3. Bioinformatics Analysis

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| **Standard Analysis** |
| Demultiplex BCL files from a sequencer into FASTQs |
| Summary metrics (key metrics about the barcoding and sequencing process: gems\_detected, snps\_phased, number\_reads et al.) |
| Alignment, de-duplication and filtering |
| Calling and phasing of SNPs, indels, and structural variants |
| Visualization |