Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 07:12:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240222.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_SRR6240222 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240222.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 07:12:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240222.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,252,048
Mapped reads	1,762,737 / 78.27%
Unmapped reads	489,311 / 21.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,092 / 0.94%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	288,223 / 12.8%
Duplication rate	11.78%
Clipped reads	901,403 / 40.03%

2.2. ACGT Content

Number/percentage of A's	32,703,754 / 28.32%
Number/percentage of C's	21,271,740 / 18.42%
Number/percentage of T's	36,936,391 / 31.99%
Number/percentage of G's	24,556,886 / 21.27%
Number/percentage of N's	9,955 / 0.01%
GC Percentage	39.69%

2.3. Coverage

Mean	0.0373

Standard Deviation	0.5191

2.4. Mapping Quality

Mean Mapping Quality	46.37

2.5. Mismatches and indels

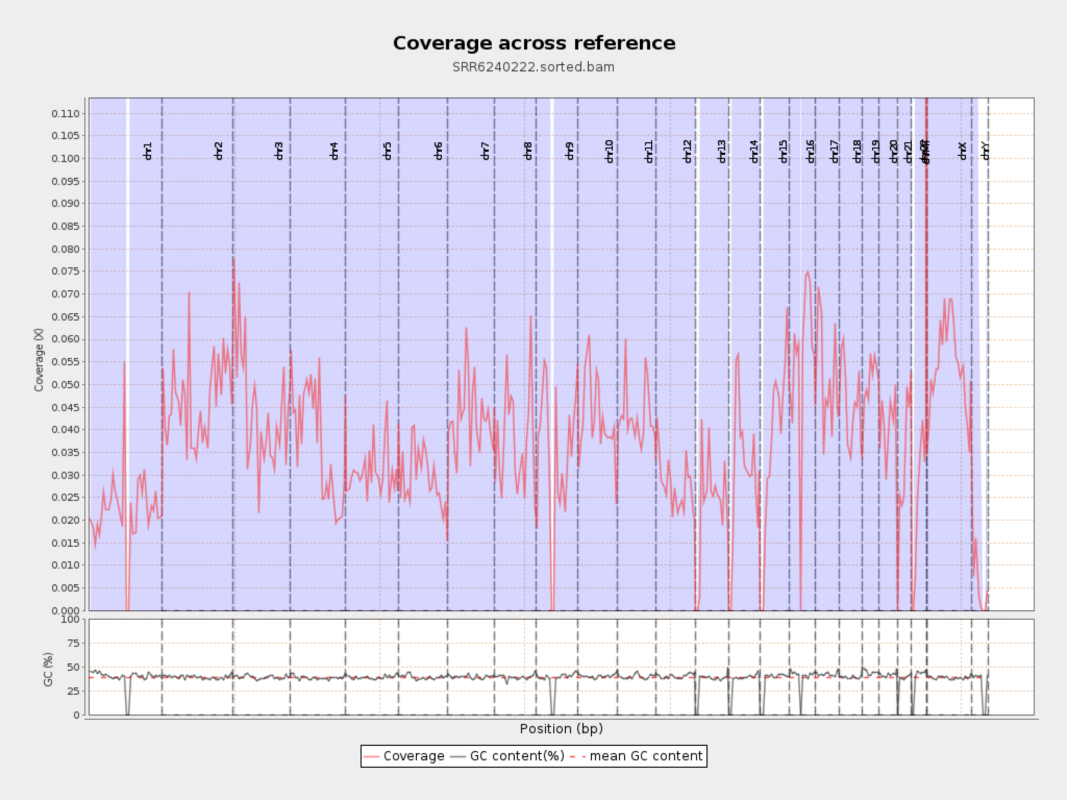
General error rate	0.86%
Mismatches	976,637
Insertions	8,567
Mapped reads with at least one insertion	0.48%
Deletions	36,246
Mapped reads with at least one deletion	2.03%
Homopolymer indels	45.02%

2.6. Chromosome stats

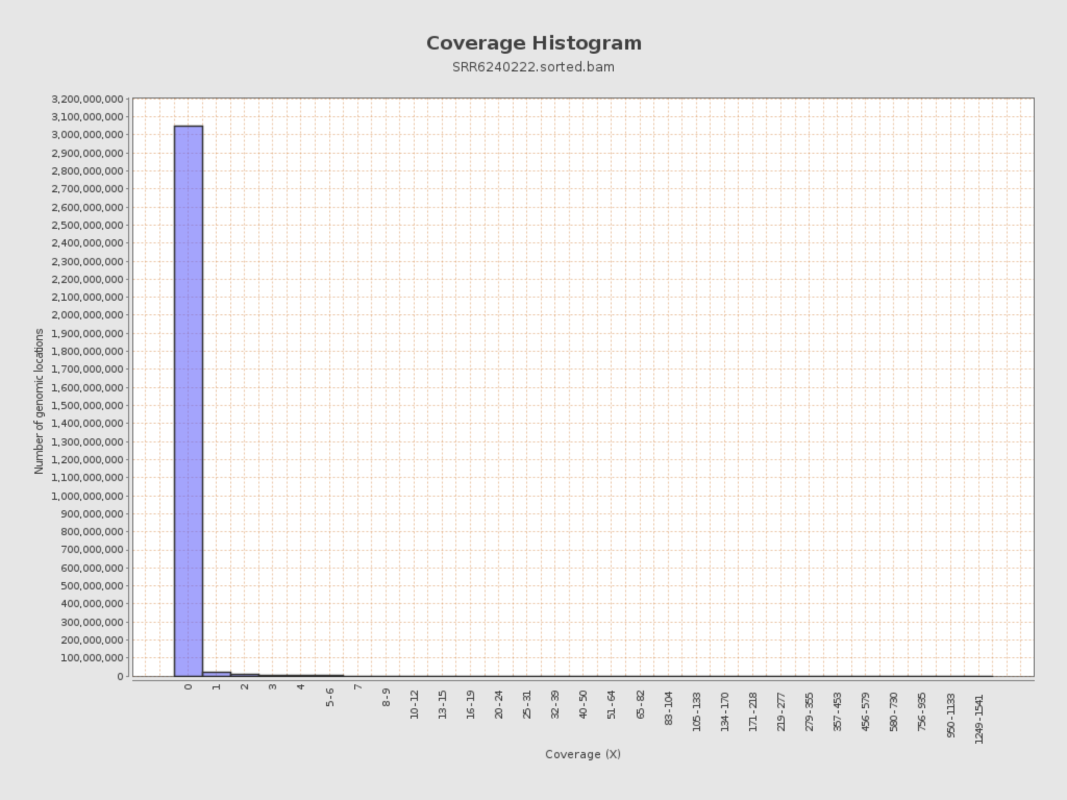
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5558688	0.0223	0.6857
chr2	243199373	11371940	0.0468	0.5445
chr3	198022430	8881227	0.0448	0.4363
chr4	191154276	7017520	0.0367	0.4
chr5	180915260	5588576	0.0309	0.3708
chr6	171115067	5099600	0.0298	0.382
chr7	159138663	6874037	0.0432	0.5621

chr8	146364022	5502544	0.0376	0.9961
chr9	141213431	4827842	0.0342	0.5077
chr10	135534747	5817464	0.0429	0.4642
chr11	135006516	5786779	0.0429	0.4792
chr12	133851895	3736769	0.0279	0.3603
chr13	115169878	2672781	0.0232	0.3252
chr14	107349540	3219935	0.03	0.394
chr15	102531392	3774966	0.0368	0.3929
chr16	90354753	5006630	0.0554	0.5053
chr17	81195210	4162797	0.0513	0.4575
chr18	78077248	3629418	0.0465	0.8057
chr19	59128983	2989303	0.0506	0.5808
chr20	63025520	2552841	0.0405	0.4067
chr21	48129895	1557278	0.0324	0.3735
chr22	51304566	1193148	0.0233	0.3063
chrMT	16571	22607	1.3643	2.0828
chrX	155270560	8346345	0.0538	0.4946
chrY	59373566	351035	0.0059	0.158

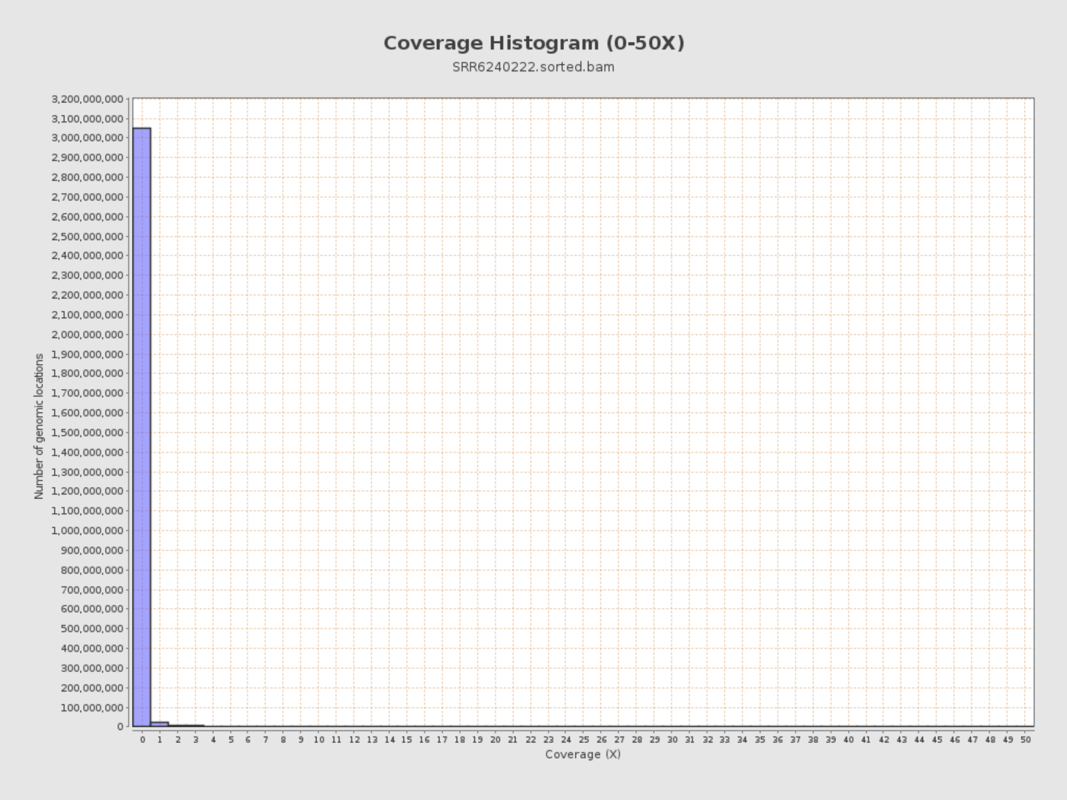
3. Results : Coverage across reference



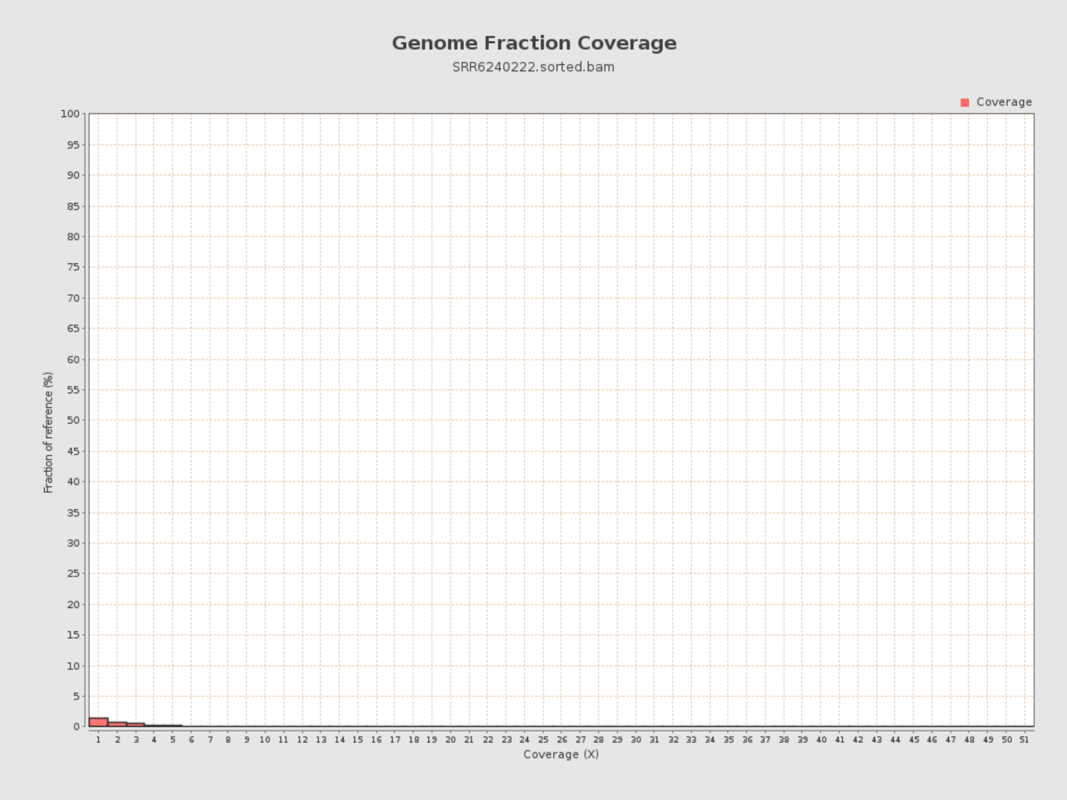
4. Results : Coverage Histogram



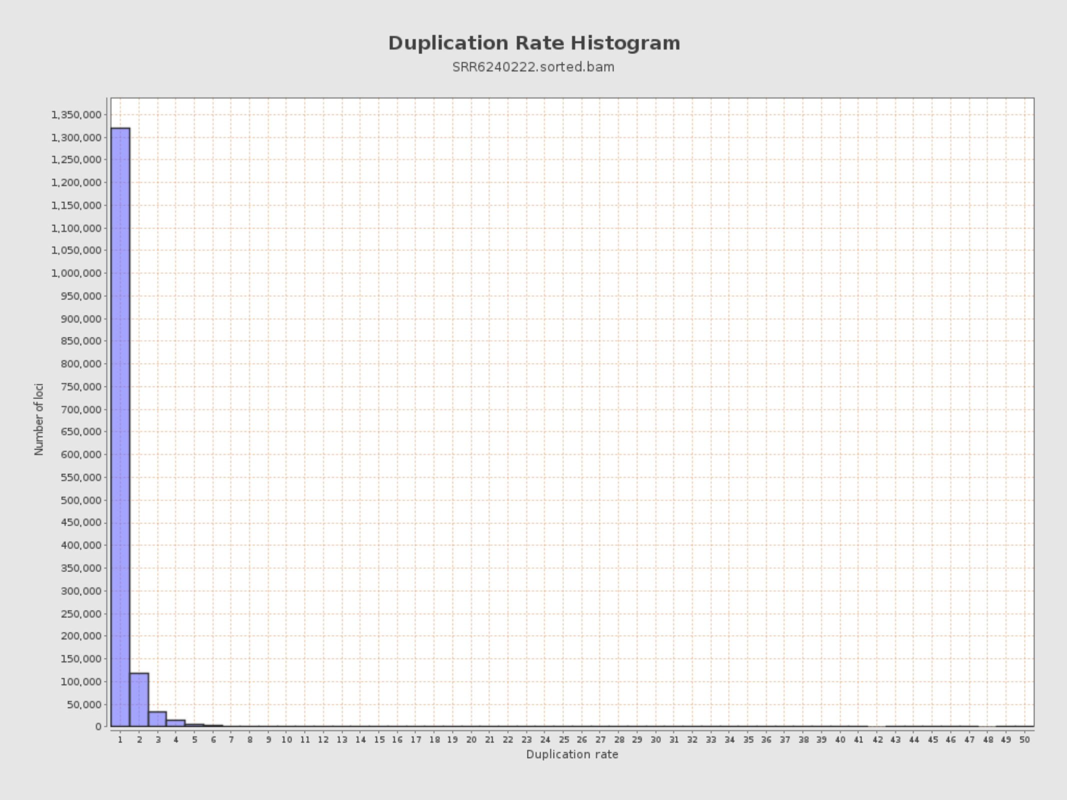
5. Results : Coverage Histogram (0-50X)



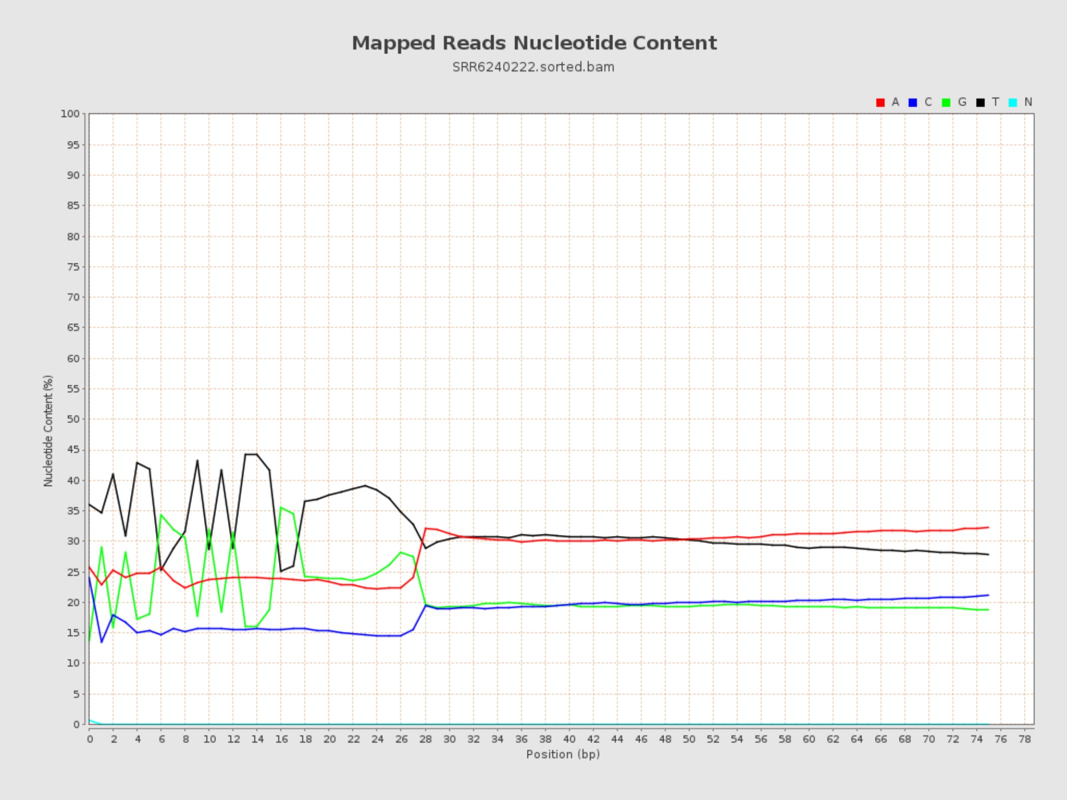
6. Results : Genome Fraction Coverage



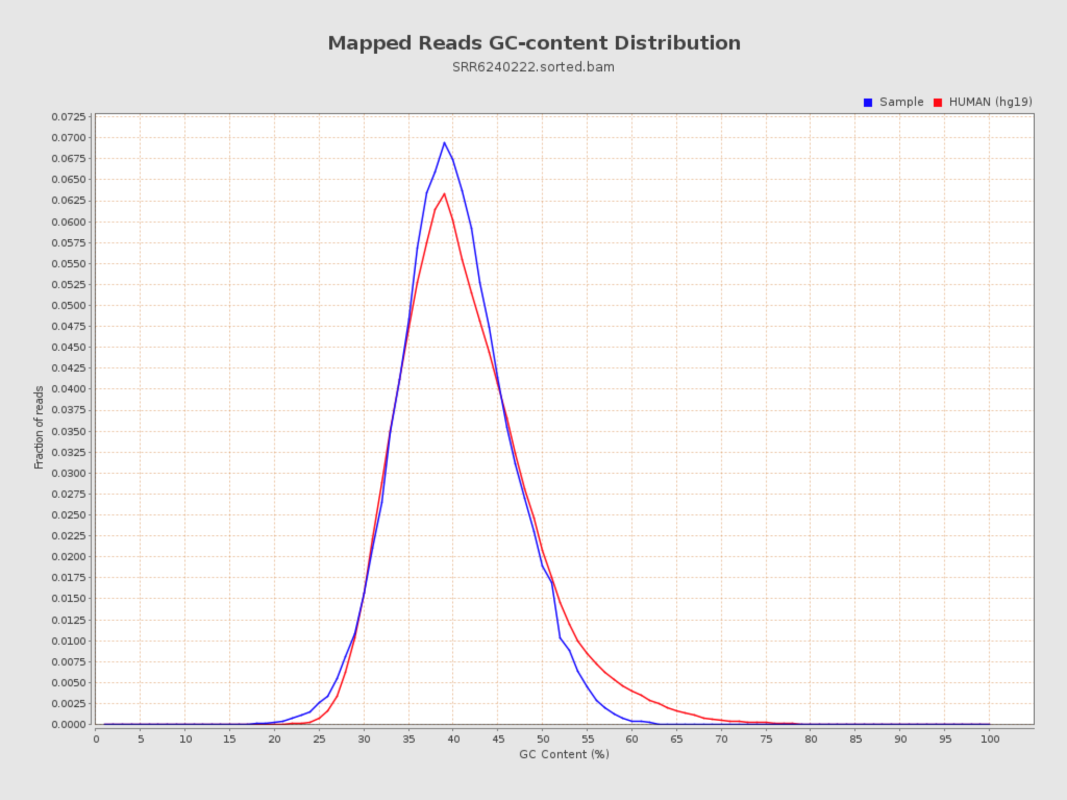
7. Results : Duplication Rate Histogram



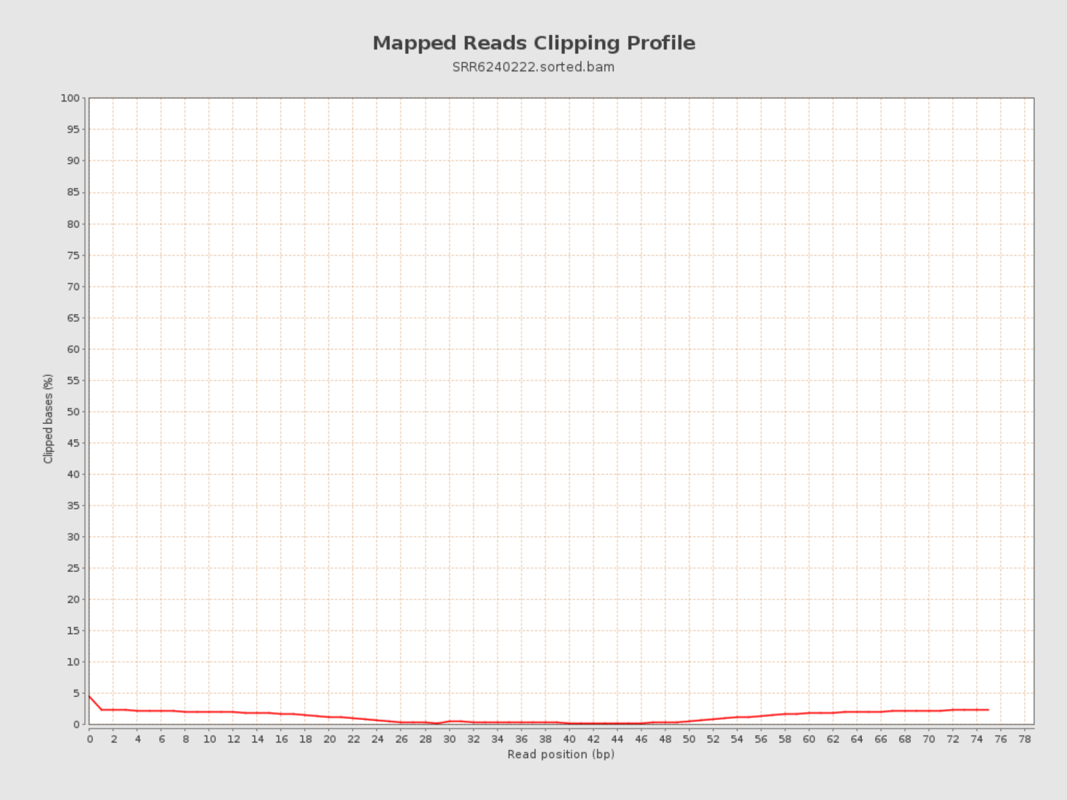
8. Results : Mapped Reads Nucleotide Content



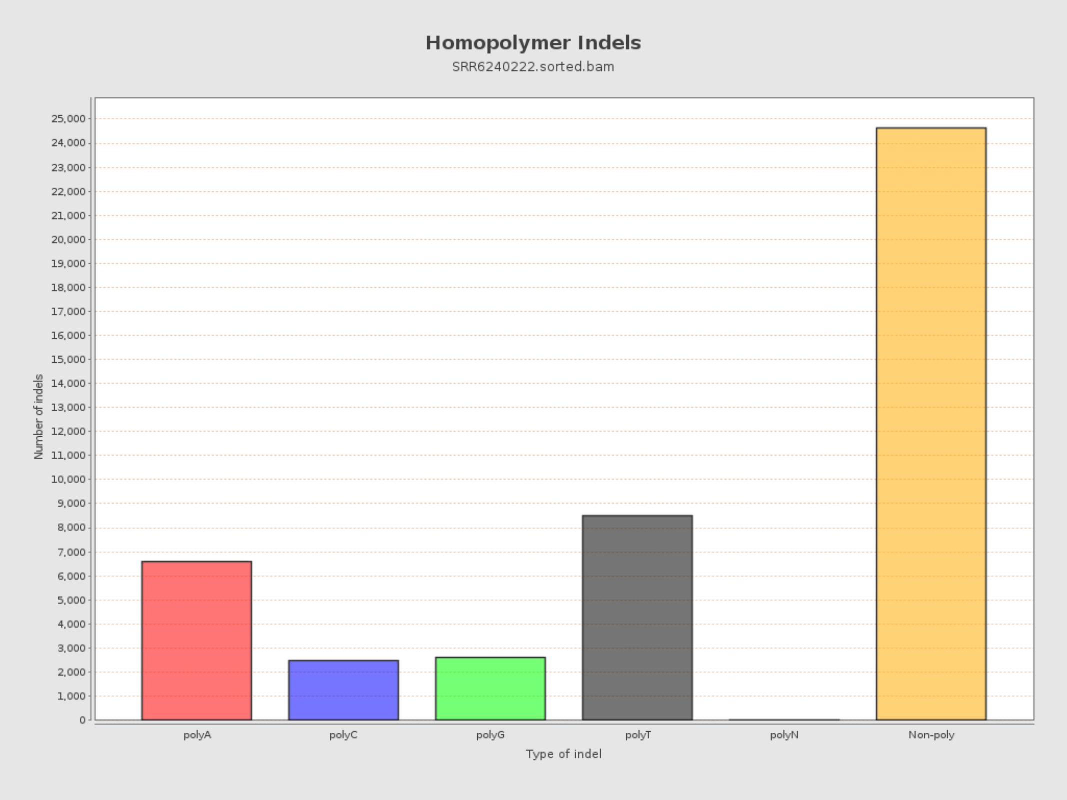
9. Results : Mapped Reads GC-content Distribution



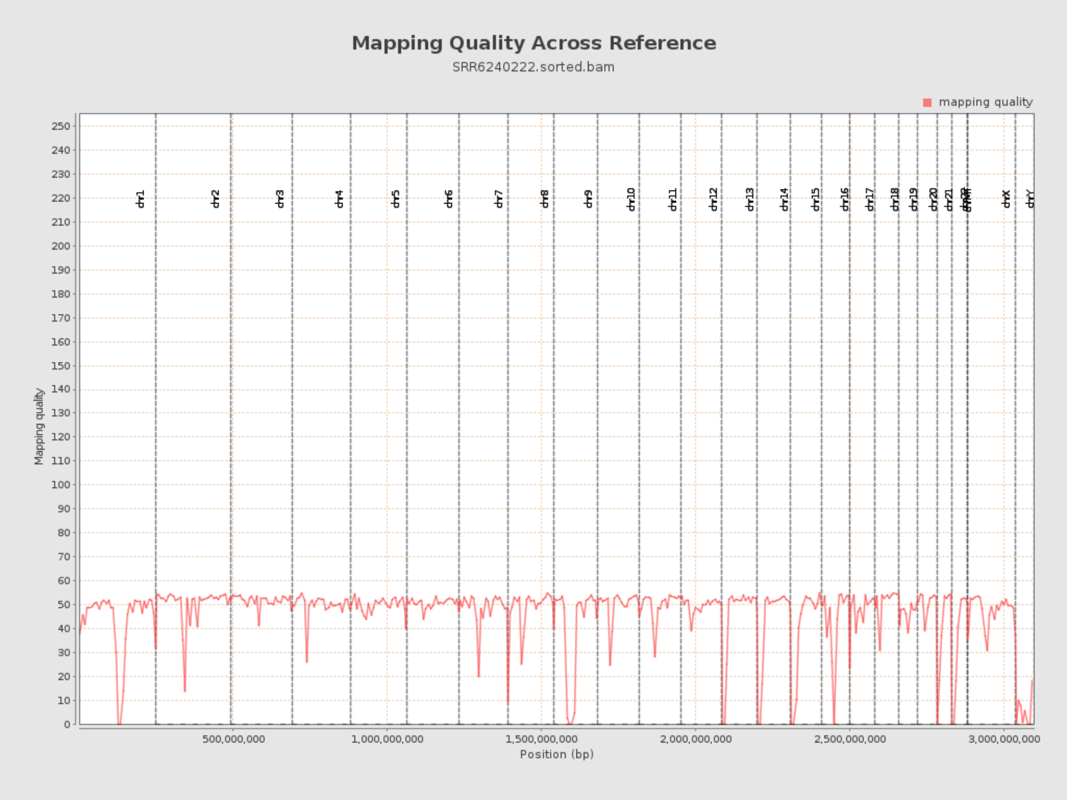
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram