**S5 Table.** Example of parameter information in the GATK tool that extracts personally identifiable information

| **Copy Number Variant Discovery** | |
|---|---|
| Tools that analyze read coverage to detect copy number variants. | |
| **Name** | **Summary** |
| AnnotateIntervals | Annotates intervals with GC content, mappability, and segmental-duplication content |
| CallCopyRatioSegments | Calls copy-ratio segments as amplified, deleted, or copy-number neutral |
| CreateReadCountPanelOfNormals | Creates a panel of normals for read-count denoising |
| DenoiseReadCounts | Denoises read counts to produce denoised copy ratios |
| DetermineGermlineContigPloidy | Determines the baseline contig ploidy for germline samples given counts data |
| FilterIntervals | Filters intervals based on annotations and/or count statistics |
| GermlineCNVCaller | Calls copy-number variants in germline samples given their counts and the output of DetermineGermlineContigPloidy |
| ModelSegments | Models segmented copy ratios from denoised copy ratios and segmented minor-allele fractions from allelic counts |
| PlotDenoisedCopyRatios | Creates plots of denoised copy ratios |
| PlotModeledSegments | Creates plots of denoised and segmented copy-ratio and minor-allele-fraction estimates |
| PostprocessGermlineCNVCalls GermlineCNVCaller | Postprocesses the output of GermlineCNVCaller and generates VCFs and denoised copy ratios |
| **Read Data Manipulation** | |
| Tools that manipulate read data in SAM, BAM or CRAM format. | |
| **Name** | **Summary** |
| SamToFastq (Picard) | Converts a SAM/BAM/CRAM file to FASTQ |

| **Reference** | |
|---|---|
| Tools that analyze and manipulate FASTA format references. | |
| **Name** | **Summary** |
| ComposeSTRTableFile | Composes a genome-wide STR location table used for DragSTR model auto-calibration |

| **Short Variant Discovery** | |
|---|---|
| Tools that perform variant calling and genotyping for short variants (SNPs, SNVs and Indels). | |
| **Name** | **Summary** |
| RampedHaplotypeCaller | **EXPERIMENTAL** Call germline SNPs and indels via local re-assembly of |

| | |
|---|---|
| | haplotypes (ramped version) |

| **Variant Annotations** | |
|---|---|
| Available to HaplotypeCaller, Mutect2, VariantAnnotator and GenotypeGVCFs. | |
| **Name** | **Summary** |
| InbreedingCoeff: | Likelihood-based test for the consanguinity among samples (InbreedingCoeff) |
| TandemRepeat: | Tandem repeat unit composition and counts per allele (STR, RU, RPA) |

SNP, single nucleotide polymorphism; SNV, single nucleotide variant; STR, short tandem repeat.