The following articles for this Special Issue were published after the original collection was released. They can be found in their respective issues or online:

Matching whole genomes to rare genetic disorders: Identification of potential causative variants using phenotype-weighted knowledge in the CAGI SickKids5 clinical genomes challenge (41: 2) https://doi.org/10.1002/humu.23933

LEAP: Using machine learning to support variant classification in a clinical setting https://doi.org/10.1002/humu.24011