Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 04:57:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240068.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_SRR6240068 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240068.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 04:57:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240068.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,057,481
Mapped reads	718,647 / 67.96%
Unmapped reads	338,834 / 32.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,105 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	90,863 / 8.59%
Duplication rate	9.51%
Clipped reads	430,243 / 40.69%

2.2. ACGT Content

Number/percentage of A's	12,863,557 / 28.25%
Number/percentage of C's	8,254,271 / 18.13%
Number/percentage of T's	14,659,064 / 32.19%
Number/percentage of G's	9,733,484 / 21.37%
Number/percentage of N's	28,592 / 0.06%
GC Percentage	39.5%

2.3. Coverage

Mean	0.0147

Standard Deviation	0.2305

2.4. Mapping Quality

Mean Mapping Quality	46

2.5. Mismatches and indels

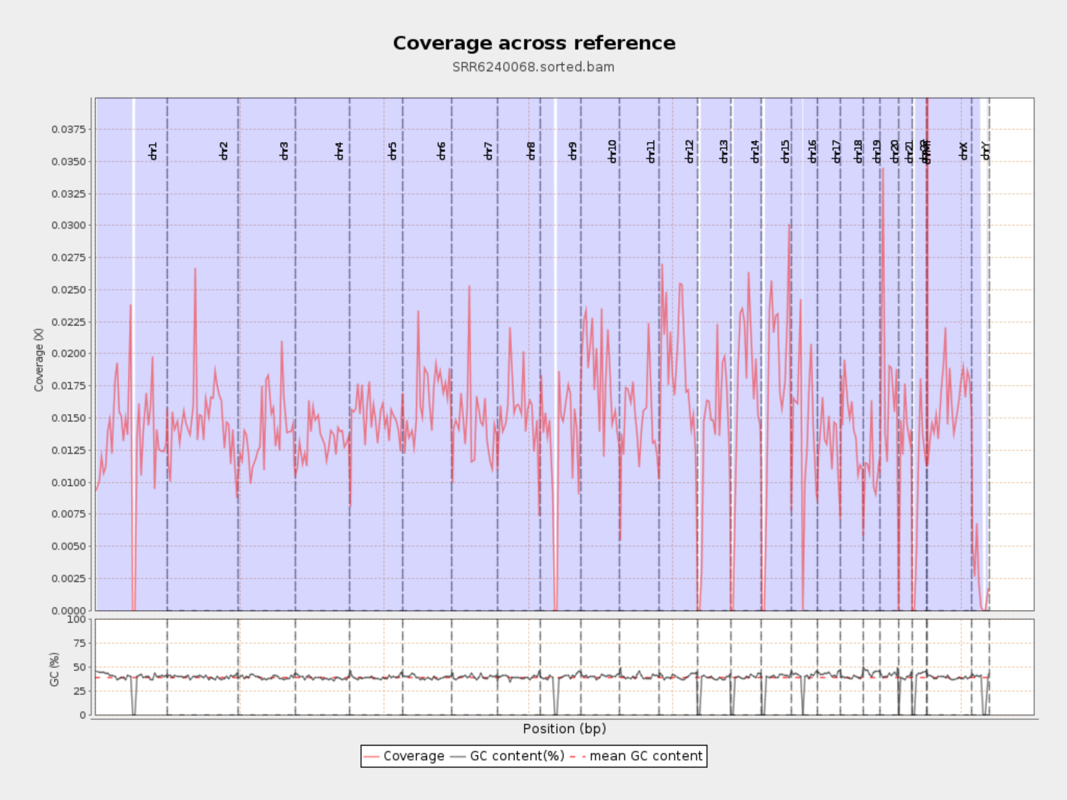
General error rate	0.97%
Mismatches	436,616
Insertions	3,358
Mapped reads with at least one insertion	0.46%
Deletions	13,525
Mapped reads with at least one deletion	1.86%
Homopolymer indels	48.23%

2.6. Chromosome stats

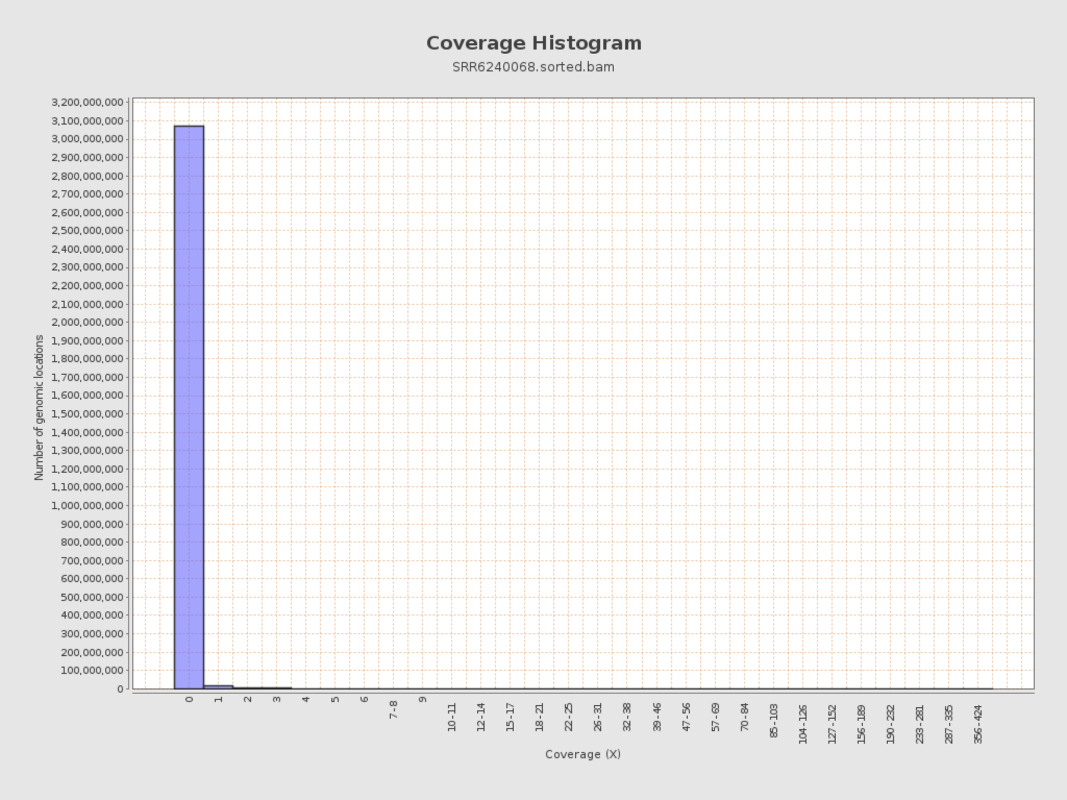
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3303125	0.0133	0.292
chr2	243199373	3614439	0.0149	0.2336
chr3	198022430	2768772	0.014	0.1879
chr4	191154276	2543375	0.0133	0.192
chr5	180915260	2744468	0.0152	0.1975
chr6	171115067	2820912	0.0165	0.2233
chr7	159138663	2324254	0.0146	0.2483

chr8	146364022	2270927	0.0155	0.3257
chr9	141213431	1839034	0.013	0.2128
chr10	135534747	2506249	0.0185	0.2381
chr11	135006516	2026317	0.015	0.2222
chr12	133851895	2571457	0.0192	0.2403
chr13	115169878	1568934	0.0136	0.1968
chr14	107349540	1783775	0.0166	0.2271
chr15	102531392	1810697	0.0177	0.2433
chr16	90354753	1258480	0.0139	0.1947
chr17	81195210	1069540	0.0132	0.1933
chr18	78077248	1131424	0.0145	0.306
chr19	59128983	660387	0.0112	0.2125
chr20	63025520	1148329	0.0182	0.2323
chr21	48129895	627363	0.013	0.1904
chr22	51304566	481297	0.0094	0.1536
chrMT	16571	24451	1.4755	2.0812
chrX	155270560	2534072	0.0163	0.2143
chrY	59373566	130164	0.0022	0.0801

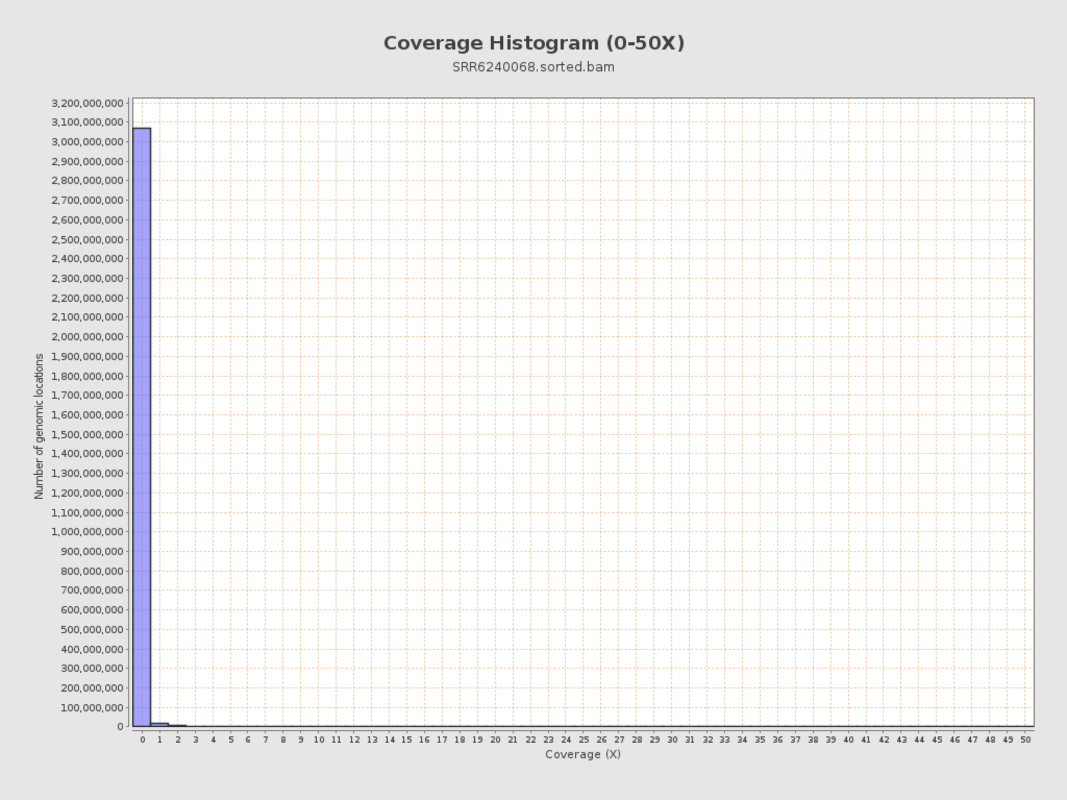
3. Results : Coverage across reference



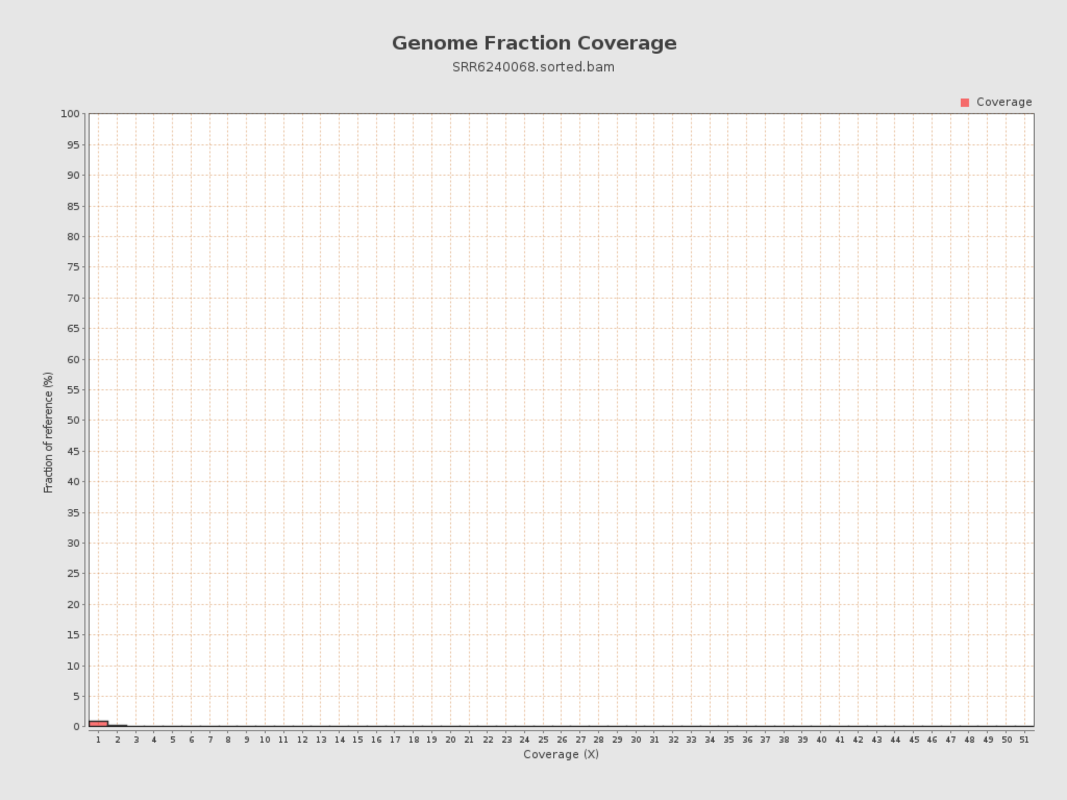
4. Results : Coverage Histogram



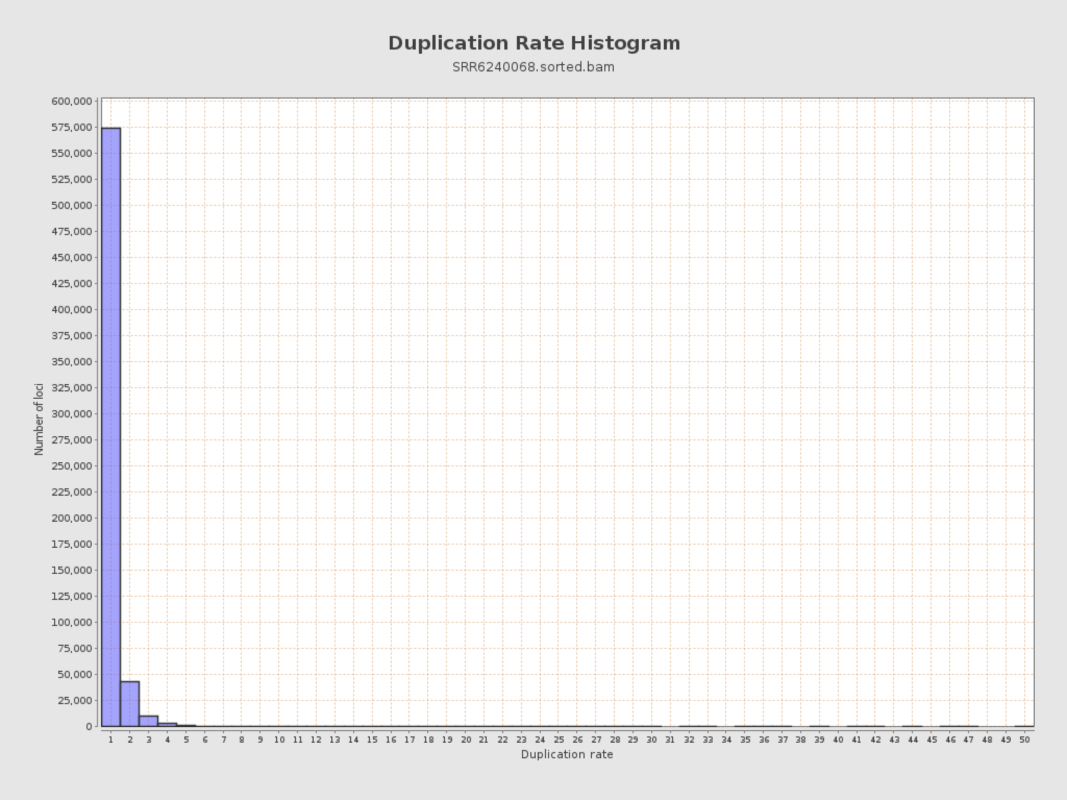
5. Results : Coverage Histogram (0-50X)



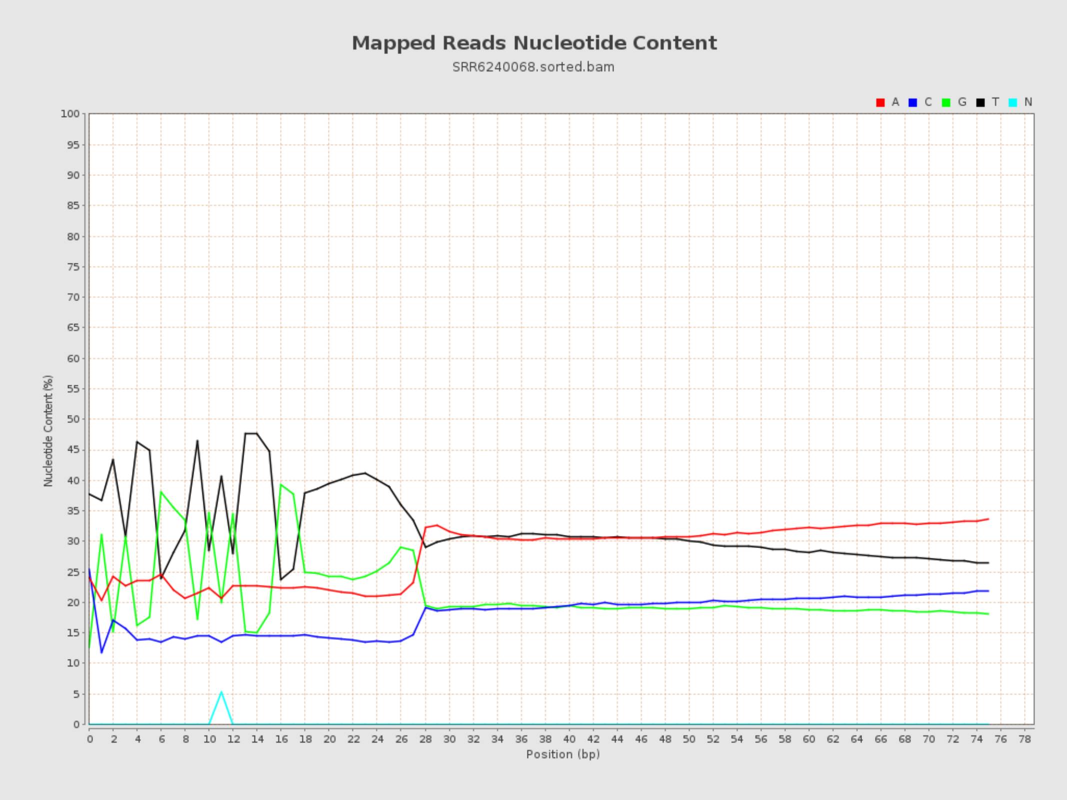
6. Results : Genome Fraction Coverage



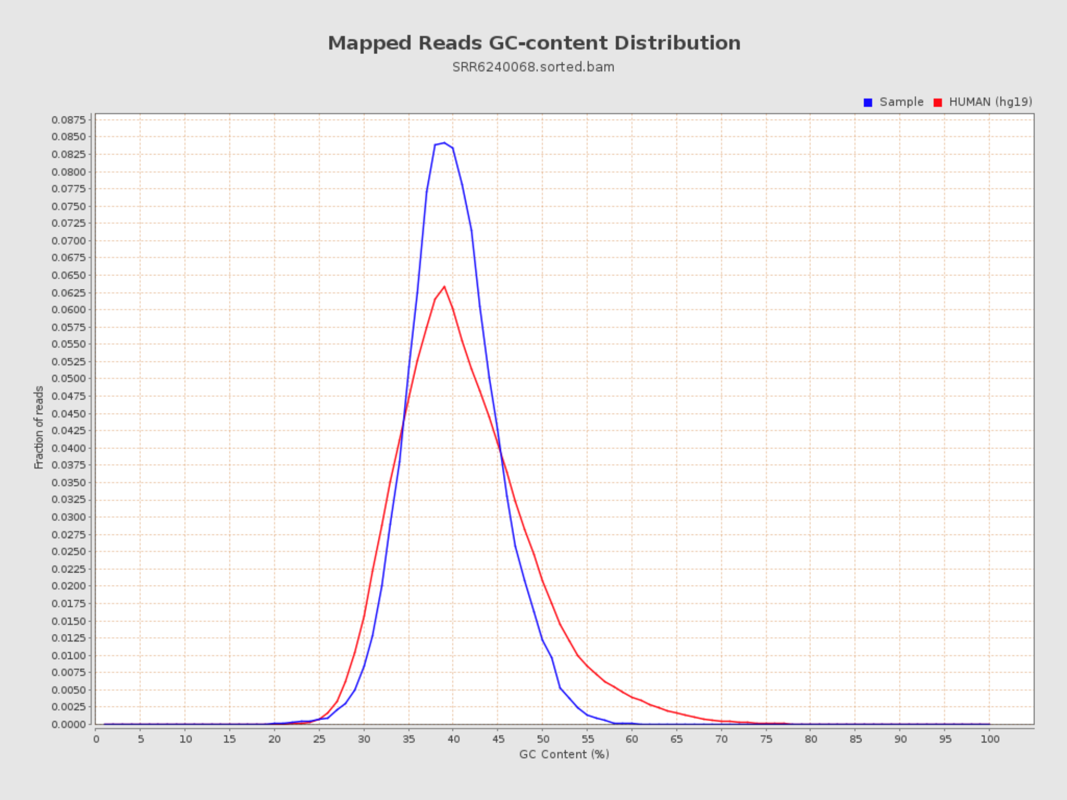
7. Results : Duplication Rate Histogram



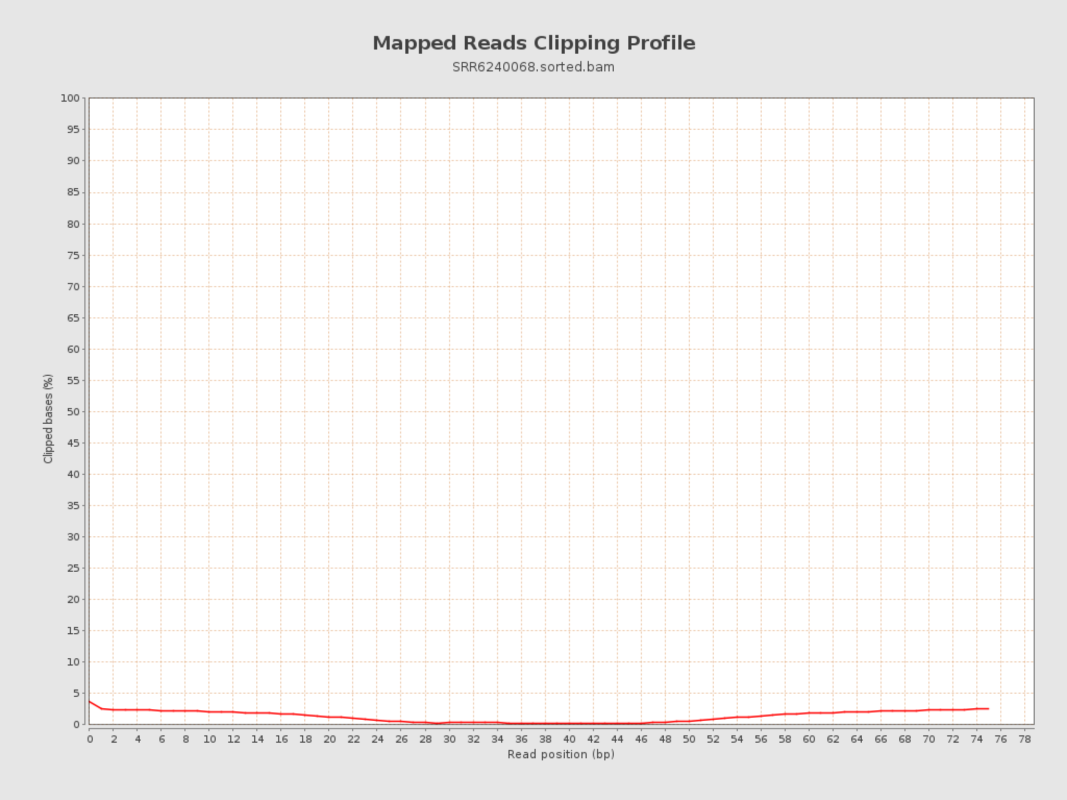
8. Results : Mapped Reads Nucleotide Content



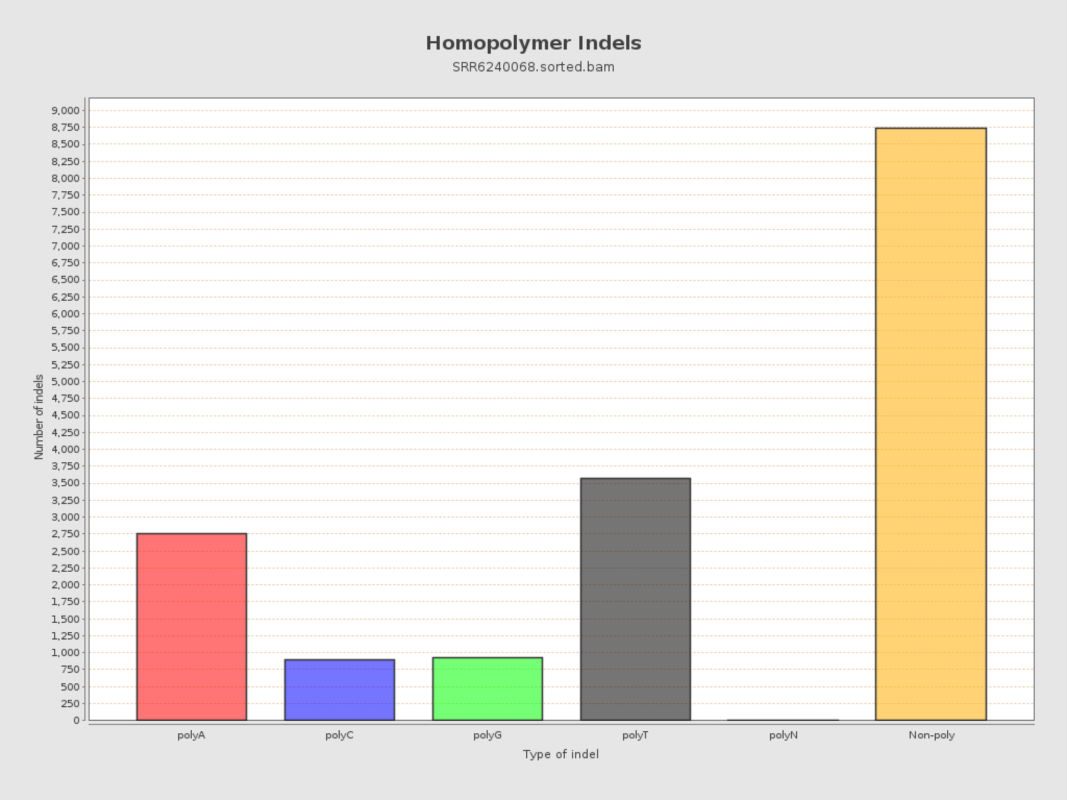
9. Results : Mapped Reads GC-content Distribution



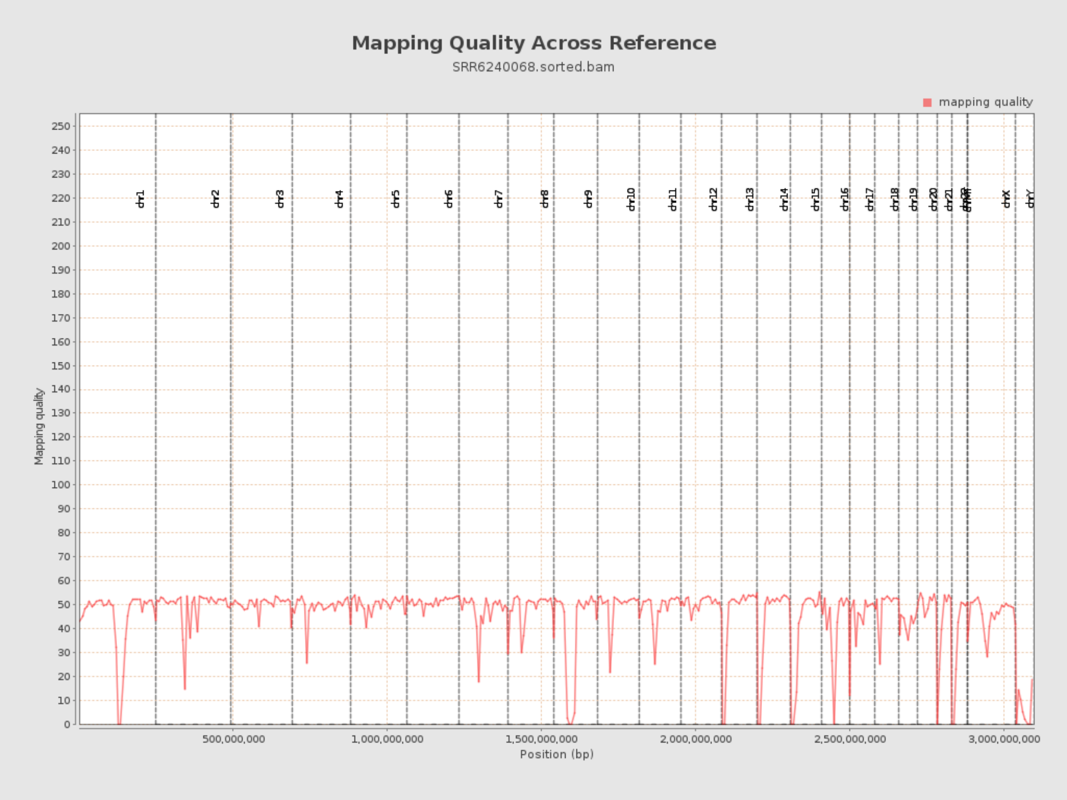
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram