Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 11:21:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068122.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR6068122 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068122.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 11:21:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068122.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,455,394
Mapped reads	4,161,534 / 93.4%
Unmapped reads	293,860 / 6.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	25,412 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	480,160 / 10.78%
Duplication rate	9.35%
Clipped reads	2,190,038 / 49.15%

2.2. ACGT Content

Number/percentage of A's	70,510,012 / 26.13%
Number/percentage of C's	49,394,837 / 18.31%
Number/percentage of T's	86,203,737 / 31.95%
Number/percentage of G's	63,661,933 / 23.6%
Number/percentage of N's	30,600 / 0.01%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0872

Standard Deviation	0.8728

2.4. Mapping Quality

Mean Mapping Quality	43.92

2.5. Mismatches and indels

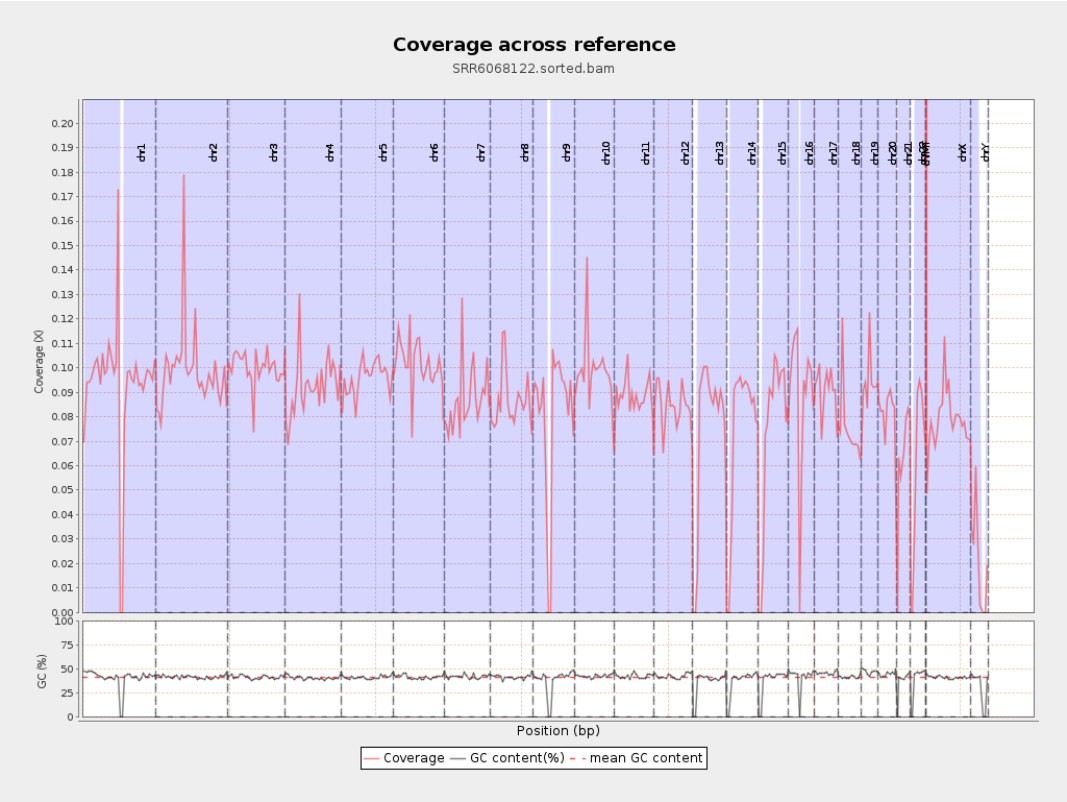
General error rate	0.63%
Mismatches	1,654,217
Insertions	19,681
Mapped reads with at least one insertion	0.47%
Deletions	70,343
Mapped reads with at least one deletion	1.67%
Homopolymer indels	45.69%

2.6. Chromosome stats

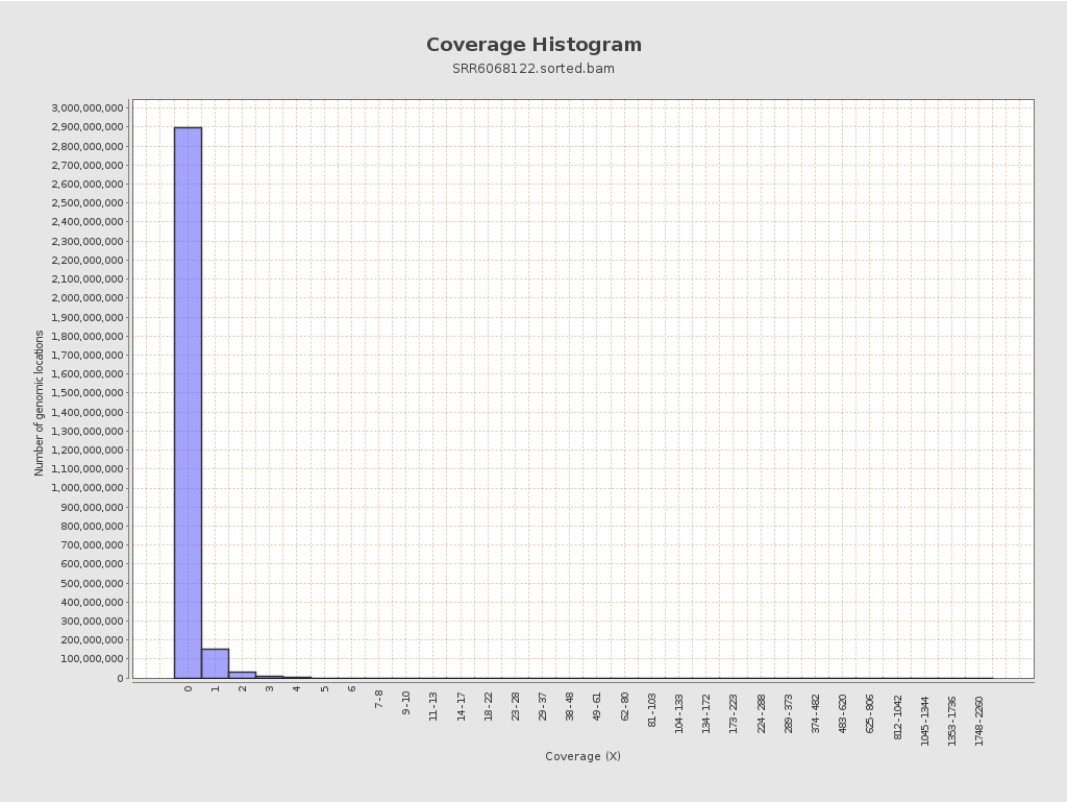
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	23217737	0.0932	1.9197
chr2	243199373	24008328	0.0987	1.0754
chr3	198022430	19791451	0.0999	0.4211
chr4	191154276	17716591	0.0927	0.4704
chr5	180915260	17312125	0.0957	0.415
chr6	171115067	17369637	0.1015	0.522
chr7	159138663	13862950	0.0871	0.9079

chr8	146364022	12635367	0.0863	1.2405
chr9	141213431	11391371	0.0807	0.7511
chr10	135534747	13411498	0.099	0.7118
chr11	135006516	11928530	0.0884	0.6288
chr12	133851895	11386200	0.0851	0.4088
chr13	115169878	8611964	0.0748	0.3696
chr14	107349540	8089827	0.0754	0.4378
chr15	102531392	7418514	0.0724	0.4255
chr16	90354753	7870420	0.0871	0.4659
chr17	81195210	7436186	0.0916	0.4654
chr18	78077248	5936188	0.076	1.4419
chr19	59128983	5554235	0.0939	1.3122
chr20	63025520	5161400	0.0819	0.4295
chr21	48129895	3076175	0.0639	0.399
chr22	51304566	3104121	0.0605	0.3258
chrMT	16571	161647	9.7548	7.176
chrX	155270560	12220776	0.0787	0.4517
chrY	59373566	1254022	0.0211	0.3448

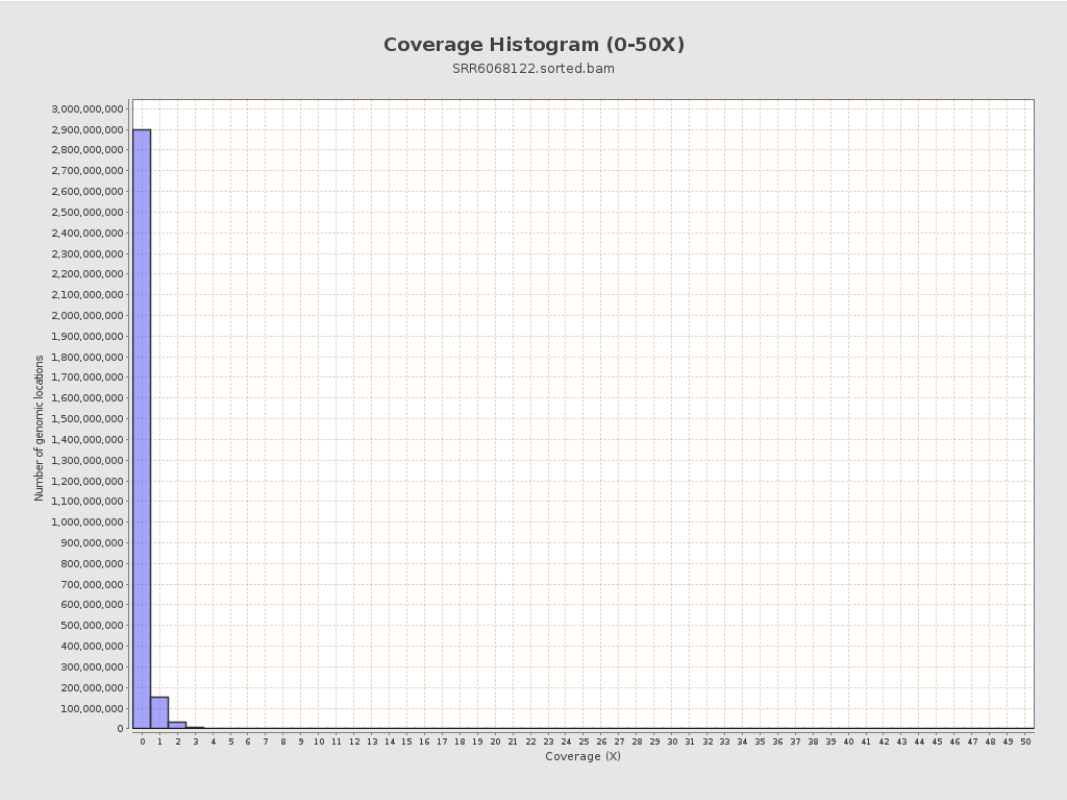
3. Results : Coverage across reference



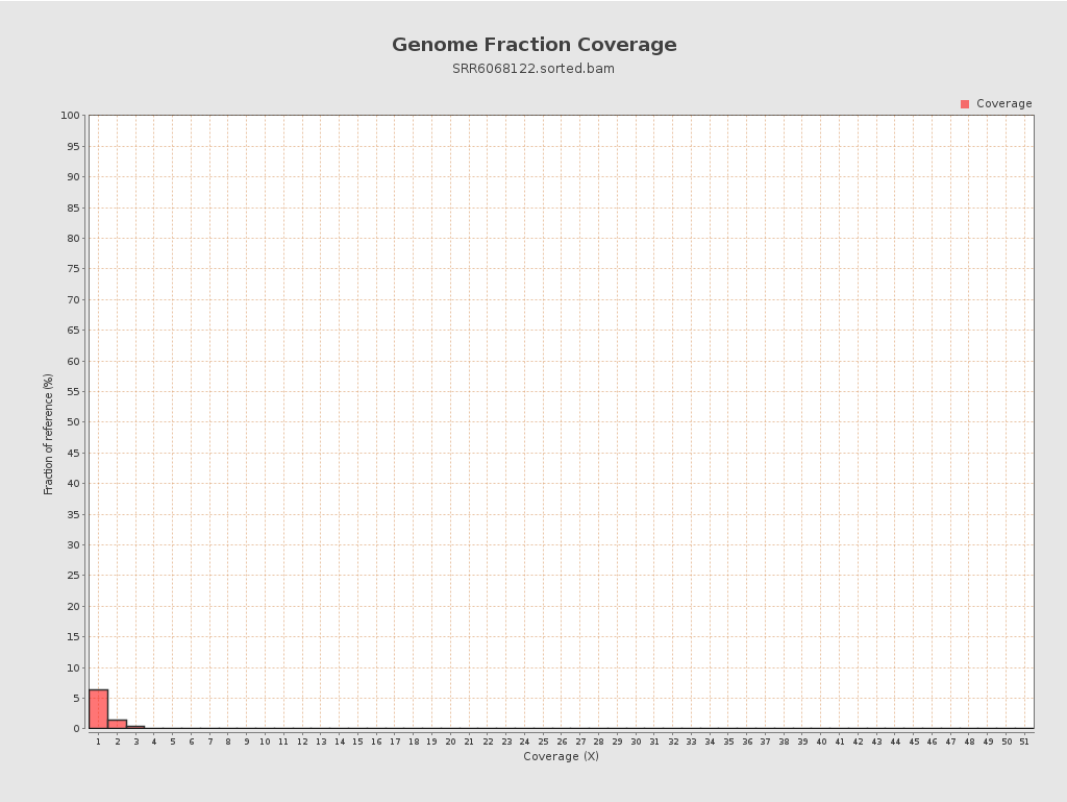
4. Results : Coverage Histogram



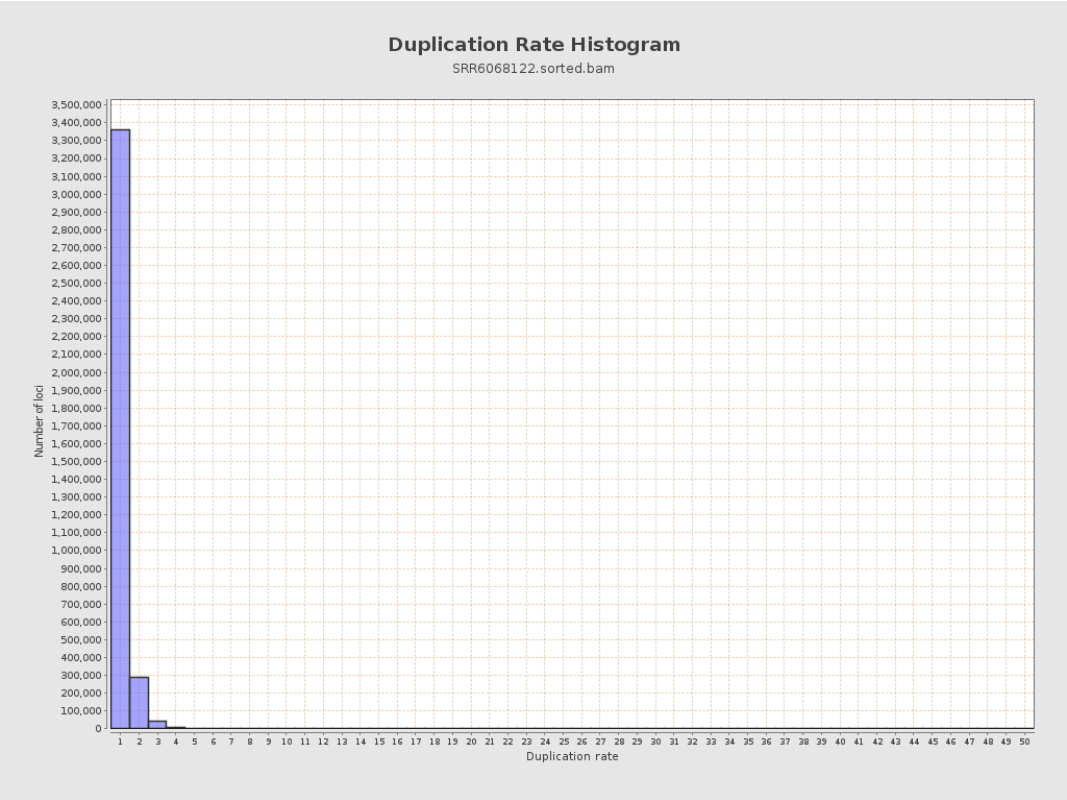
5. Results : Coverage Histogram (0-50X)



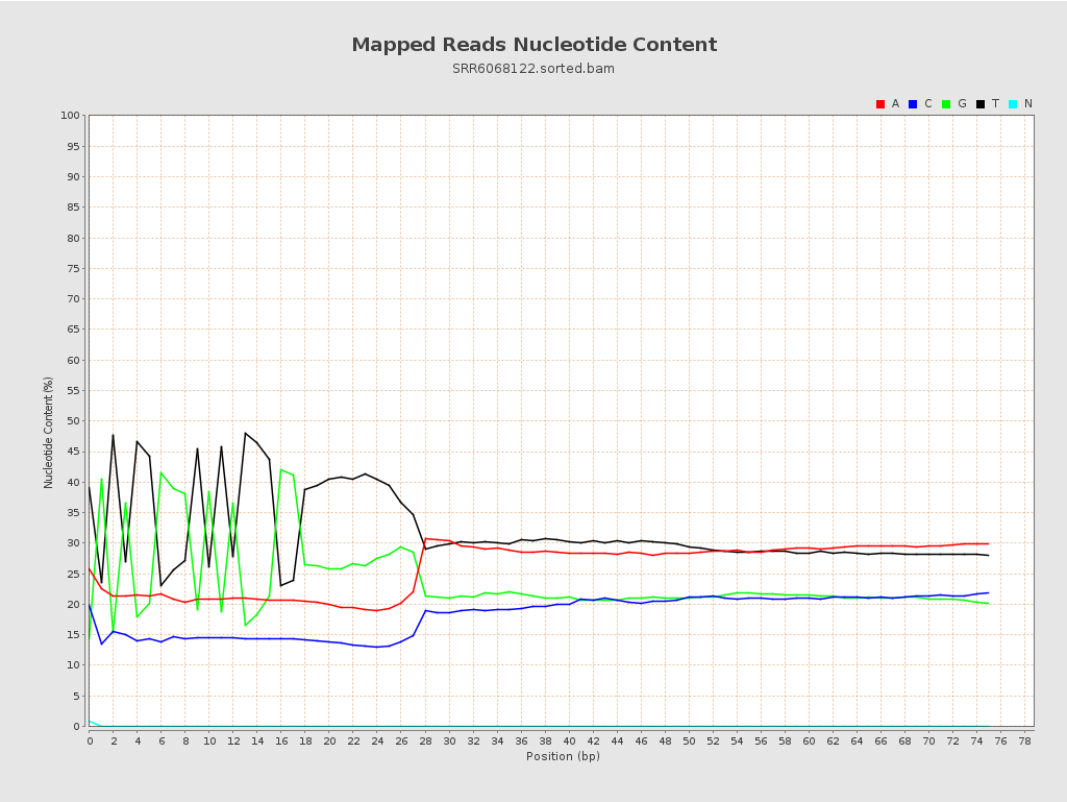
6. Results : Genome Fraction Coverage



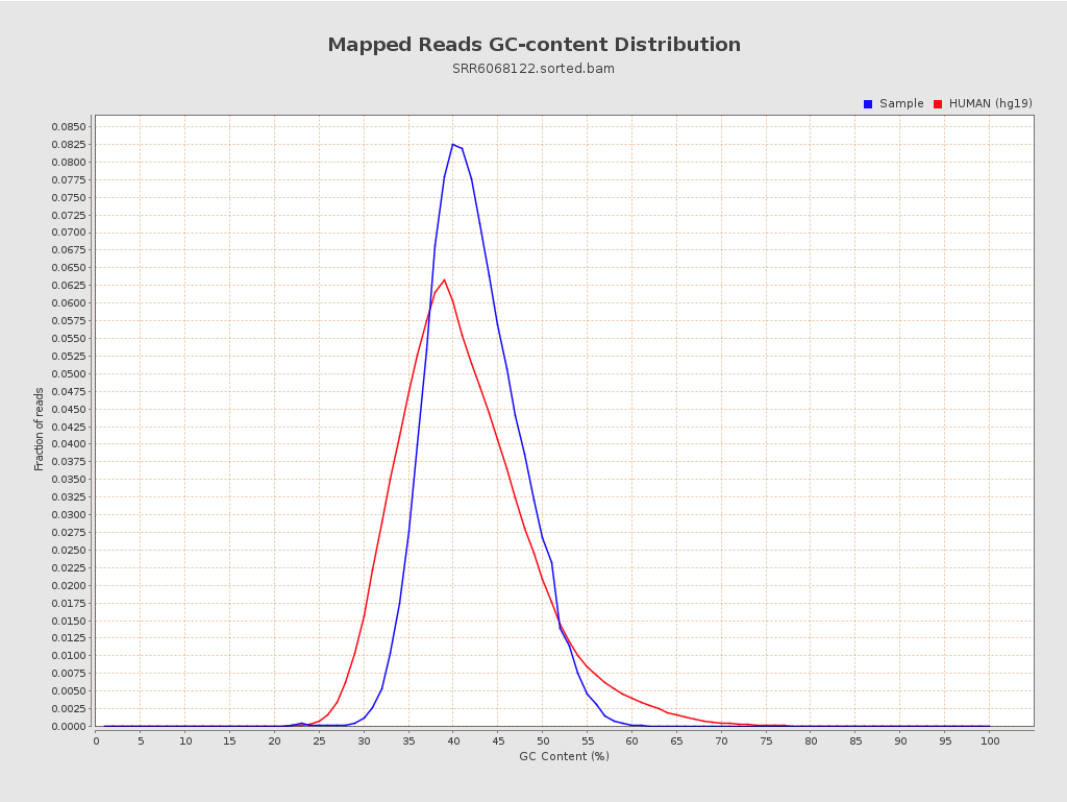
7. Results : Duplication Rate Histogram



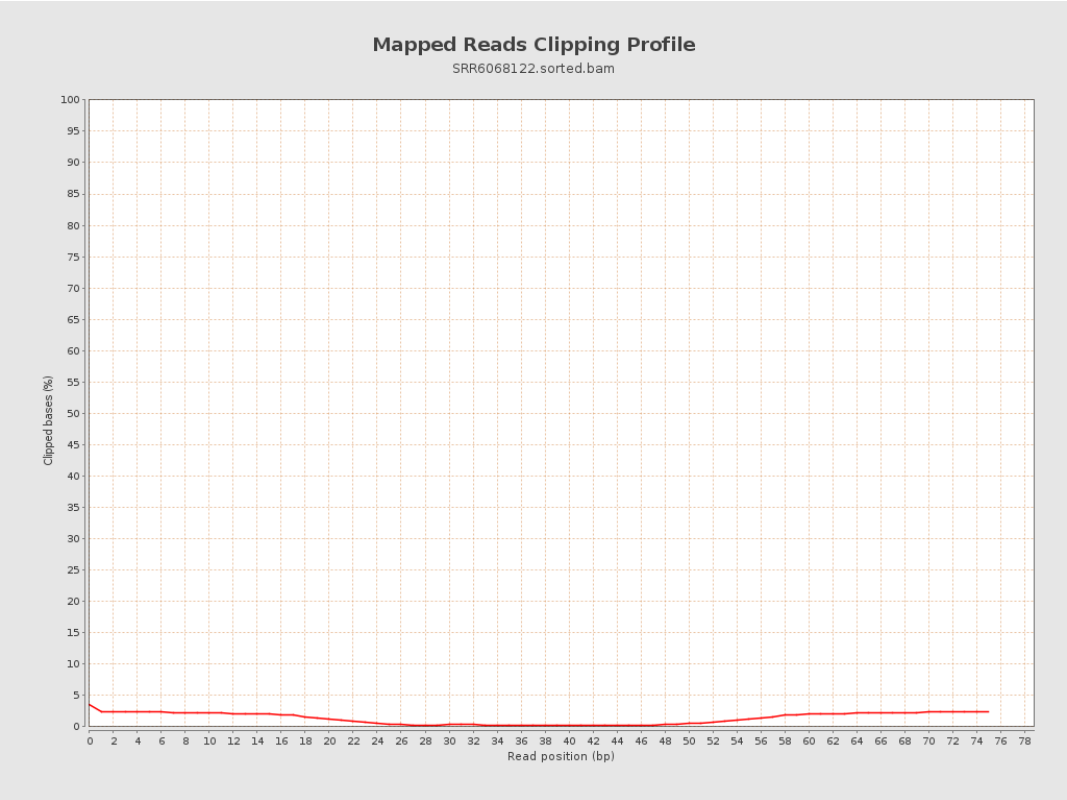
8. Results : Mapped Reads Nucleotide Content



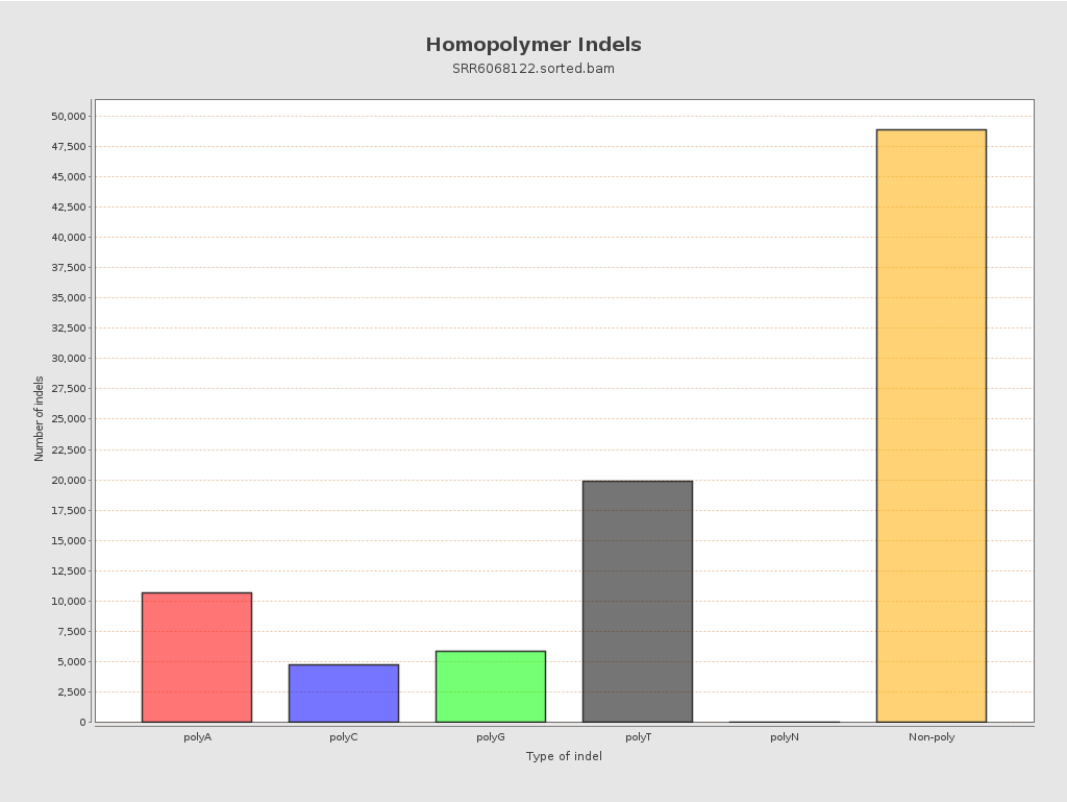
9. Results : Mapped Reads GC-content Distribution



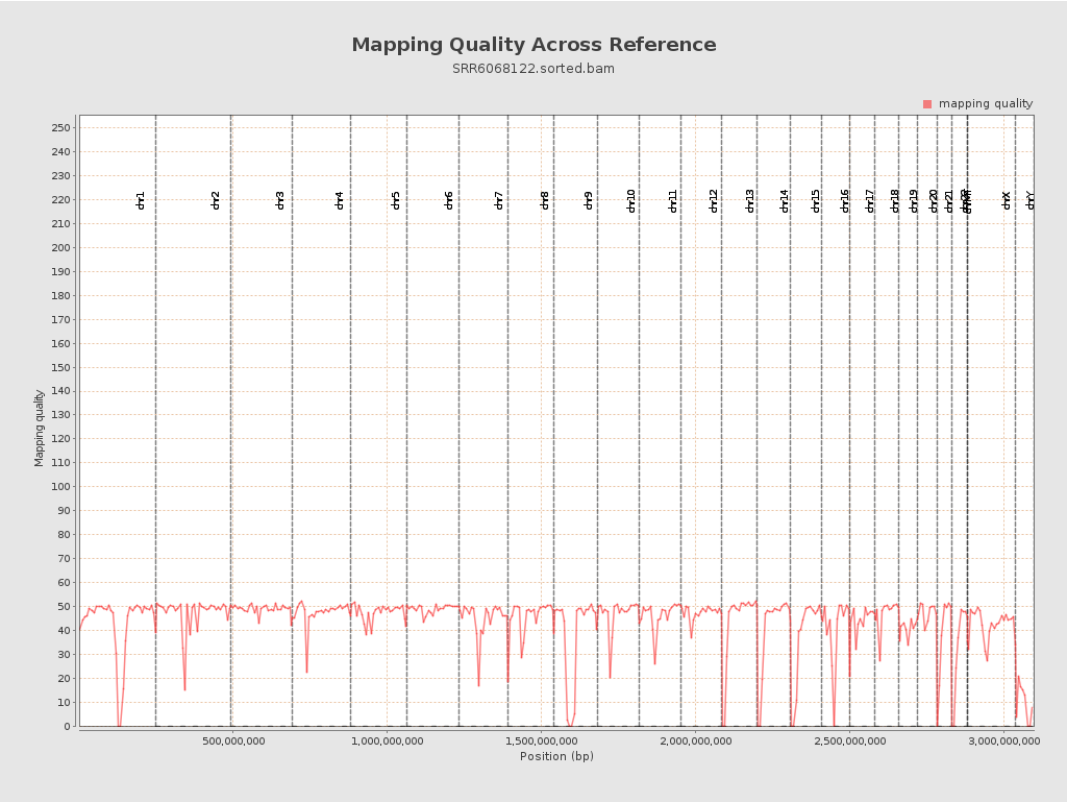
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram