Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/18 06:38:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6240211.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_SRR6240211 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6240211.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 18 06:38:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6240211.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,165,328
Mapped reads	1,731,822 / 79.98%
Unmapped reads	433,506 / 20.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,810 / 0.87%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	193,114 / 8.92%
Duplication rate	8.77%
Clipped reads	869,484 / 40.15%

2.2. ACGT Content

Number/percentage of A's	32,510,184 / 28.54%
Number/percentage of C's	21,384,272 / 18.77%
Number/percentage of T's	35,823,931 / 31.45%
Number/percentage of G's	24,169,037 / 21.22%
Number/percentage of N's	10,203 / 0.01%
GC Percentage	39.99%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3801

2.4. Mapping Quality

Mean Mapping Quality	46.41

2.5. Mismatches and indels

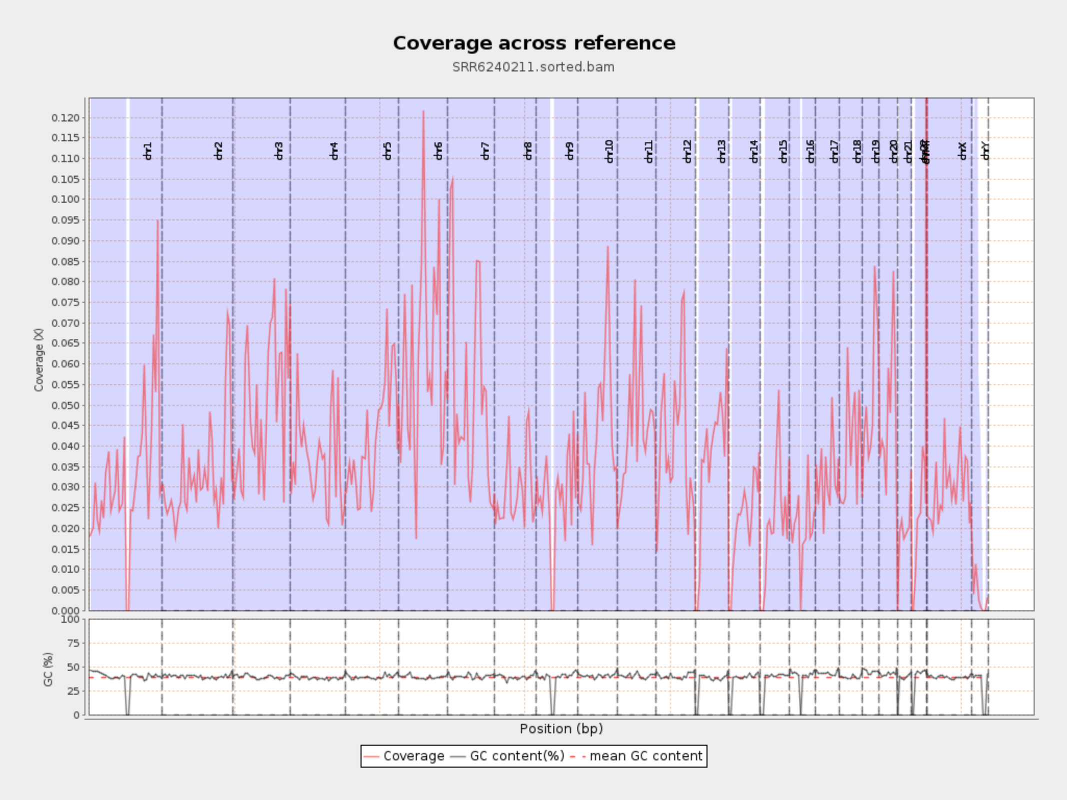
General error rate	0.8%
Mismatches	895,188
Insertions	8,078
Mapped reads with at least one insertion	0.46%
Deletions	29,140
Mapped reads with at least one deletion	1.66%
Homopolymer indels	46.63%

2.6. Chromosome stats

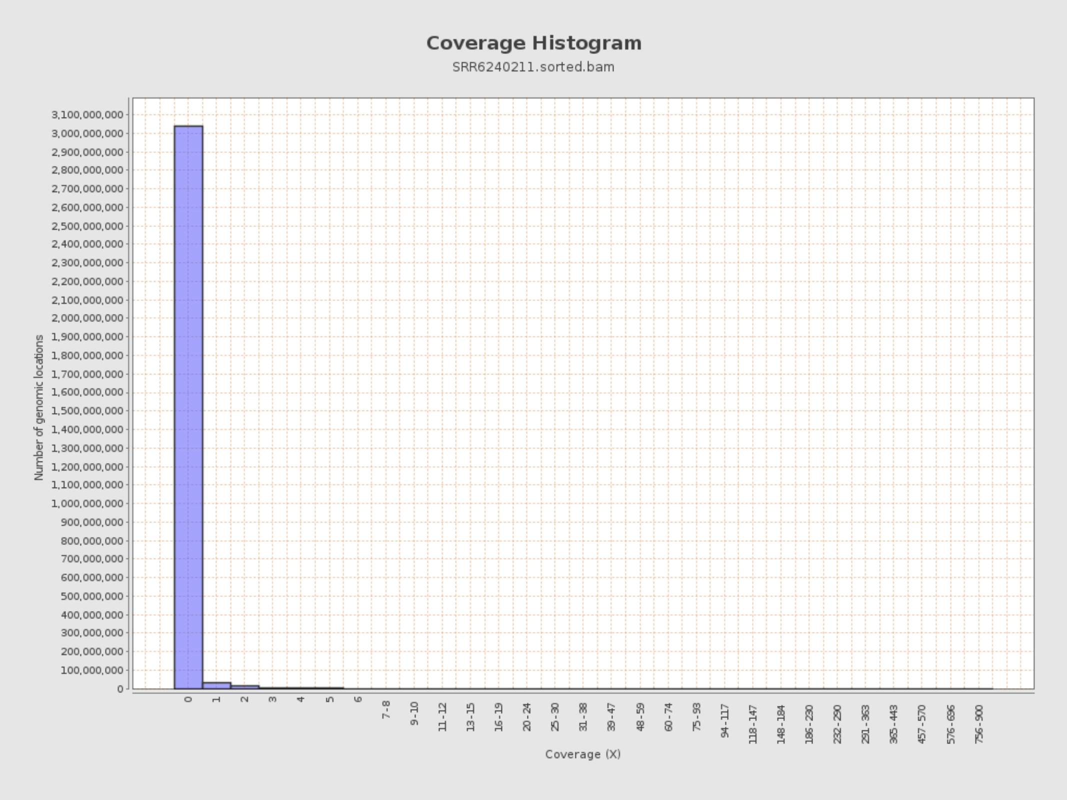
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8189088	0.0329	0.4671
chr2	243199373	8082117	0.0332	0.3738
chr3	198022430	9748761	0.0492	0.375
chr4	191154276	7018155	0.0367	0.3345
chr5	180915260	7614106	0.0421	0.3546
chr6	171115067	10394676	0.0607	0.4431
chr7	159138663	8368229	0.0526	0.4467

chr8	146364022	4264212	0.0291	0.6065
chr9	141213431	3810267	0.027	0.3071
chr10	135534747	5882379	0.0434	0.3845
chr11	135006516	6020491	0.0446	0.3911
chr12	133851895	5437043	0.0406	0.3559
chr13	115169878	4216028	0.0366	0.3318
chr14	107349540	2317381	0.0216	0.2565
chr15	102531392	2156209	0.021	0.2512
chr16	90354753	1830117	0.0203	0.2447
chr17	81195210	2633282	0.0324	0.312
chr18	78077248	3068918	0.0393	0.4763
chr19	59128983	3055926	0.0517	0.4146
chr20	63025520	3030792	0.0481	0.374
chr21	48129895	924421	0.0192	0.2334
chr22	51304566	1061550	0.0207	0.2314
chrMT	16571	9398	0.5671	1.177
chrX	155270560	4588436	0.0296	0.3019
chrY	59373566	225979	0.0038	0.1063

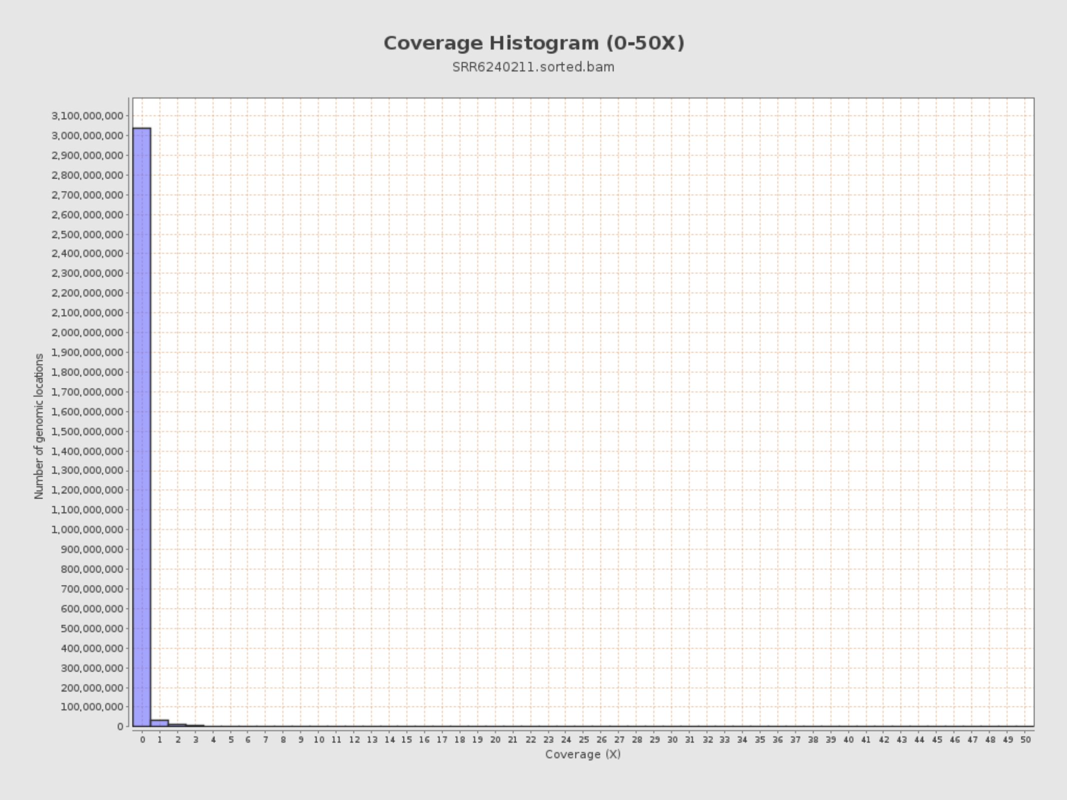
3. Results : Coverage across reference



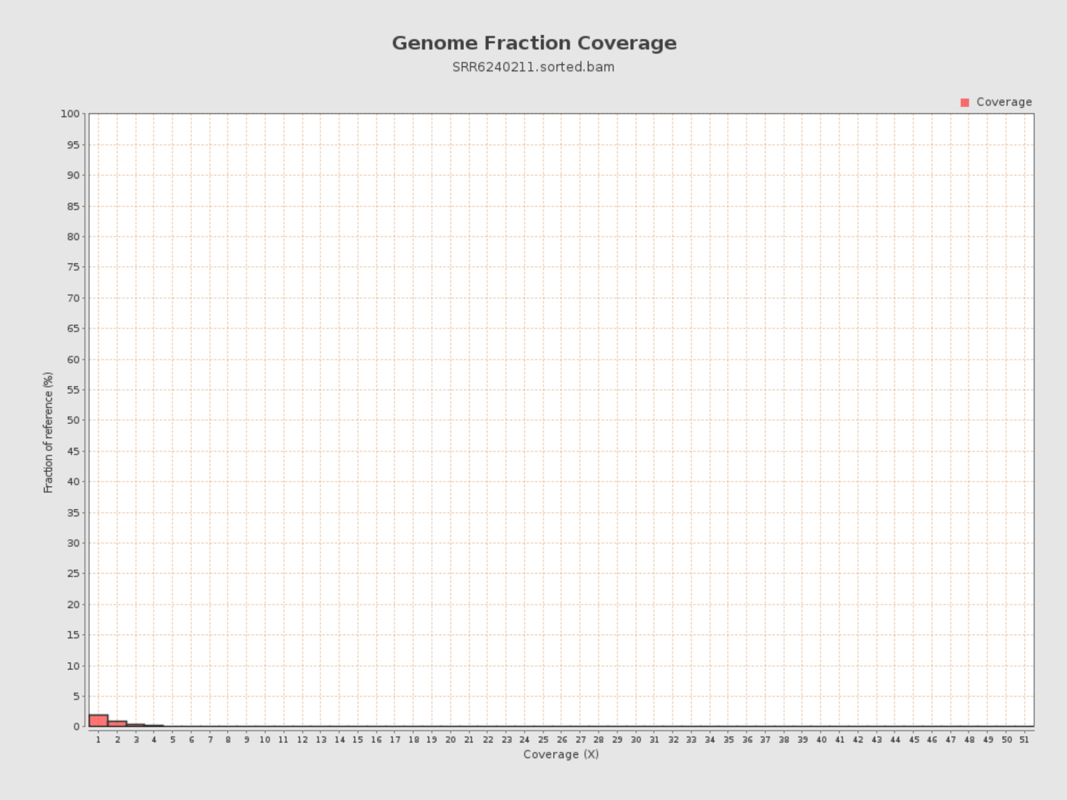
4. Results : Coverage Histogram



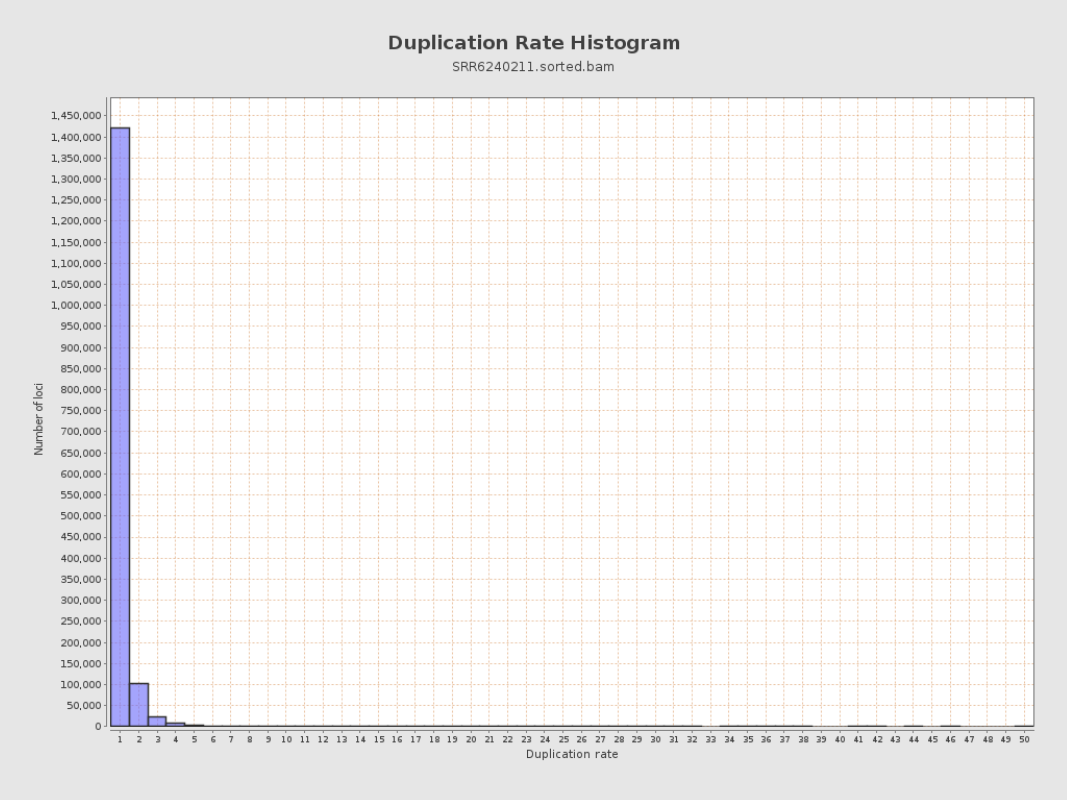
5. Results : Coverage Histogram (0-50X)



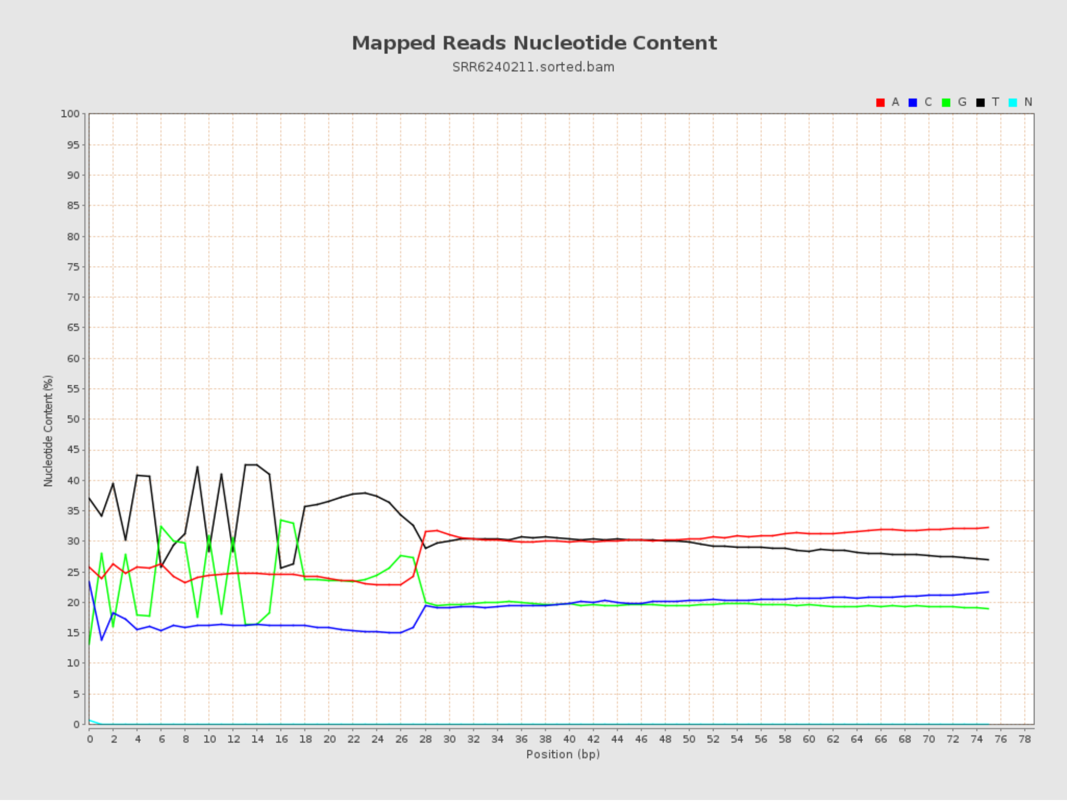
6. Results : Genome Fraction Coverage



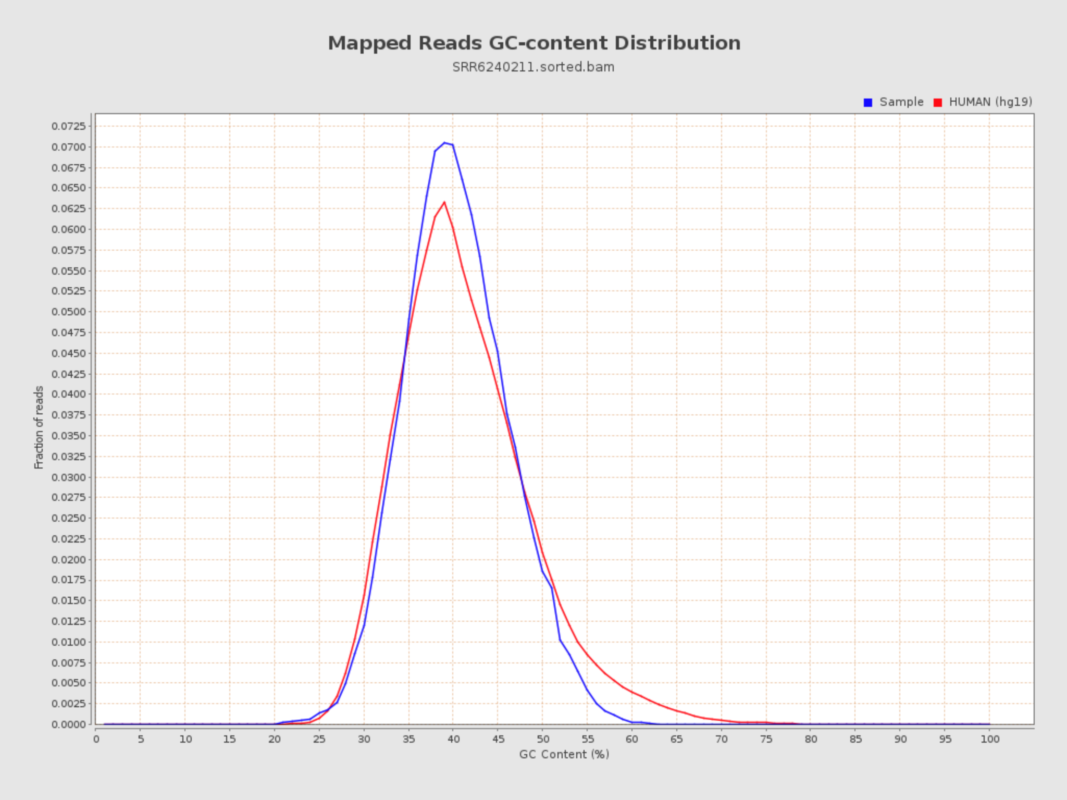
7. Results : Duplication Rate Histogram



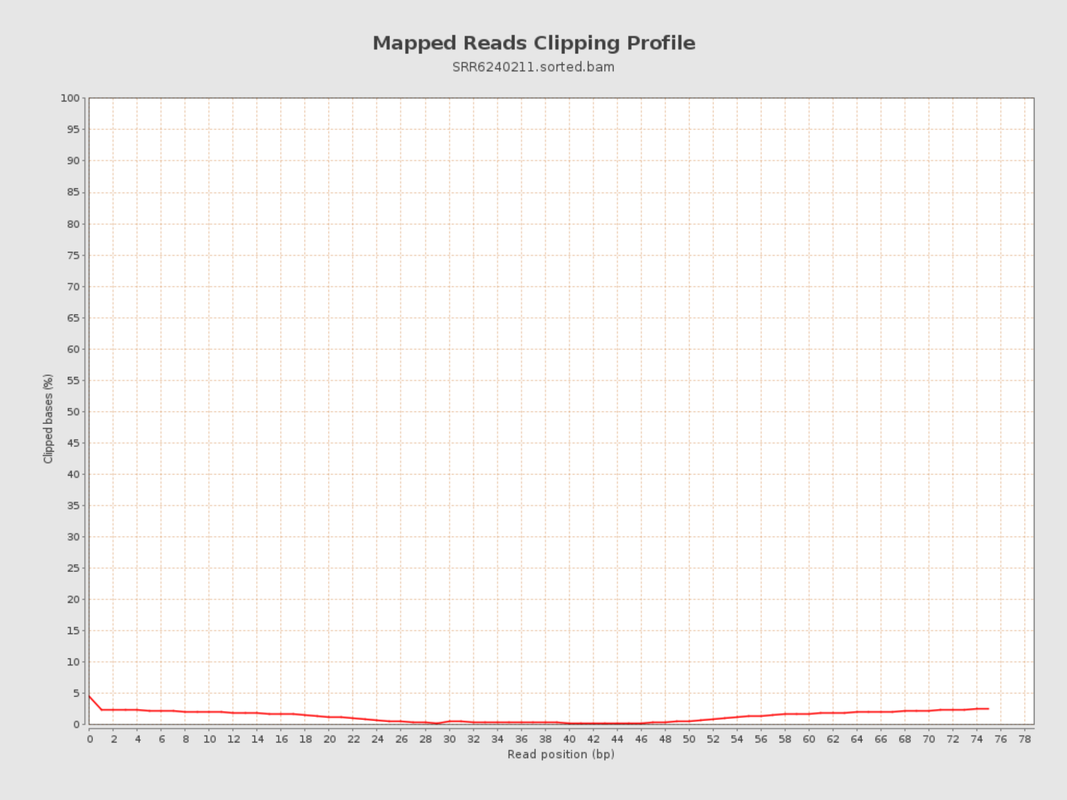
8. Results : Mapped Reads Nucleotide Content



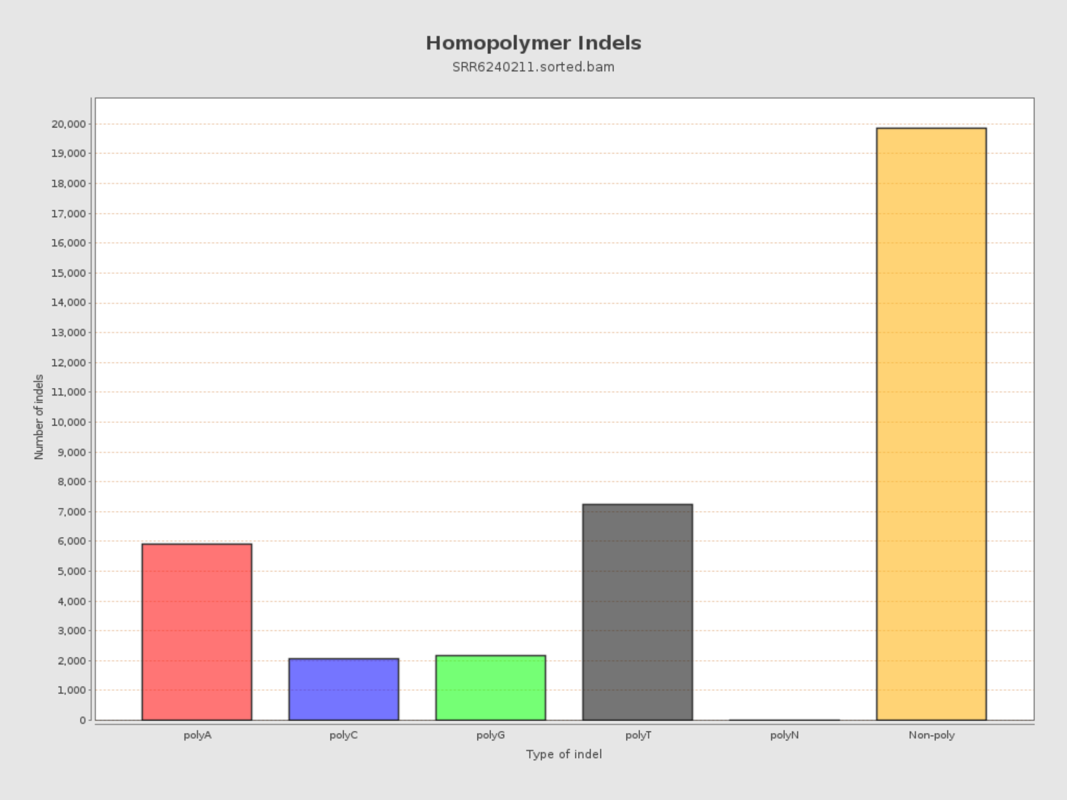
9. Results : Mapped Reads GC-content Distribution



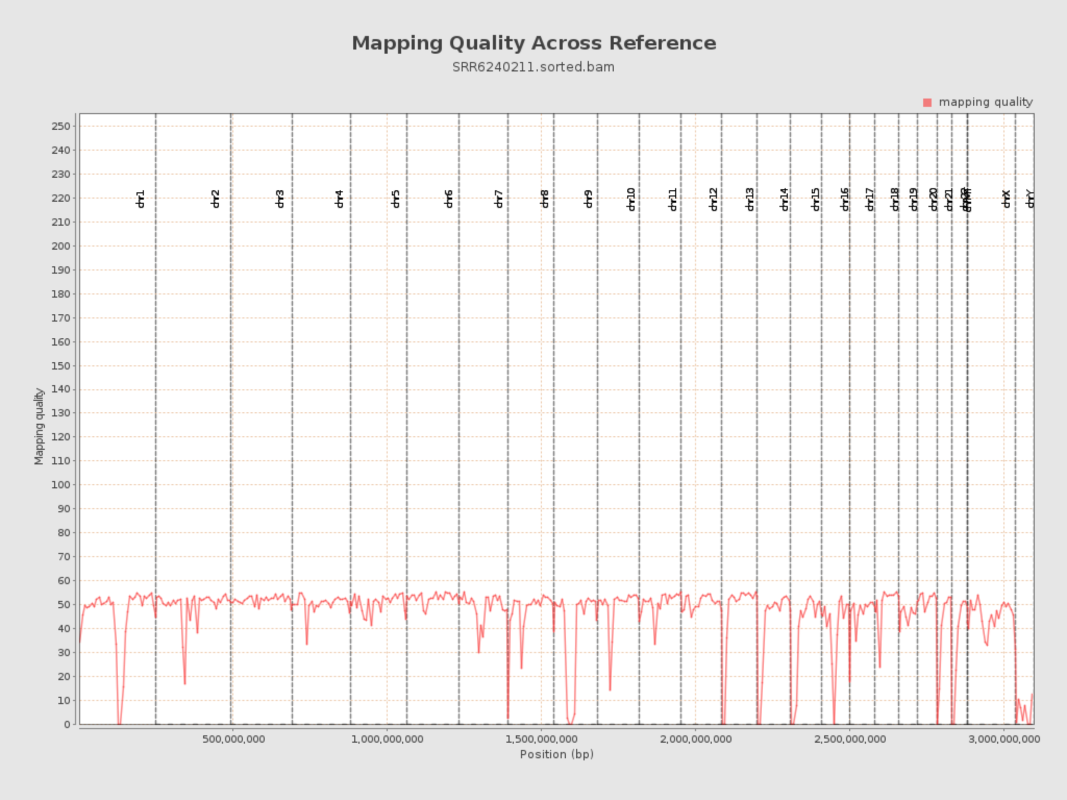
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram