Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 14:54:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525051.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_SRR10525051 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525051.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 14:54:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525051.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	495,207
Mapped reads	424,526 / 85.73%
Unmapped reads	70,681 / 14.27%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,117 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	16,181 / 3.27%
Duplication rate	3.25%
Clipped reads	424,476 / 85.72%

2.2. ACGT Content

Number/percentage of A's	6,449,119 / 26.03%
Number/percentage of C's	4,317,510 / 17.43%
Number/percentage of T's	7,908,583 / 31.92%
Number/percentage of G's	6,096,810 / 24.61%
Number/percentage of N's	2,476 / 0.01%
GC Percentage	42.04%

2.3. Coverage

Mean	0.008

Standard Deviation	0.1128

2.4. Mapping Quality

Mean Mapping Quality	46.38

2.5. Mismatches and indels

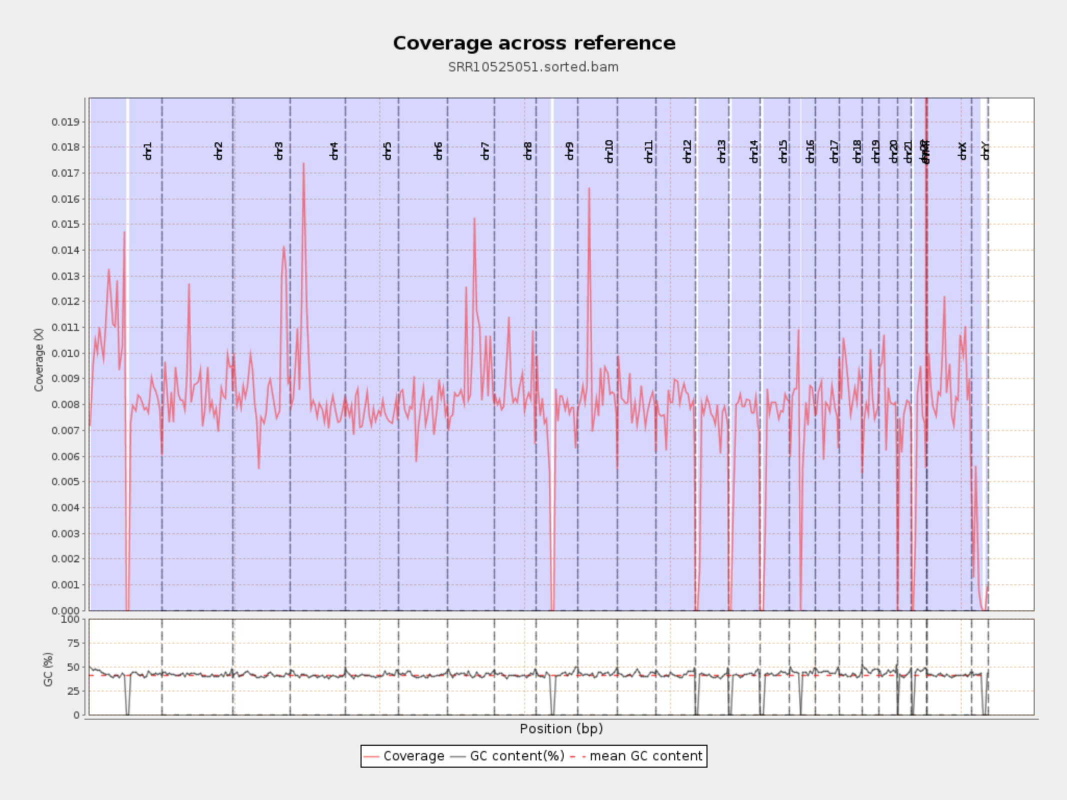
General error rate	0.5%
Mismatches	121,584
Insertions	1,763
Mapped reads with at least one insertion	0.41%
Deletions	5,159
Mapped reads with at least one deletion	1.21%
Homopolymer indels	44.63%

2.6. Chromosome stats

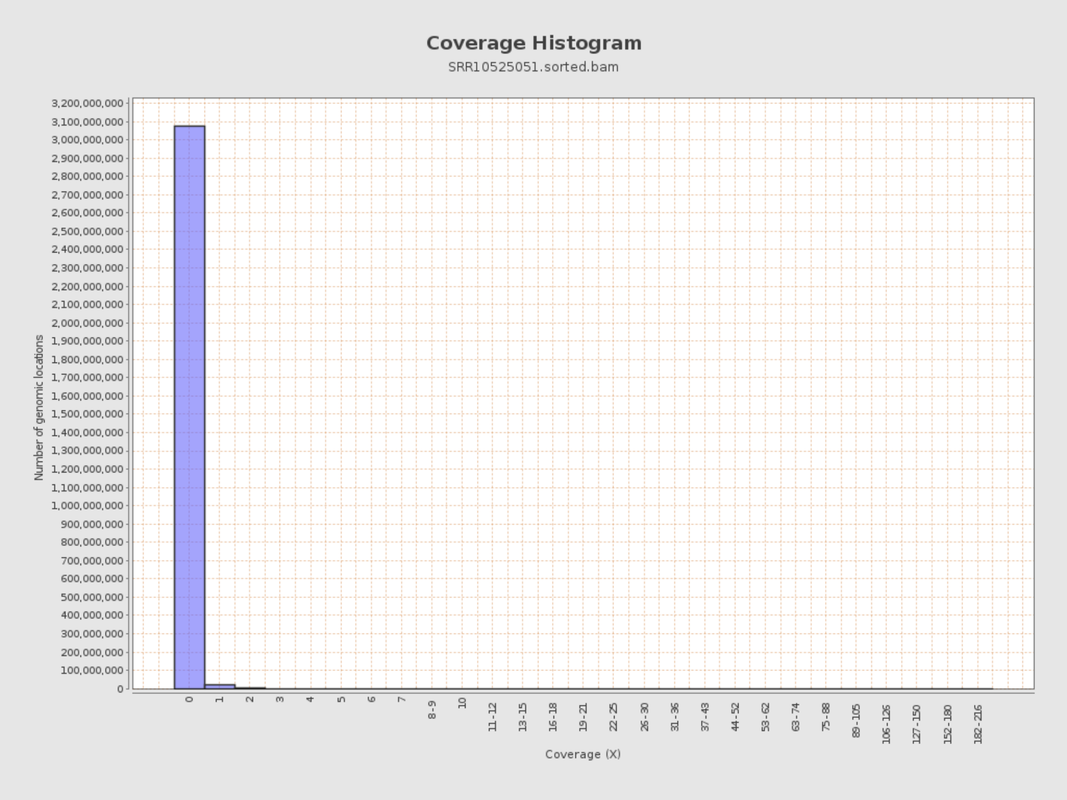
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2238455	0.009	0.1797
chr2	243199373	2077618	0.0085	0.1312
chr3	198022430	1751981	0.0088	0.0989
chr4	191154276	1683942	0.0088	0.1048
chr5	180915260	1395167	0.0077	0.0929
chr6	171115067	1355110	0.0079	0.0967
chr7	159138663	1495952	0.0094	0.1202

chr8	146364022	1252834	0.0086	0.1324
chr9	141213431	967301	0.0068	0.0948
chr10	135534747	1189596	0.0088	0.115
chr11	135006516	1089414	0.0081	0.1014
chr12	133851895	1083142	0.0081	0.0968
chr13	115169878	735754	0.0064	0.0844
chr14	107349540	712155	0.0066	0.087
chr15	102531392	668094	0.0065	0.0848
chr16	90354753	671404	0.0074	0.0933
chr17	81195210	632724	0.0078	0.0938
chr18	78077248	695049	0.0089	0.1384
chr19	59128983	473431	0.008	0.1204
chr20	63025520	533601	0.0085	0.0983
chr21	48129895	328106	0.0068	0.0911
chr22	51304566	285312	0.0056	0.0788
chrMT	16571	3873	0.2337	0.4914
chrX	155270560	1378632	0.0089	0.1028
chrY	59373566	84039	0.0014	0.0608

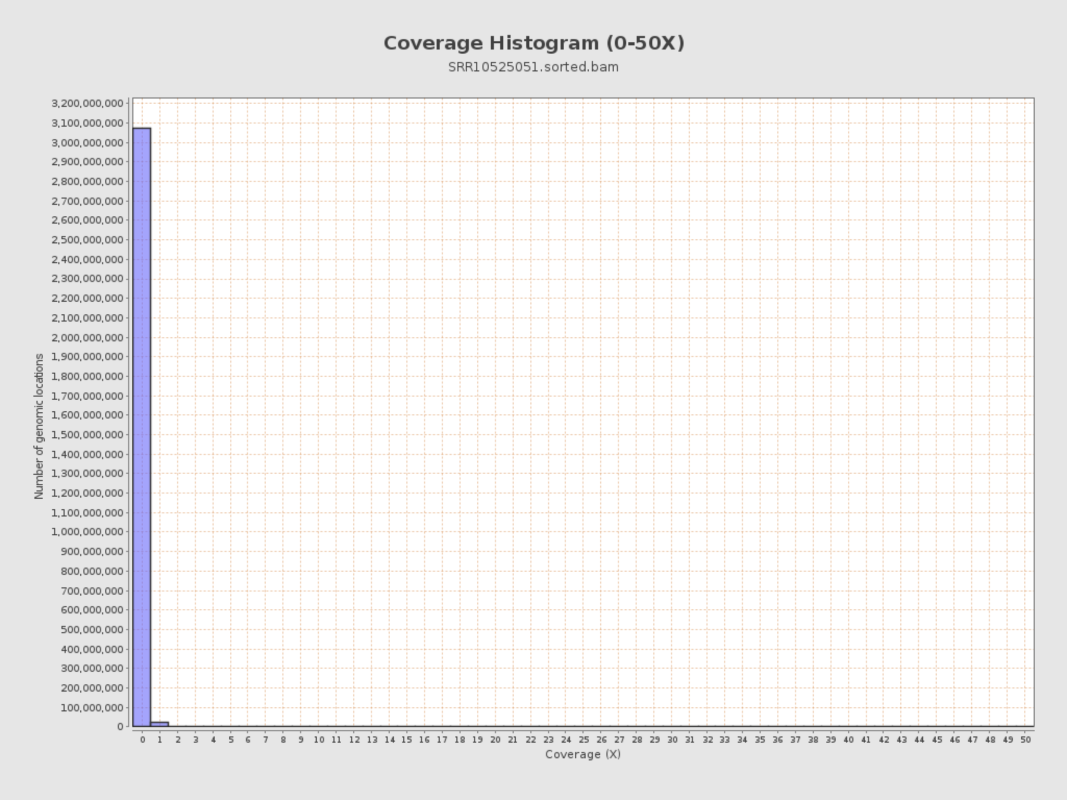
3. Results : Coverage across reference



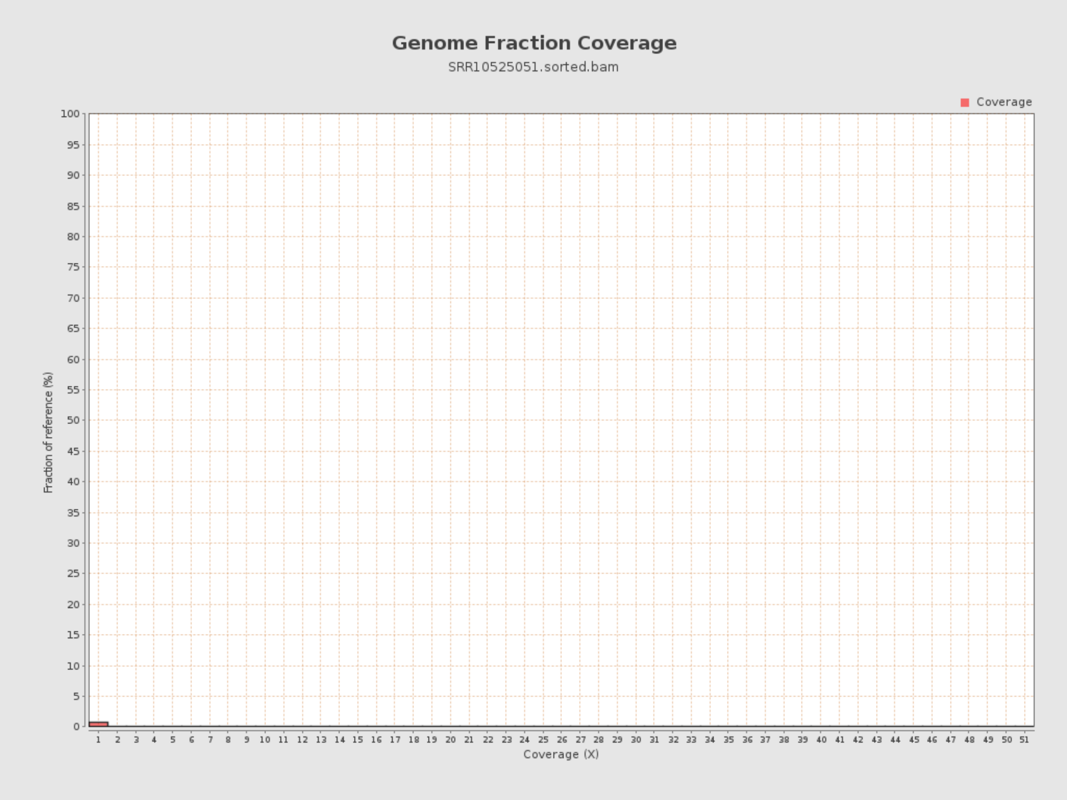
4. Results : Coverage Histogram



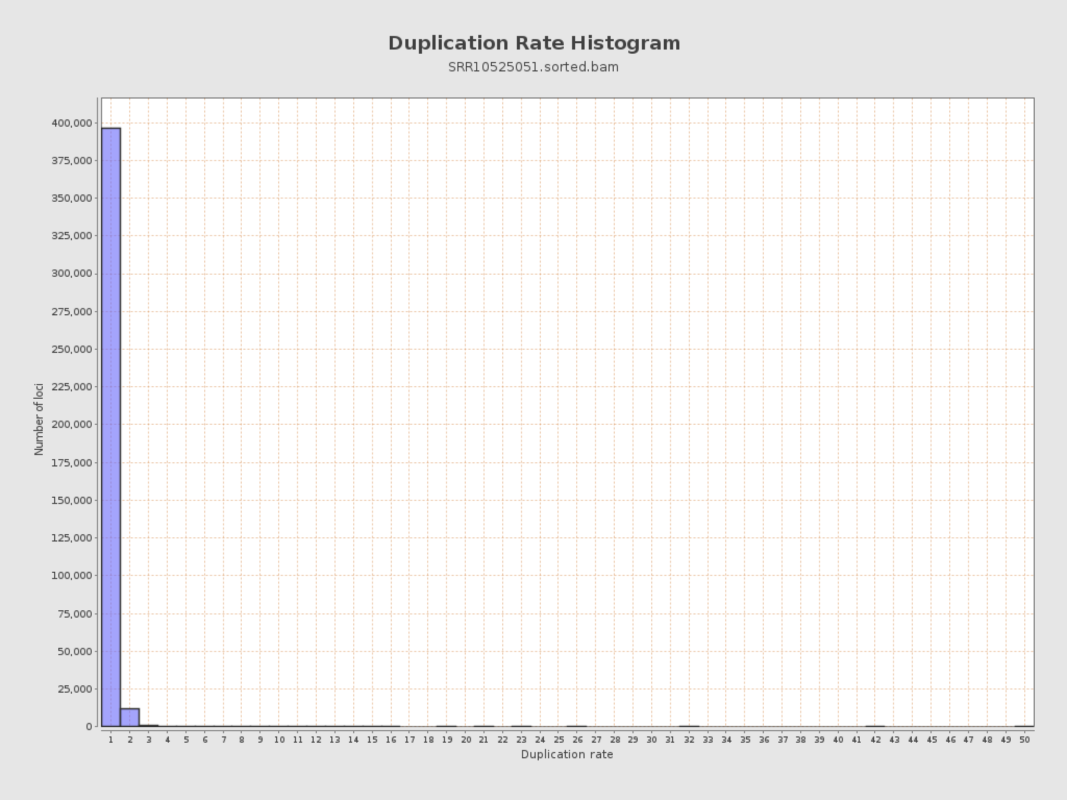
5. Results : Coverage Histogram (0-50X)



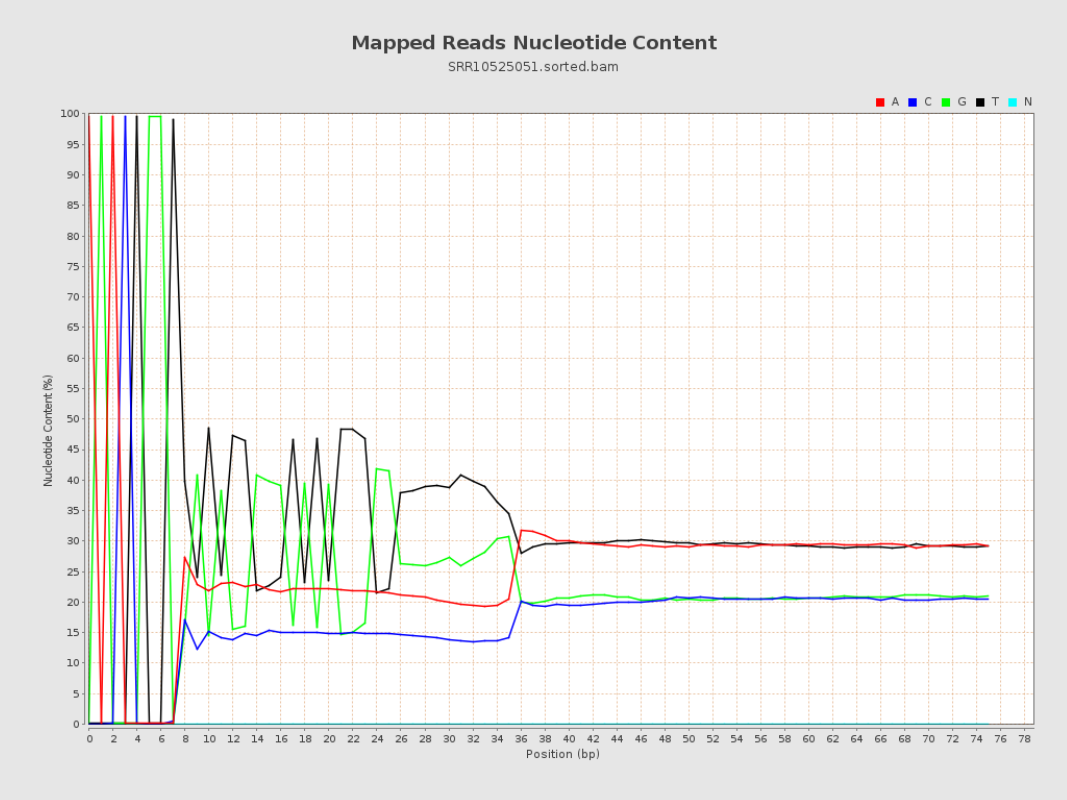
6. Results : Genome Fraction Coverage



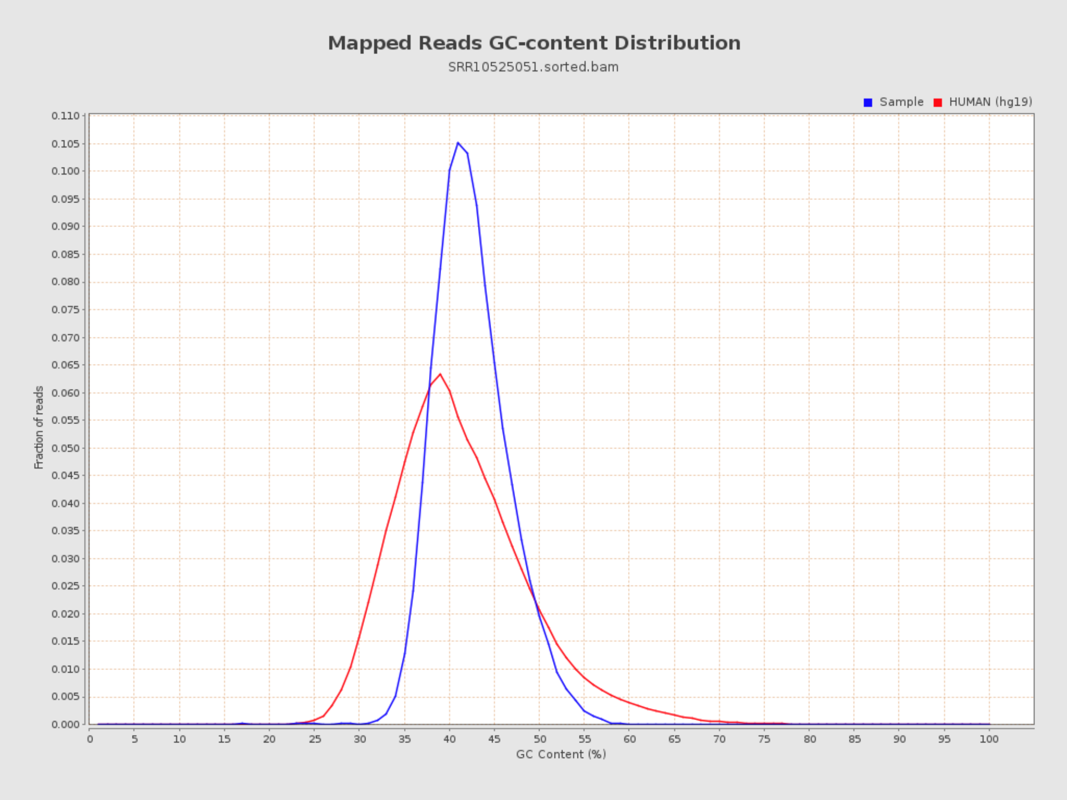
7. Results : Duplication Rate Histogram



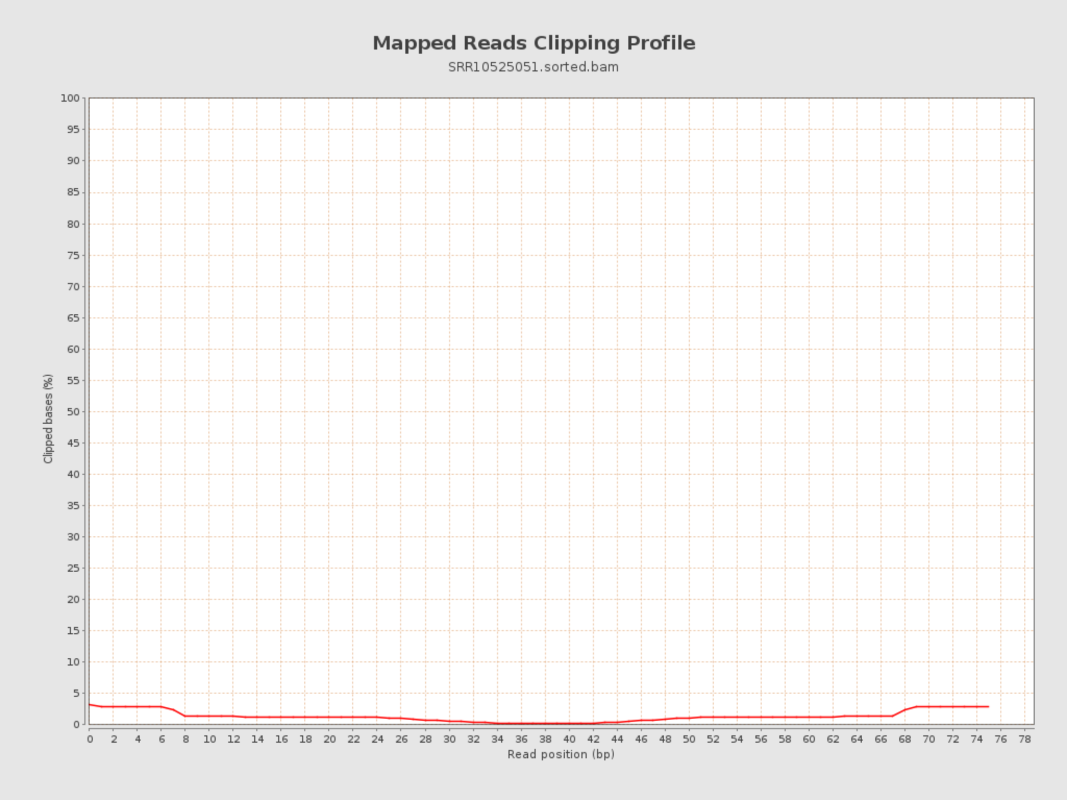
8. Results : Mapped Reads Nucleotide Content



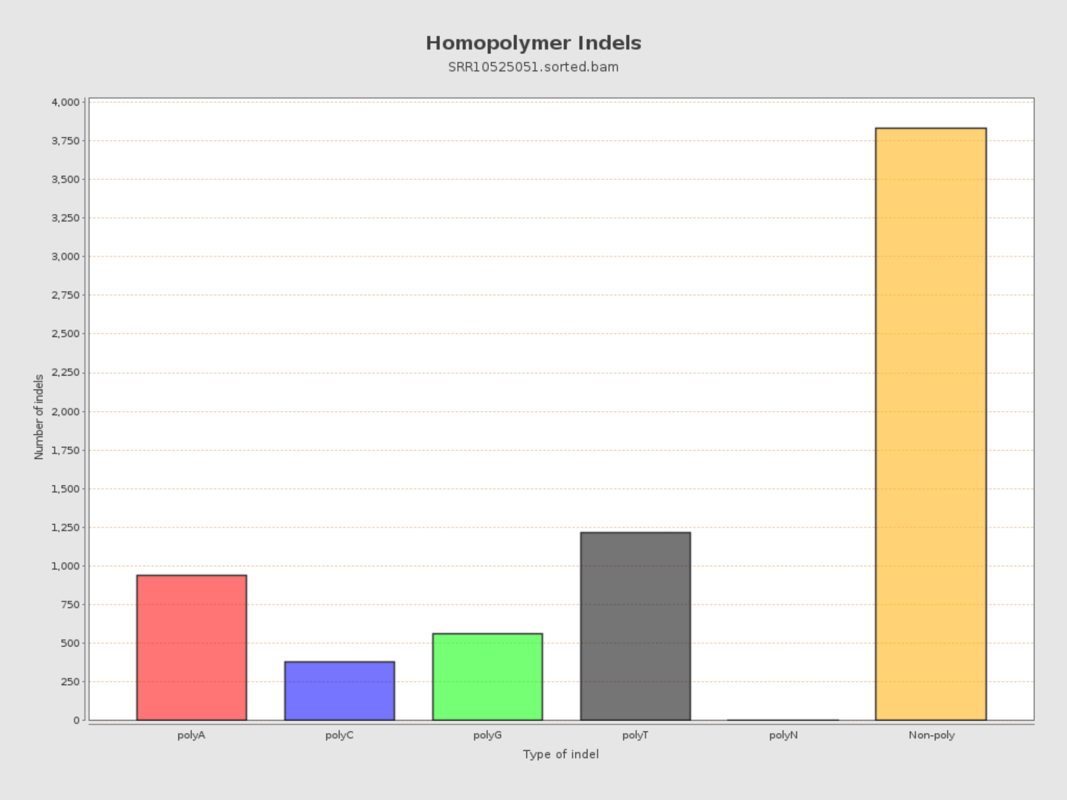
9. Results : Mapped Reads GC-content Distribution



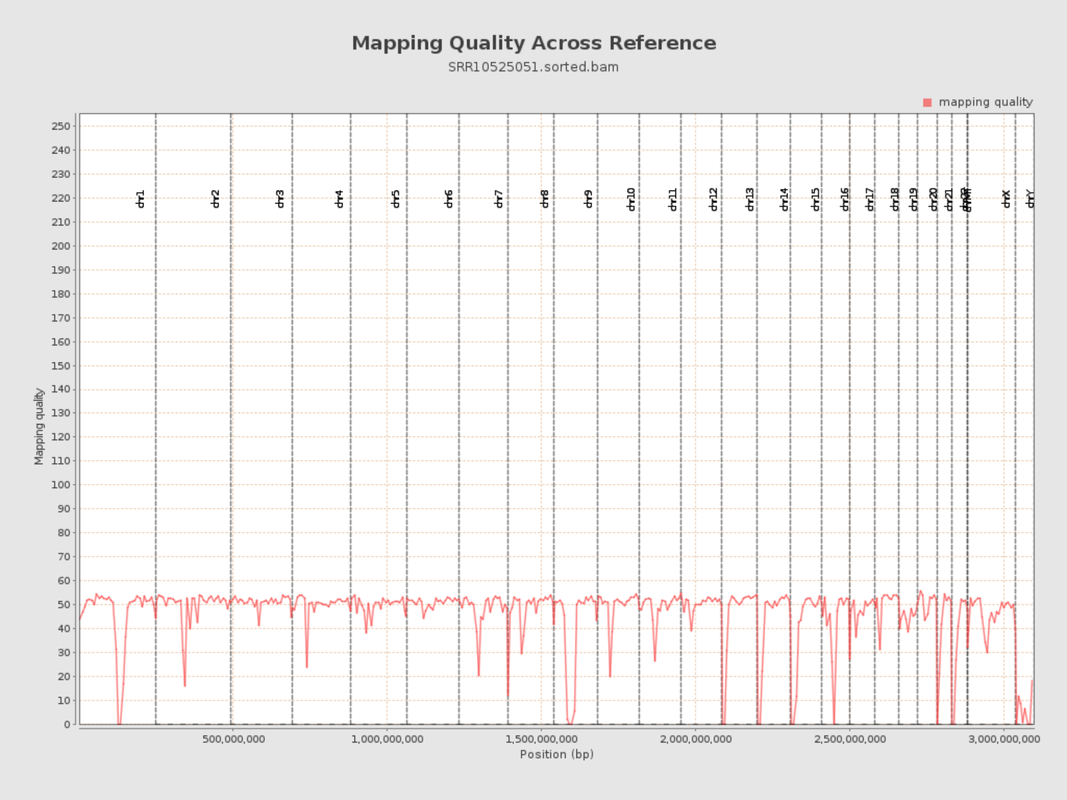
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram