Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 07:12:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6063608.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_SRR6063608 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6063608.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 07:12:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6063608.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,947,467
Mapped reads	4,661,636 / 94.22%
Unmapped reads	285,831 / 5.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,432 / 0.62%
Read min/max/mean length	30 / 76 / 76.21
Duplicated reads (estimated)	510,345 / 10.32%
Duplication rate	8.71%
Clipped reads	2,547,980 / 51.5%

2.2. ACGT Content

Number/percentage of A's	77,683,752 / 26.05%
Number/percentage of C's	53,397,141 / 17.9%
Number/percentage of T's	97,455,598 / 32.67%
Number/percentage of G's	69,691,061 / 23.37%
Number/percentage of N's	33,138 / 0.01%
GC Percentage	41.27%

2.3. Coverage

Mean	0.0964

Standard Deviation	1.1673

2.4. Mapping Quality

Mean Mapping Quality	45.12

2.5. Mismatches and indels

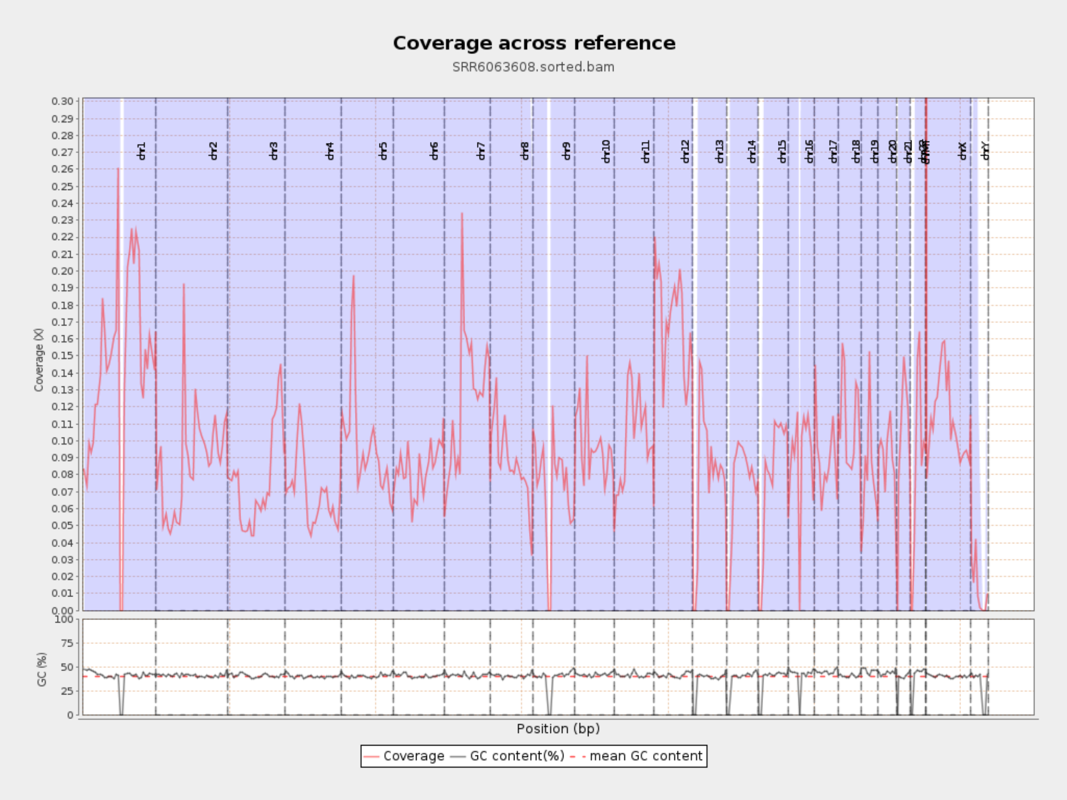
General error rate	0.58%
Mismatches	1,688,504
Insertions	19,248
Mapped reads with at least one insertion	0.41%
Deletions	72,397
Mapped reads with at least one deletion	1.54%
Homopolymer indels	44.41%

2.6. Chromosome stats

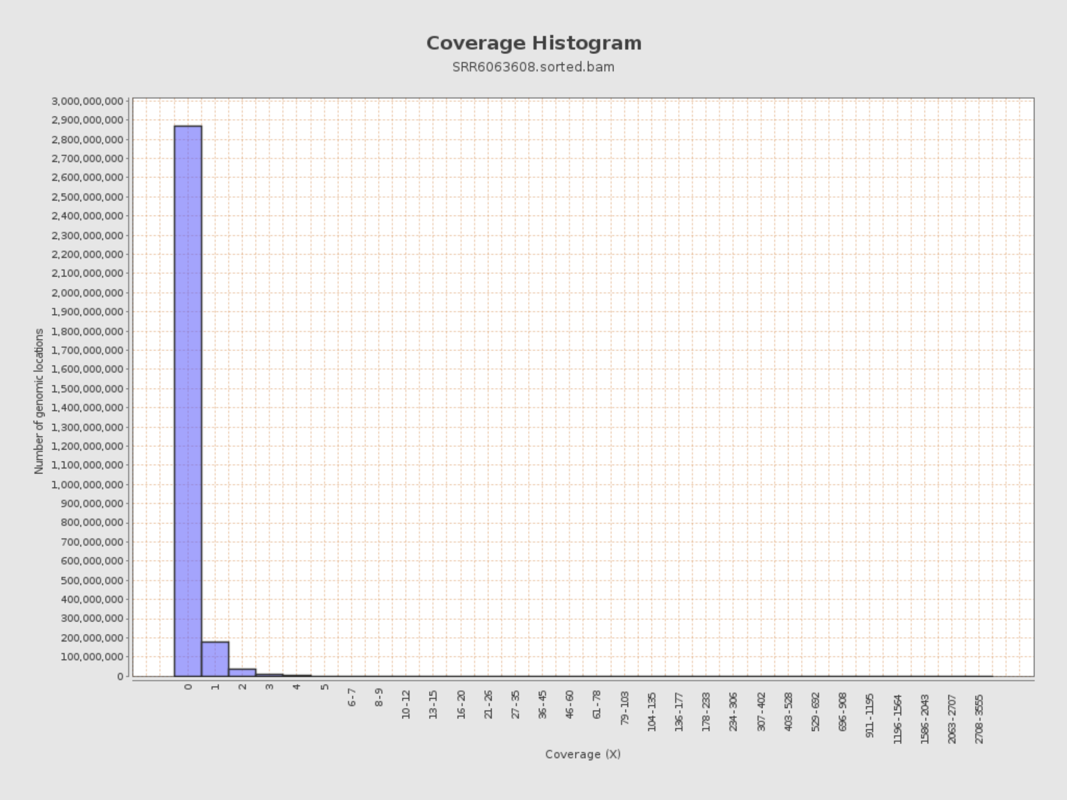
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	36025690	0.1445	2.7887
chr2	243199373	21338824	0.0877	1.619
chr3	198022430	15159188	0.0766	0.3605
chr4	191154276	13345704	0.0698	0.3896
chr5	180915260	17700247	0.0978	0.4076
chr6	171115067	14256927	0.0833	0.5208
chr7	159138663	19953863	0.1254	1.5915

chr8	146364022	12699091	0.0868	1.0983
chr9	141213431	10150411	0.0719	0.8599
chr10	135534747	13224562	0.0976	0.7637
chr11	135006516	13806284	0.1023	0.8368
chr12	133851895	23042098	0.1721	0.5641
chr13	115169878	9325630	0.081	0.4058
chr14	107349540	7825712	0.0729	0.4341
chr15	102531392	8061389	0.0786	0.4124
chr16	90354753	7970441	0.0882	0.4604
chr17	81195210	7414355	0.0913	0.4862
chr18	78077248	8753702	0.1121	1.6271
chr19	59128983	4838112	0.0818	1.917
chr20	63025520	5751424	0.0913	0.4329
chr21	48129895	4912465	0.1021	0.4411
chr22	51304566	4351419	0.0848	0.366
chrMT	16571	262611	15.8476	9.2729
chrX	155270560	17454924	0.1124	0.5595
chrY	59373566	761248	0.0128	0.3441

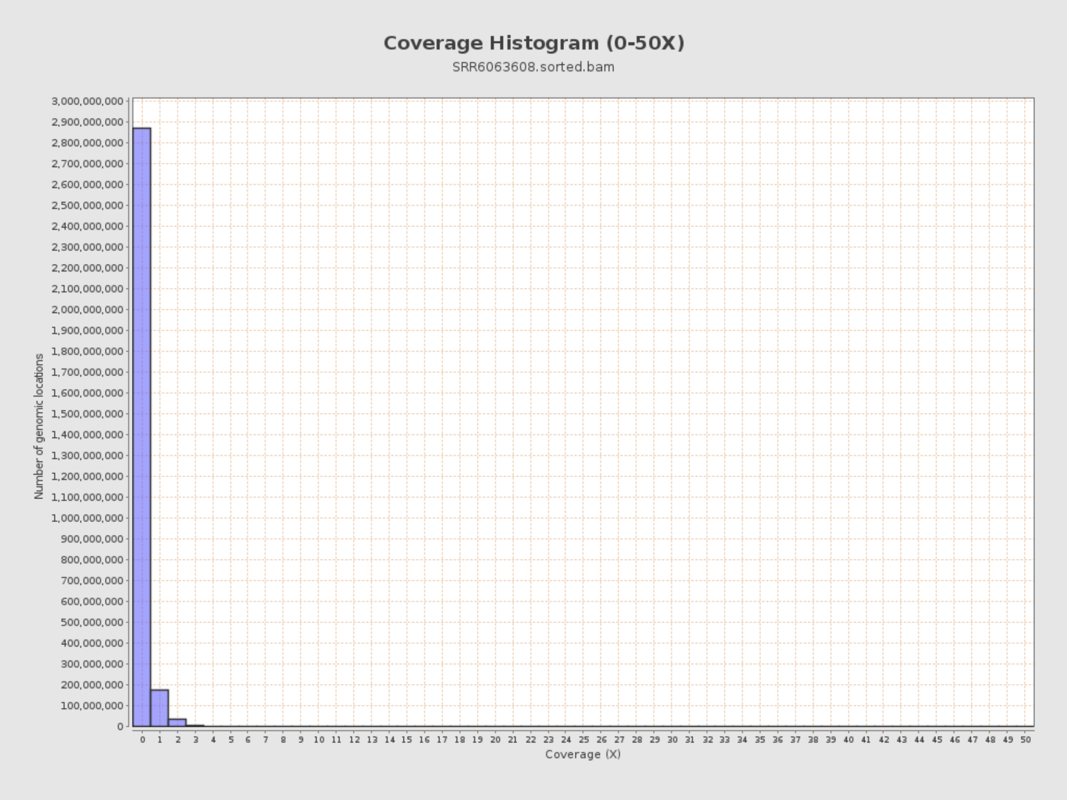
3. Results : Coverage across reference



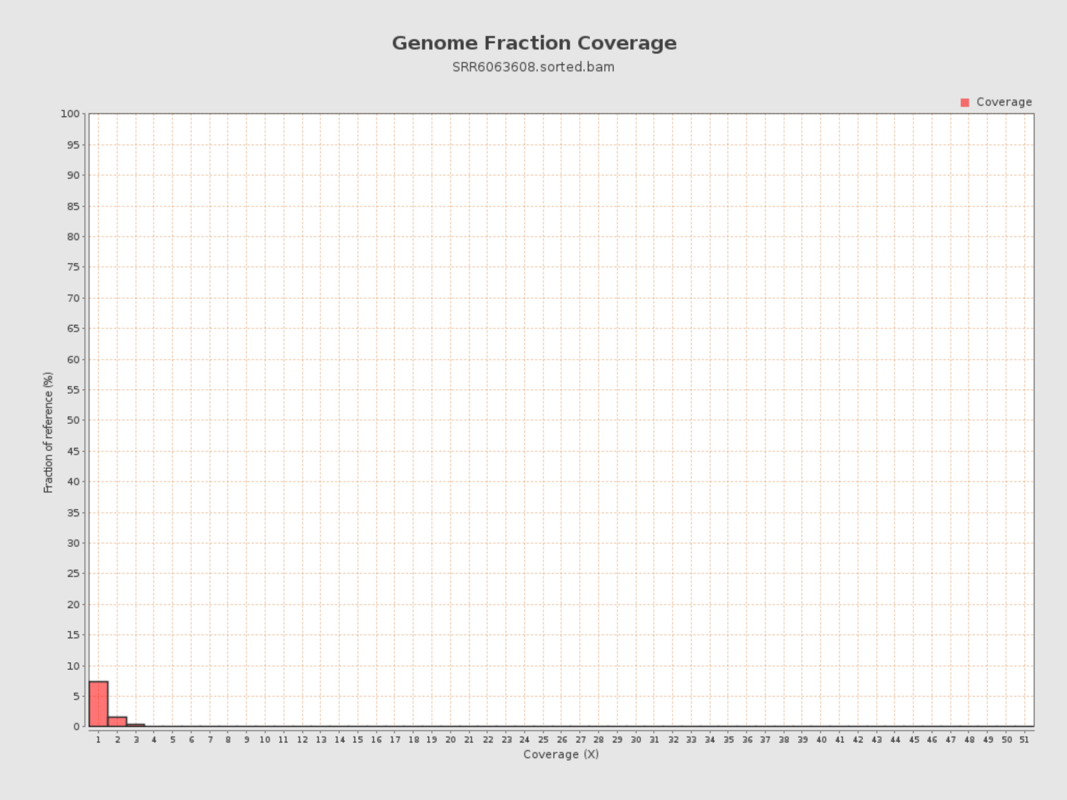
4. Results : Coverage Histogram



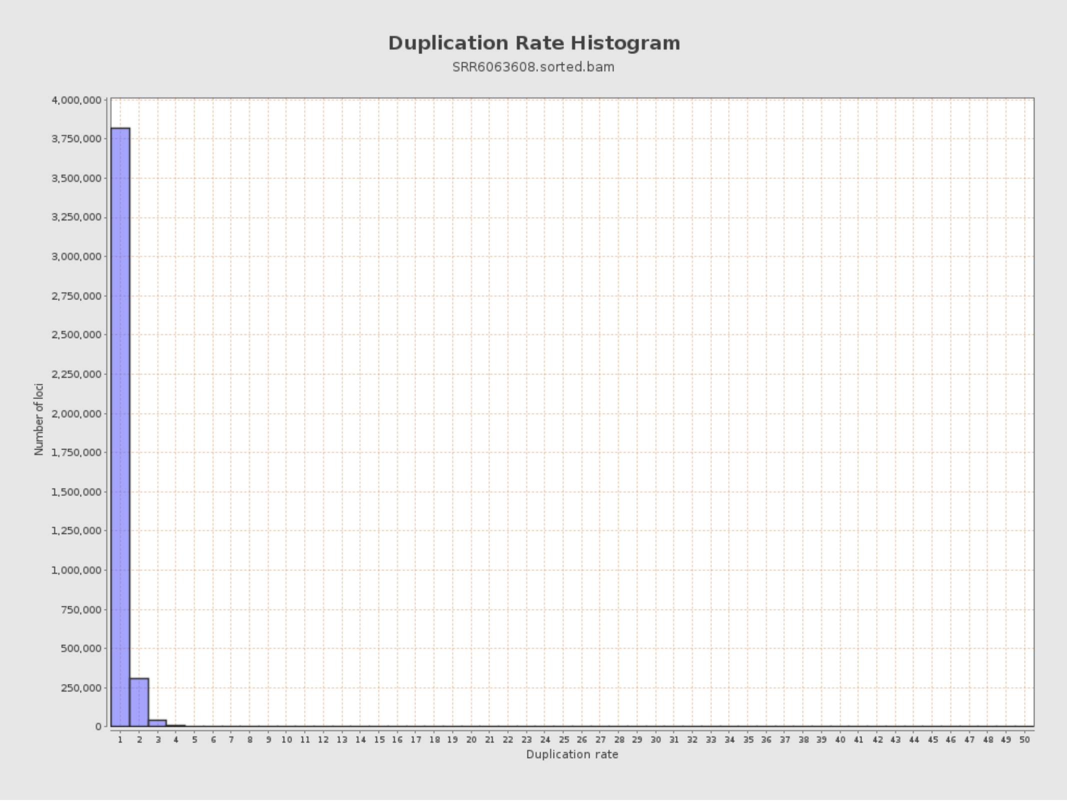
5. Results : Coverage Histogram (0-50X)



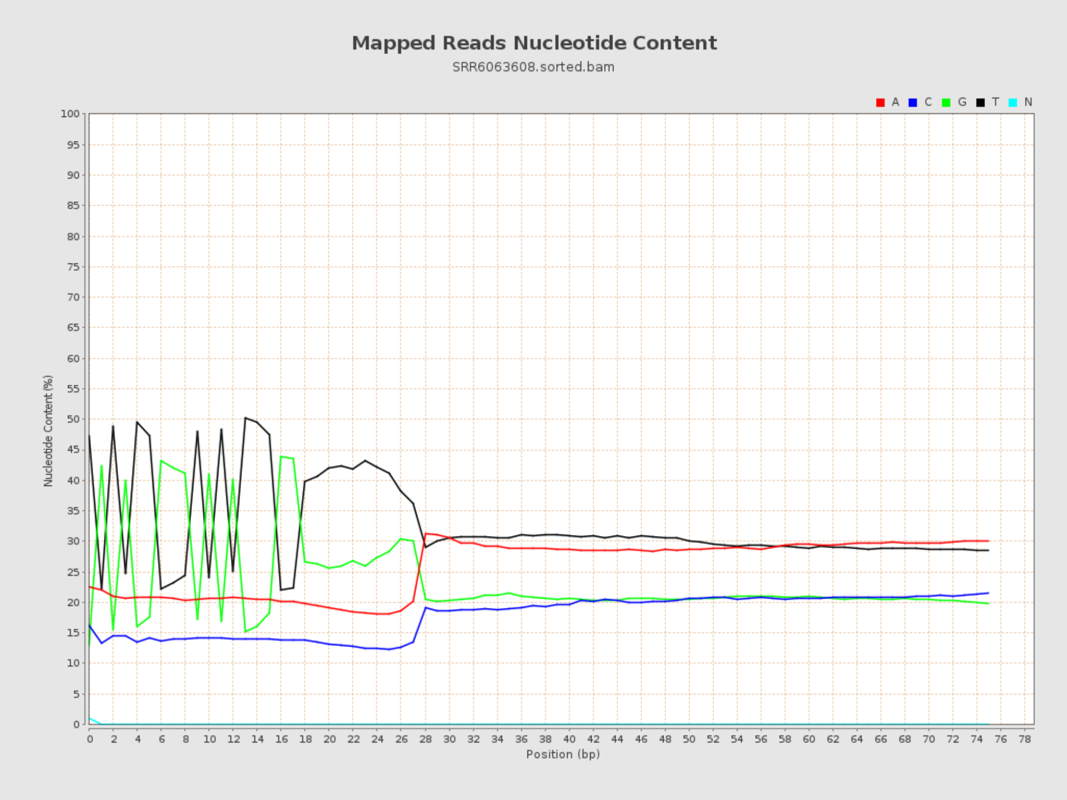
6. Results : Genome Fraction Coverage



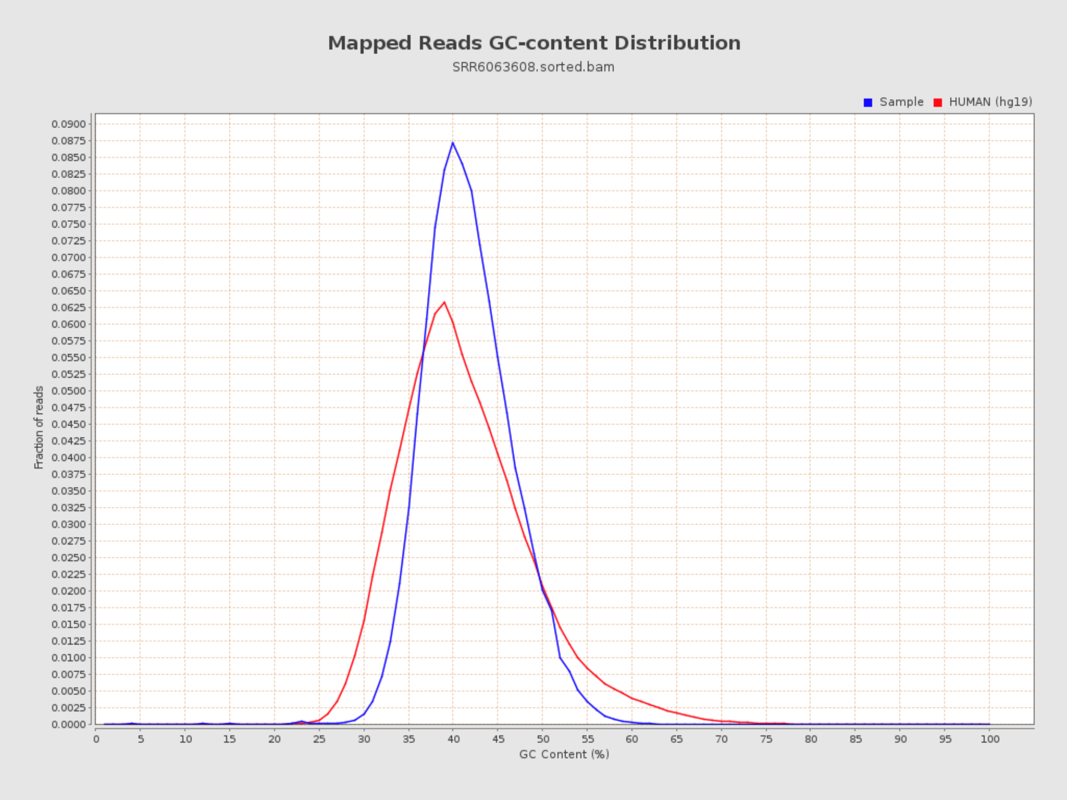
7. Results : Duplication Rate Histogram



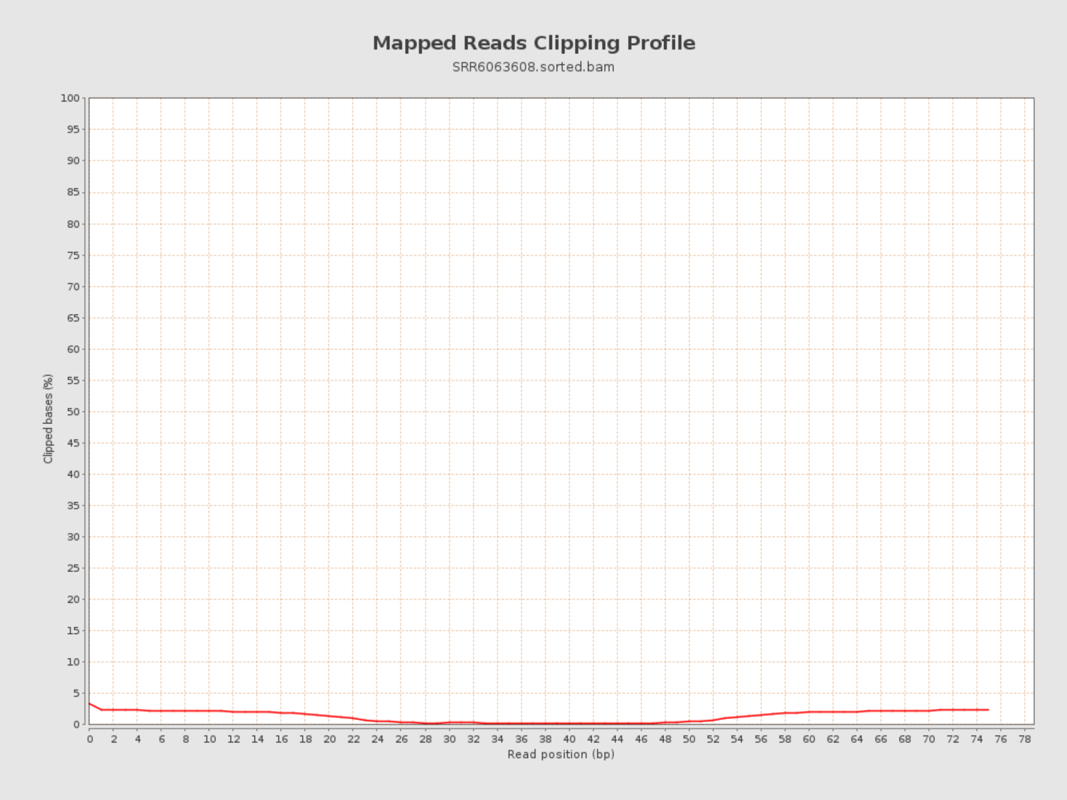
8. Results : Mapped Reads Nucleotide Content



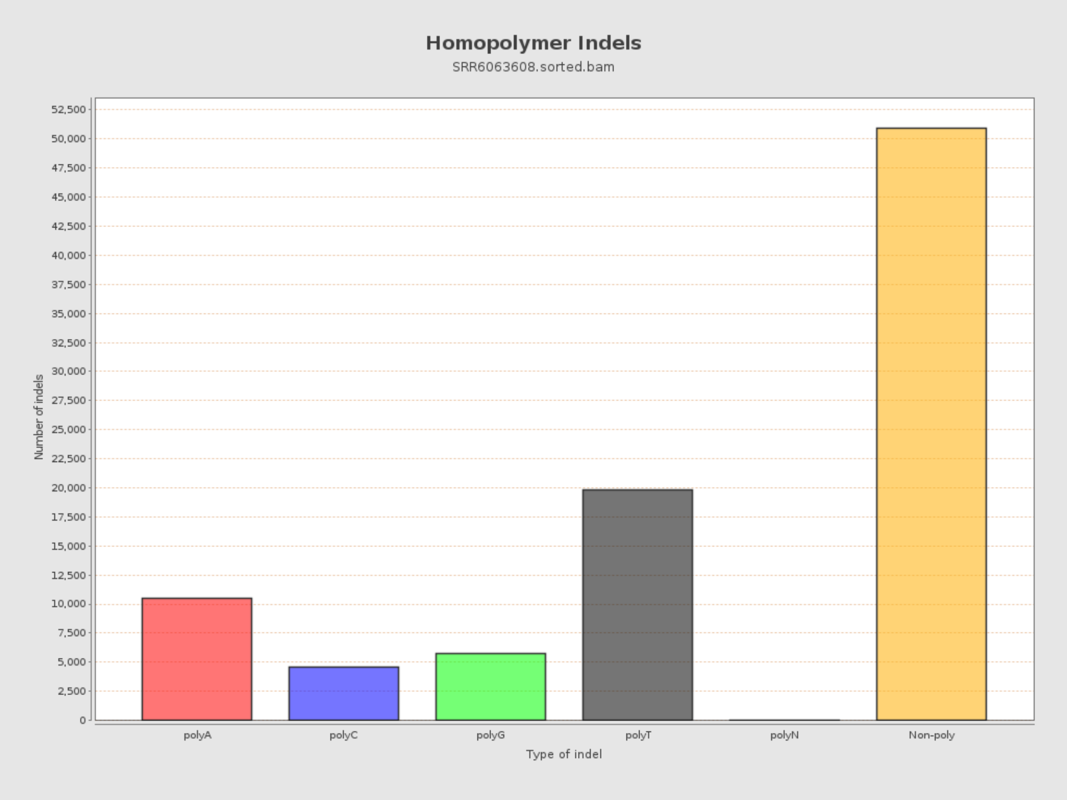
9. Results : Mapped Reads GC-content Distribution



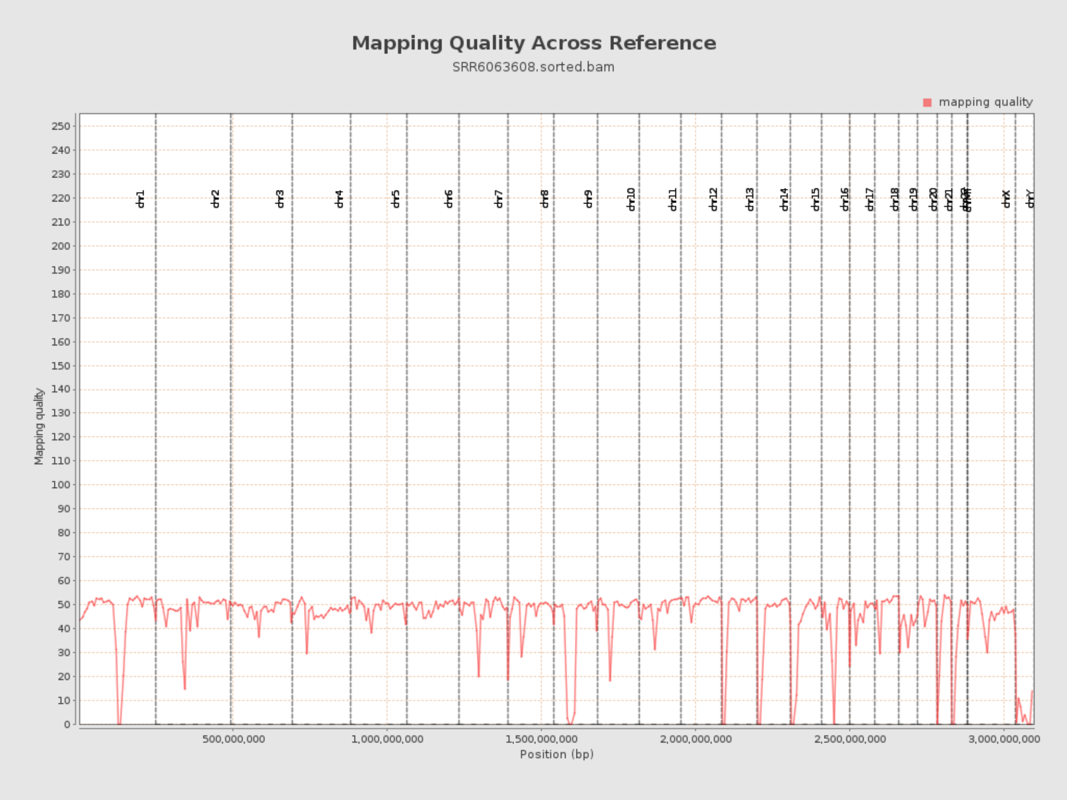
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram