Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:49:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819099.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_SRR1819099 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819099.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:49:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819099.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,337,884
Mapped reads	1,227,321 / 91.74%
Unmapped reads	110,563 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,865 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	44,756 / 3.35%
Duplication rate	2.76%
Clipped reads	1,228,961 / 91.86%

2.2. ACGT Content

Number/percentage of A's	18,450,375 / 25.67%
Number/percentage of C's	14,157,104 / 19.7%
Number/percentage of T's	22,387,791 / 31.15%
Number/percentage of G's	16,878,755 / 23.48%
Number/percentage of N's	1,097 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0232

Standard Deviation	0.2281

2.4. Mapping Quality

Mean Mapping Quality	45.22

2.5. Mismatches and indels

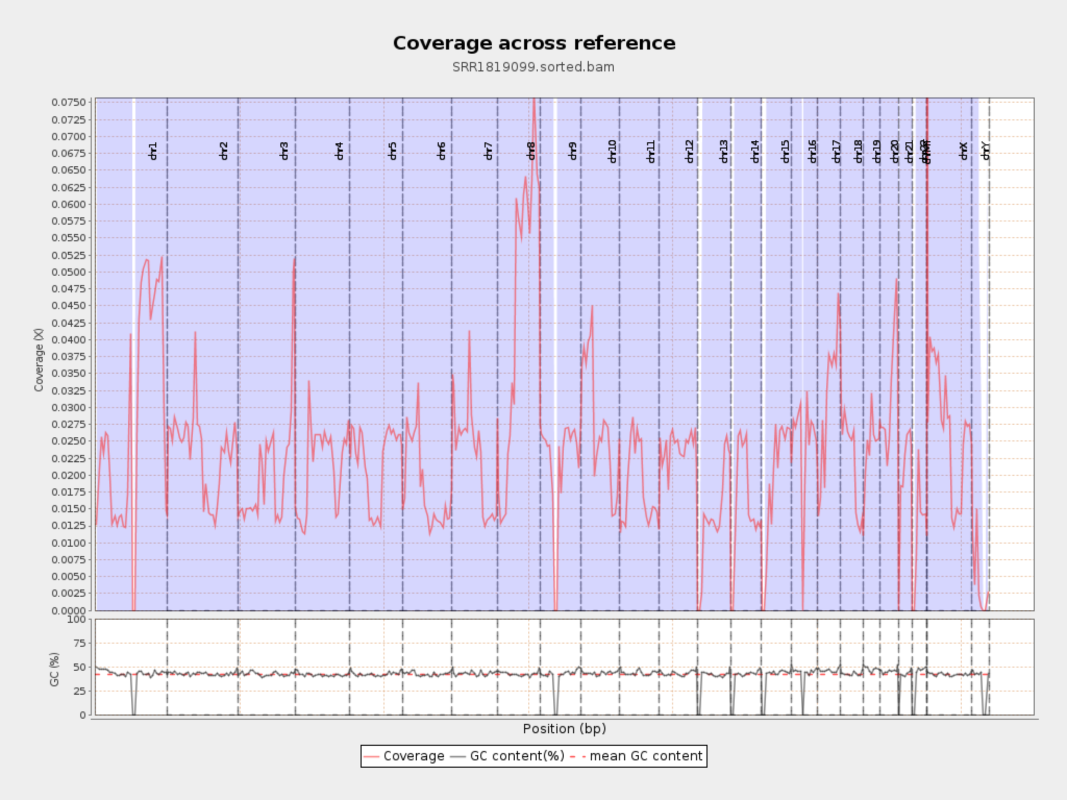
General error rate	0.52%
Mismatches	361,886
Insertions	5,099
Mapped reads with at least one insertion	0.41%
Deletions	13,808
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.79%

2.6. Chromosome stats

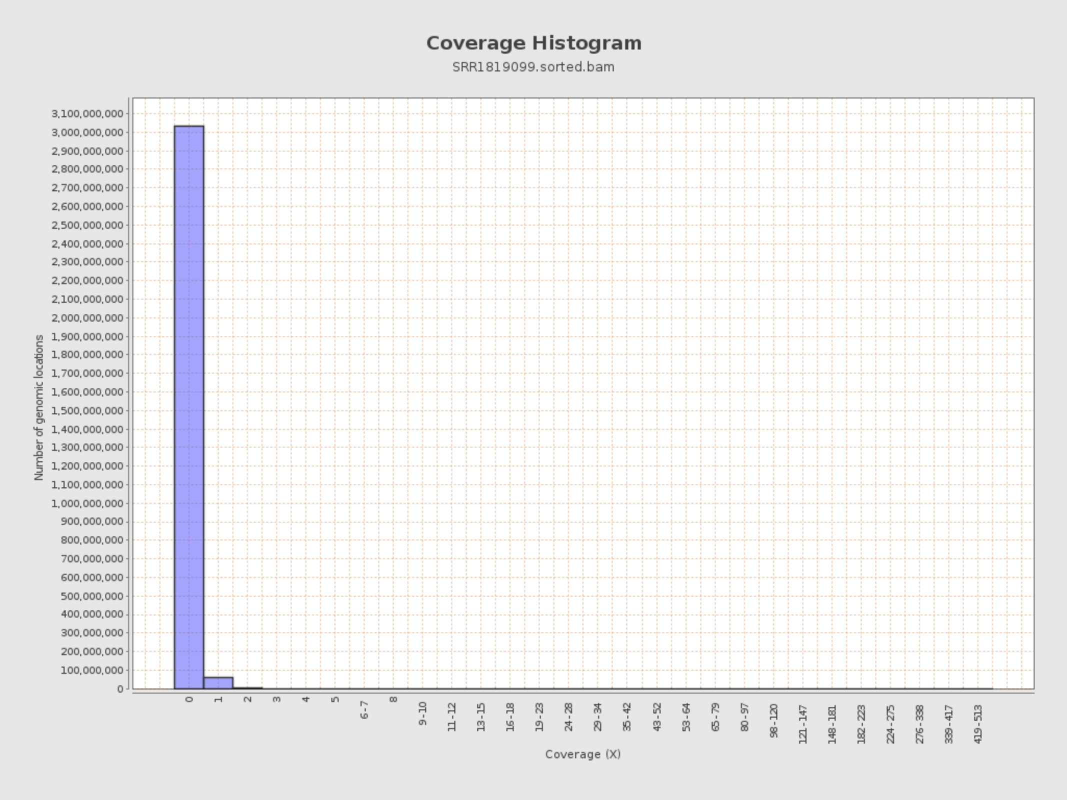
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7023972	0.0282	0.4078
chr2	243199373	5735901	0.0236	0.2566
chr3	198022430	3977357	0.0201	0.1545
chr4	191154276	4101212	0.0215	0.1781
chr5	180915260	3975081	0.022	0.1601
chr6	171115067	3116970	0.0182	0.1808
chr7	159138663	3654398	0.023	0.282

chr8	146364022	6562805	0.0448	0.2651
chr9	141213431	3043926	0.0216	0.1963
chr10	135534747	3802887	0.0281	0.2404
chr11	135006516	2482150	0.0184	0.2032
chr12	133851895	3235534	0.0242	0.1694
chr13	115169878	1577819	0.0137	0.1269
chr14	107349540	1685951	0.0157	0.1374
chr15	102531392	1934653	0.0189	0.1496
chr16	90354753	2204046	0.0244	0.1762
chr17	81195210	2523105	0.0311	0.1987
chr18	78077248	1705063	0.0218	0.3354
chr19	59128983	1456794	0.0246	0.2775
chr20	63025520	2039873	0.0324	0.1966
chr21	48129895	989540	0.0206	0.1688
chr22	51304566	601940	0.0117	0.116
chrMT	16571	8426	0.5085	0.8618
chrX	155270560	4211785	0.0271	0.1917
chrY	59373566	247018	0.0042	0.132

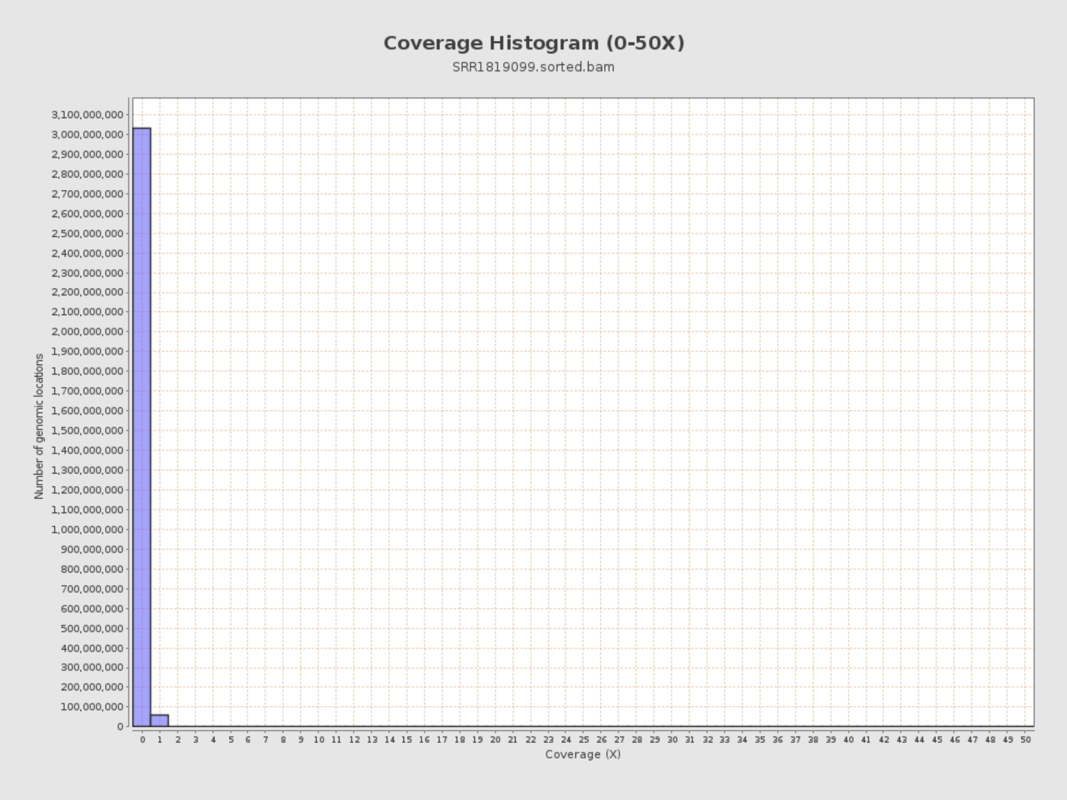
3. Results : Coverage across reference



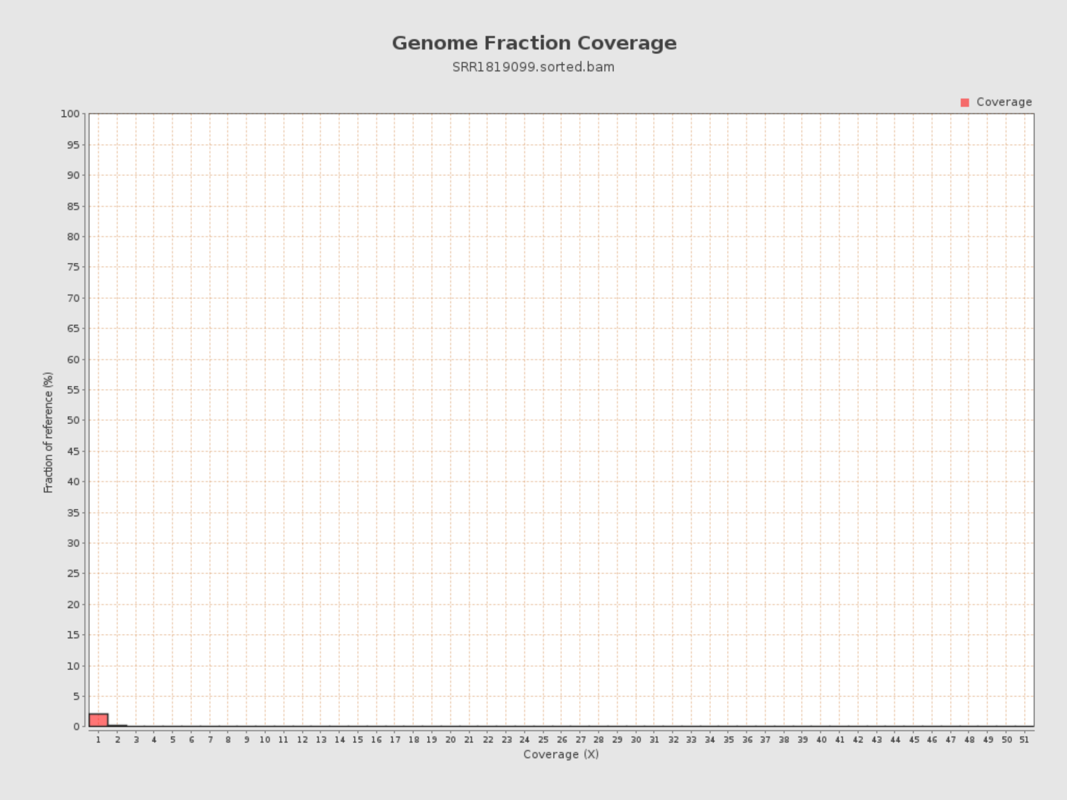
4. Results : Coverage Histogram



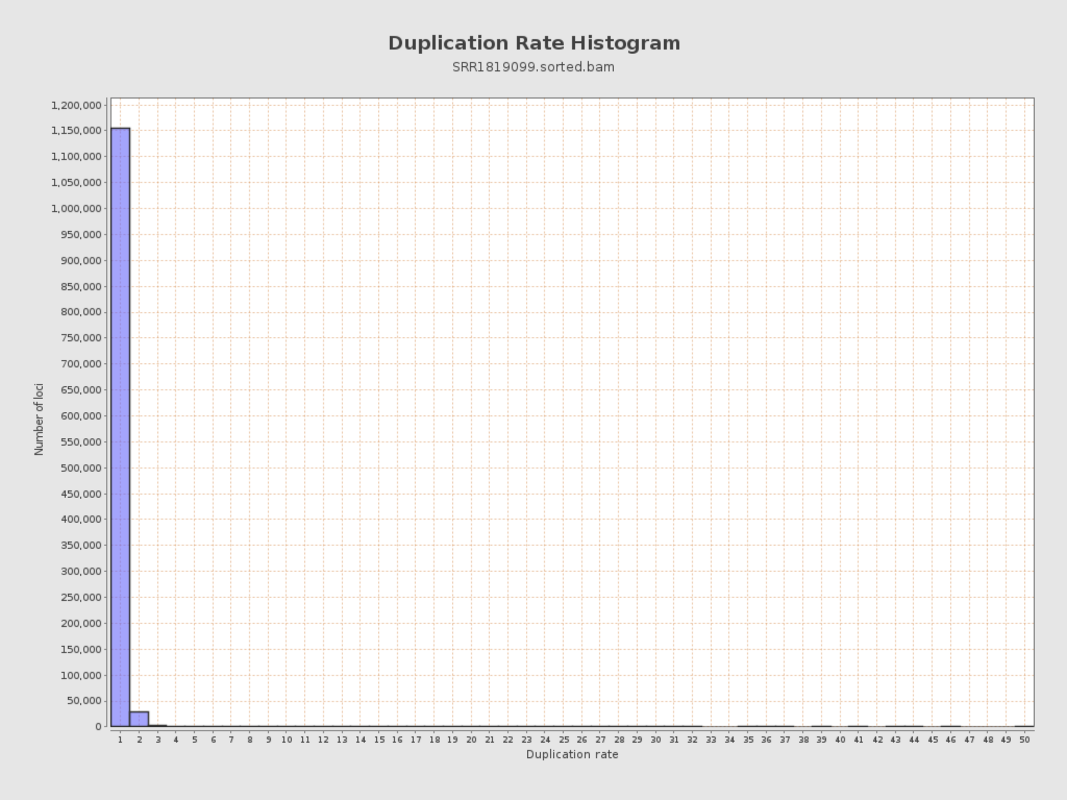
5. Results : Coverage Histogram (0-50X)



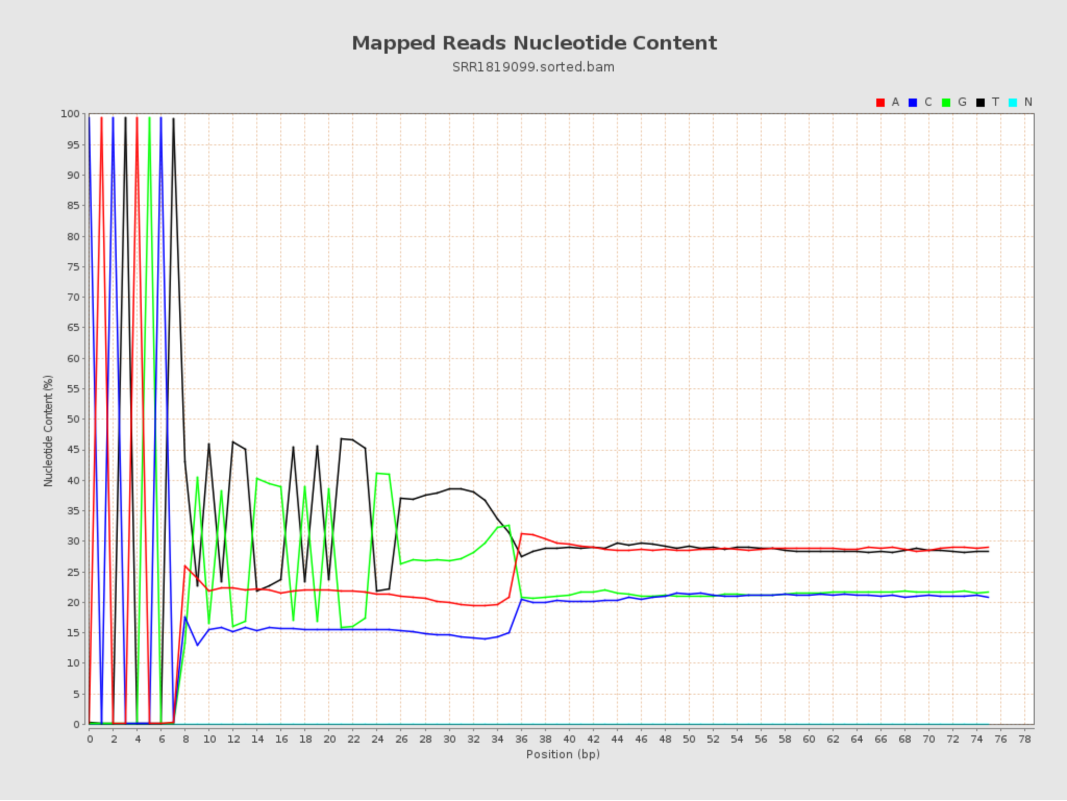
6. Results : Genome Fraction Coverage



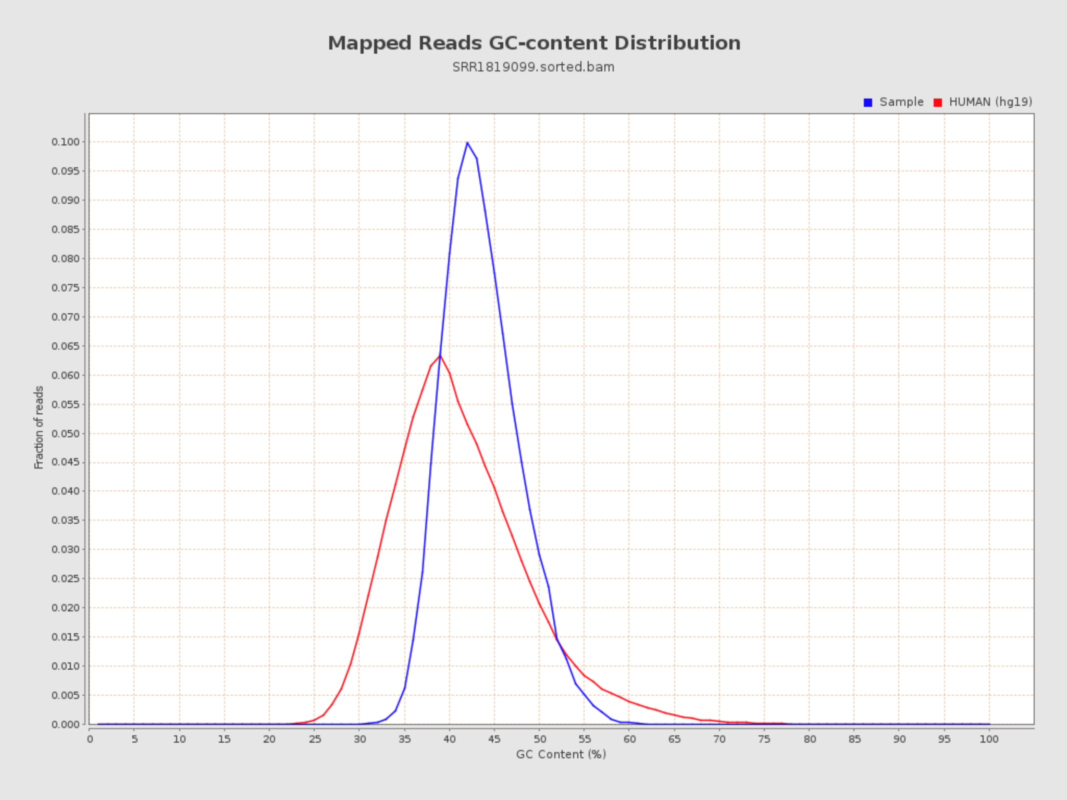
7. Results : Duplication Rate Histogram



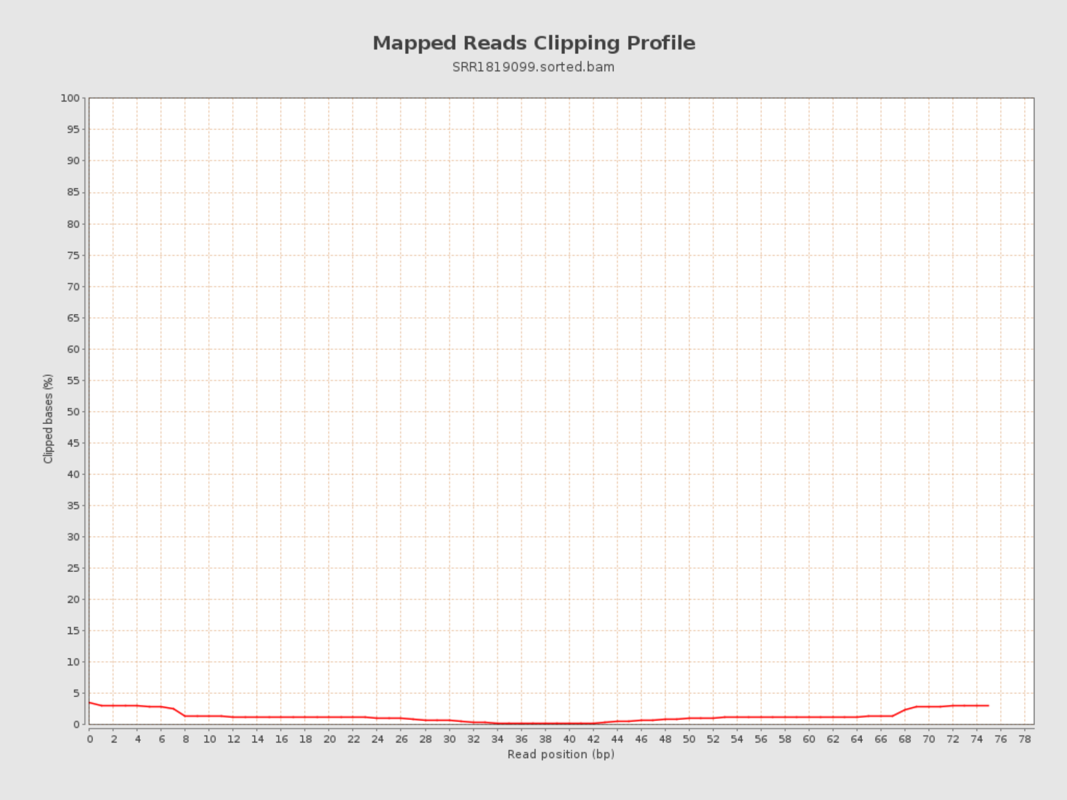
8. Results : Mapped Reads Nucleotide Content



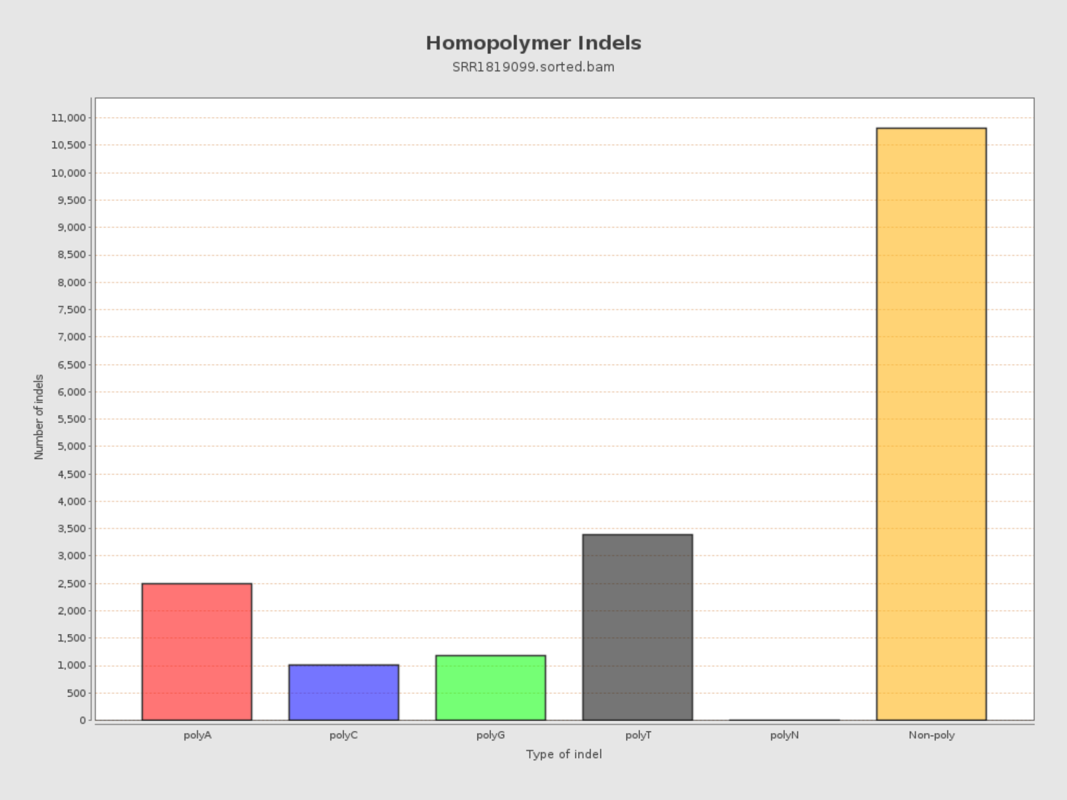
9. Results : Mapped Reads GC-content Distribution



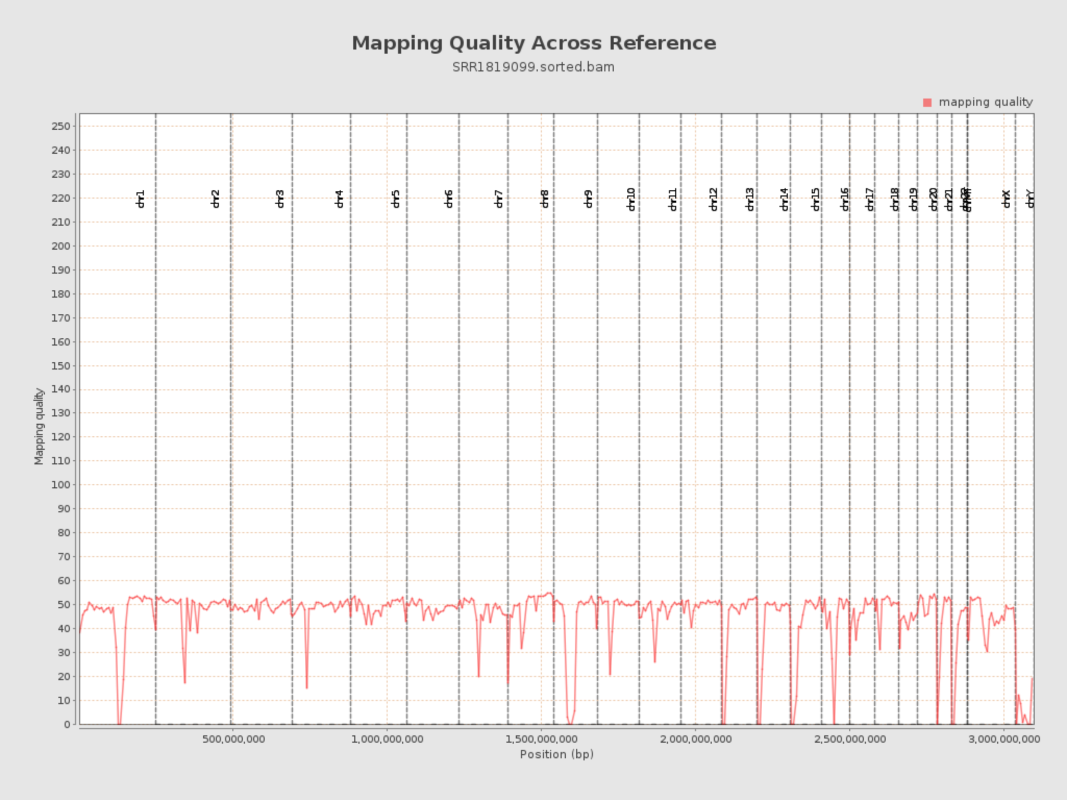
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram