Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 15:27:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068184.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_SRR6068184 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068184.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 15:27:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068184.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,036,768
Mapped reads	659,048 / 63.57%
Unmapped reads	377,720 / 36.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,579 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	162,684 / 15.69%
Duplication rate	15.93%
Clipped reads	469,424 / 45.28%

2.2. ACGT Content

Number/percentage of A's	10,898,169 / 27.28%
Number/percentage of C's	6,942,019 / 17.38%
Number/percentage of T's	13,128,449 / 32.86%
Number/percentage of G's	8,944,342 / 22.39%
Number/percentage of N's	39,480 / 0.1%
GC Percentage	39.76%

2.3. Coverage

Mean	0.0129

Standard Deviation	0.2546

2.4. Mapping Quality

Mean Mapping Quality	45.59

2.5. Mismatches and indels

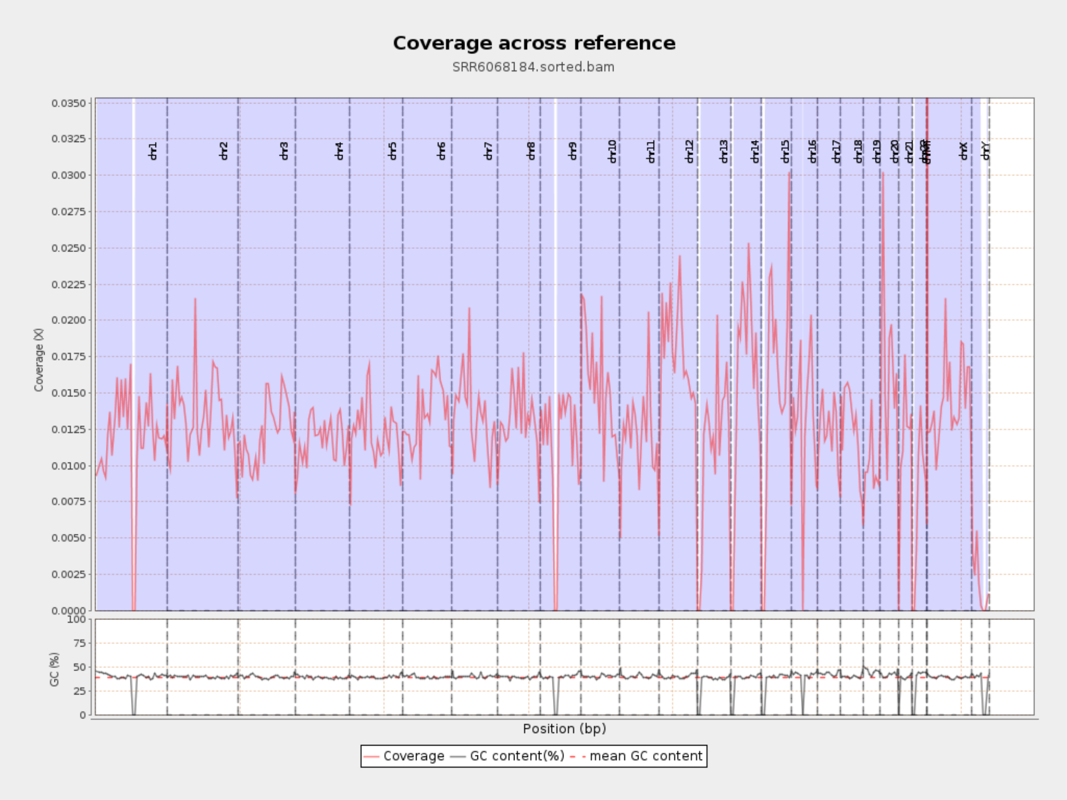
General error rate	1.08%
Mismatches	427,299
Insertions	2,808
Mapped reads with at least one insertion	0.42%
Deletions	13,946
Mapped reads with at least one deletion	2.09%
Homopolymer indels	49.22%

2.6. Chromosome stats

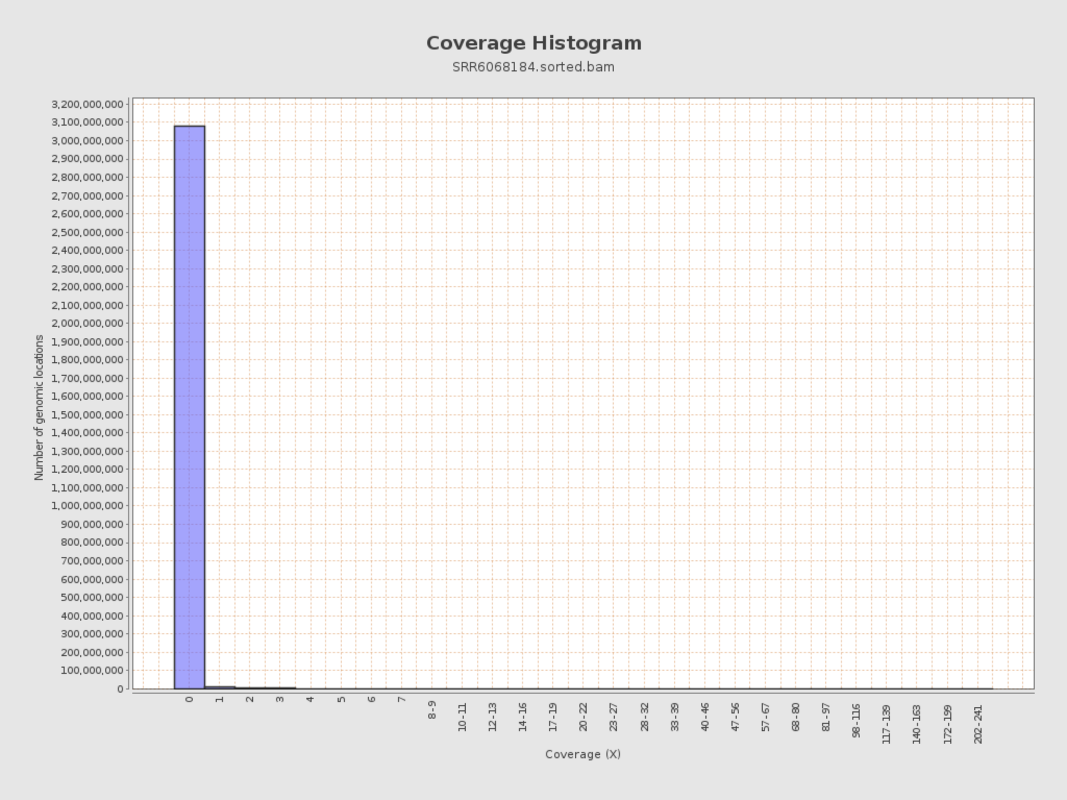
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2933710	0.0118	0.2662
chr2	243199373	3279657	0.0135	0.2591
chr3	198022430	2440362	0.0123	0.2347
chr4	191154276	2249856	0.0118	0.2394
chr5	180915260	2223345	0.0123	0.2356
chr6	171115067	2325034	0.0136	0.2556
chr7	159138663	2159623	0.0136	0.2891

chr8	146364022	1922674	0.0131	0.2775
chr9	141213431	1616601	0.0114	0.2344
chr10	135534747	2100376	0.0155	0.2742
chr11	135006516	1658274	0.0123	0.2467
chr12	133851895	2374543	0.0177	0.2952
chr13	115169878	1287652	0.0112	0.2305
chr14	107349540	1673371	0.0156	0.2815
chr15	102531392	1588956	0.0155	0.2828
chr16	90354753	1165878	0.0129	0.2326
chr17	81195210	1006459	0.0124	0.2343
chr18	78077248	991483	0.0127	0.2863
chr19	59128983	586419	0.0099	0.21
chr20	63025520	1058764	0.0168	0.2821
chr21	48129895	560027	0.0116	0.2232
chr22	51304566	389502	0.0076	0.1746
chrMT	16571	30743	1.8552	3.2075
chrX	155270560	2246222	0.0145	0.2556
chrY	59373566	107500	0.0018	0.1091

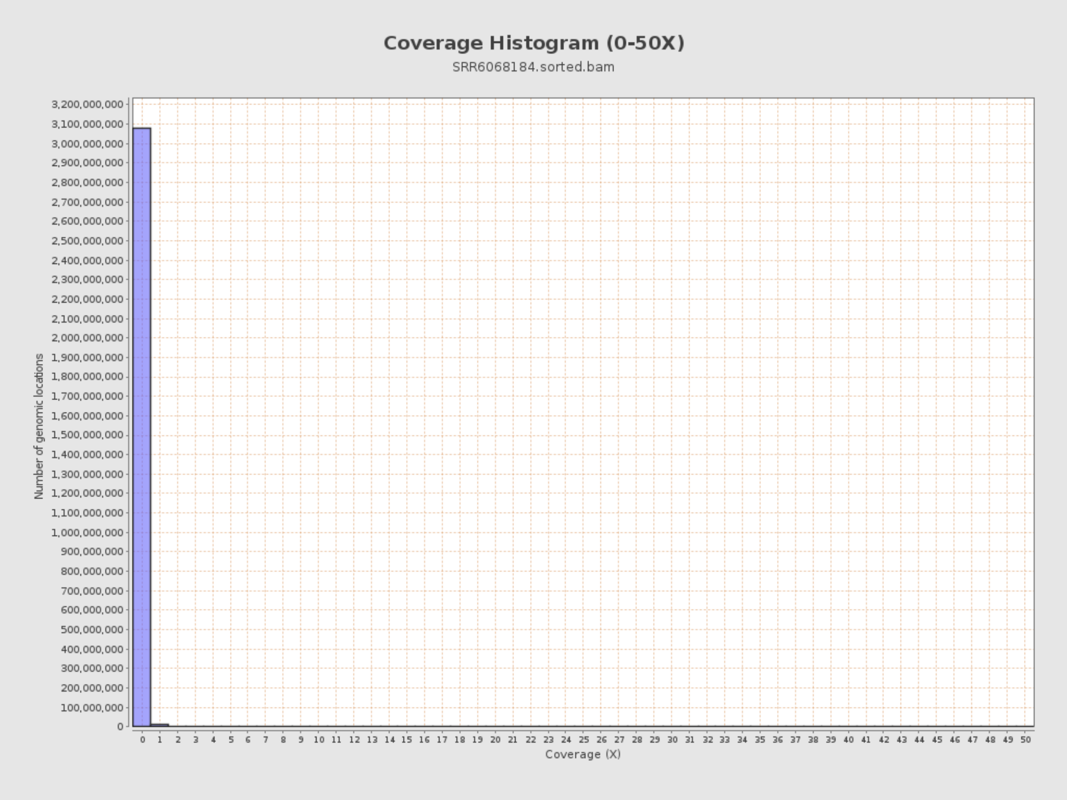
3. Results : Coverage across reference



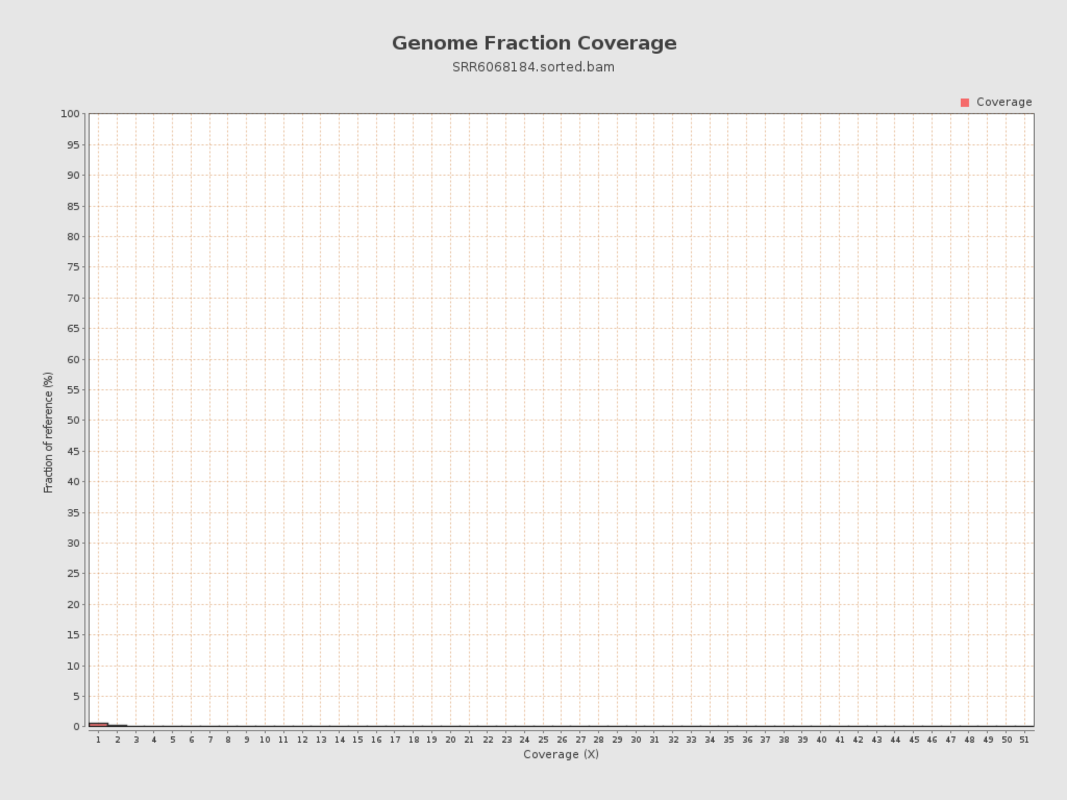
4. Results : Coverage Histogram



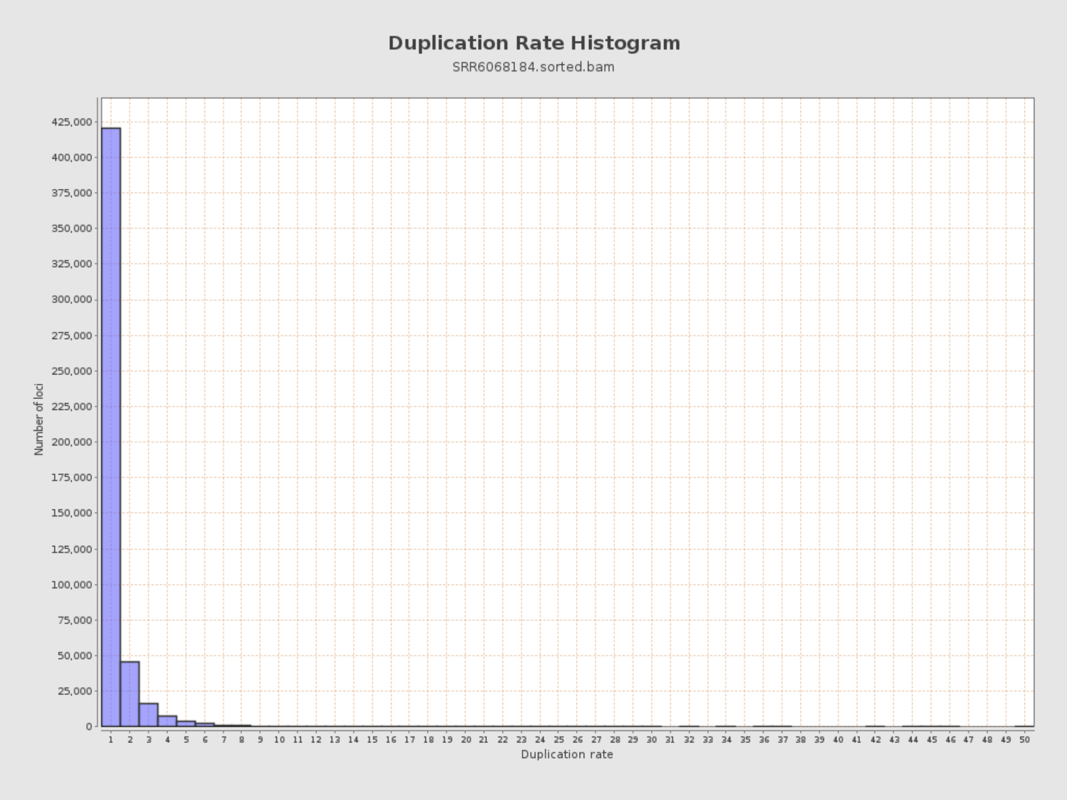
5. Results : Coverage Histogram (0-50X)



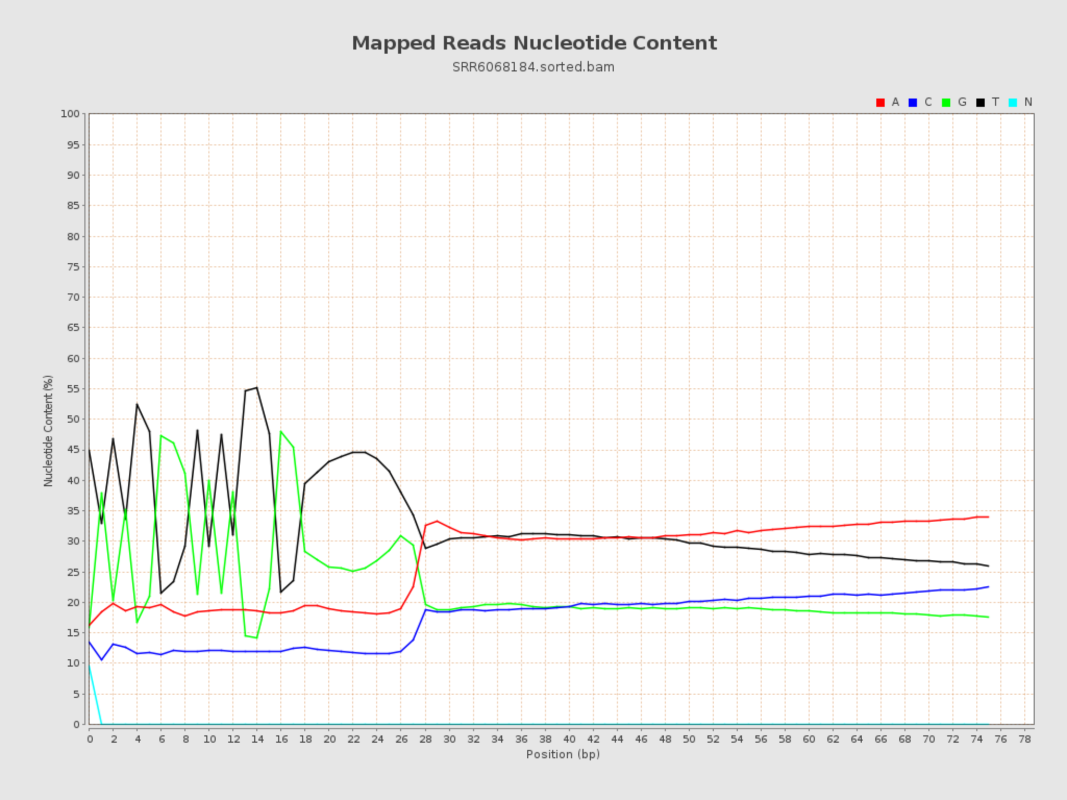
6. Results : Genome Fraction Coverage



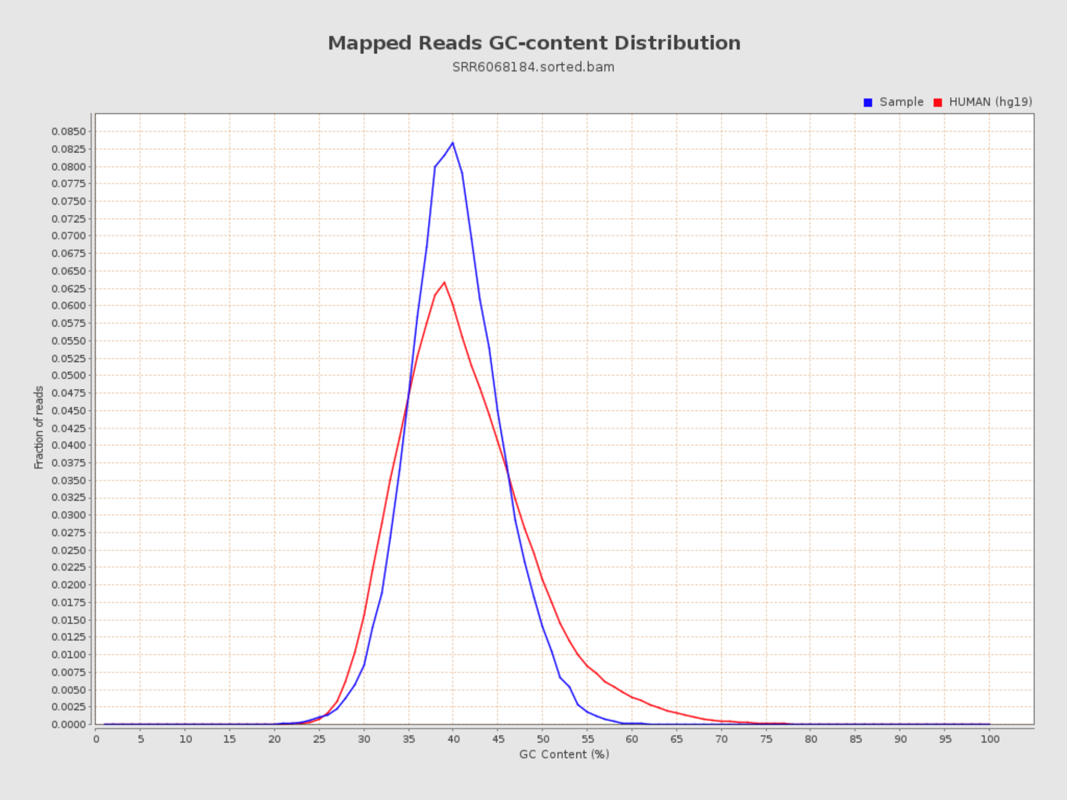
7. Results : Duplication Rate Histogram



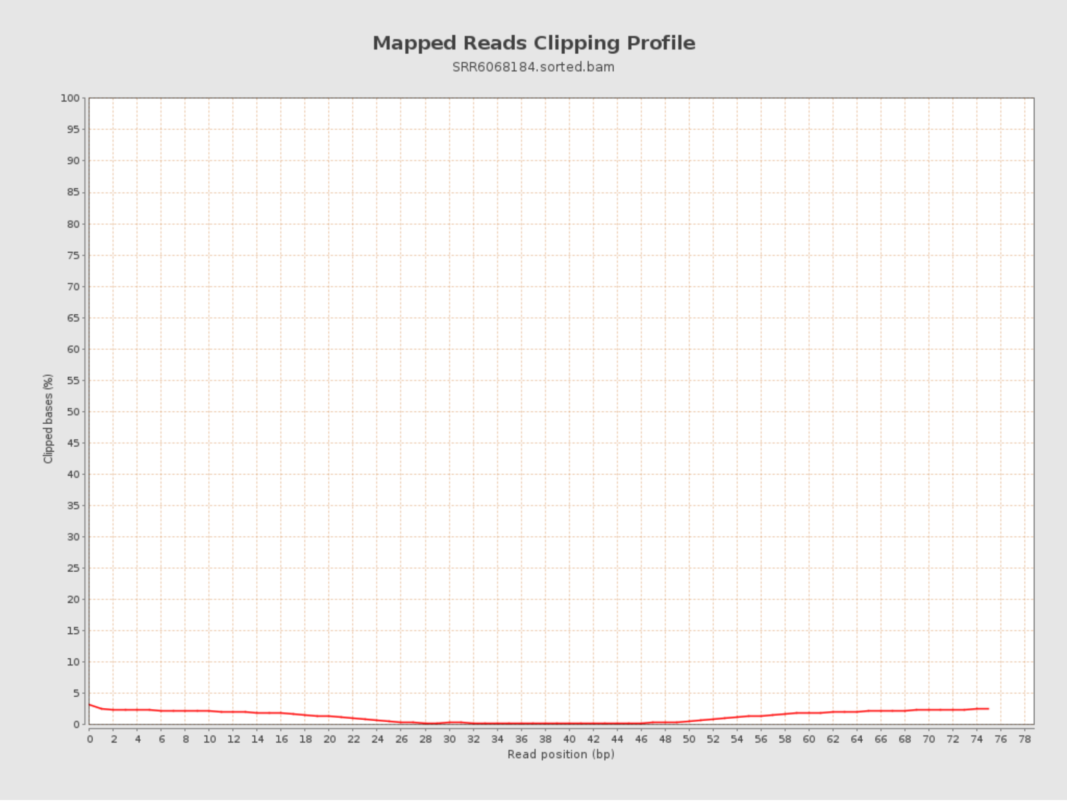
8. Results : Mapped Reads Nucleotide Content



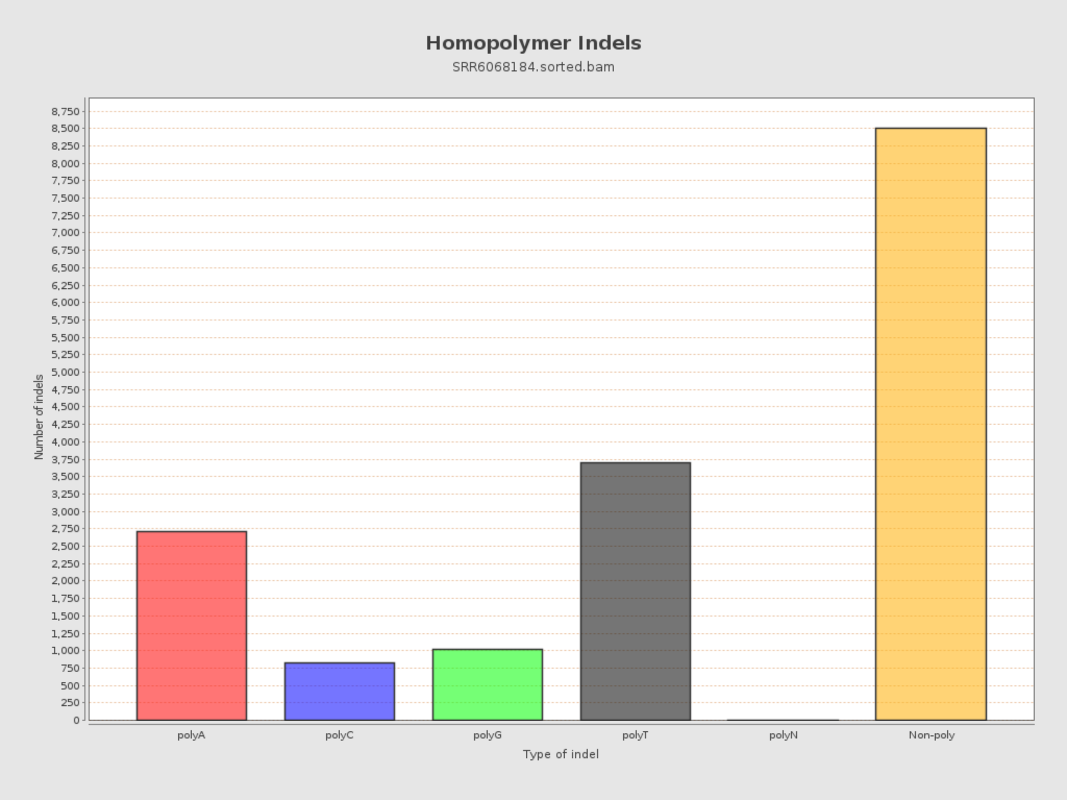
9. Results : Mapped Reads GC-content Distribution



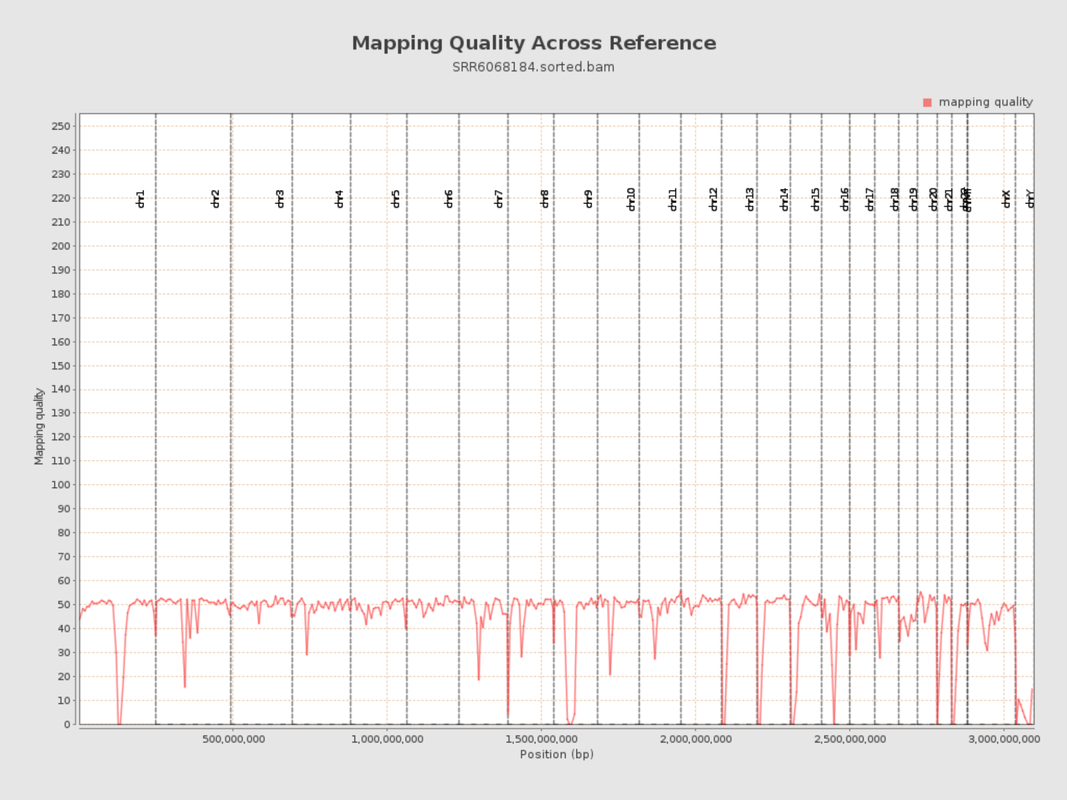
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram