Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:39:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068064.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_SRR6068064 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068064.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:39:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068064.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,481,458
Mapped reads	2,202,913 / 88.77%
Unmapped reads	278,545 / 11.23%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,337 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	162,016 / 6.53%
Duplication rate	5.59%
Clipped reads	1,169,023 / 47.11%

2.2. ACGT Content

Number/percentage of A's	38,241,721 / 26.75%
Number/percentage of C's	28,005,074 / 19.59%
Number/percentage of T's	43,531,105 / 30.45%
Number/percentage of G's	33,177,813 / 23.21%
Number/percentage of N's	2,659 / 0%
GC Percentage	42.8%

2.3. Coverage

Mean	0.0462

Standard Deviation	0.8109

2.4. Mapping Quality

Mean Mapping Quality	42.18

2.5. Mismatches and indels

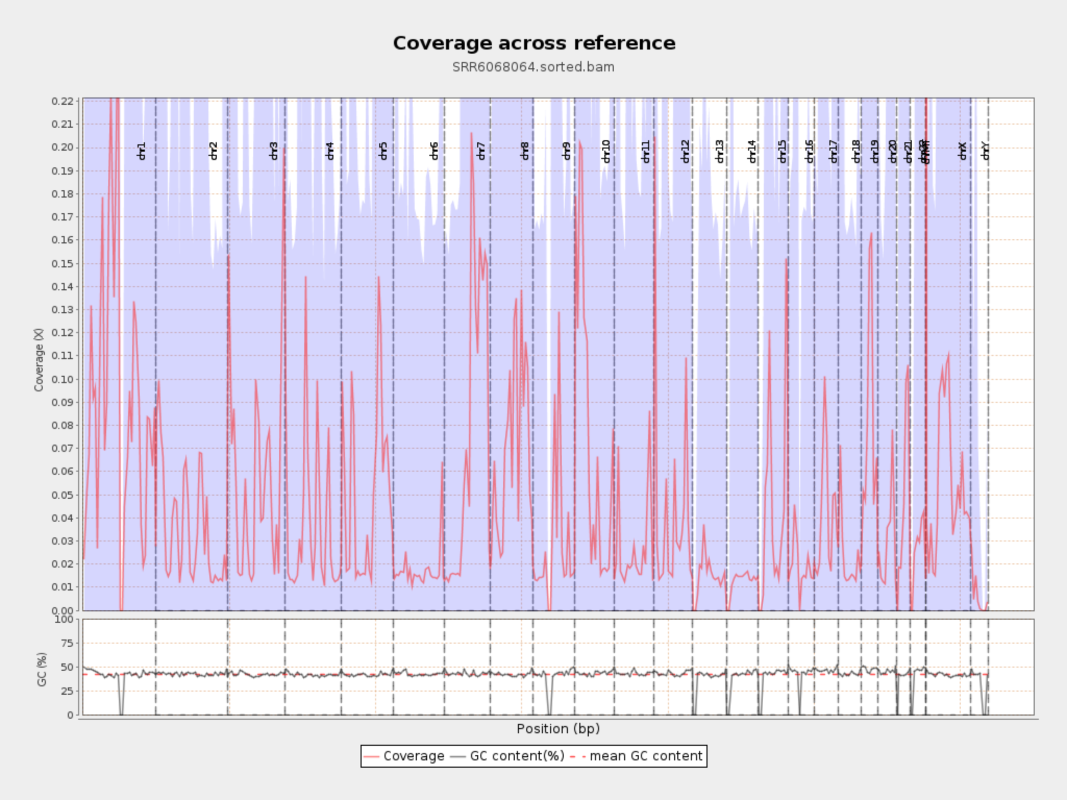
General error rate	0.76%
Mismatches	1,067,823
Insertions	9,736
Mapped reads with at least one insertion	0.44%
Deletions	31,333
Mapped reads with at least one deletion	1.41%
Homopolymer indels	45.54%

2.6. Chromosome stats

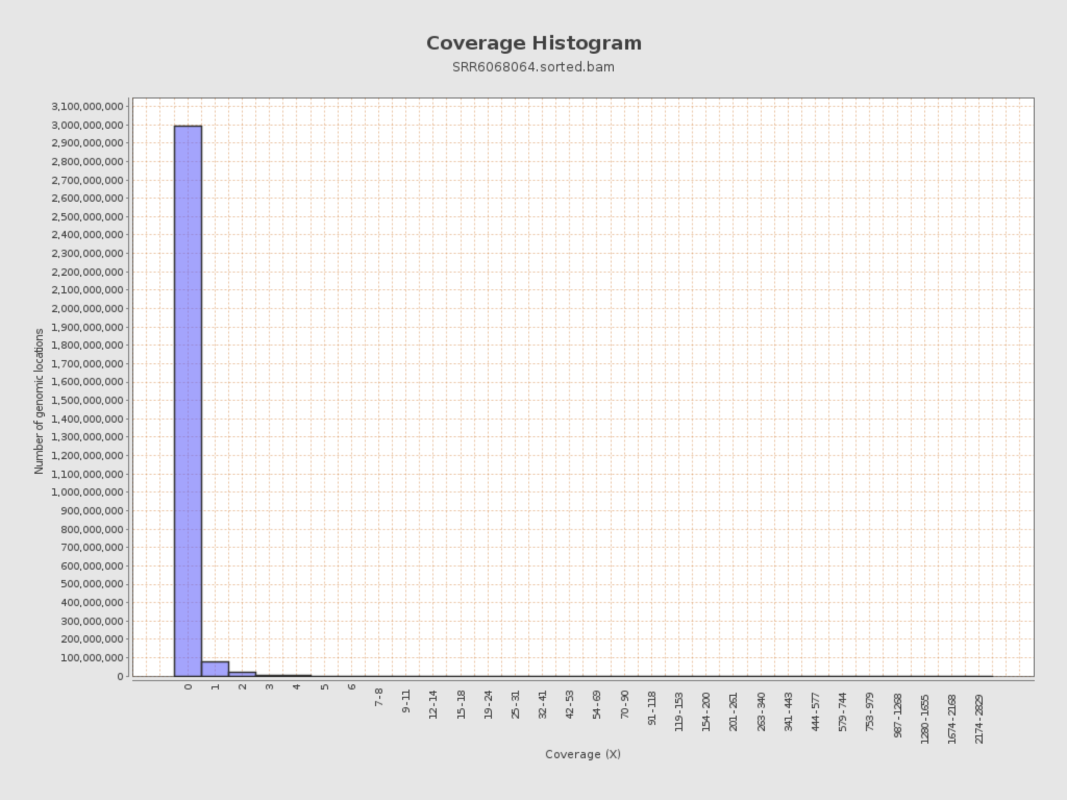
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23147856	0.0929	2.4984
chr2	243199373	8728948	0.0359	0.4478
chr3	198022430	11435516	0.0577	0.3255
chr4	191154276	7033666	0.0368	0.2701
chr5	180915260	9443779	0.0522	0.3018
chr6	171115067	3033406	0.0177	0.1929
chr7	159138663	12226360	0.0768	0.4186

chr8	146364022	10434528	0.0713	0.3737
chr9	141213431	4057223	0.0287	0.3526
chr10	135534747	10099016	0.0745	0.6551
chr11	135006516	3724831	0.0276	0.2817
chr12	133851895	5700816	0.0426	0.2912
chr13	115169878	1719509	0.0149	0.1585
chr14	107349540	1343690	0.0125	0.1921
chr15	102531392	4628678	0.0451	0.2918
chr16	90354753	1671786	0.0185	0.2254
chr17	81195210	3368365	0.0415	0.291
chr18	78077248	1836388	0.0235	0.6536
chr19	59128983	4834158	0.0818	1.5053
chr20	63025520	1960747	0.0311	0.2371
chr21	48129895	2304187	0.0479	0.3115
chr22	51304566	1334107	0.026	0.2093
chrMT	16571	79367	4.7895	3.5012
chrX	155270560	8505250	0.0548	0.3463
chrY	59373566	357273	0.006	0.1332

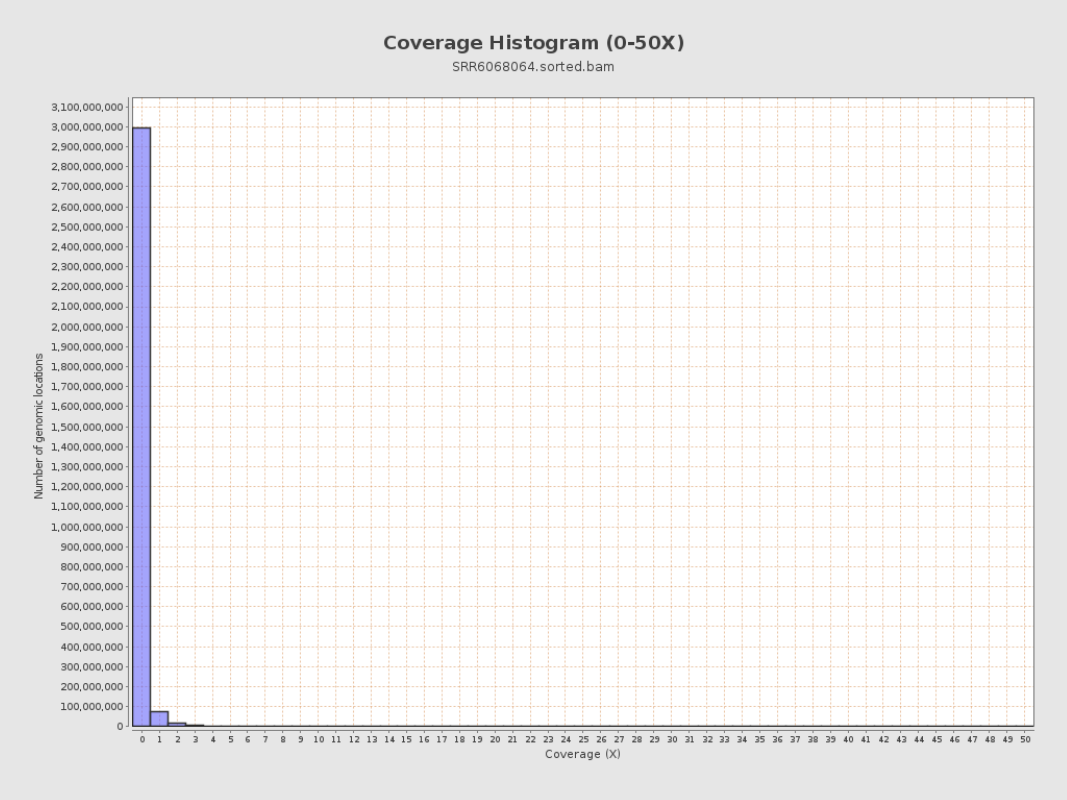
3. Results : Coverage across reference



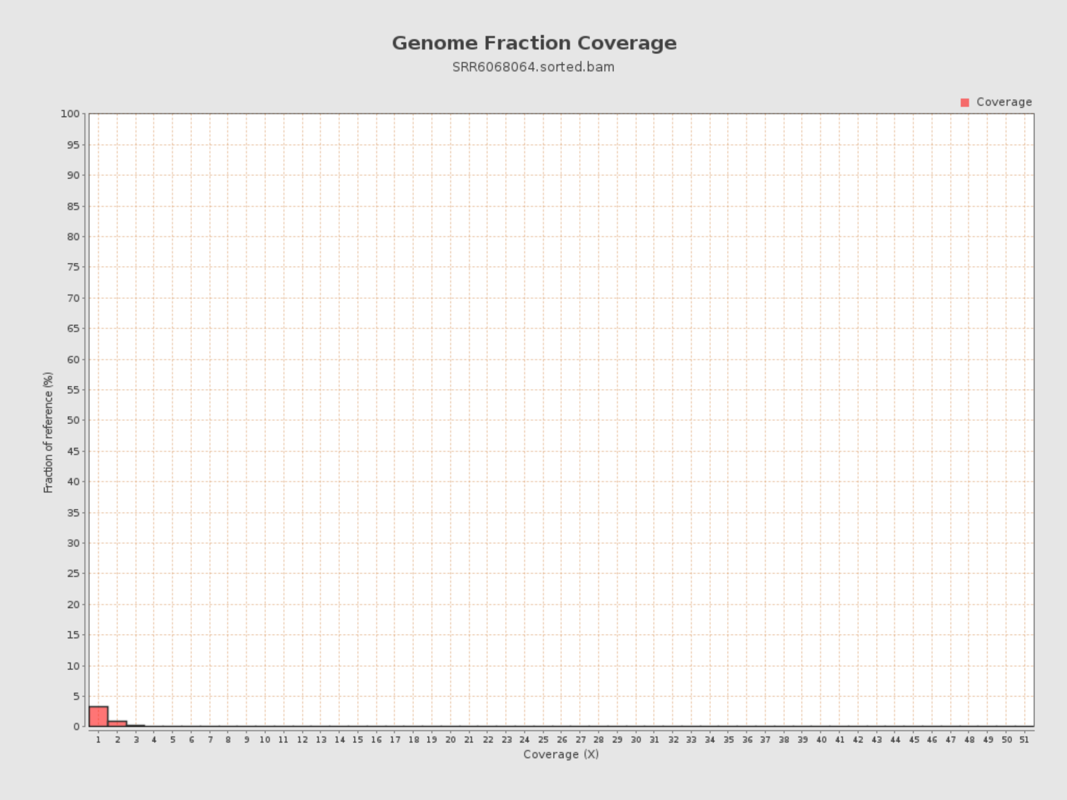
4. Results : Coverage Histogram



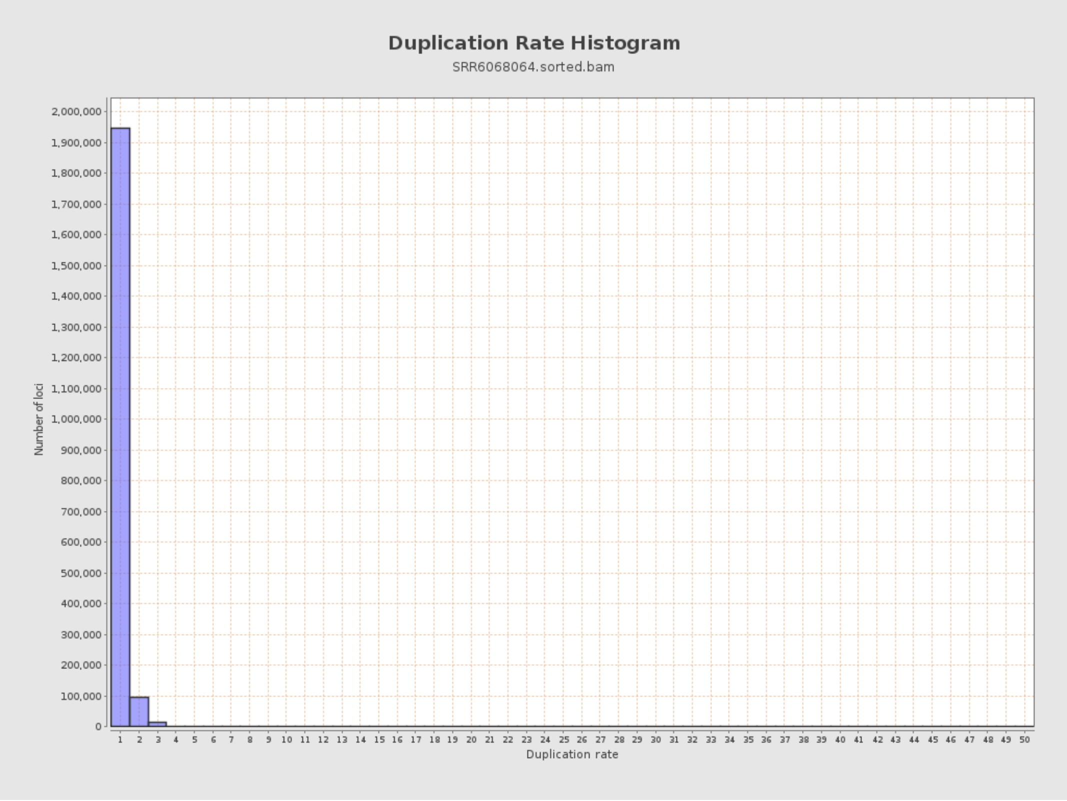
5. Results : Coverage Histogram (0-50X)



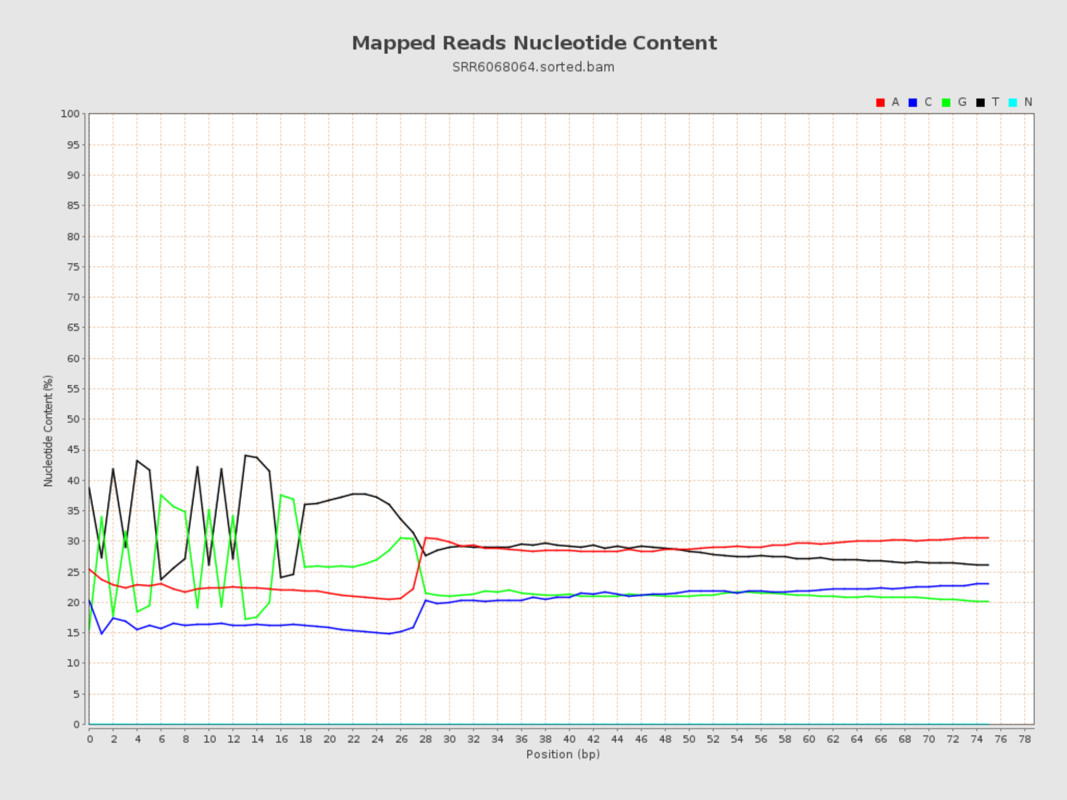
6. Results : Genome Fraction Coverage



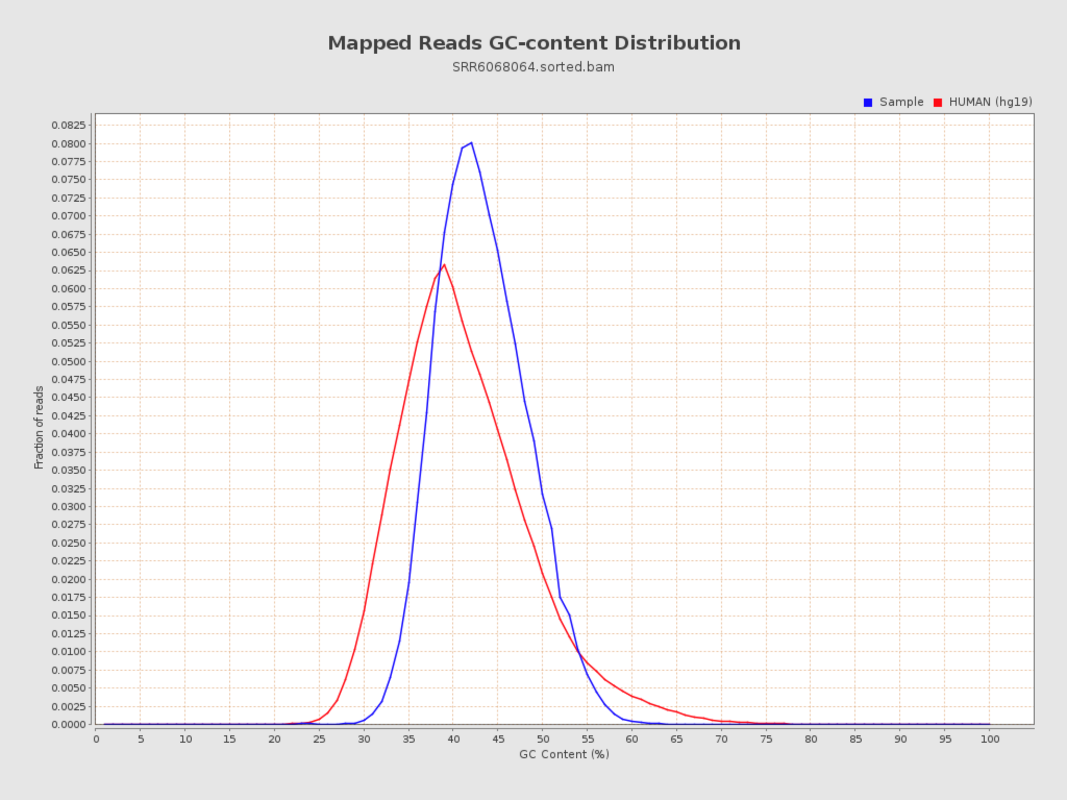
7. Results : Duplication Rate Histogram



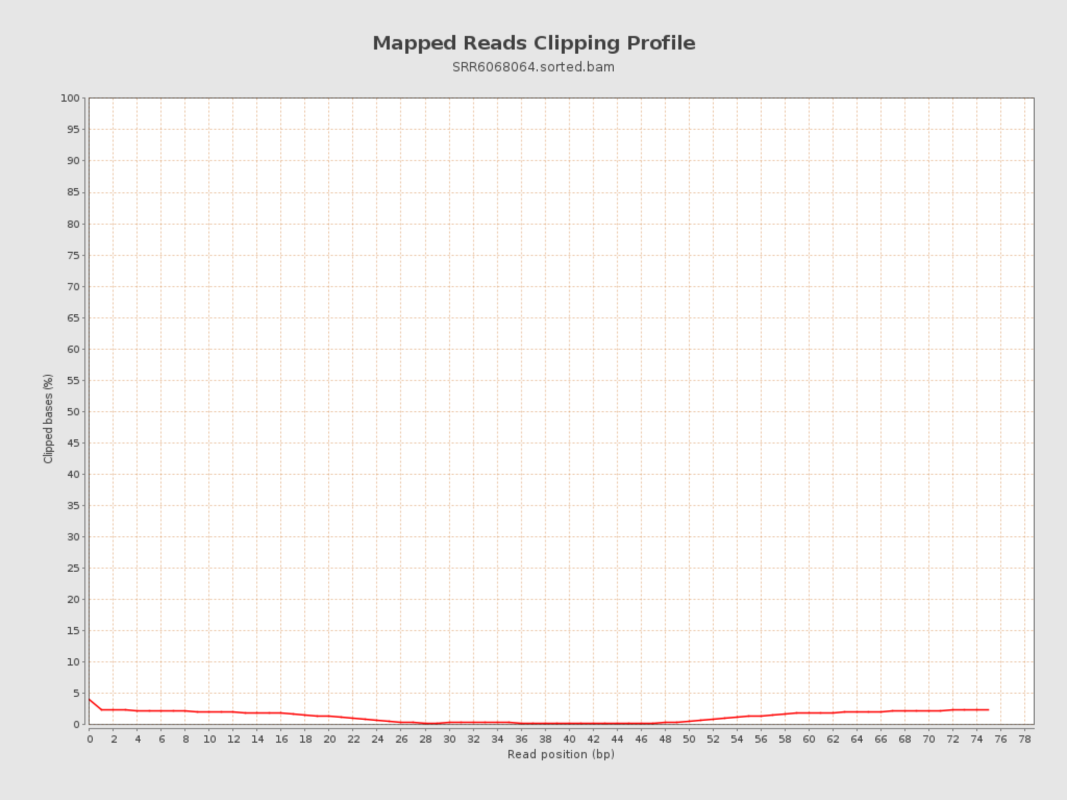
8. Results : Mapped Reads Nucleotide Content



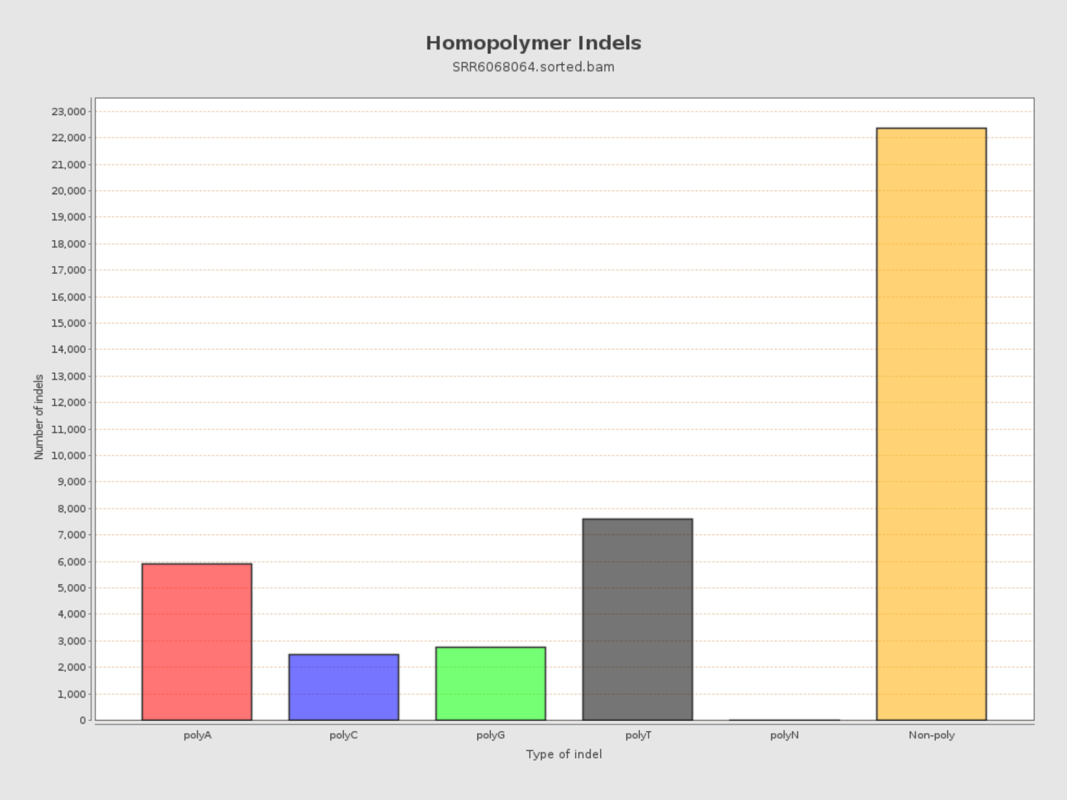
9. Results : Mapped Reads GC-content Distribution



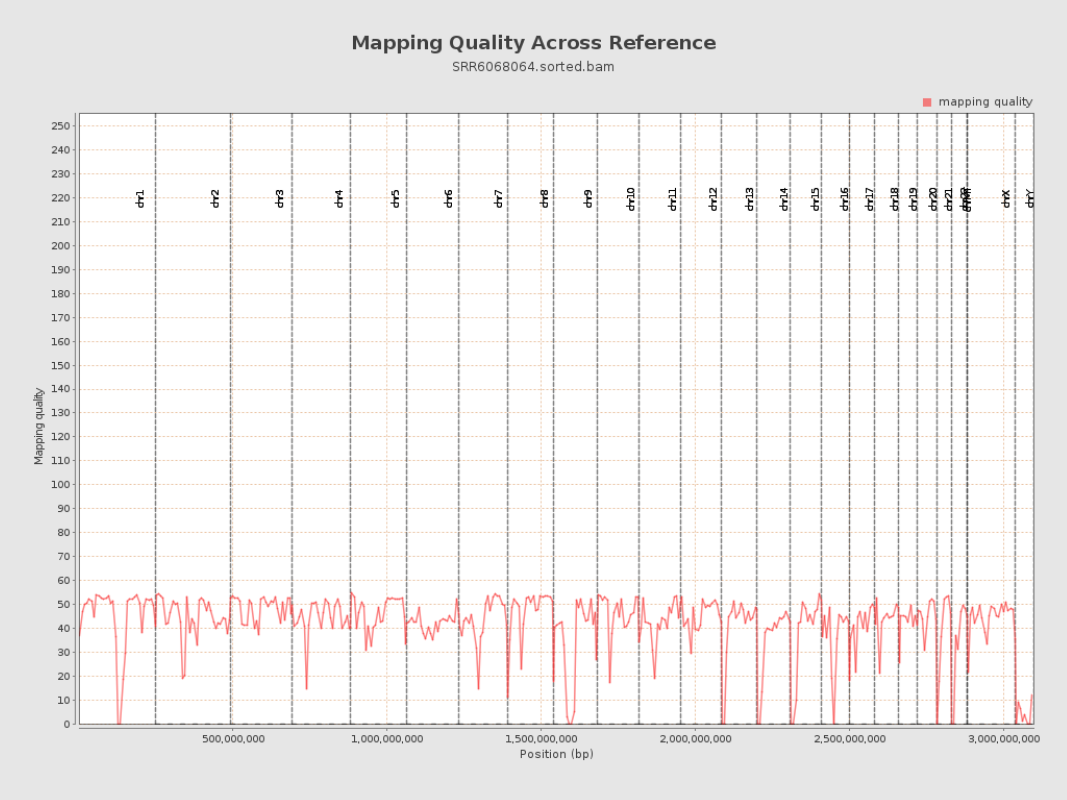
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram