
2. PGM semiconductor sequencer (Ion Torrent, Life Technologies).
3. Bioinformatics: Torrent Suite 4.6 (Ion Torrent, Life Technologies), ANNOVAR¹, version 2013 Feb21 (annovar.openbioinformatics.org).

Results: Mutations were identified in 100% of familial and 88.5% of sporadic cases.

n=64 patients



Spectrum of *PHEX* mutations (n=54)
n=38 were novel



Conclusions:

- The study confirmed predominance of *PHEX* mutations among the patients with HR.
- The large size and complexity of *PHEX* gene makes the targeted NGS a feasible tool for diagnostics of HR.

References :

1. Wang K., Li M., Hakonarson H. ANNOVAR: functional annotation of genetic variants from high-throughput sequencing data. *Nucleic Acids Research*, 38:e164, 2010

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