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Special issue of Mutation Research - "DeMarini tribute"

Discovering human germ cell mutagens with whole genome sequencing: insights from power calculations reveal the importance of controlling for between family variability

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Highlights

- Pedigree whole genome sequencing may be used to identify human germ cell mutagens
- Power analyses were performed to determine sample size to identify germ cell mutagens
- Modeling inter-family variability of the mutation-by-paternal age effect increased power
- Sufficient power is achieved by sampling 4-28 multi-sibling families per treatment group

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