Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:41:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240212.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_SRR6240212 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240212.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:41:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240212.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,427,655
Mapped reads	2,034,382 / 83.8%
Unmapped reads	393,273 / 16.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,974 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	147,847 / 6.09%
Duplication rate	5.87%
Clipped reads	929,407 / 38.28%

2.2. ACGT Content

Number/percentage of A's	38,118,821 / 28.14%
Number/percentage of C's	25,133,315 / 18.56%
Number/percentage of T's	42,998,514 / 31.75%
Number/percentage of G's	29,182,189 / 21.55%
Number/percentage of N's	13,214 / 0.01%
GC Percentage	40.1%

2.3. Coverage

Mean	0.0438

Standard Deviation	0.4207

2.4. Mapping Quality

Mean Mapping Quality	46.76

2.5. Mismatches and indels

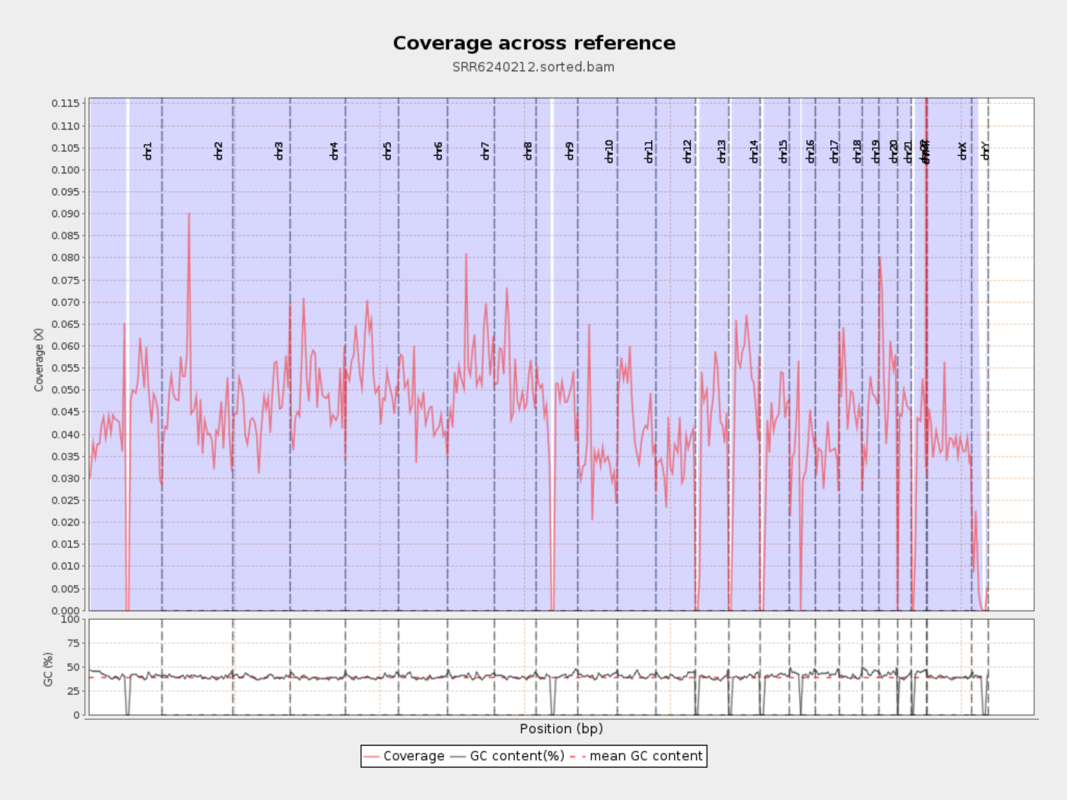
General error rate	0.81%
Mismatches	1,075,098
Insertions	10,636
Mapped reads with at least one insertion	0.52%
Deletions	31,139
Mapped reads with at least one deletion	1.51%
Homopolymer indels	47.82%

2.6. Chromosome stats

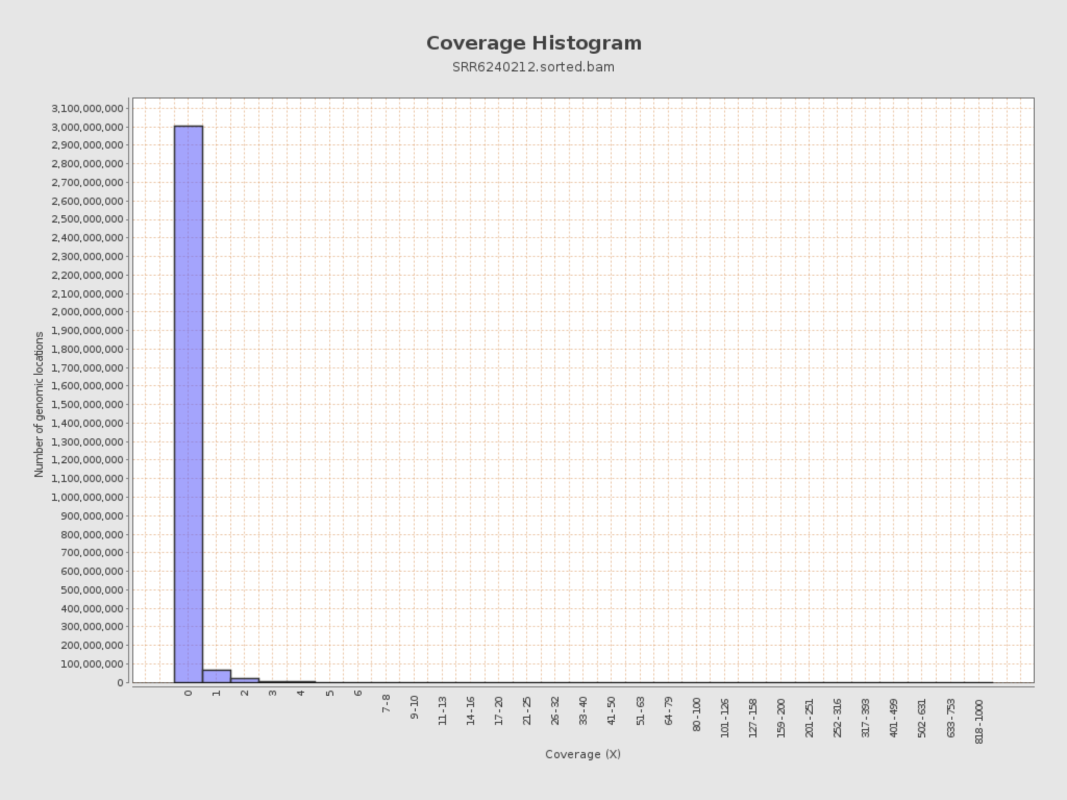
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10543725	0.0423	0.6183
chr2	243199373	11215736	0.0461	0.4706
chr3	198022430	9178114	0.0463	0.2998
chr4	191154276	9473145	0.0496	0.3334
chr5	180915260	9833760	0.0544	0.3246
chr6	171115067	7935258	0.0464	0.3383
chr7	159138663	8910027	0.056	0.5421

chr8	146364022	7710293	0.0527	0.6924
chr9	141213431	6040572	0.0428	0.4104
chr10	135534747	4654891	0.0343	0.353
chr11	135006516	6046693	0.0448	0.378
chr12	133851895	4673897	0.0349	0.2616
chr13	115169878	4483589	0.0389	0.2746
chr14	107349540	4970664	0.0463	0.3175
chr15	102531392	3805323	0.0371	0.27
chr16	90354753	3172438	0.0351	0.2846
chr17	81195210	2838135	0.035	0.2745
chr18	78077248	3843885	0.0492	0.8227
chr19	59128983	2632240	0.0445	0.4347
chr20	63025520	3536023	0.0561	0.3369
chr21	48129895	2011929	0.0418	0.3053
chr22	51304566	1602213	0.0312	0.2364
chrMT	16571	16217	0.9786	1.5737
chrX	155270560	5979519	0.0385	0.3006
chrY	59373566	393517	0.0066	0.1734

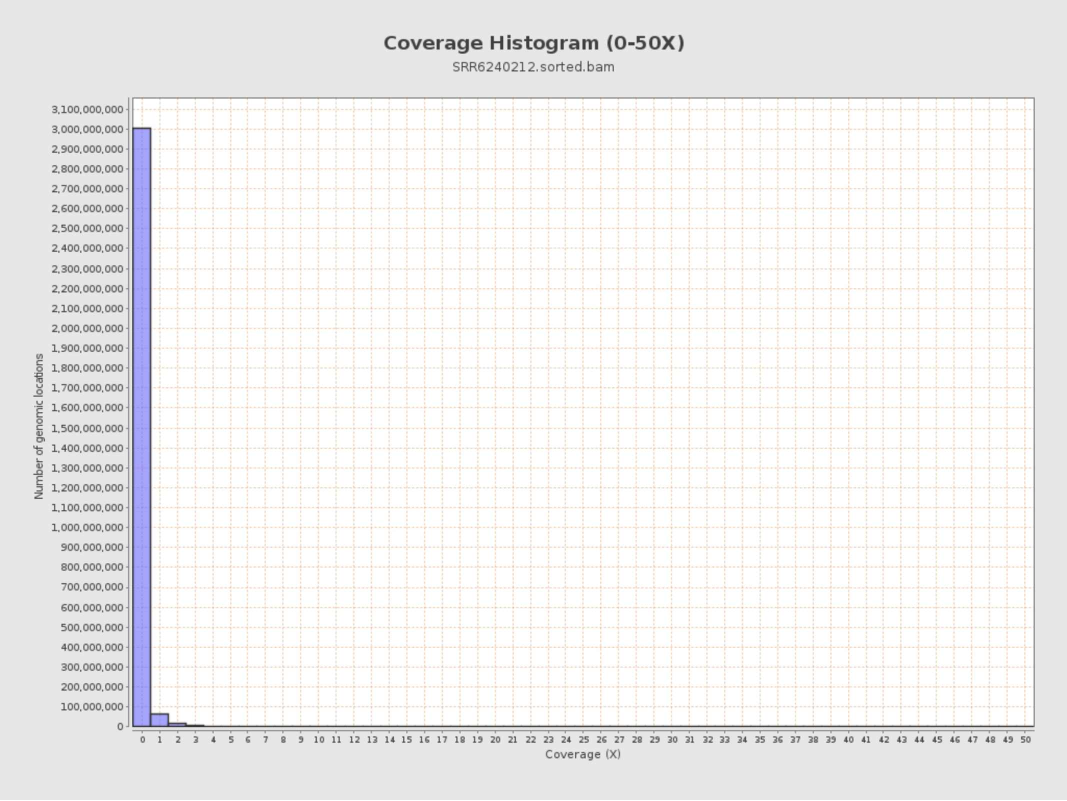
3. Results : Coverage across reference



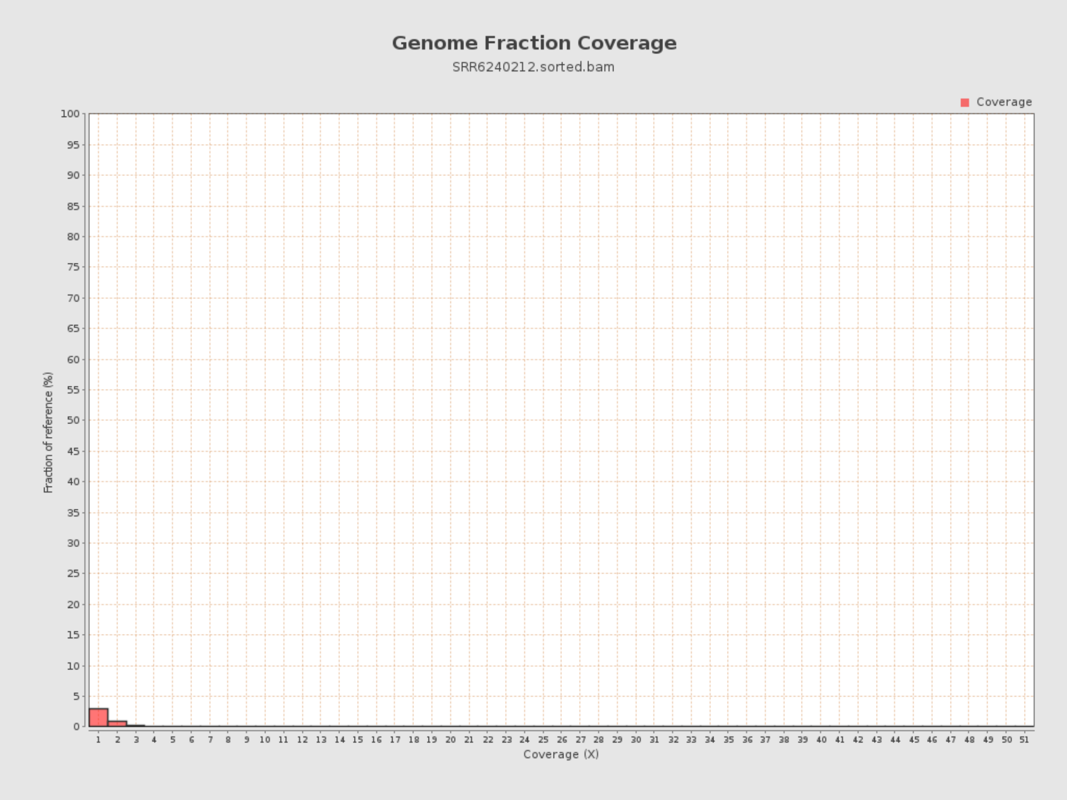
4. Results : Coverage Histogram



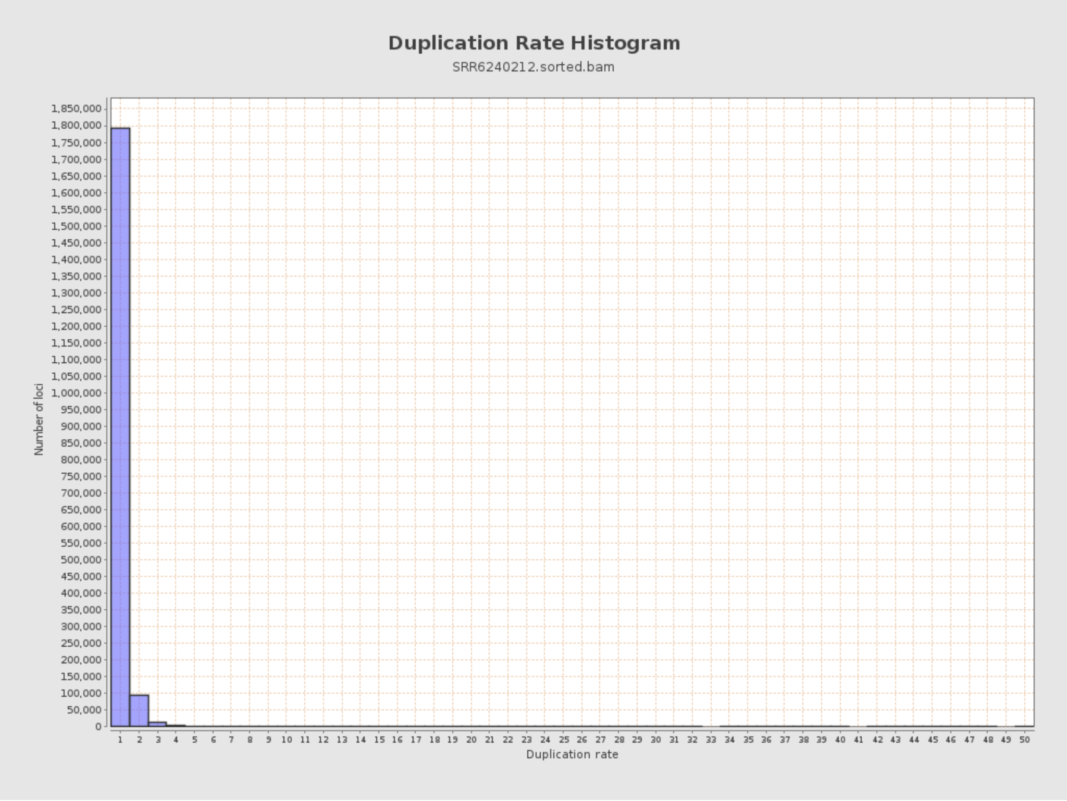
5. Results : Coverage Histogram (0-50X)



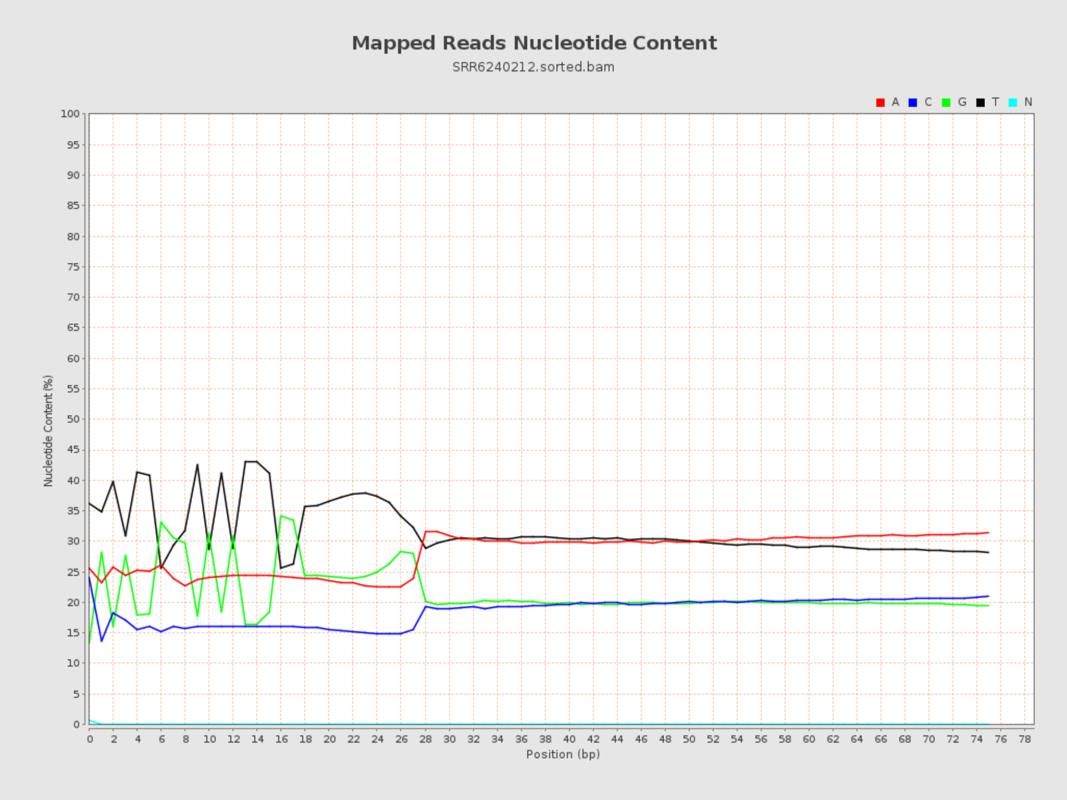
6. Results : Genome Fraction Coverage



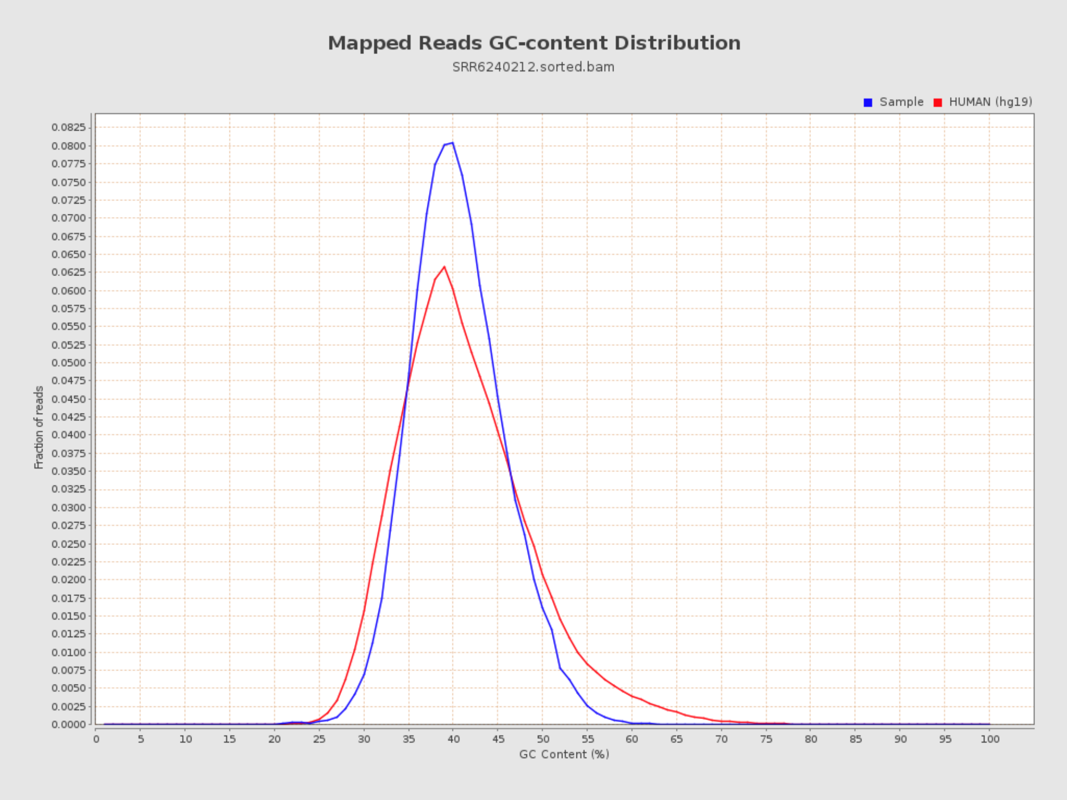
7. Results : Duplication Rate Histogram



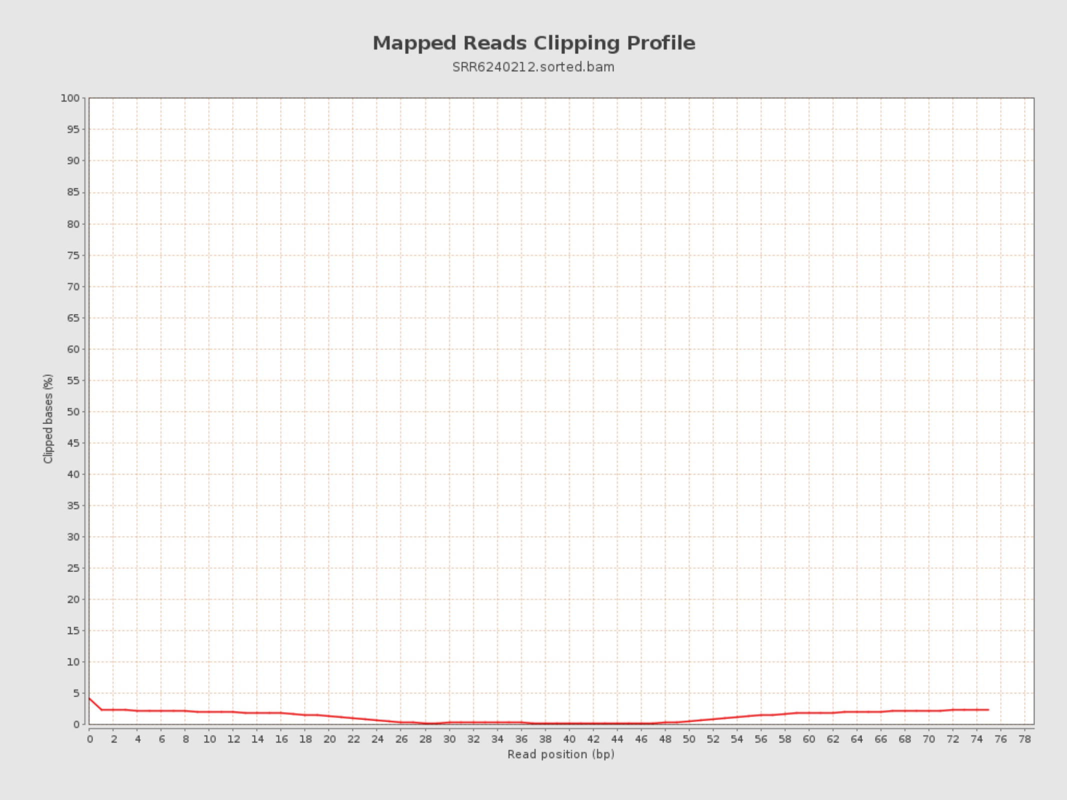
8. Results : Mapped Reads Nucleotide Content



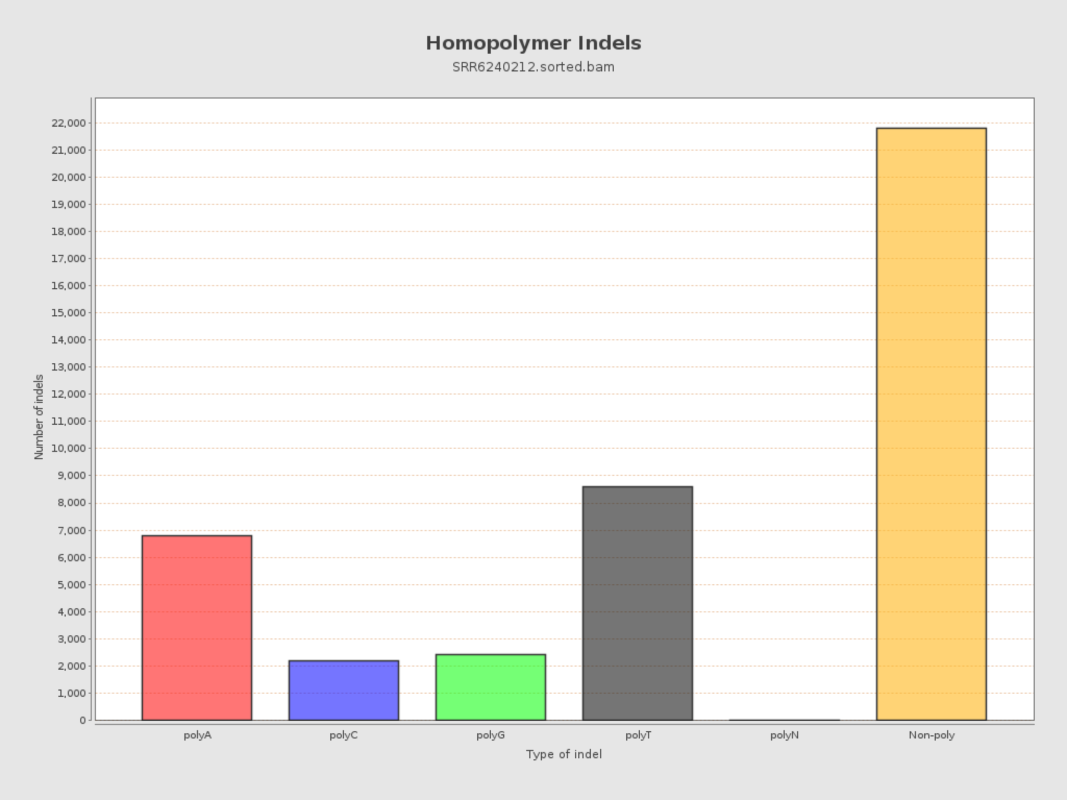
9. Results : Mapped Reads GC-content Distribution



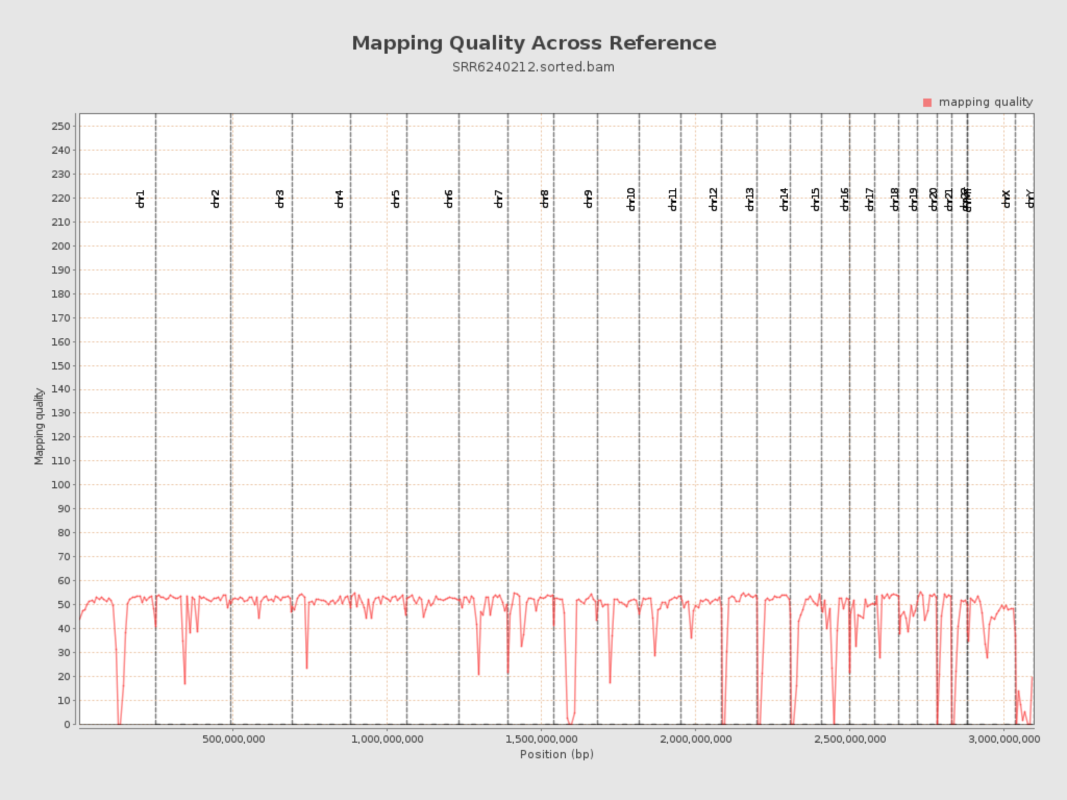
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram