Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 20:42:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8751210.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_SRR8751210 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8751210.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 20:42:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8751210.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,191,034
Mapped reads	5,624,308 / 90.85%
Unmapped reads	566,726 / 9.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	317,517 / 5.13%
Read min/max/mean length	30 / 101 / 103.12
Duplicated reads (estimated)	206,121 / 3.33%
Duplication rate	2.13%
Clipped reads	1,425,378 / 23.02%

2.2. ACGT Content

Number/percentage of A's	160,120,244 / 29.06%
Number/percentage of C's	114,924,496 / 20.86%
Number/percentage of T's	161,223,735 / 29.26%
Number/percentage of G's	114,682,471 / 20.82%
Number/percentage of N's	2,988 / 0%
GC Percentage	41.67%

2.3. Coverage

Mean	0.178

Standard Deviation	1.5828

2.4. Mapping Quality

Mean Mapping Quality	51.14

2.5. Mismatches and indels

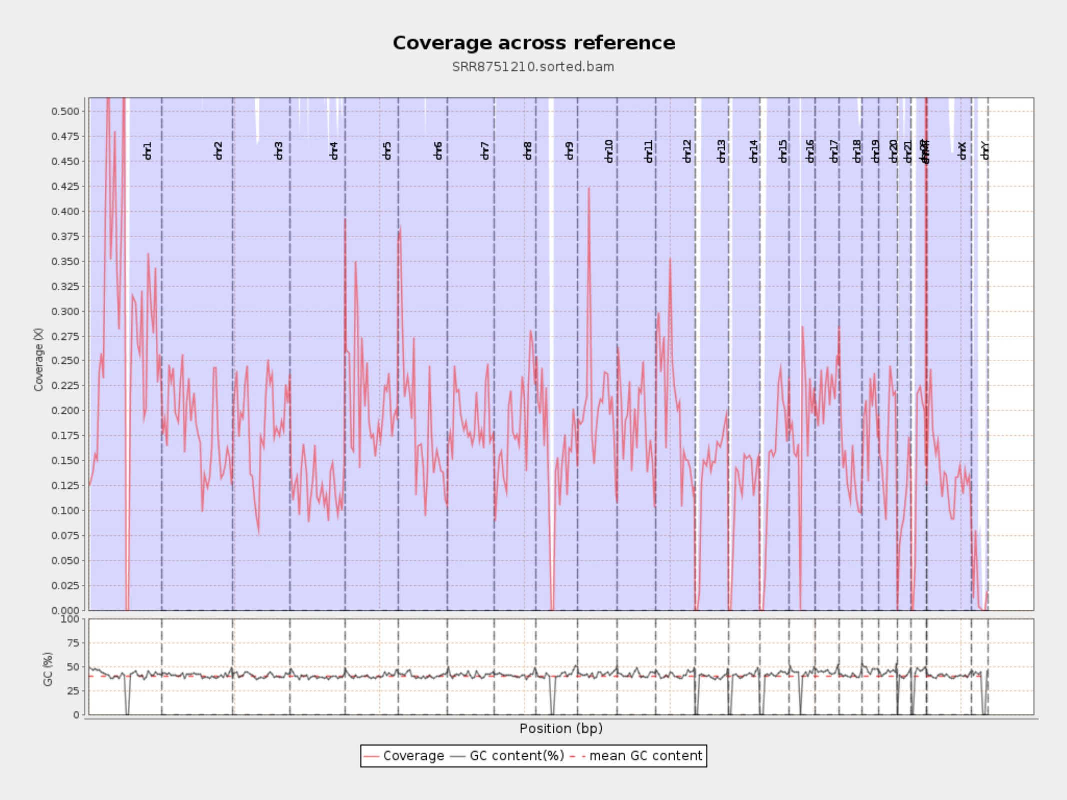
General error rate	0.49%
Mismatches	2,142,681
Insertions	392,888
Mapped reads with at least one insertion	6.69%
Deletions	84,984
Mapped reads with at least one deletion	1.48%
Homopolymer indels	53.43%

2.6. Chromosome stats

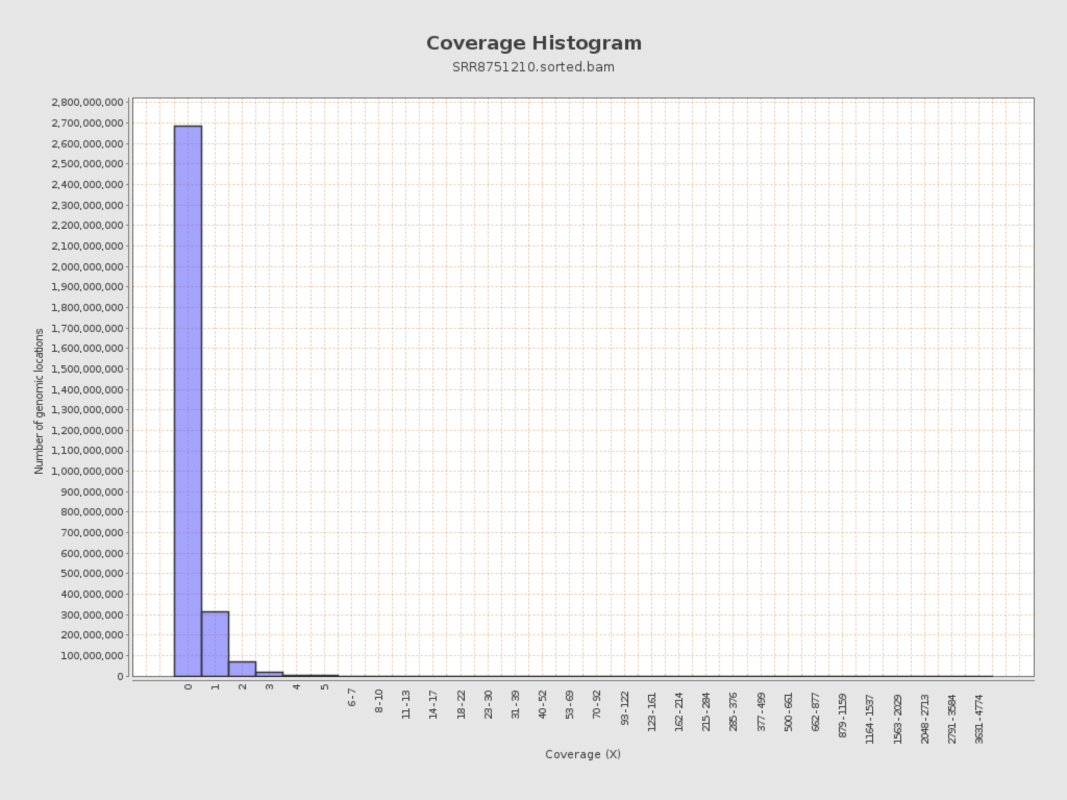
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	69846405	0.2802	4.464
chr2	243199373	44534456	0.1831	0.7402
chr3	198022430	36804610	0.1859	0.6144
chr4	191154276	23432184	0.1226	0.5758
chr5	180915260	38295256	0.2117	0.5651
chr6	171115067	32410275	0.1894	0.9426
chr7	159138663	30377027	0.1909	0.9195

chr8	146364022	26814677	0.1832	0.6382
chr9	141213431	21054500	0.1491	0.8429
chr10	135534747	28232298	0.2083	2.3063
chr11	135006516	25139998	0.1862	0.7999
chr12	133851895	27858020	0.2081	0.5659
chr13	115169878	15239631	0.1323	0.4447
chr14	107349540	12449283	0.116	0.4427
chr15	102531392	14771353	0.1441	0.4623
chr16	90354753	16331922	0.1808	1.0433
chr17	81195210	17959889	0.2212	0.7783
chr18	78077248	11051049	0.1415	1.5136
chr19	59128983	11494609	0.1944	3.0094
chr20	63025520	10699309	0.1698	0.5219
chr21	48129895	4815576	0.1001	0.4627
chr22	51304566	7227845	0.1409	0.4648
chrMT	16571	1313000	79.2348	27.2813
chrX	155270560	21822127	0.1405	0.5296
chrY	59373566	1167131	0.0197	0.7152

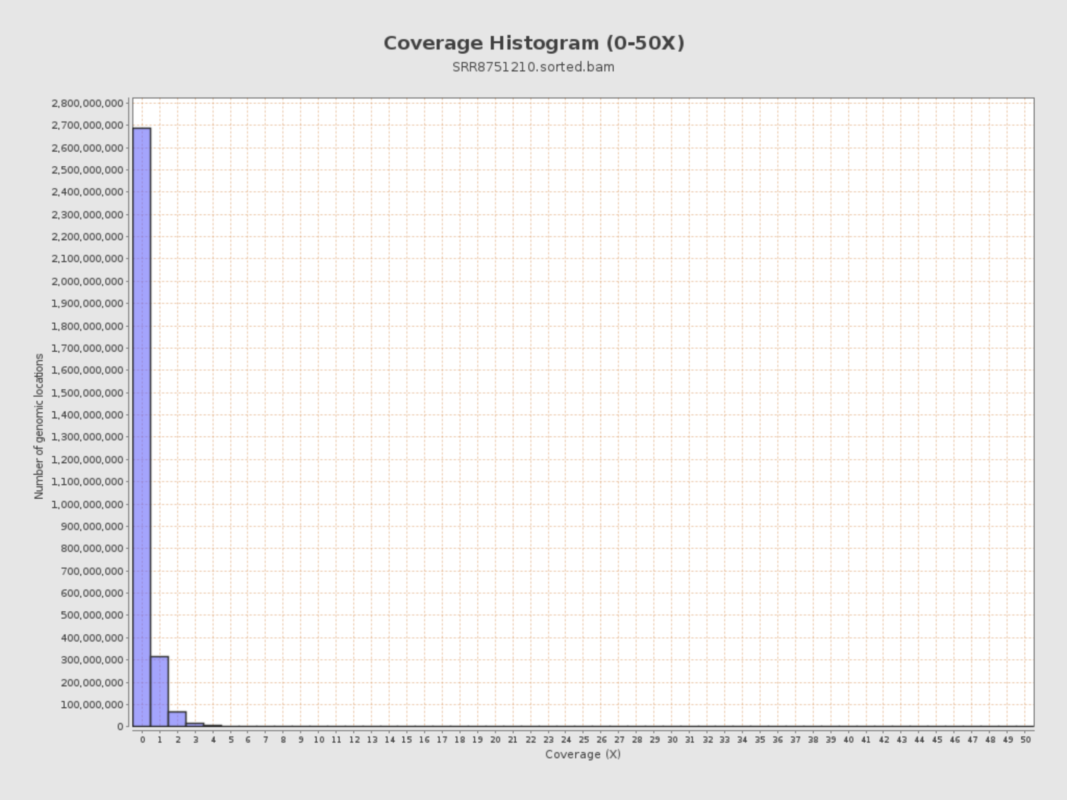
3. Results : Coverage across reference



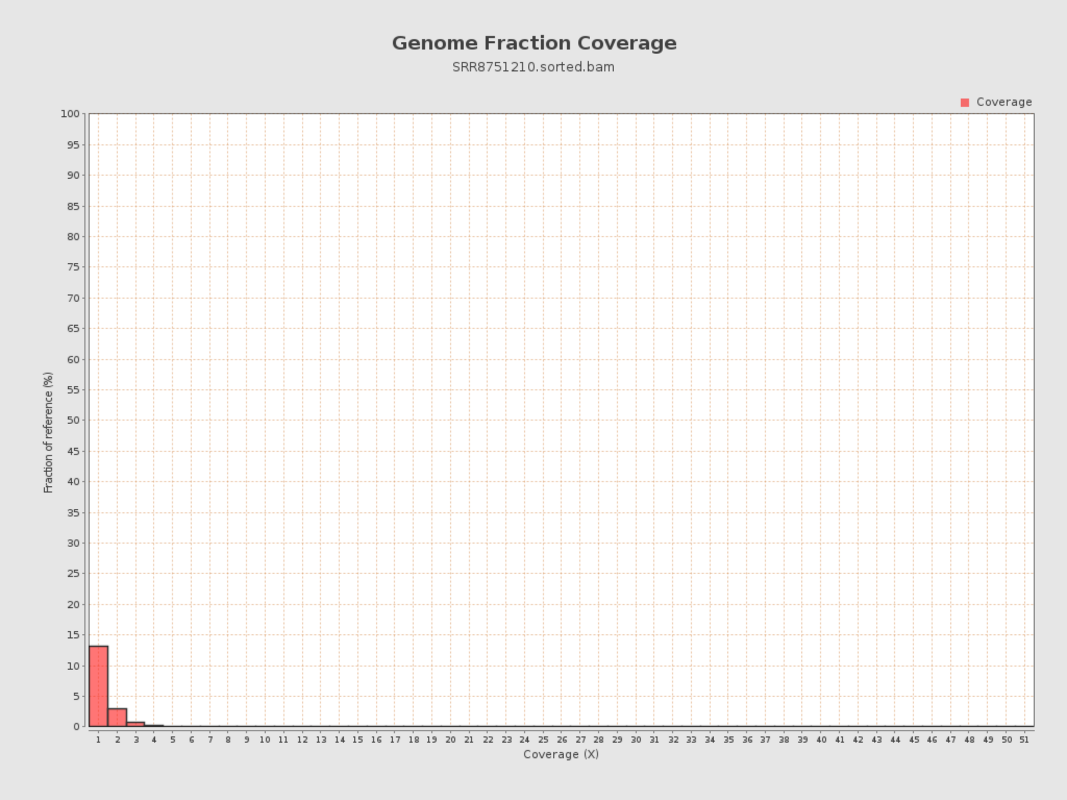
4. Results : Coverage Histogram



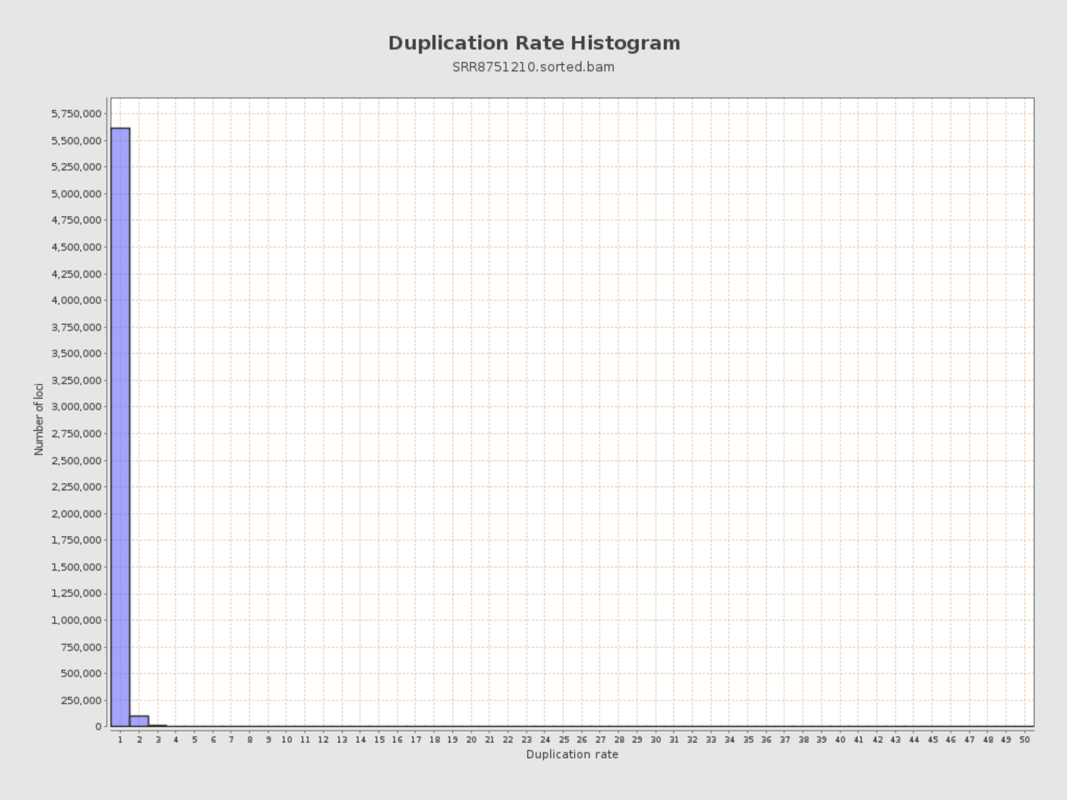
5. Results : Coverage Histogram (0-50X)



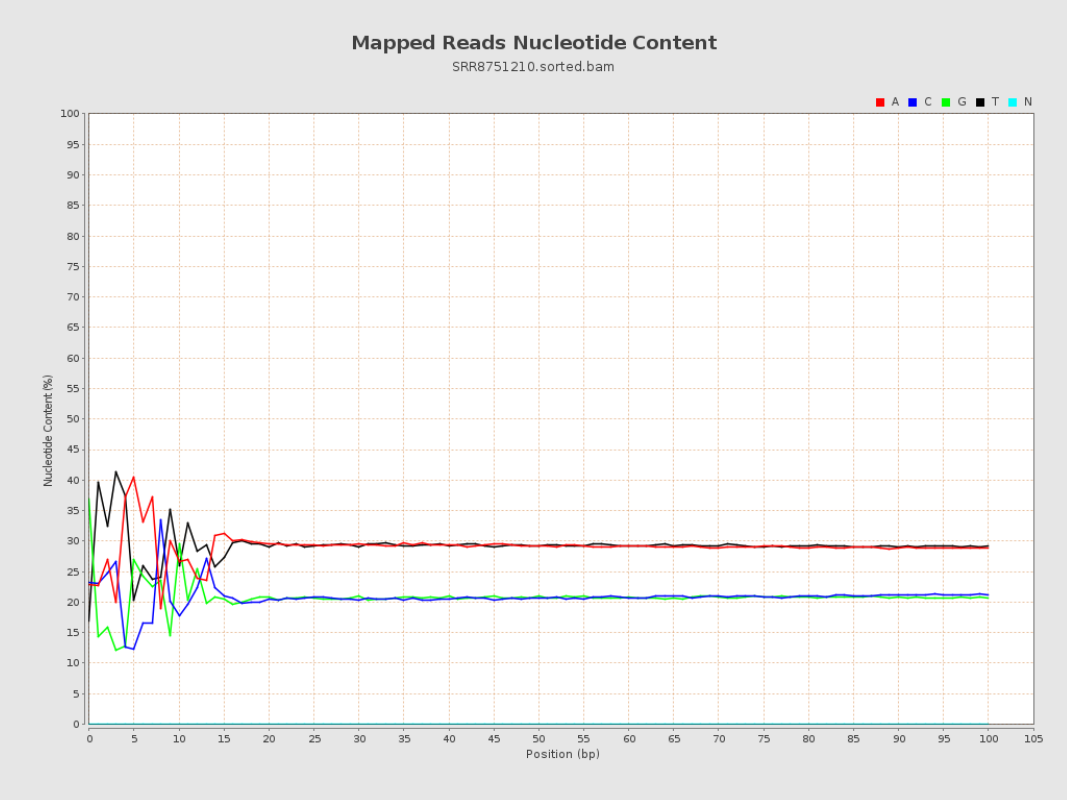
6. Results : Genome Fraction Coverage



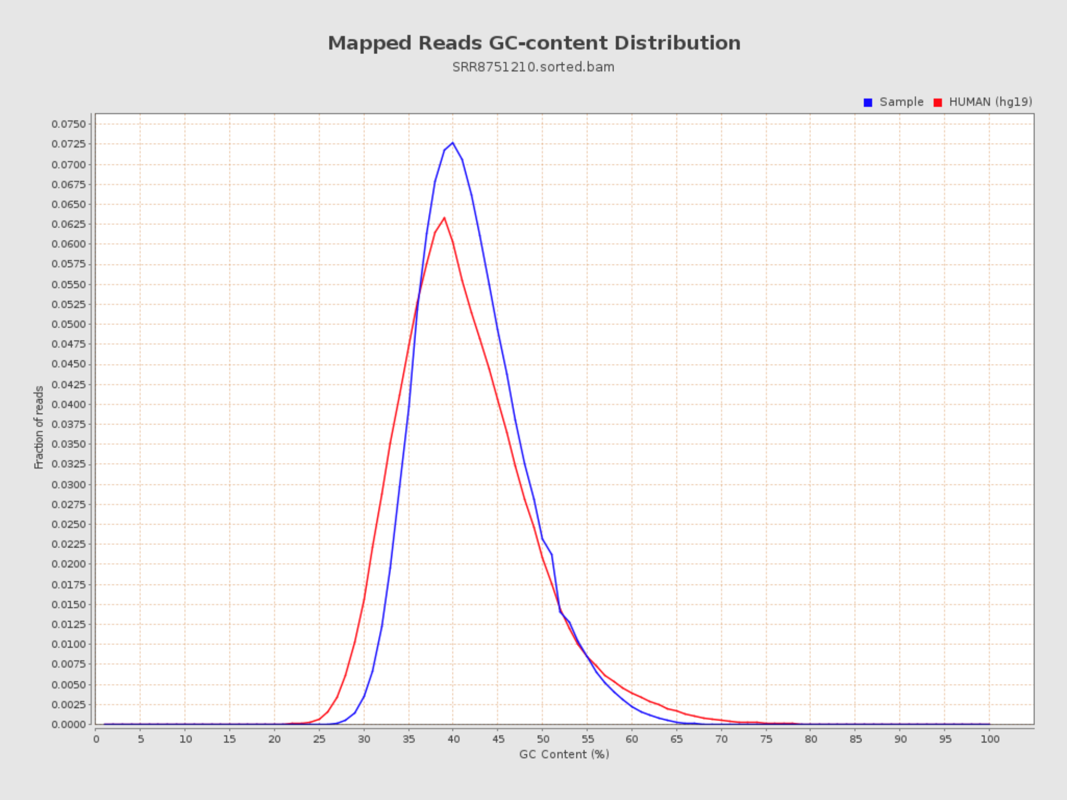
7. Results : Duplication Rate Histogram



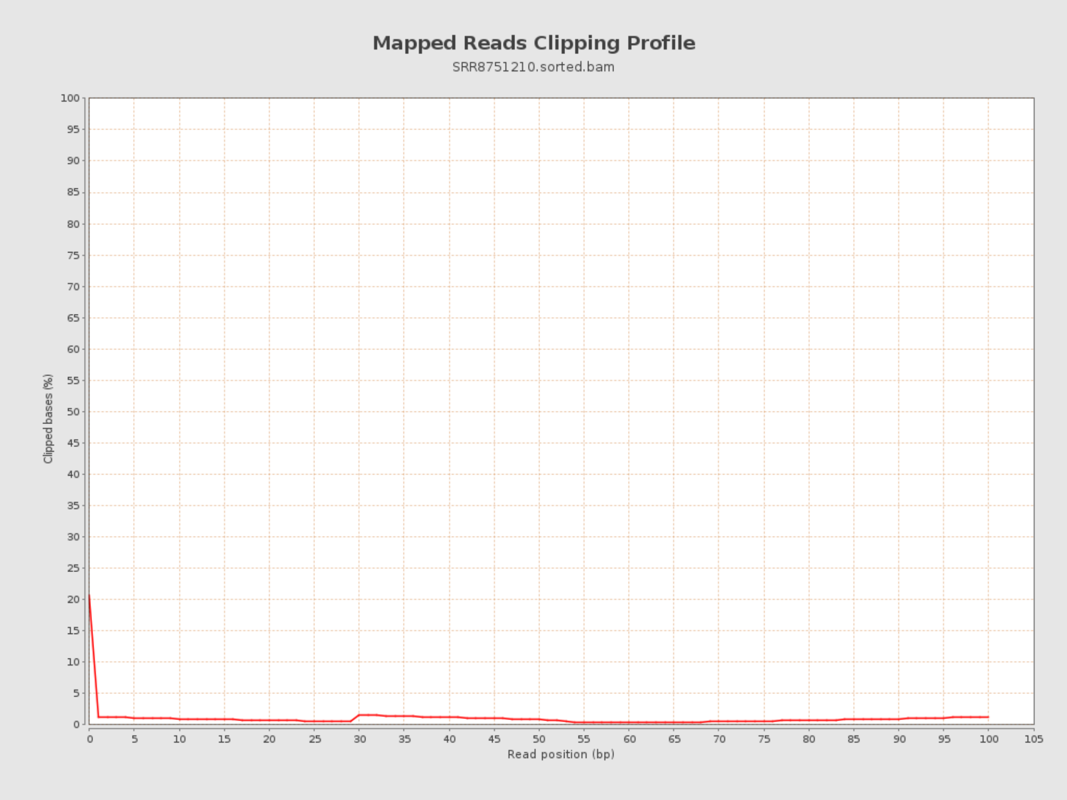
8. Results : Mapped Reads Nucleotide Content



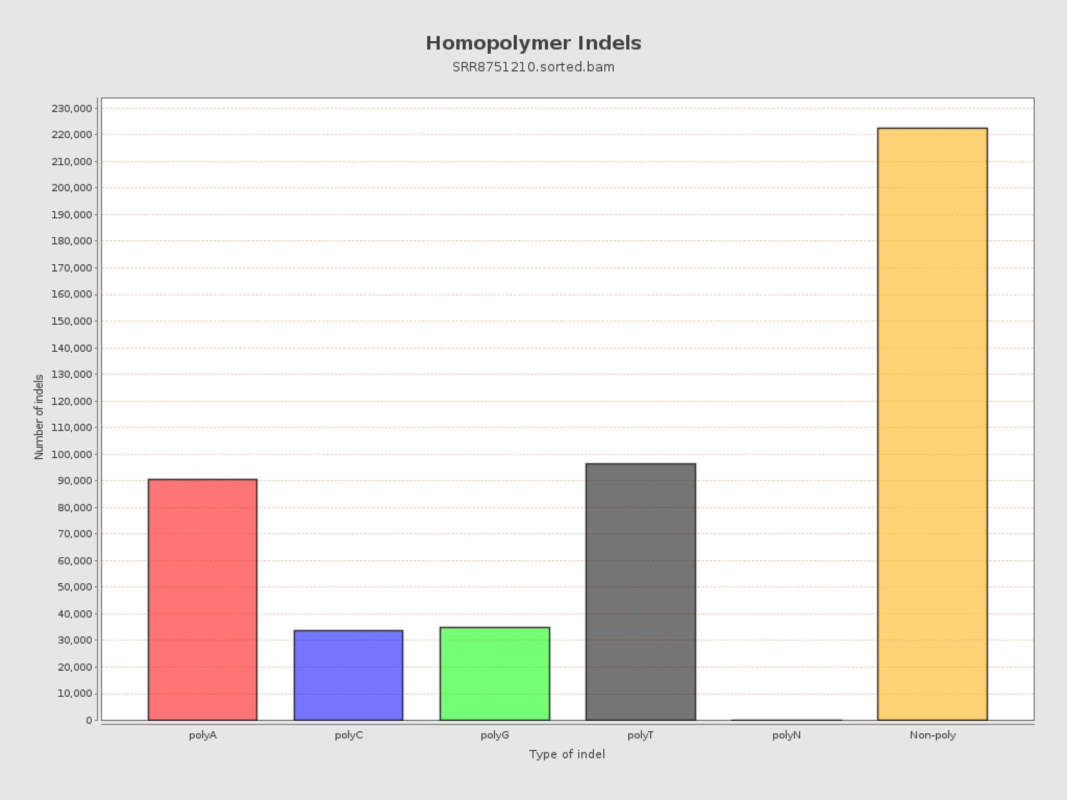
9. Results : Mapped Reads GC-content Distribution



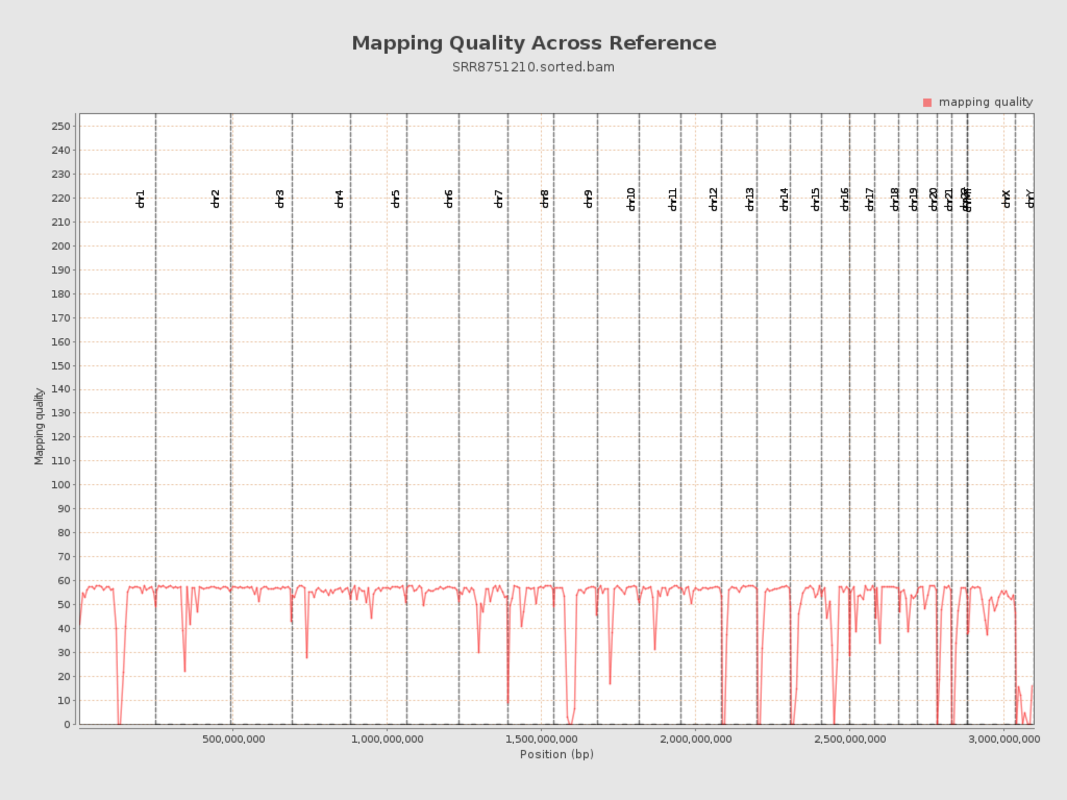
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram