Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 01:11:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525254.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_SRR10525254 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525254.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 01:11:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525254.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,518,921
Mapped reads	1,387,921 / 91.38%
Unmapped reads	131,000 / 8.62%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,353 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	44,201 / 2.91%
Duplication rate	2.25%
Clipped reads	1,391,603 / 91.62%

2.2. ACGT Content

Number/percentage of A's	19,697,589 / 24.35%
Number/percentage of C's	14,752,189 / 18.24%
Number/percentage of T's	26,417,735 / 32.66%
Number/percentage of G's	20,020,732 / 24.75%
Number/percentage of N's	1,482 / 0%
GC Percentage	42.99%

2.3. Coverage

Mean	0.0261

Standard Deviation	0.2686

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

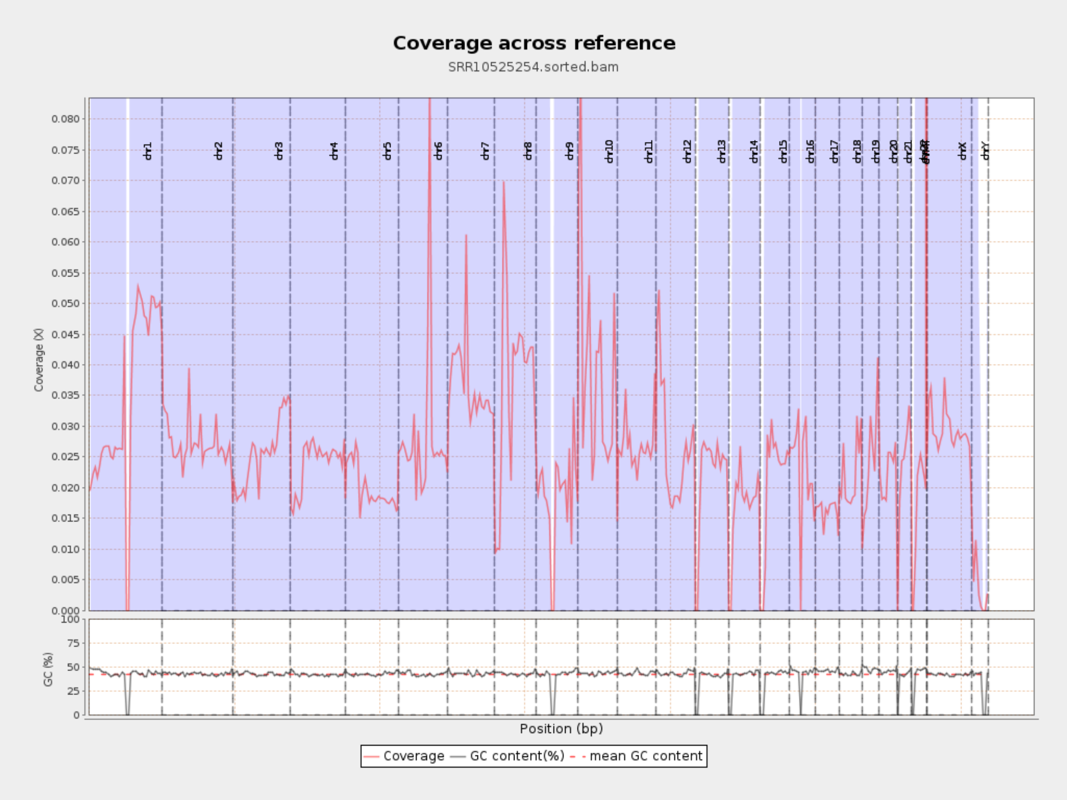
General error rate	0.52%
Mismatches	409,135
Insertions	5,342
Mapped reads with at least one insertion	0.38%
Deletions	16,899
Mapped reads with at least one deletion	1.21%
Homopolymer indels	44.98%

2.6. Chromosome stats

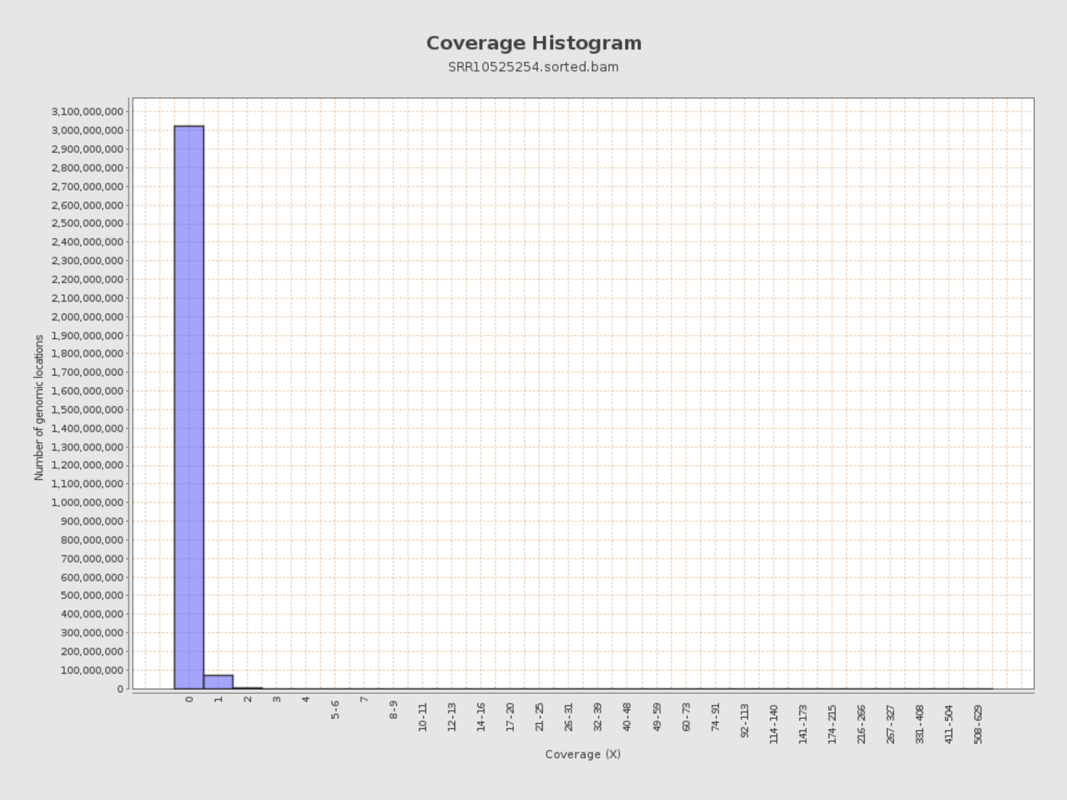
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8493757	0.0341	0.4766
chr2	243199373	6637811	0.0273	0.3177
chr3	198022430	5031684	0.0254	0.1725
chr4	191154276	4570414	0.0239	0.17
chr5	180915260	3608595	0.0199	0.1519
chr6	171115067	4903069	0.0287	0.2059
chr7	159138663	5909496	0.0371	0.4808

chr8	146364022	5347978	0.0365	0.2809
chr9	141213431	2619345	0.0185	0.1864
chr10	135534747	5359561	0.0395	0.3092
chr11	135006516	3631591	0.0269	0.2241
chr12	133851895	3581715	0.0268	0.1778
chr13	115169878	2515417	0.0218	0.16
chr14	107349540	1798918	0.0168	0.143
chr15	102531392	2142435	0.0209	0.1564
chr16	90354753	2052783	0.0227	0.1814
chr17	81195210	1312313	0.0162	0.14
chr18	78077248	1724358	0.0221	0.389
chr19	59128983	1458437	0.0247	0.3385
chr20	63025520	1394496	0.0221	0.1614
chr21	48129895	1135516	0.0236	0.1704
chr22	51304566	819758	0.016	0.1346
chrMT	16571	79873	4.82	3.4731
chrX	155270560	4560386	0.0294	0.1979
chrY	59373566	227082	0.0038	0.0979

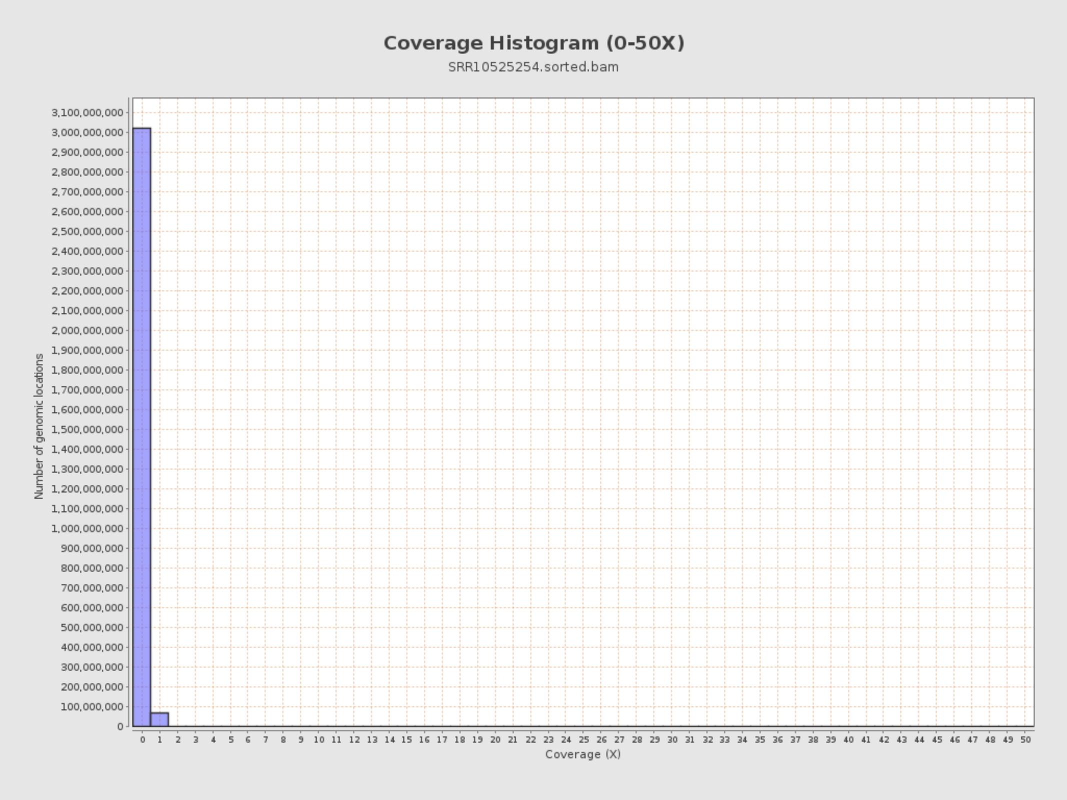
3. Results : Coverage across reference



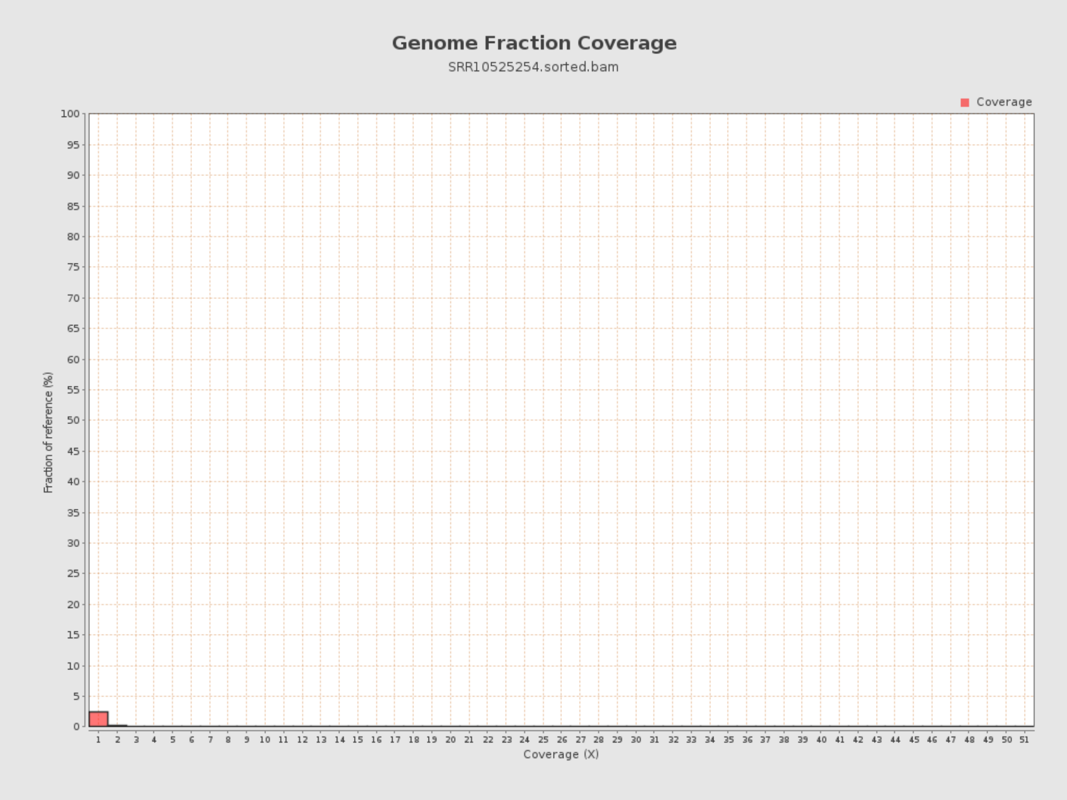
4. Results : Coverage Histogram



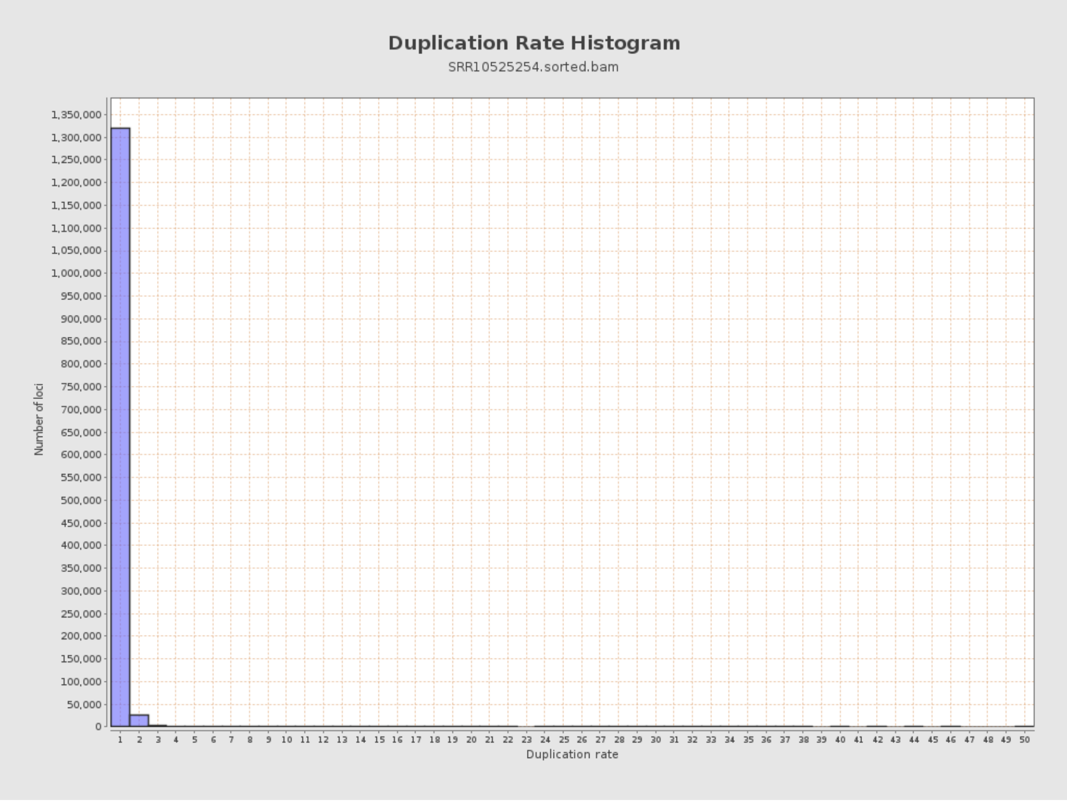
5. Results : Coverage Histogram (0-50X)



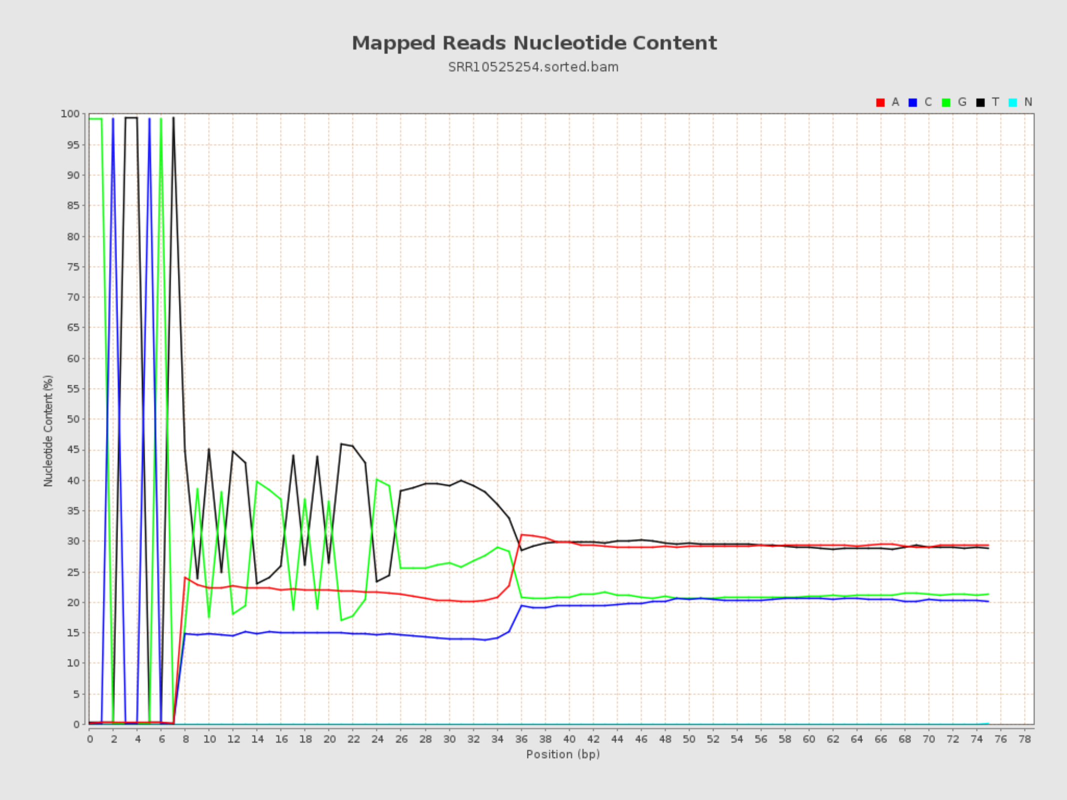
6. Results : Genome Fraction Coverage



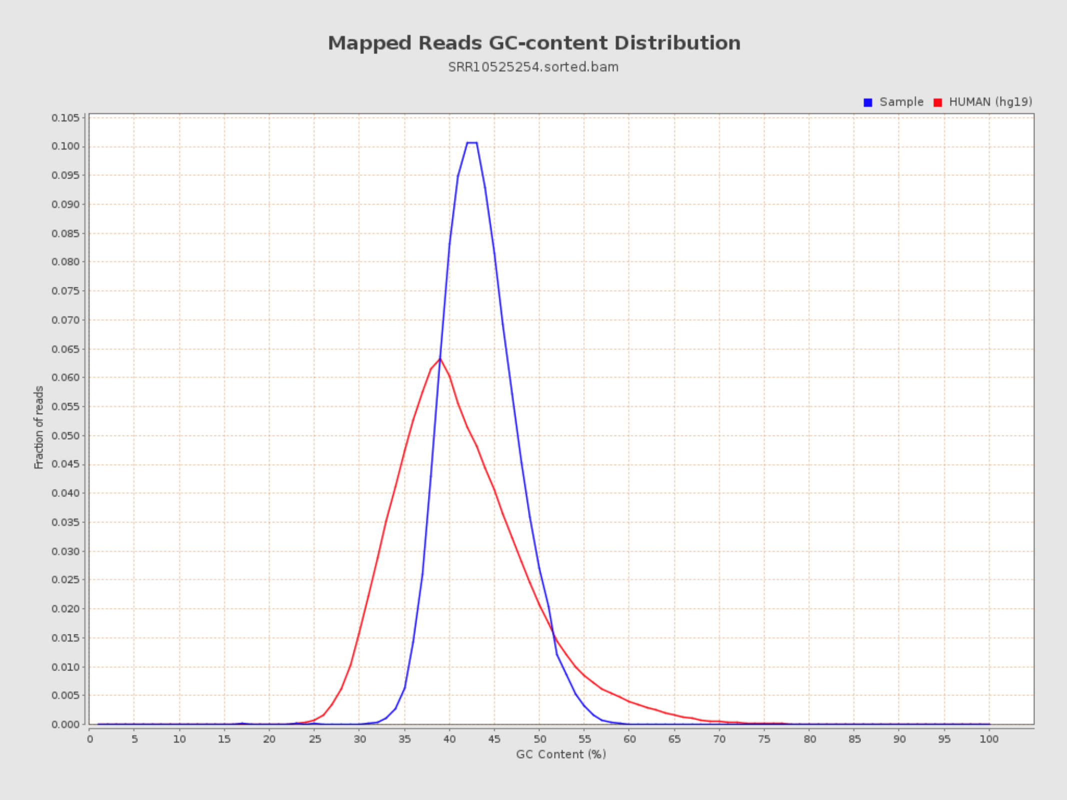
7. Results : Duplication Rate Histogram



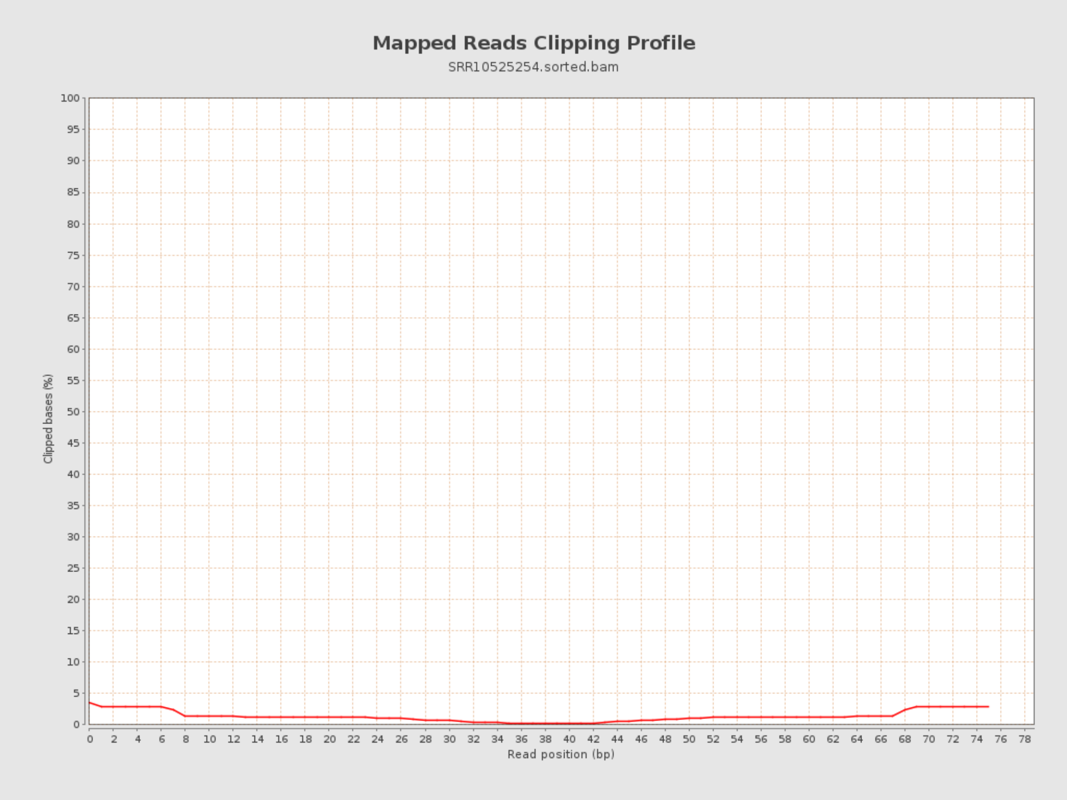
8. Results : Mapped Reads Nucleotide Content



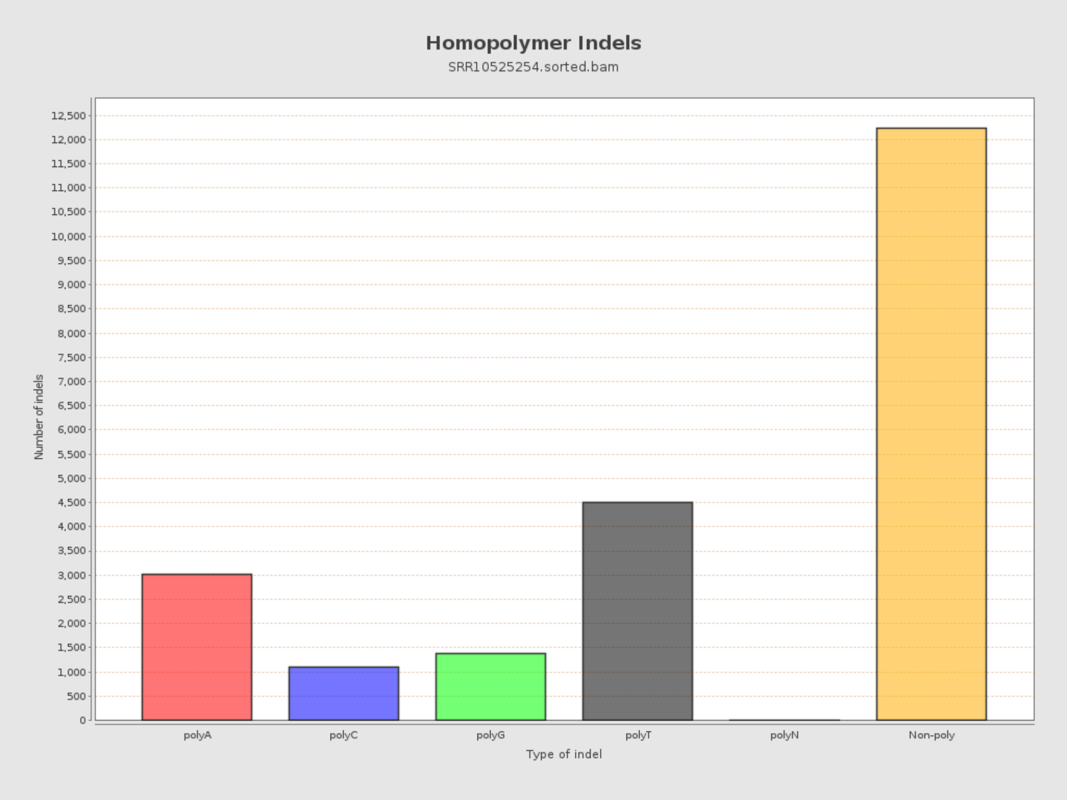
9. Results : Mapped Reads GC-content Distribution



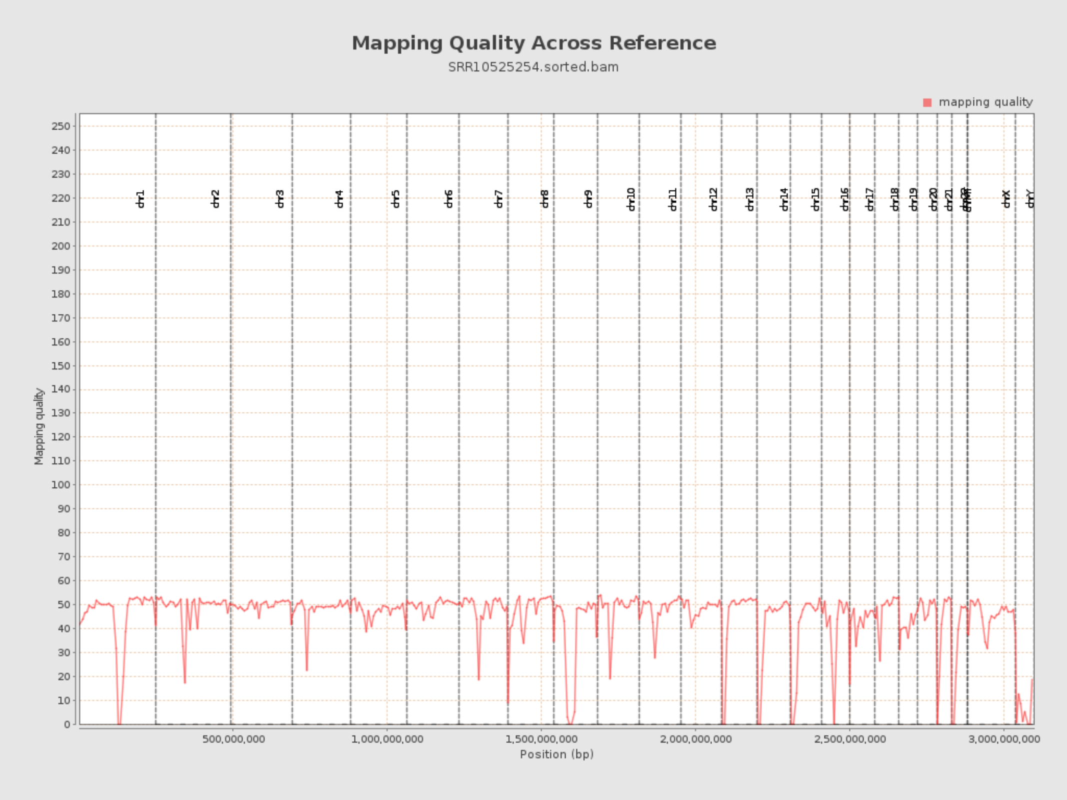
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram