Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 06:26:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008674.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_SRR6008674 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008674.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 06:26:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008674.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,754,215
Mapped reads	1,236,337 / 70.48%
Unmapped reads	517,878 / 29.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,297 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	142,996 / 8.15%
Duplication rate	9.46%
Clipped reads	719,109 / 40.99%

2.2. ACGT Content

Number/percentage of A's	20,498,253 / 26.43%
Number/percentage of C's	13,624,345 / 17.57%
Number/percentage of T's	25,216,196 / 32.51%
Number/percentage of G's	18,209,849 / 23.48%
Number/percentage of N's	13,858 / 0.02%
GC Percentage	41.04%

2.3. Coverage

Mean	0.0251

Standard Deviation	0.2763

2.4. Mapping Quality

Mean Mapping Quality	46.06

2.5. Mismatches and indels

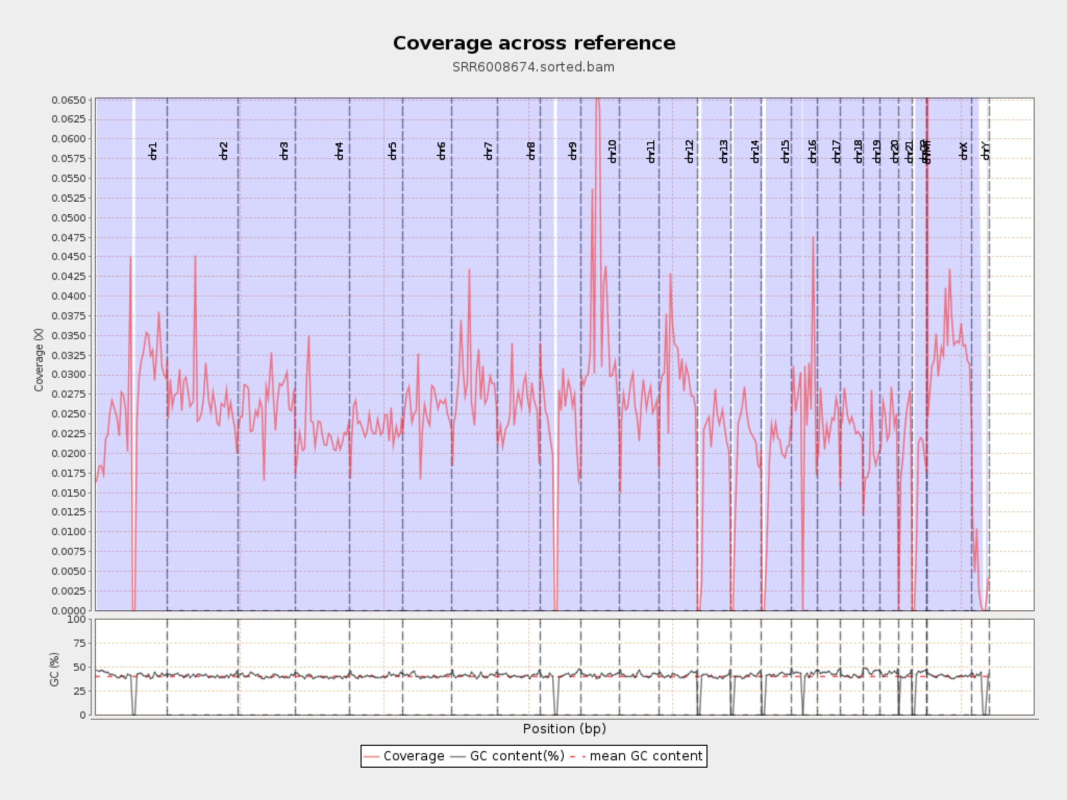
General error rate	0.88%
Mismatches	673,932
Insertions	6,314
Mapped reads with at least one insertion	0.51%
Deletions	28,843
Mapped reads with at least one deletion	2.3%
Homopolymer indels	49.67%

2.6. Chromosome stats

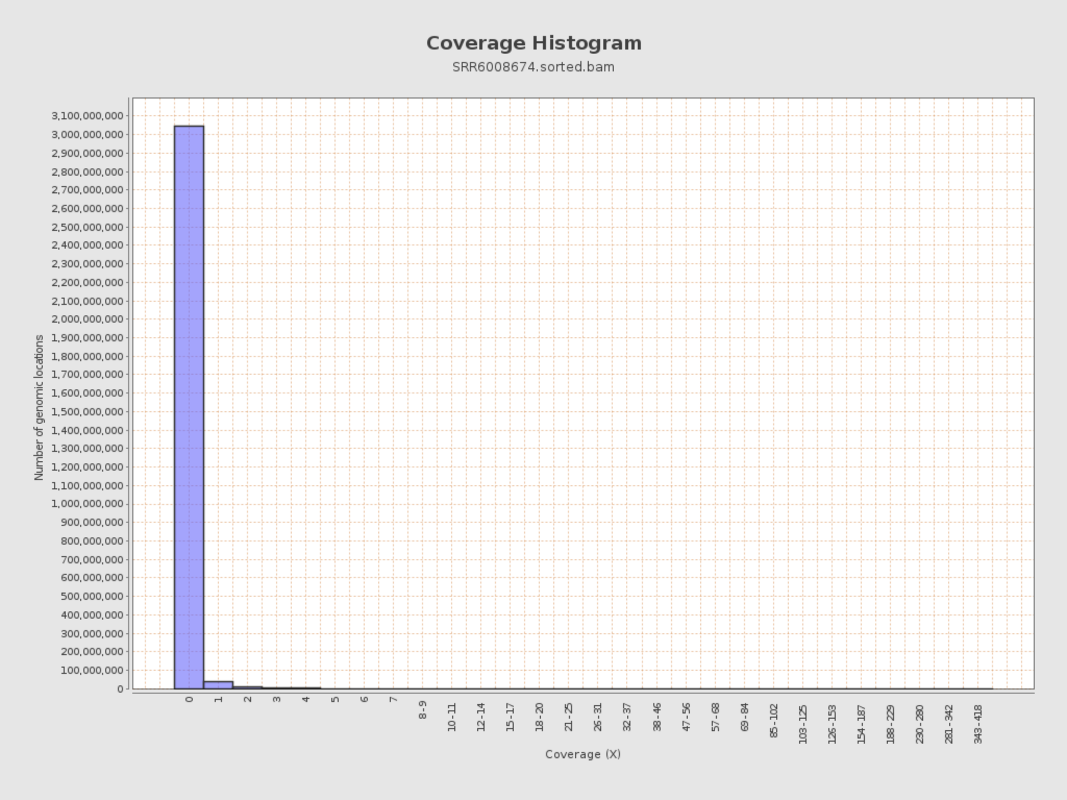
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6472859	0.026	0.4077
chr2	243199373	6566801	0.027	0.3036
chr3	198022430	5225022	0.0264	0.2303
chr4	191154276	4327910	0.0226	0.2217
chr5	180915260	4245761	0.0235	0.2144
chr6	171115067	4385494	0.0256	0.2422
chr7	159138663	4604864	0.0289	0.3508

chr8	146364022	3754880	0.0257	0.2692
chr9	141213431	3221682	0.0228	0.259
chr10	135534747	5027275	0.0371	0.3515
chr11	135006516	3532406	0.0262	0.2847
chr12	133851895	4110504	0.0307	0.2518
chr13	115169878	2259966	0.0196	0.1994
chr14	107349540	2078292	0.0194	0.2061
chr15	102531392	1768849	0.0173	0.1845
chr16	90354753	2366260	0.0262	0.2585
chr17	81195210	1909670	0.0235	0.2294
chr18	78077248	1876223	0.024	0.3824
chr19	59128983	1148525	0.0194	0.2903
chr20	63025520	1501457	0.0238	0.2213
chr21	48129895	974339	0.0202	0.2101
chr22	51304566	742323	0.0145	0.1661
chrMT	16571	65727	3.9664	3.4592
chrX	155270560	5206987	0.0335	0.2703
chrY	59373566	235150	0.004	0.0957

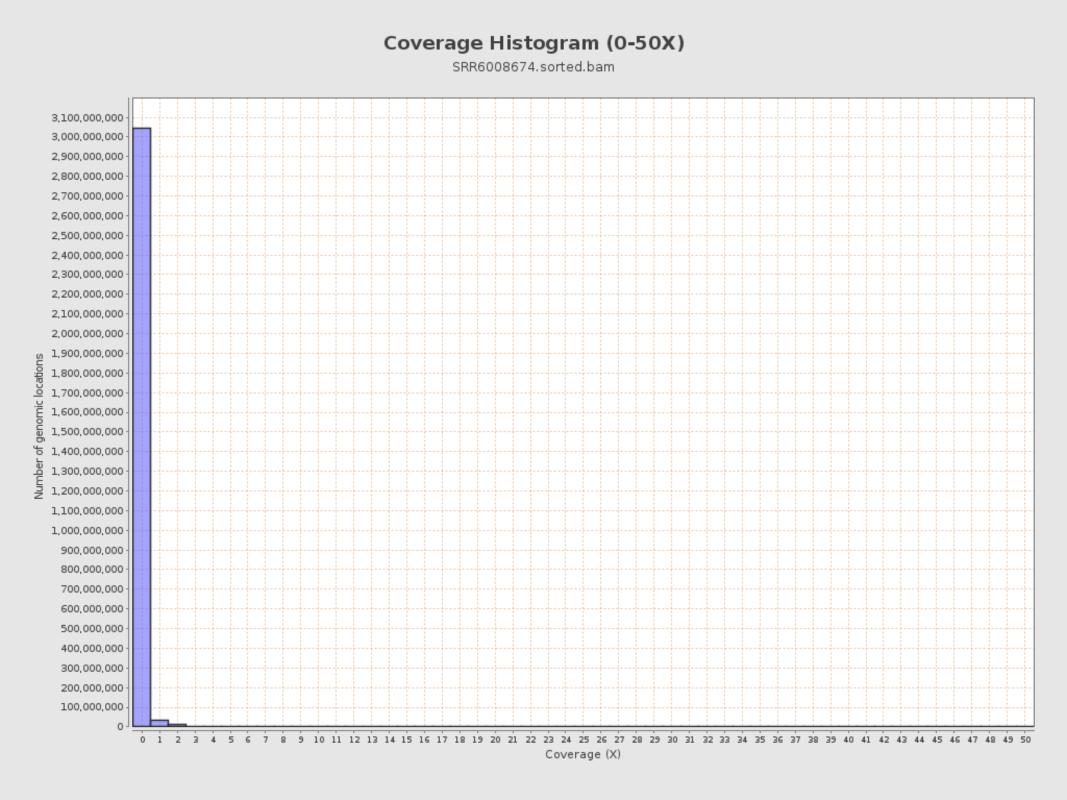
3. Results : Coverage across reference



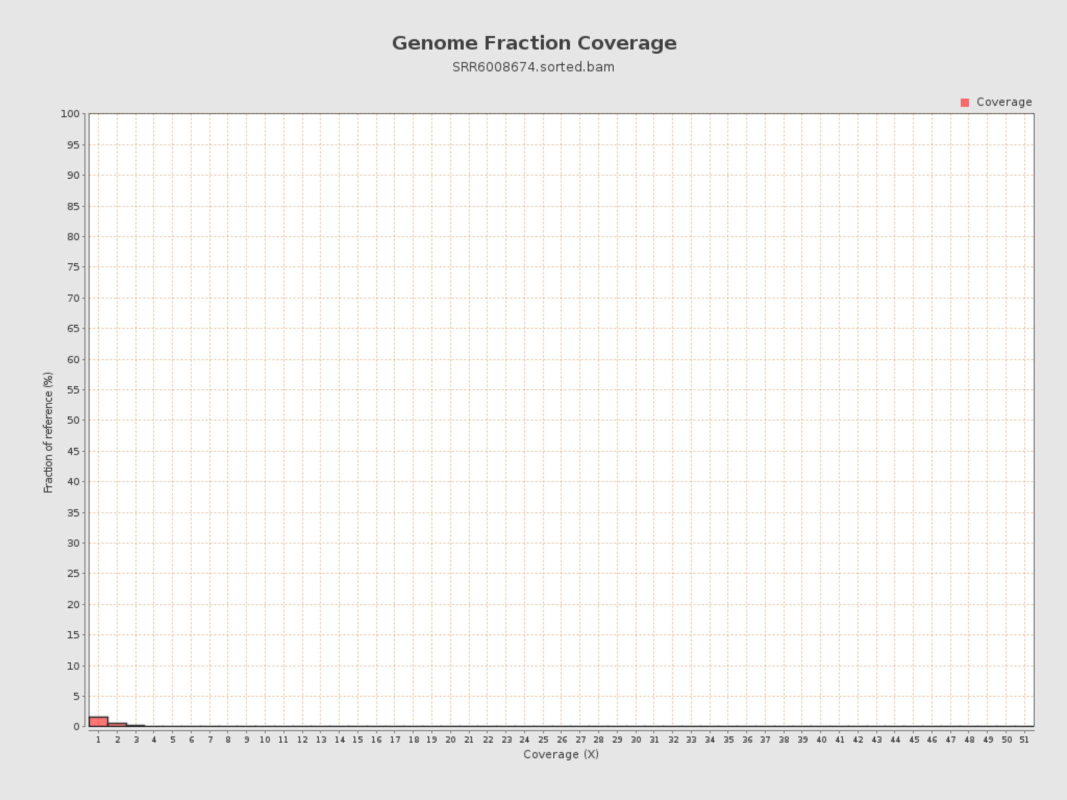
4. Results : Coverage Histogram



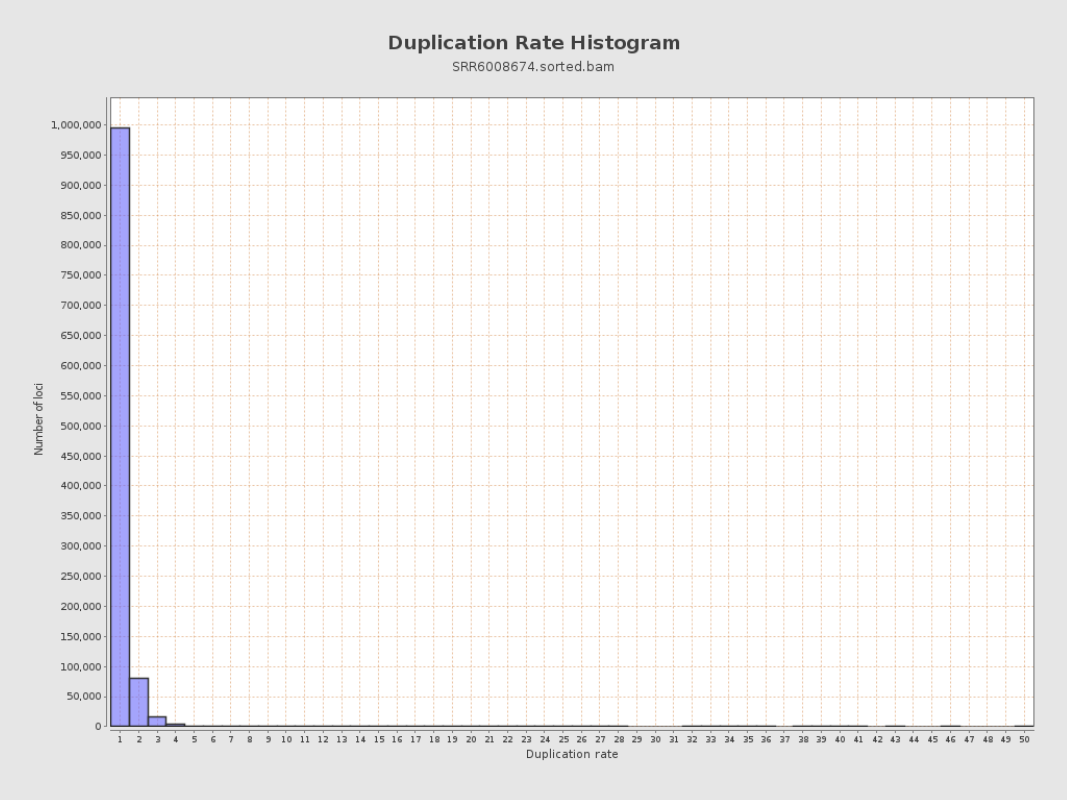
5. Results : Coverage Histogram (0-50X)



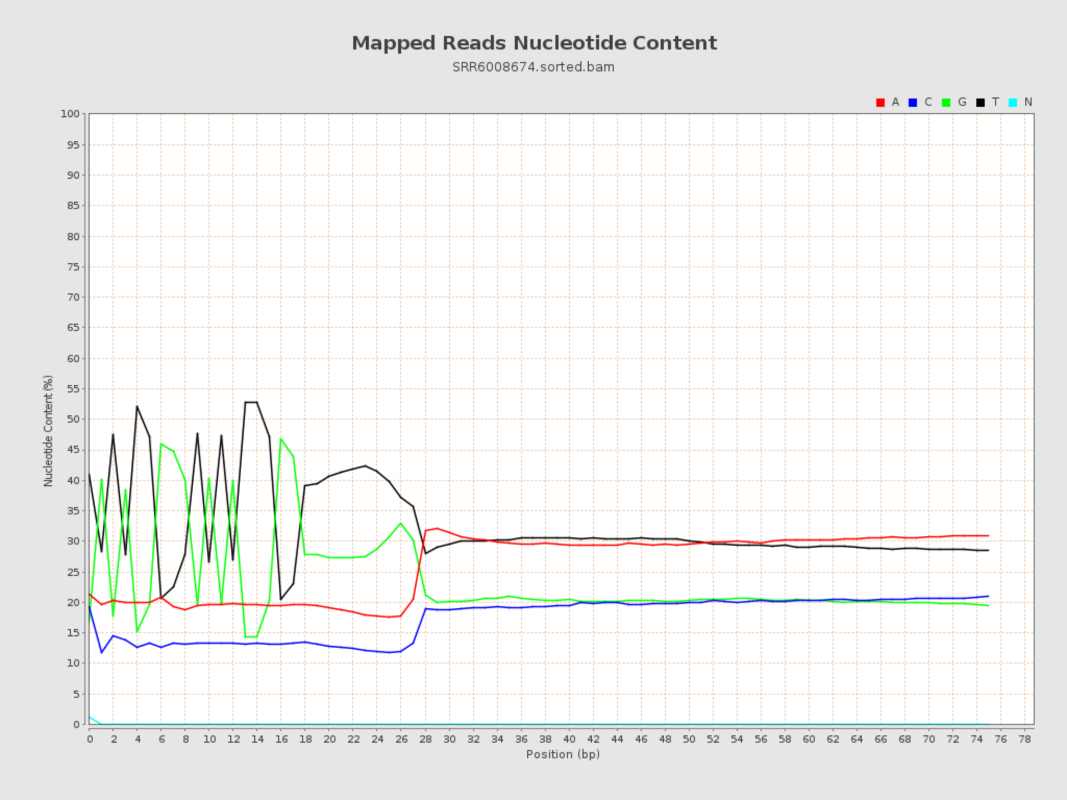
6. Results : Genome Fraction Coverage



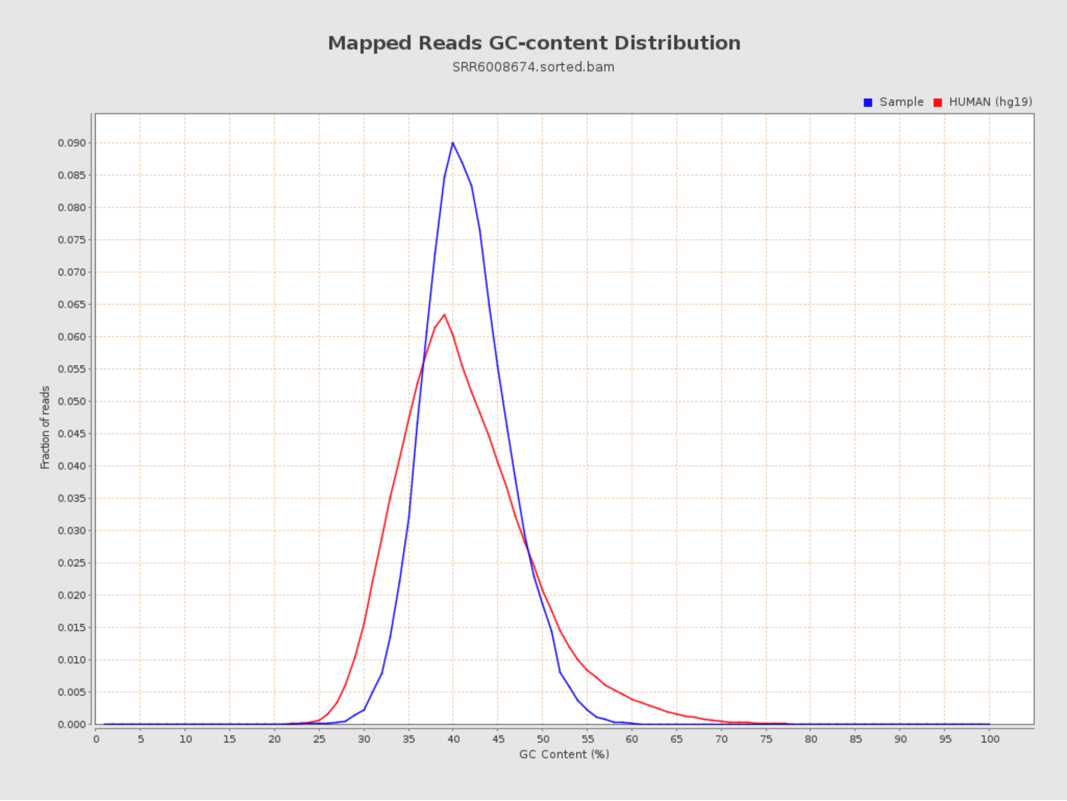
7. Results : Duplication Rate Histogram



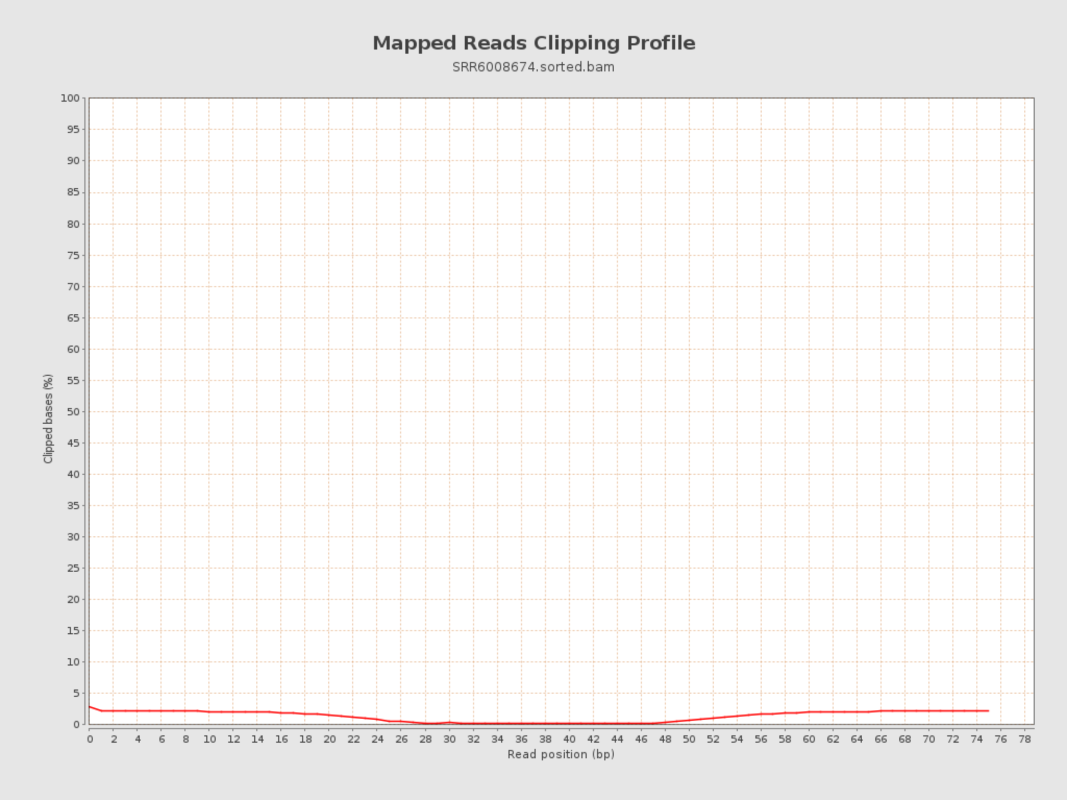
8. Results : Mapped Reads Nucleotide Content



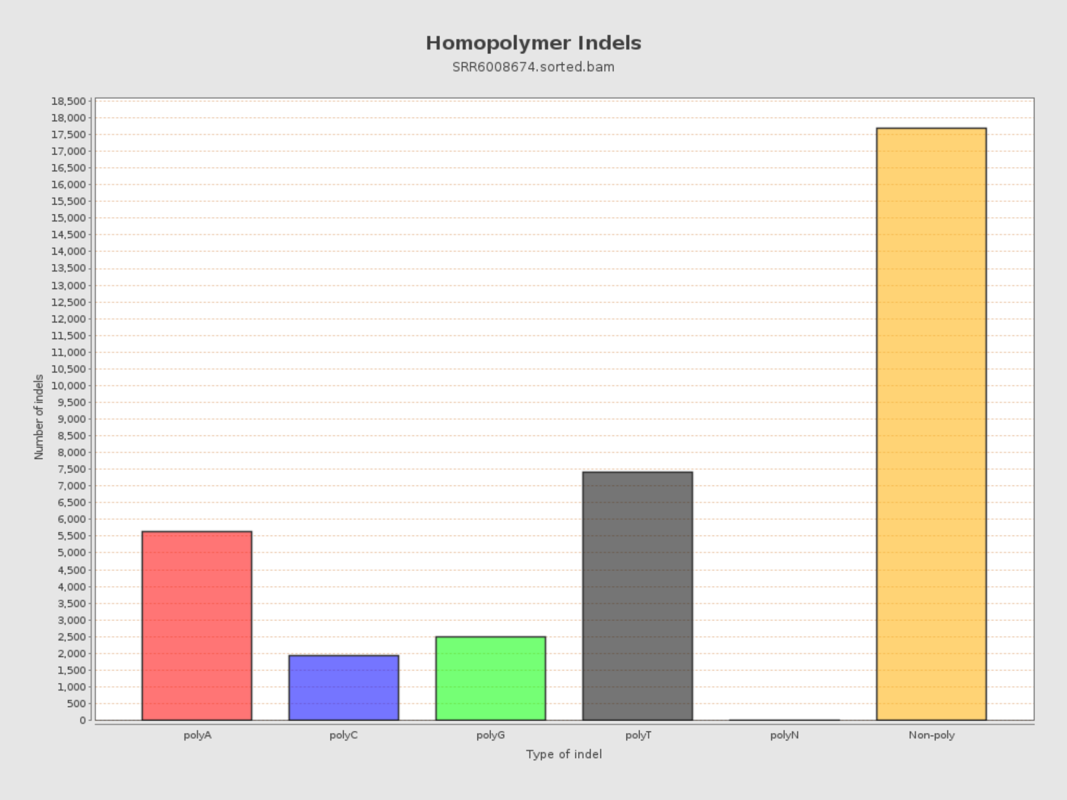
9. Results : Mapped Reads GC-content Distribution



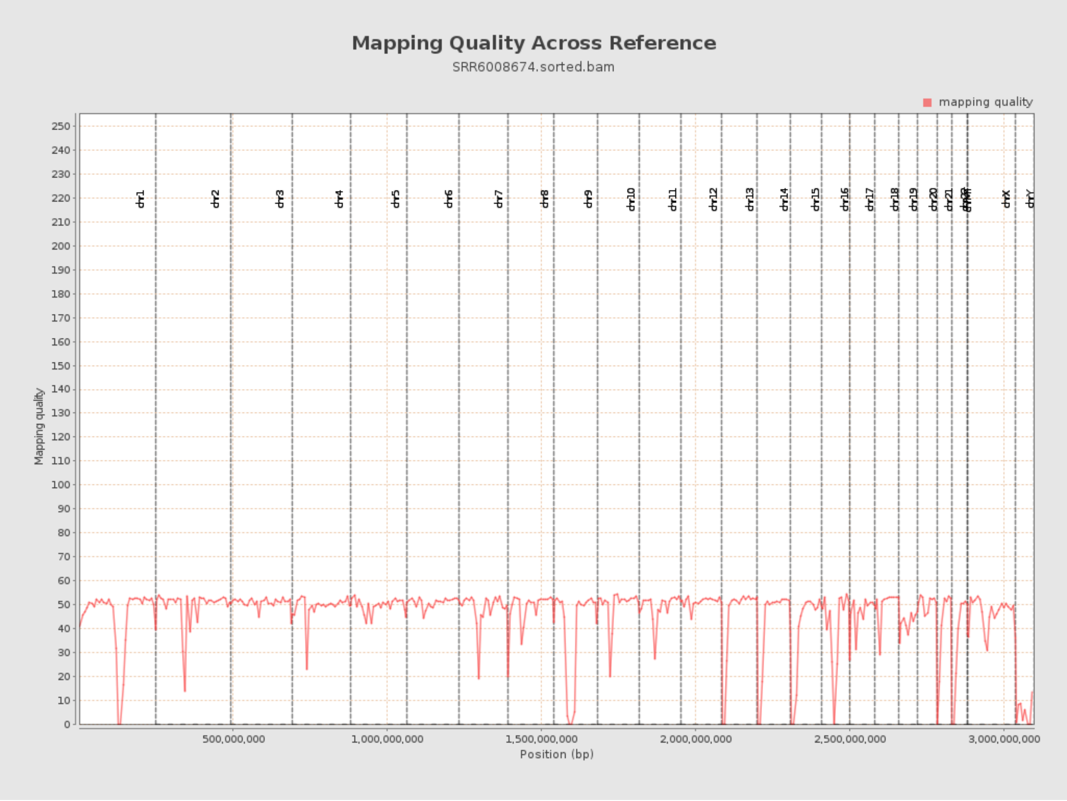
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram