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Whole exome sequencing identifies genetic variants in inherited thrombocytopenia with secondary qualitative function defects

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Contributions: BJ, GCL, ML, SPW and NVM designed the research. BJ, GCL, JF, ML, DM, MAS, ISG, SD, DB, VL, SJF, BD, JR, PH and NVM performed the research and analyzed data. GCL, DA, TB, PHB B-M, PC, NC, CG, BJ, MM, JM, SP, KT, JT, JW and MW provided patient samples and clinical data. GCL, ML, SPW and NVM undertook the research governance of the study. BJ and NVM wrote the paper and all authors critically reviewed and edited the paper. GL, PH, PG, SM, AM, MD, SPW and NVM coordinated the GAPP study.