Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 22:11:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751223.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_SRR8751223 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751223.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 22:11:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751223.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,024,655
Mapped reads	3,857,619 / 95.85%
Unmapped reads	167,036 / 4.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	57,073 / 1.42%
Read min/max/mean length	30 / 101 / 101.59
Duplicated reads (estimated)	41,076 / 1.02%
Duplication rate	1%
Clipped reads	471,595 / 11.72%

2.2. ACGT Content

Number/percentage of A's	111,587,933 / 29.31%
Number/percentage of C's	78,968,273 / 20.74%
Number/percentage of T's	112,259,435 / 29.48%
Number/percentage of G's	77,917,347 / 20.46%
Number/percentage of N's	2,075 / 0%
GC Percentage	41.21%

2.3. Coverage

Mean	0.123

Standard Deviation	0.4134

2.4. Mapping Quality

Mean Mapping Quality	51.84

2.5. Mismatches and indels

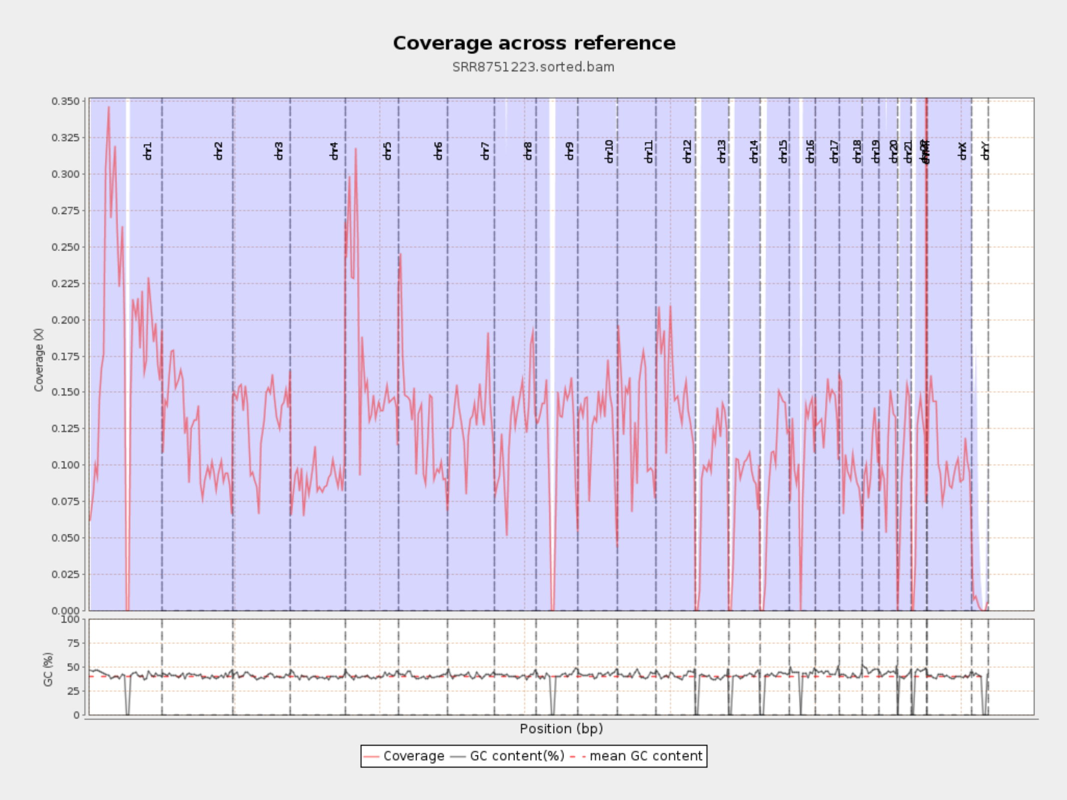
General error rate	0.28%
Mismatches	1,000,447
Insertions	41,158
Mapped reads with at least one insertion	1.06%
Deletions	43,860
Mapped reads with at least one deletion	1.12%
Homopolymer indels	47.22%

2.6. Chromosome stats

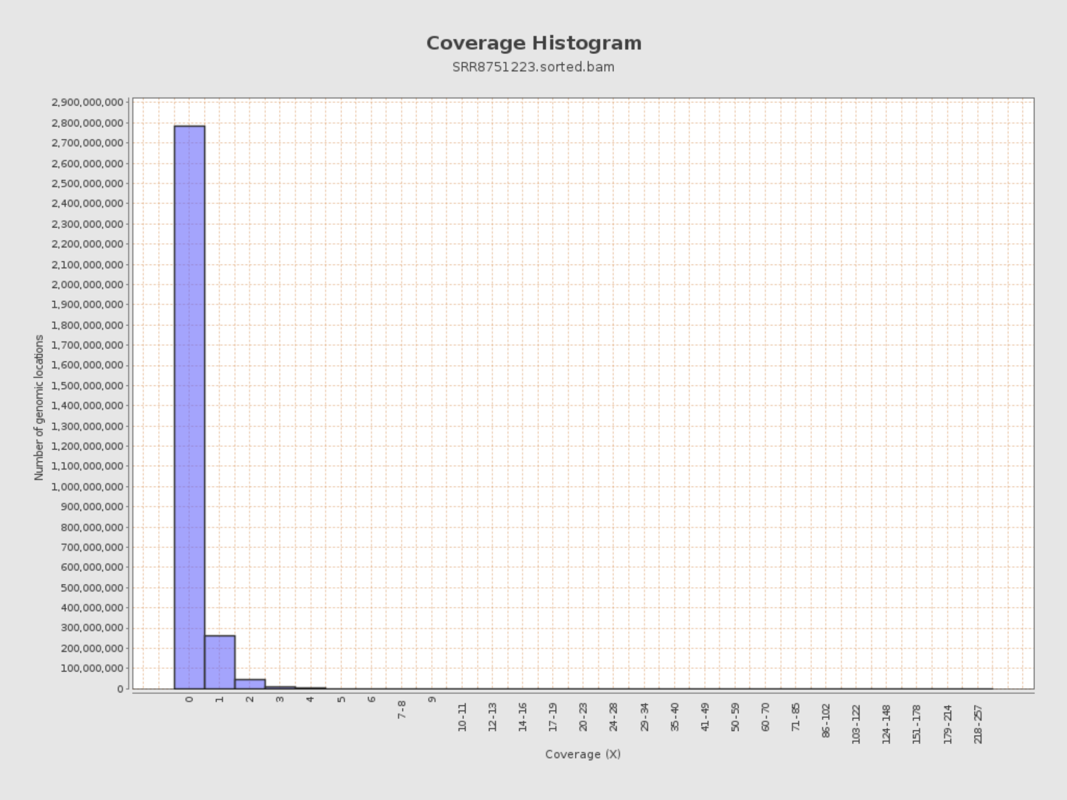
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	46487160	0.1865	0.5561
chr2	243199373	28845757	0.1186	0.3911
chr3	198022430	26293478	0.1328	0.4134
chr4	191154276	17007352	0.089	0.3351
chr5	180915260	31401571	0.1736	0.4777
chr6	171115067	22082547	0.1291	0.4159
chr7	159138663	21179189	0.1331	0.4146

chr8	146364022	18458919	0.1261	0.4029
chr9	141213431	16414119	0.1162	0.3907
chr10	135534747	17950978	0.1324	0.4326
chr11	135006516	17698185	0.1311	0.4162
chr12	133851895	20747769	0.155	0.4471
chr13	115169878	11001254	0.0955	0.3508
chr14	107349540	8451420	0.0787	0.3153
chr15	102531392	9678273	0.0944	0.3513
chr16	90354753	9446017	0.1045	0.3697
chr17	81195210	10980756	0.1352	0.4243
chr18	78077248	7828808	0.1003	0.369
chr19	59128983	6030649	0.102	0.3892
chr20	63025520	6688828	0.1061	0.3715
chr21	48129895	4774894	0.0992	0.3647
chr22	51304566	4468396	0.0871	0.3397
chrMT	16571	376036	22.6924	11.6326
chrX	155270560	16213701	0.1044	0.3655
chrY	59373566	322514	0.0054	0.1022

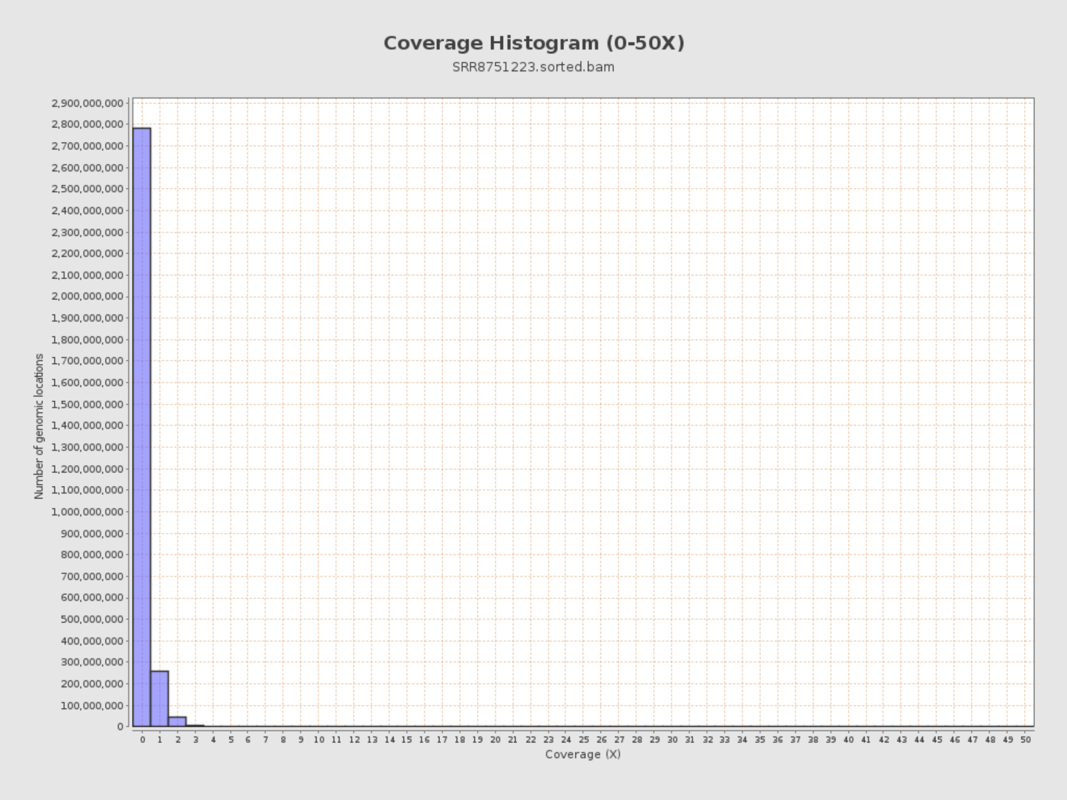
3. Results : Coverage across reference



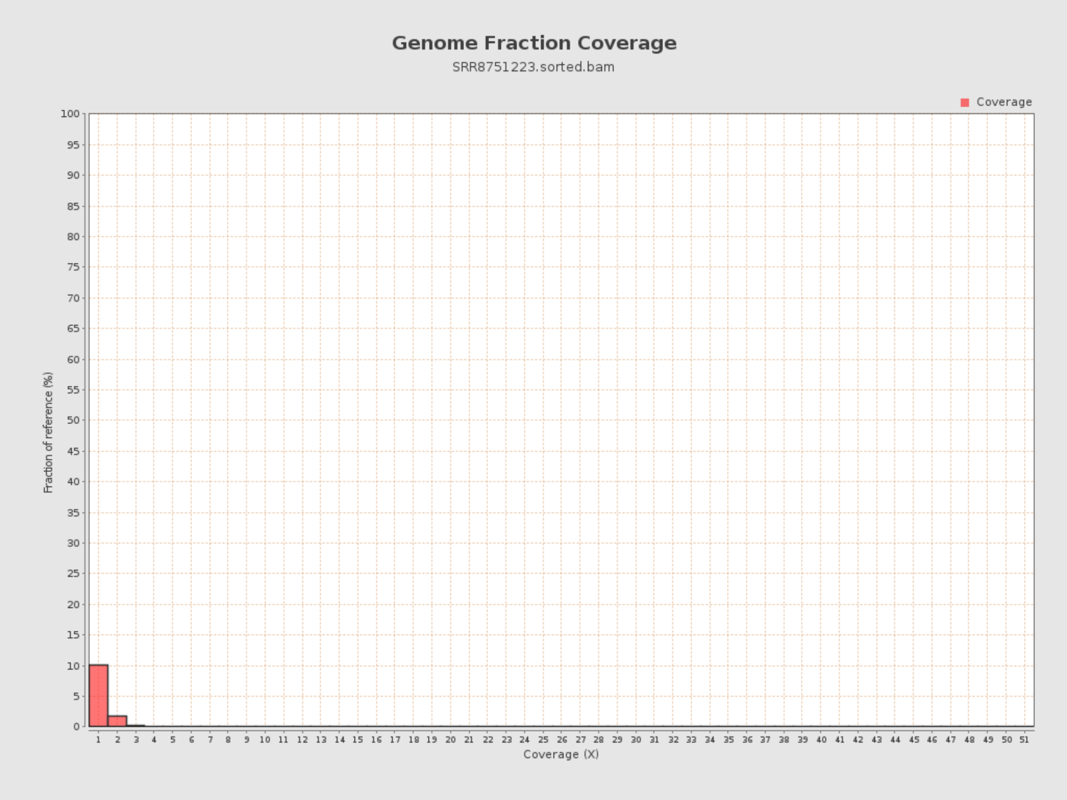
4. Results : Coverage Histogram



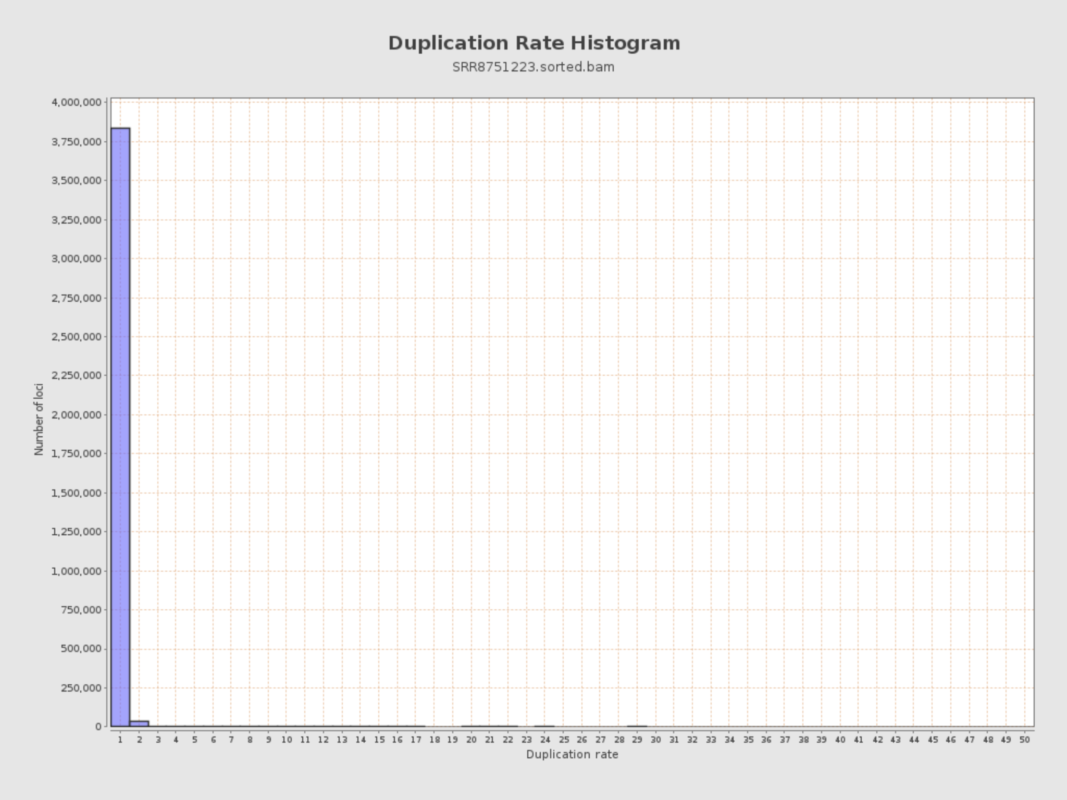
5. Results : Coverage Histogram (0-50X)



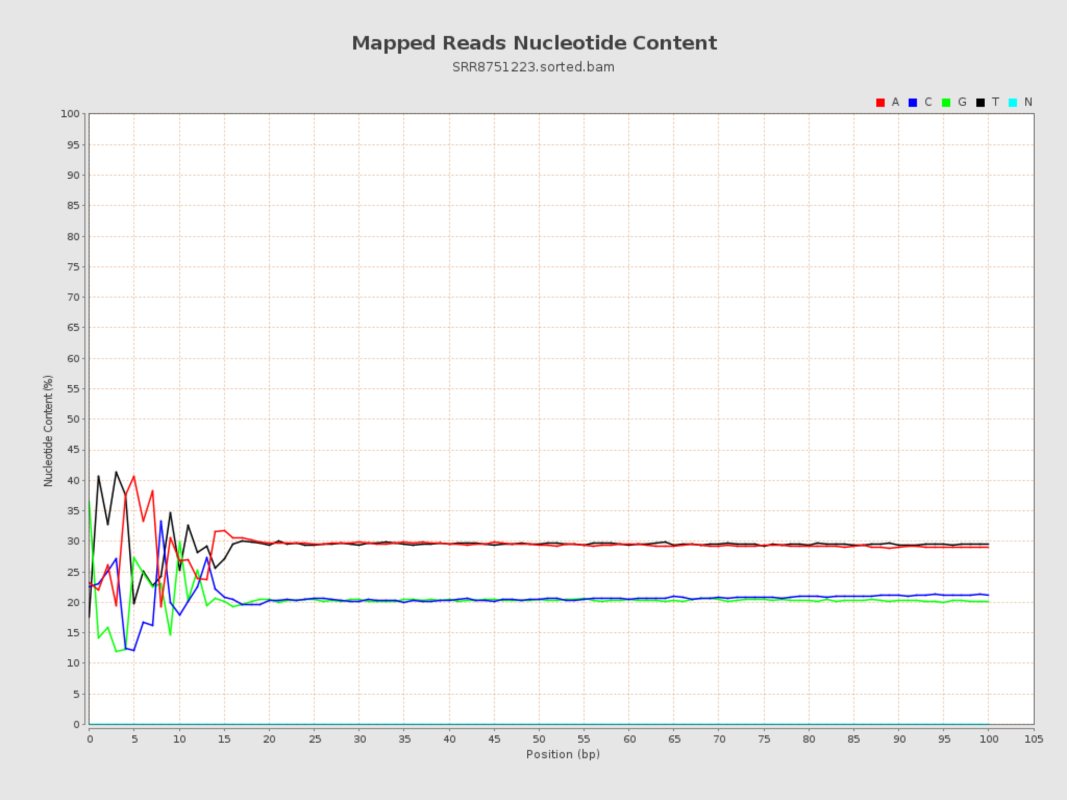
6. Results : Genome Fraction Coverage



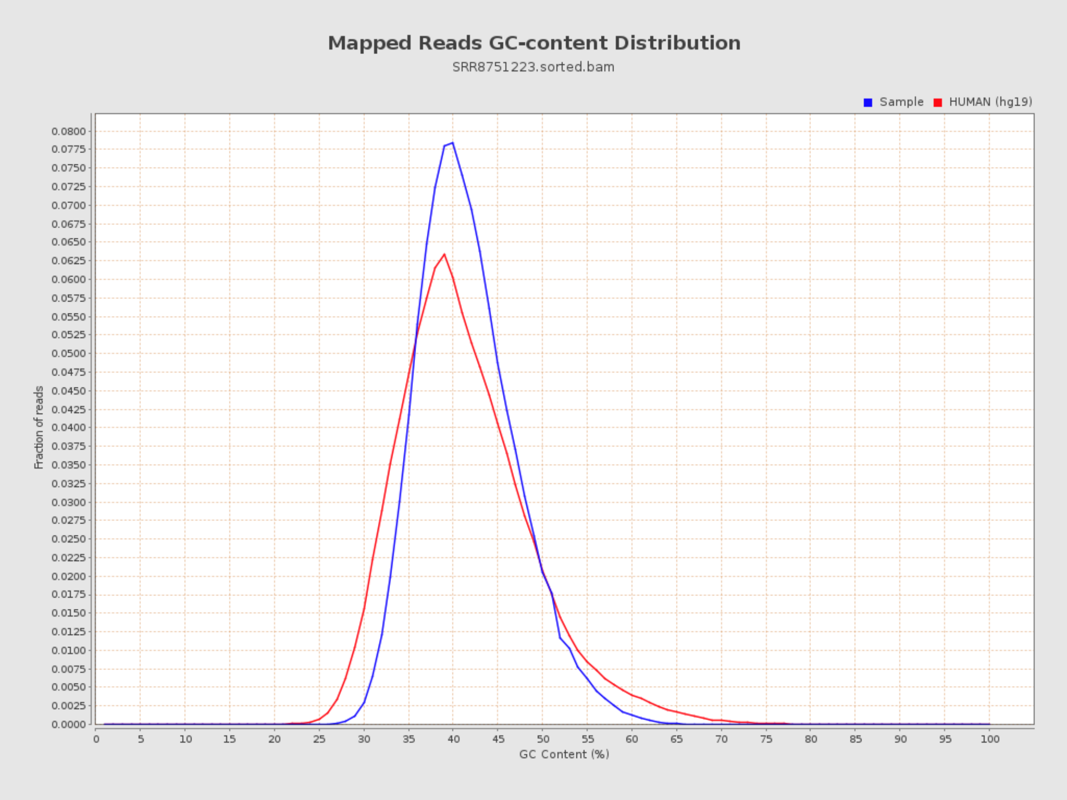
7. Results : Duplication Rate Histogram



8. Results : Mapped Reads Nucleotide Content

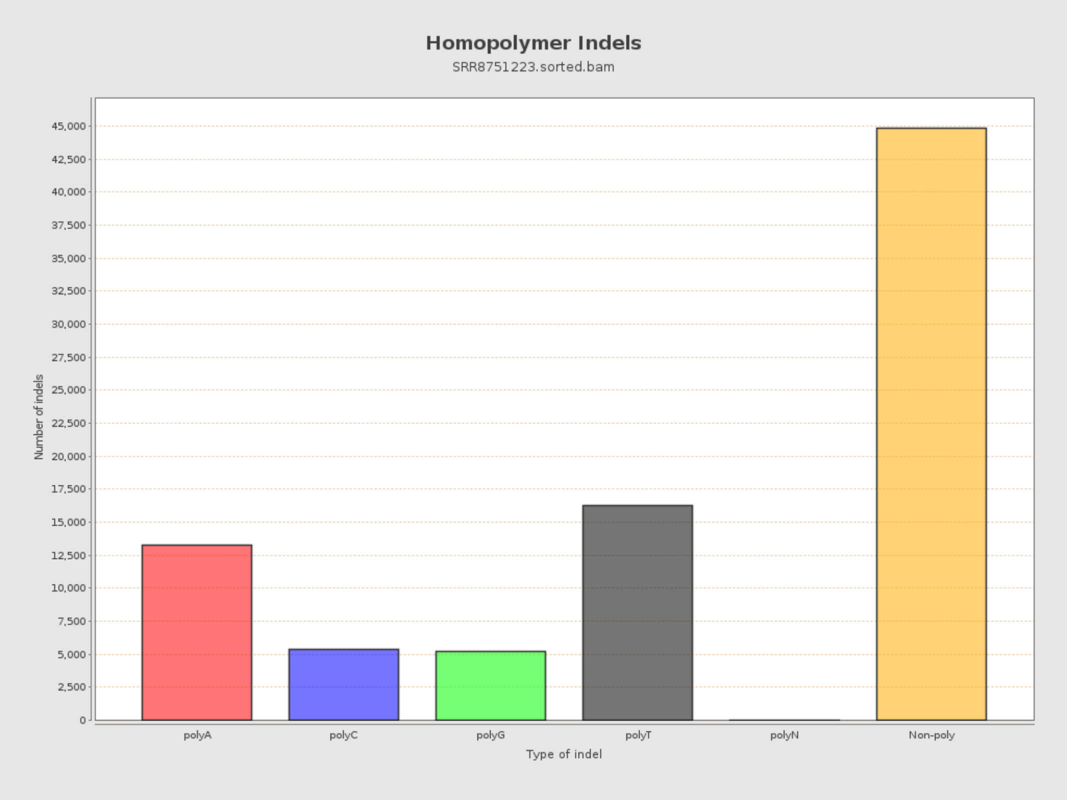


9. Results : Mapped Reads GC-content Distribution

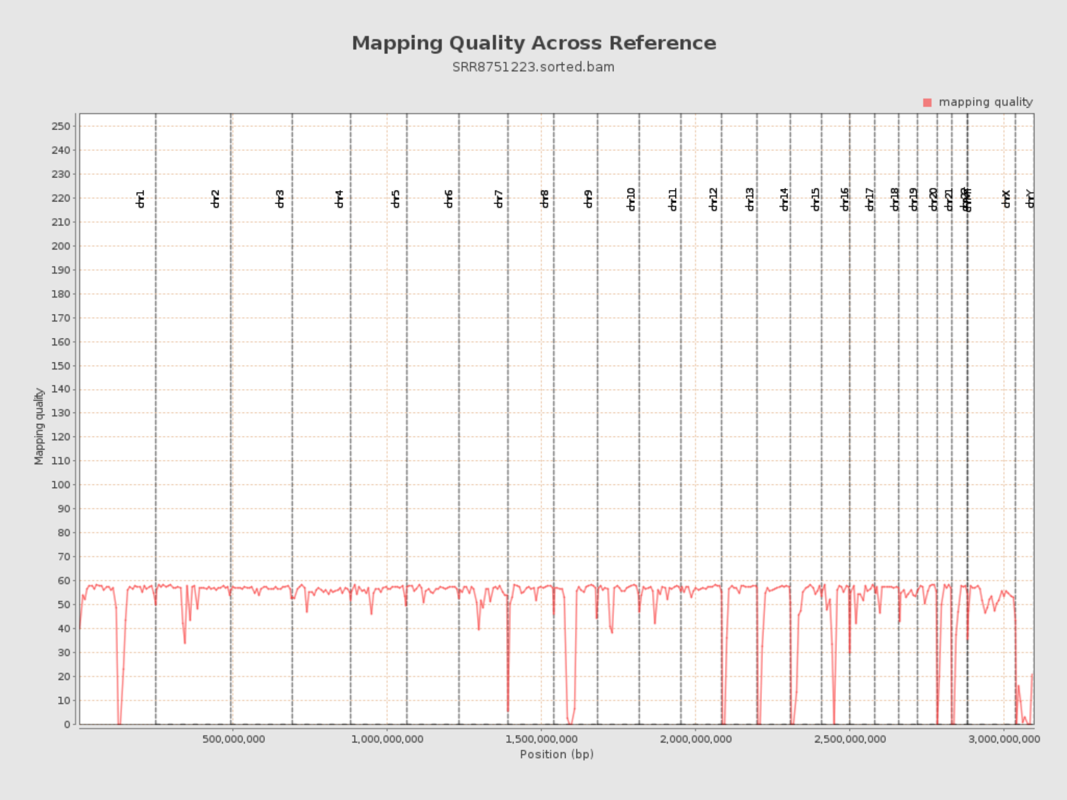


10. Results : Mapped Reads Clipping Profile

11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram