Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:29:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068185.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_SRR6068185 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068185.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:29:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068185.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,182,056
Mapped reads	992,083 / 83.93%
Unmapped reads	189,973 / 16.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,905 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	89,117 / 7.54%
Duplication rate	7.56%
Clipped reads	623,974 / 52.79%

2.2. ACGT Content

Number/percentage of A's	17,311,842 / 27.9%
Number/percentage of C's	11,229,406 / 18.1%
Number/percentage of T's	19,849,783 / 32%
Number/percentage of G's	13,589,139 / 21.9%
Number/percentage of N's	58,535 / 0.09%
GC Percentage	40%

2.3. Coverage

Mean	0.0201

Standard Deviation	0.2427

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

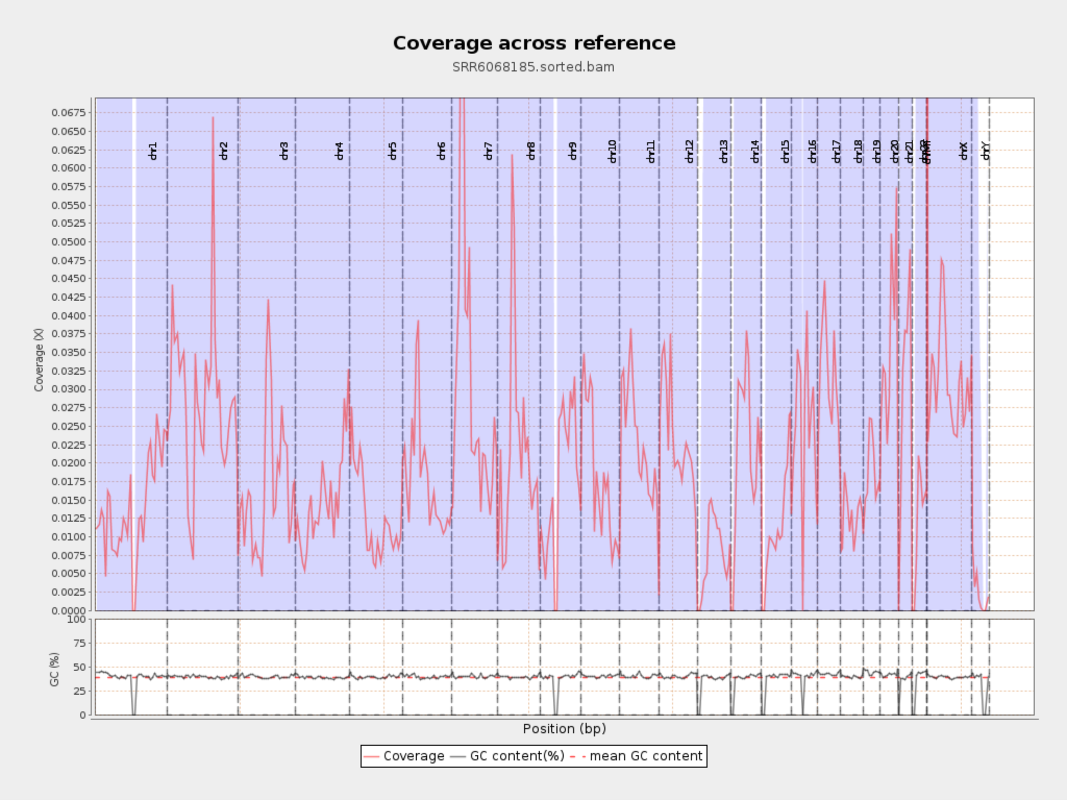
General error rate	0.99%
Mismatches	607,238
Insertions	4,402
Mapped reads with at least one insertion	0.44%
Deletions	19,579
Mapped reads with at least one deletion	1.95%
Homopolymer indels	48.39%

2.6. Chromosome stats

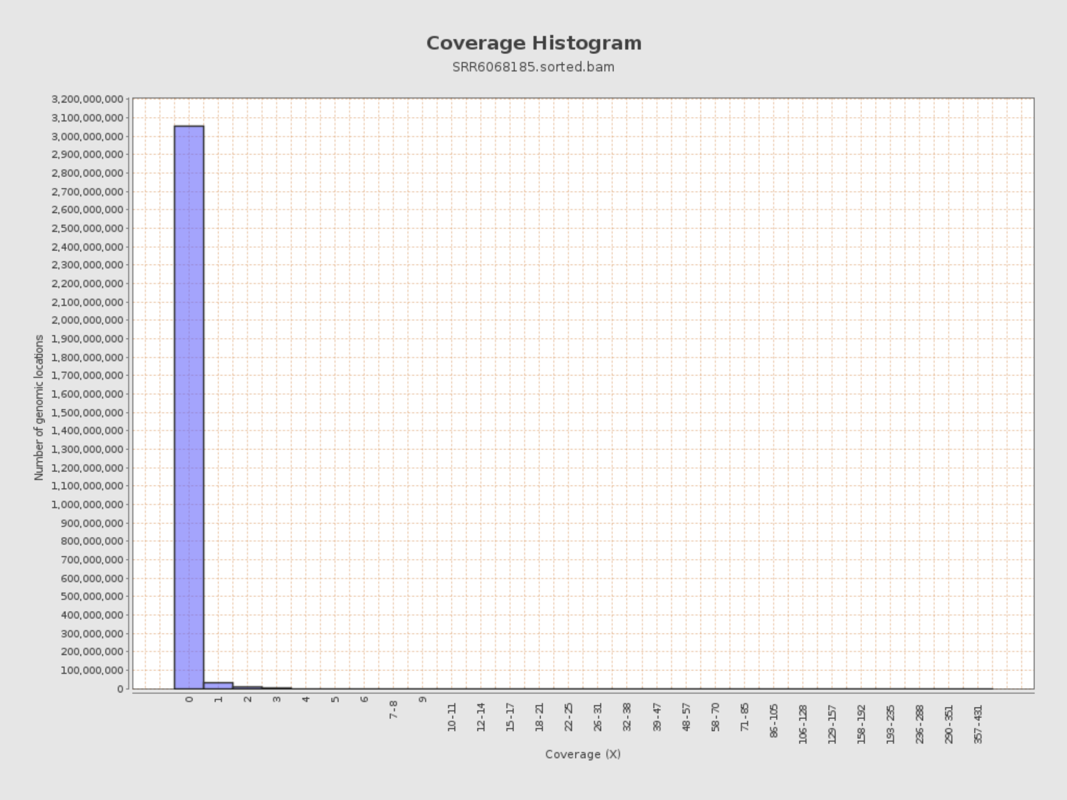
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3430931	0.0138	0.2673
chr2	243199373	7004526	0.0288	0.289
chr3	198022430	3276554	0.0165	0.1734
chr4	191154276	2868631	0.015	0.1652
chr5	180915260	2274858	0.0126	0.1514
chr6	171115067	3071809	0.018	0.233
chr7	159138663	5087303	0.032	0.4809

chr8	146364022	3170070	0.0217	0.266
chr9	141213431	2436448	0.0173	0.2175
chr10	135534747	2527377	0.0186	0.2261
chr11	135006516	3119159	0.0231	0.2429
chr12	133851895	3145962	0.0235	0.2071
chr13	115169878	891591	0.0077	0.1174
chr14	107349540	2348820	0.0219	0.2052
chr15	102531392	1143668	0.0112	0.1411
chr16	90354753	2226490	0.0246	0.2177
chr17	81195210	2609911	0.0321	0.2692
chr18	78077248	977583	0.0125	0.2594
chr19	59128983	1128593	0.0191	0.238
chr20	63025520	2268591	0.036	0.2587
chr21	48129895	1473560	0.0306	0.2396
chr22	51304566	627937	0.0122	0.1428
chrMT	16571	7117	0.4295	0.9287
chrX	155270560	4815723	0.031	0.251
chrY	59373566	138913	0.0023	0.0608

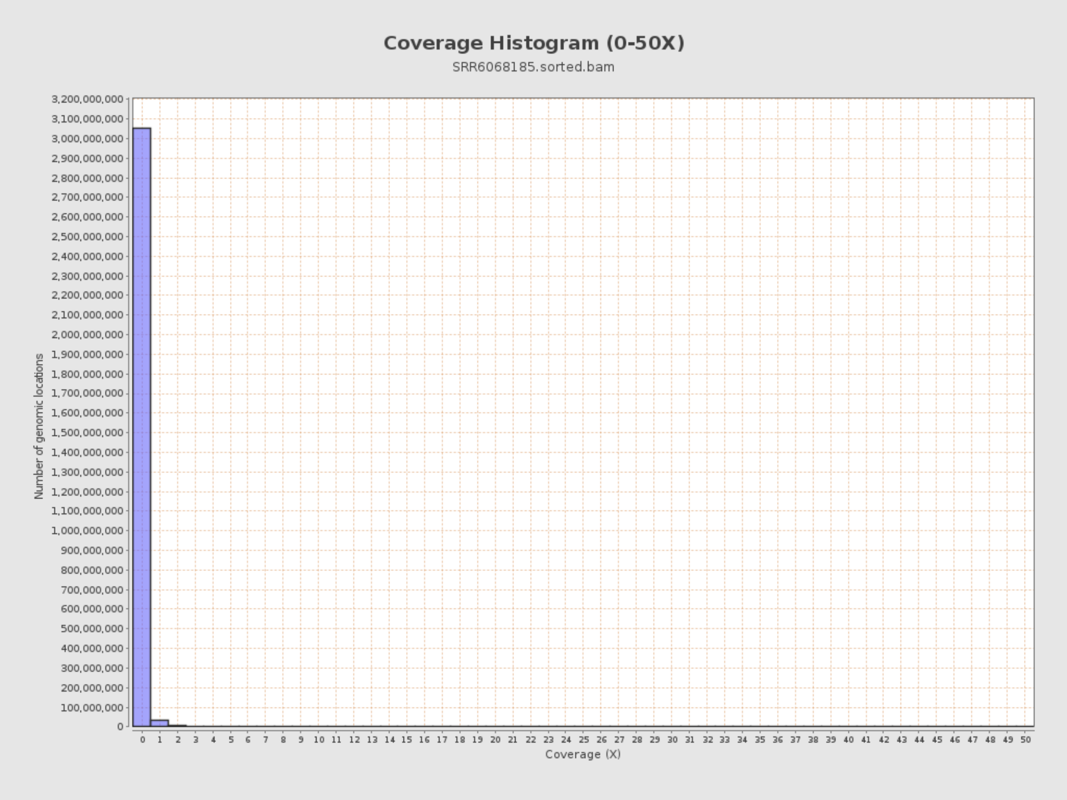
3. Results : Coverage across reference



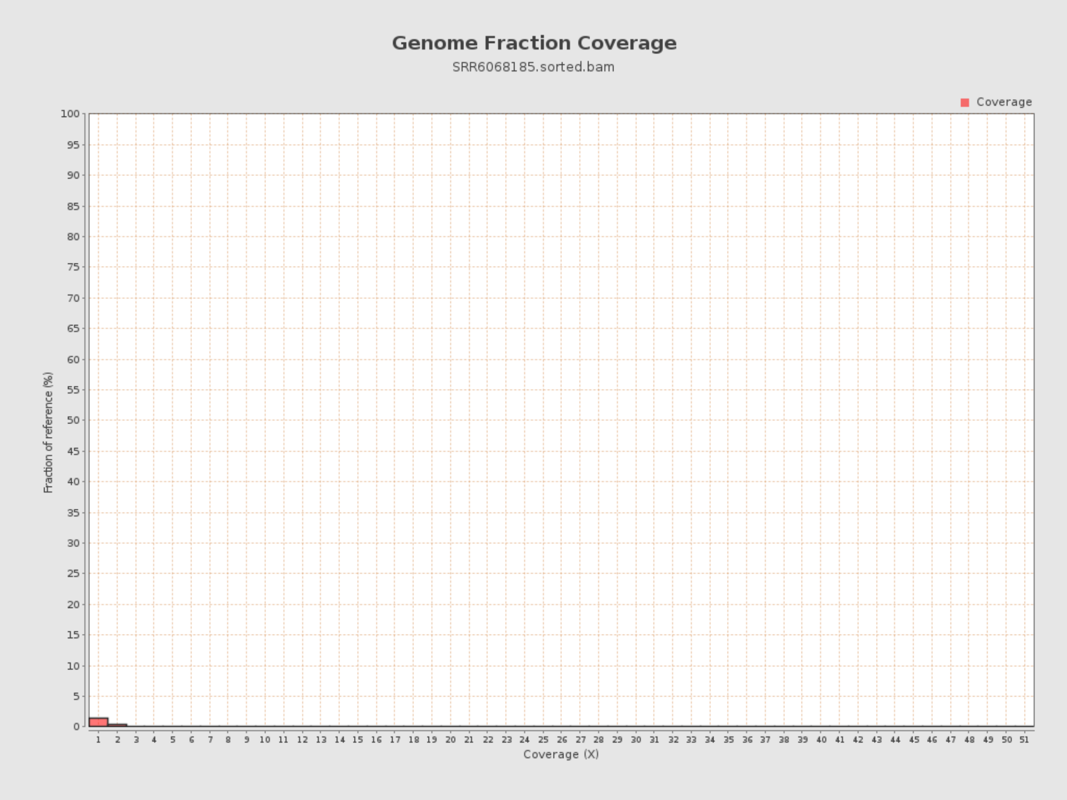
4. Results : Coverage Histogram



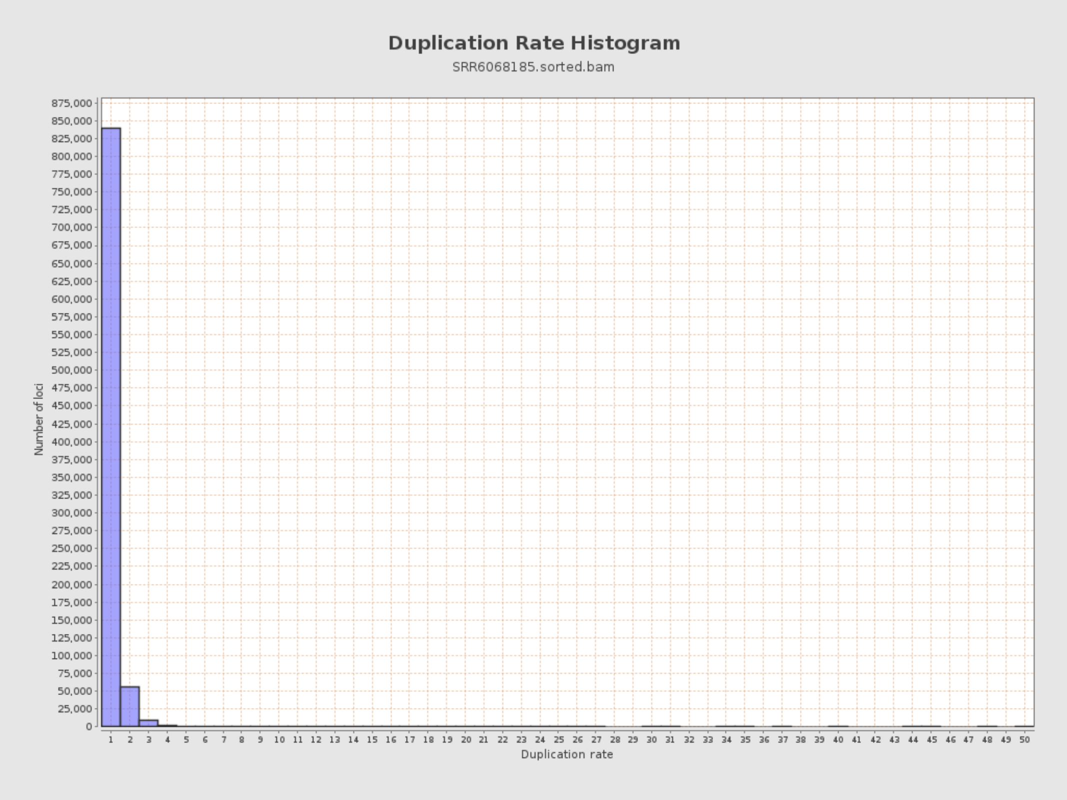
5. Results : Coverage Histogram (0-50X)



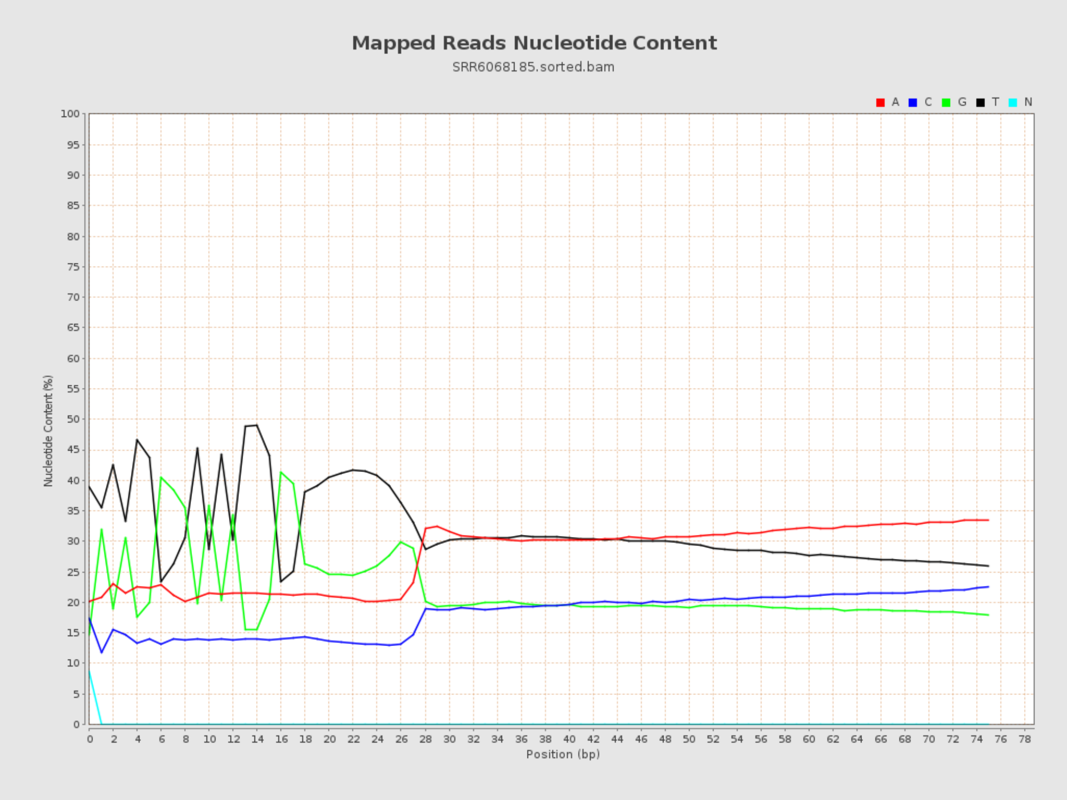
6. Results : Genome Fraction Coverage



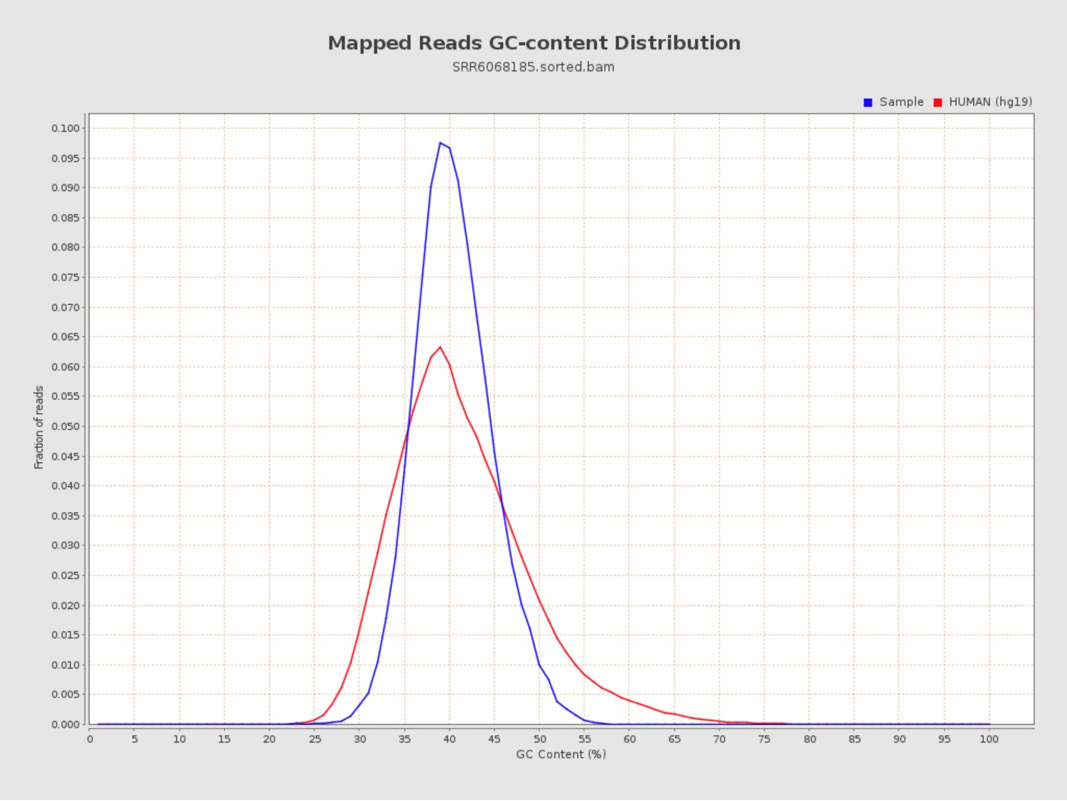
7. Results : Duplication Rate Histogram



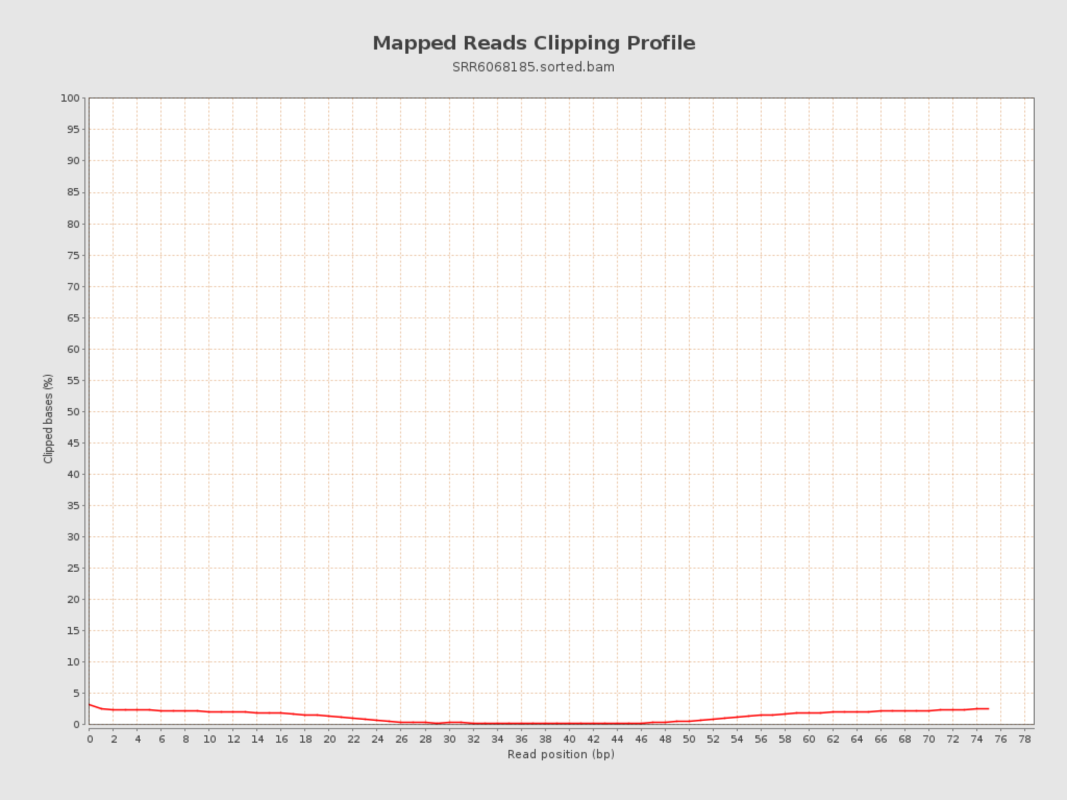
8. Results : Mapped Reads Nucleotide Content



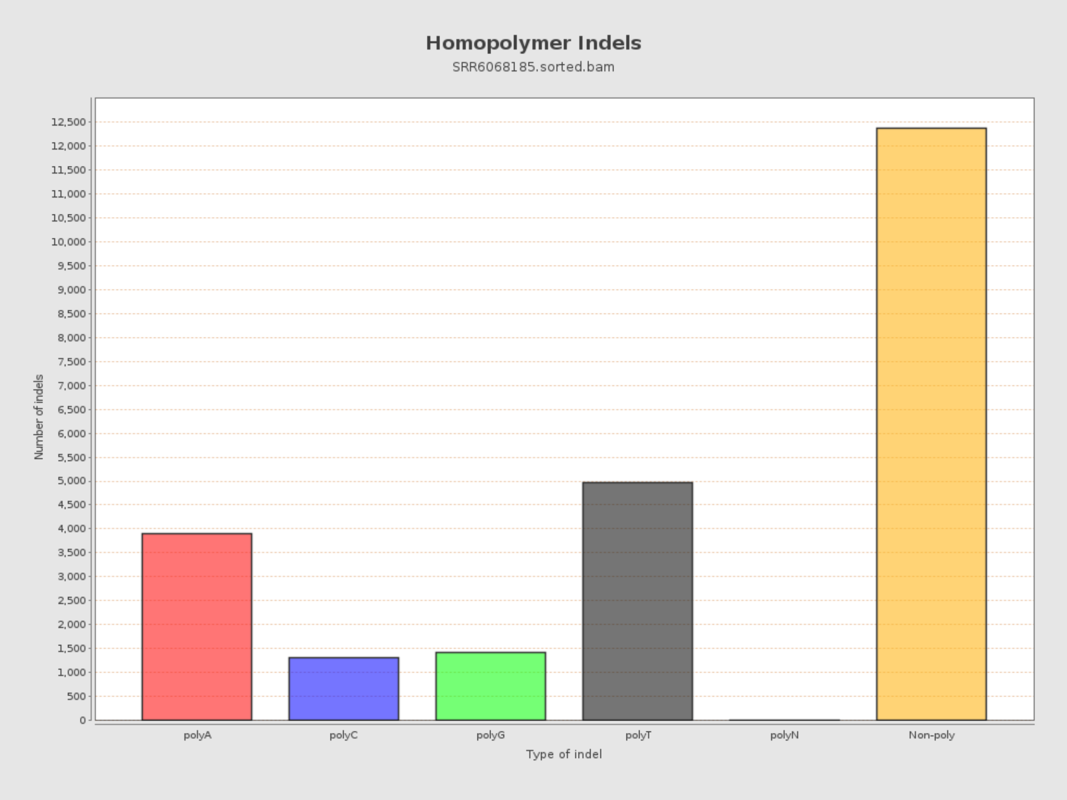
9. Results : Mapped Reads GC-content Distribution



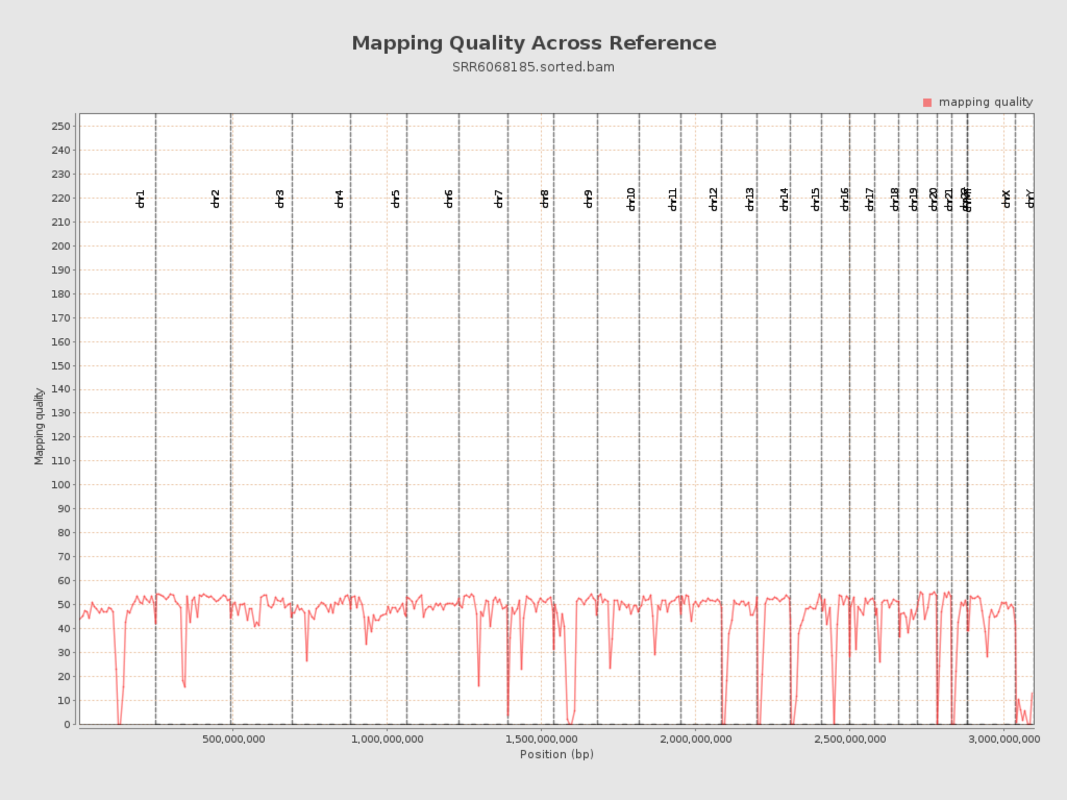
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram