Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 08:00:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818769.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_SRR1818769 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818769.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 08:00:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818769.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	285,828
Mapped reads	265,574 / 92.91%
Unmapped reads	20,254 / 7.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,263 / 0.79%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	34,682 / 12.13%
Duplication rate	11.92%
Clipped reads	265,149 / 92.77%

2.2. ACGT Content

Number/percentage of A's	5,273,274 / 29.3%
Number/percentage of C's	3,666,814 / 20.37%
Number/percentage of T's	5,118,447 / 28.44%
Number/percentage of G's	3,939,648 / 21.89%
Number/percentage of N's	1,248 / 0.01%
GC Percentage	42.26%

2.3. Coverage

Mean	0.0058

Standard Deviation	0.1061

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Mismatches and indels

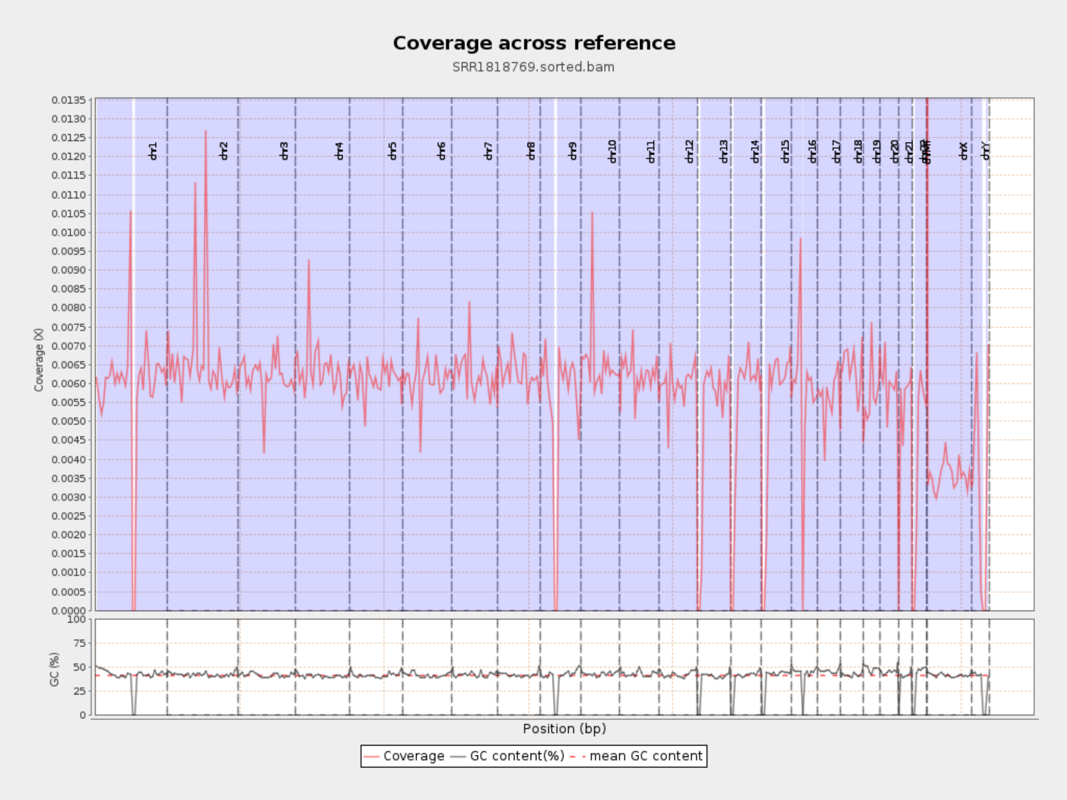
General error rate	0.55%
Mismatches	94,267
Insertions	2,189
Mapped reads with at least one insertion	0.81%
Deletions	4,675
Mapped reads with at least one deletion	1.74%
Homopolymer indels	42.76%

2.6. Chromosome stats

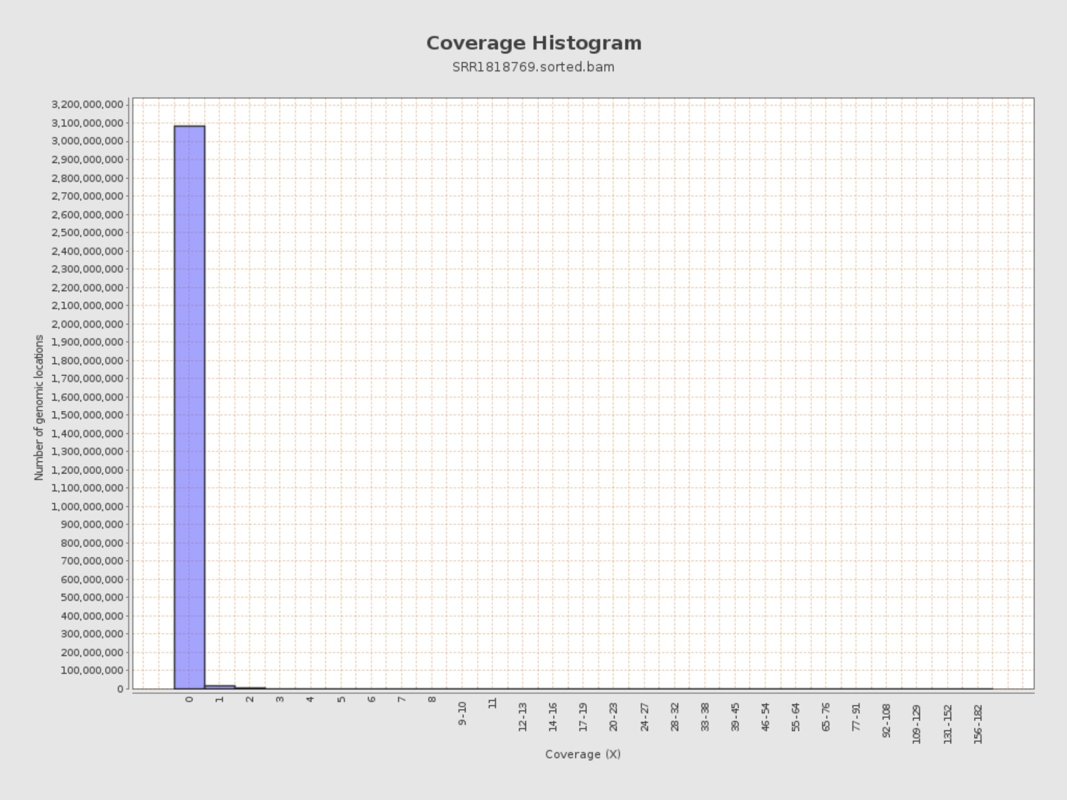
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1469089	0.0059	0.1396
chr2	243199373	1616672	0.0066	0.1529
chr3	198022430	1226373	0.0062	0.0924
chr4	191154276	1217294	0.0064	0.0979
chr5	180915260	1114272	0.0062	0.0923
chr6	171115067	1050706	0.0061	0.095
chr7	159138663	997107	0.0063	0.1035

chr8	146364022	927113	0.0063	0.0989
chr9	141213431	767908	0.0054	0.0917
chr10	135534747	891636	0.0066	0.1124
chr11	135006516	847058	0.0063	0.0966
chr12	133851895	803660	0.006	0.0942
chr13	115169878	578622	0.005	0.0827
chr14	107349540	566026	0.0053	0.0906
chr15	102531392	524112	0.0051	0.0843
chr16	90354753	517299	0.0057	0.1095
chr17	81195210	458654	0.0056	0.089
chr18	78077248	499249	0.0064	0.115
chr19	59128983	339215	0.0057	0.1214
chr20	63025520	376809	0.006	0.0935
chr21	48129895	248796	0.0052	0.0878
chr22	51304566	206882	0.004	0.0786
chrMT	16571	11264	0.6797	1.0674
chrX	155270560	556175	0.0036	0.0723
chrY	59373566	195087	0.0033	0.1359

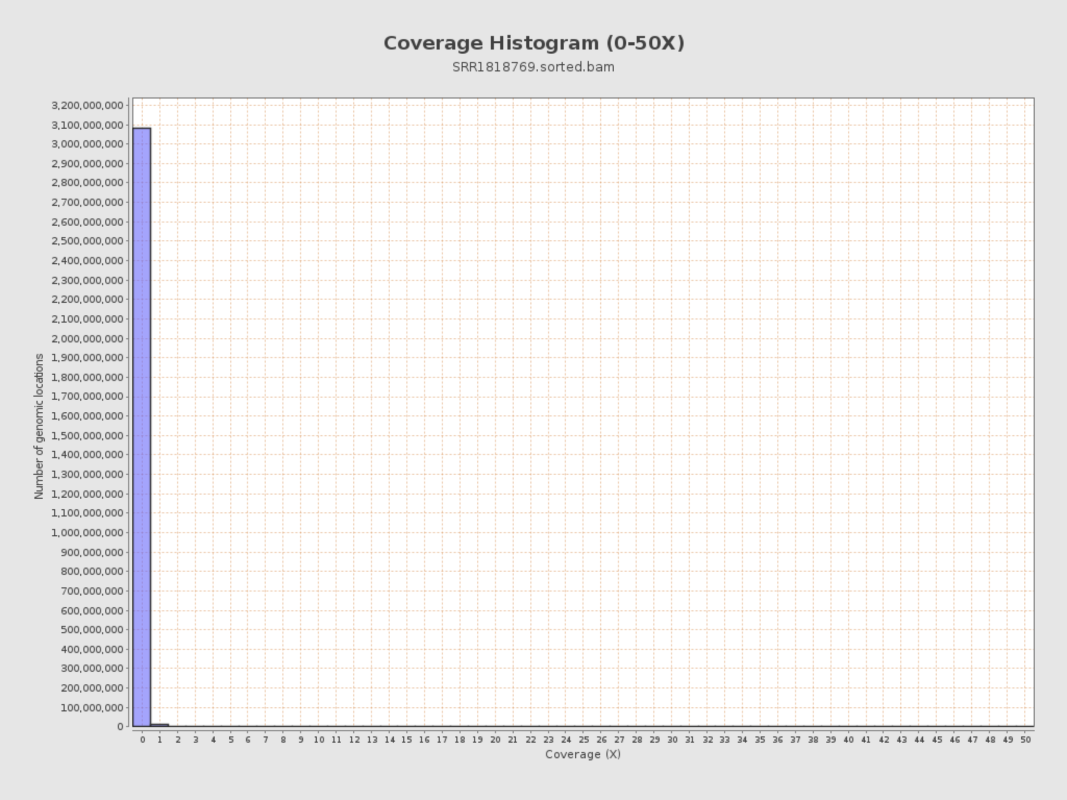
3. Results : Coverage across reference



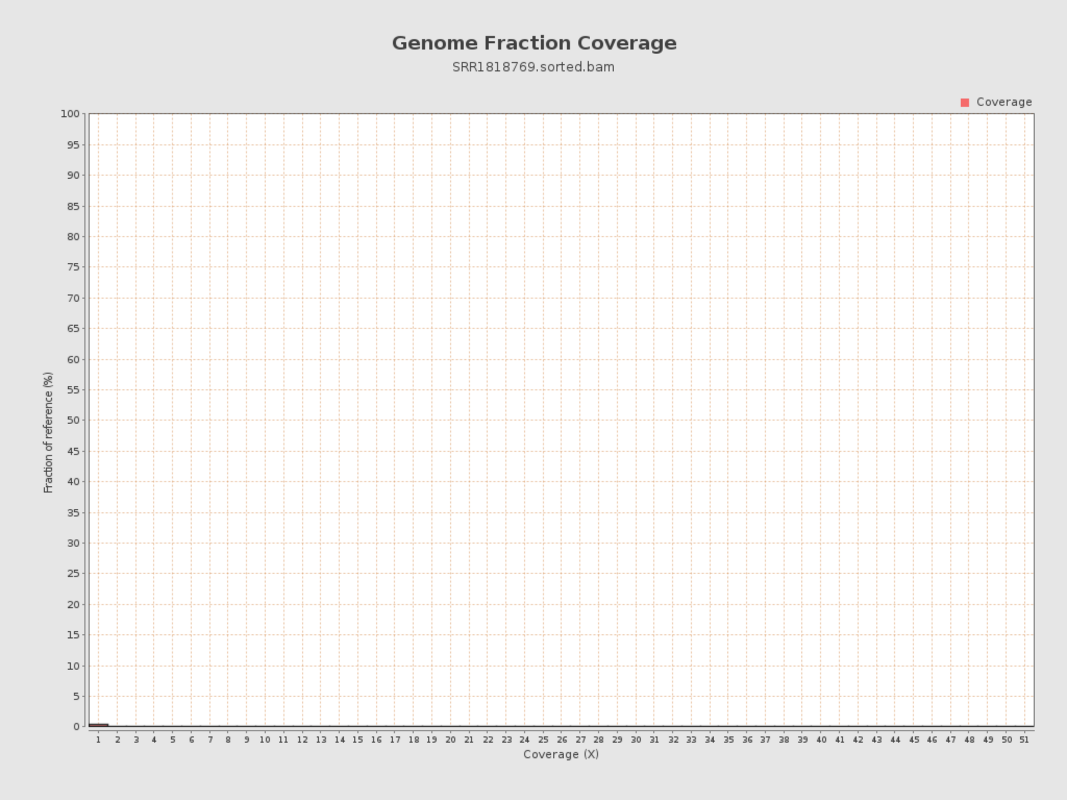
4. Results : Coverage Histogram



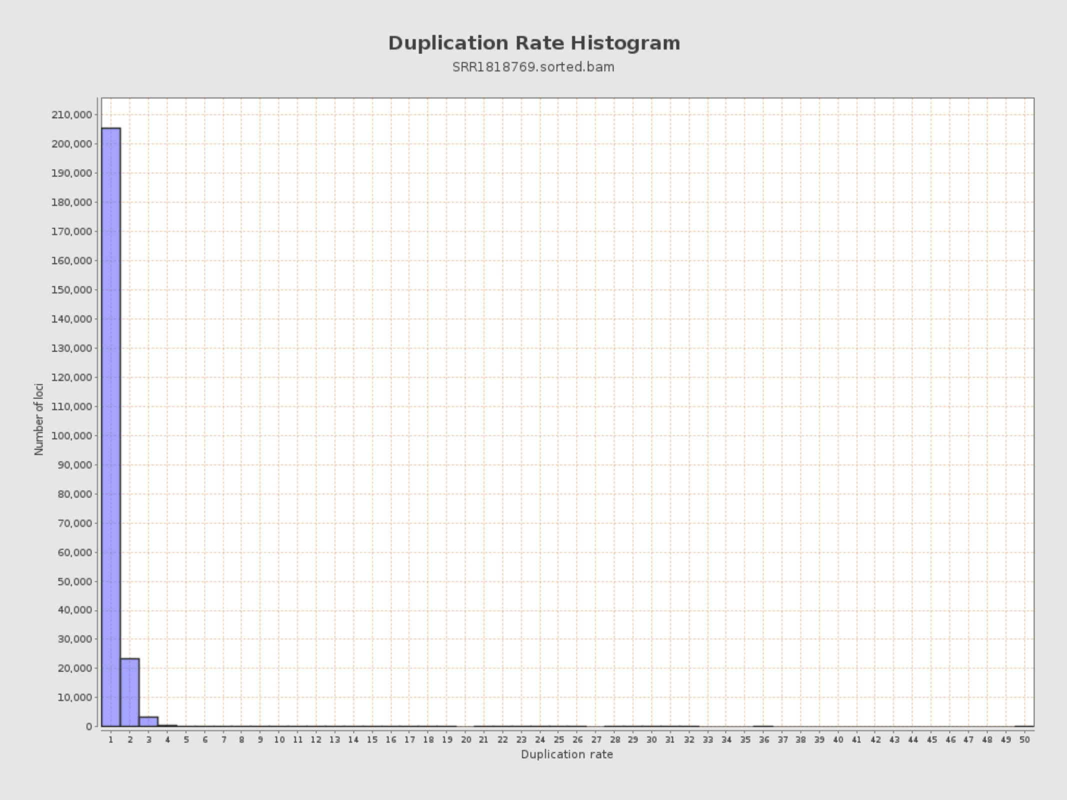
5. Results : Coverage Histogram (0-50X)



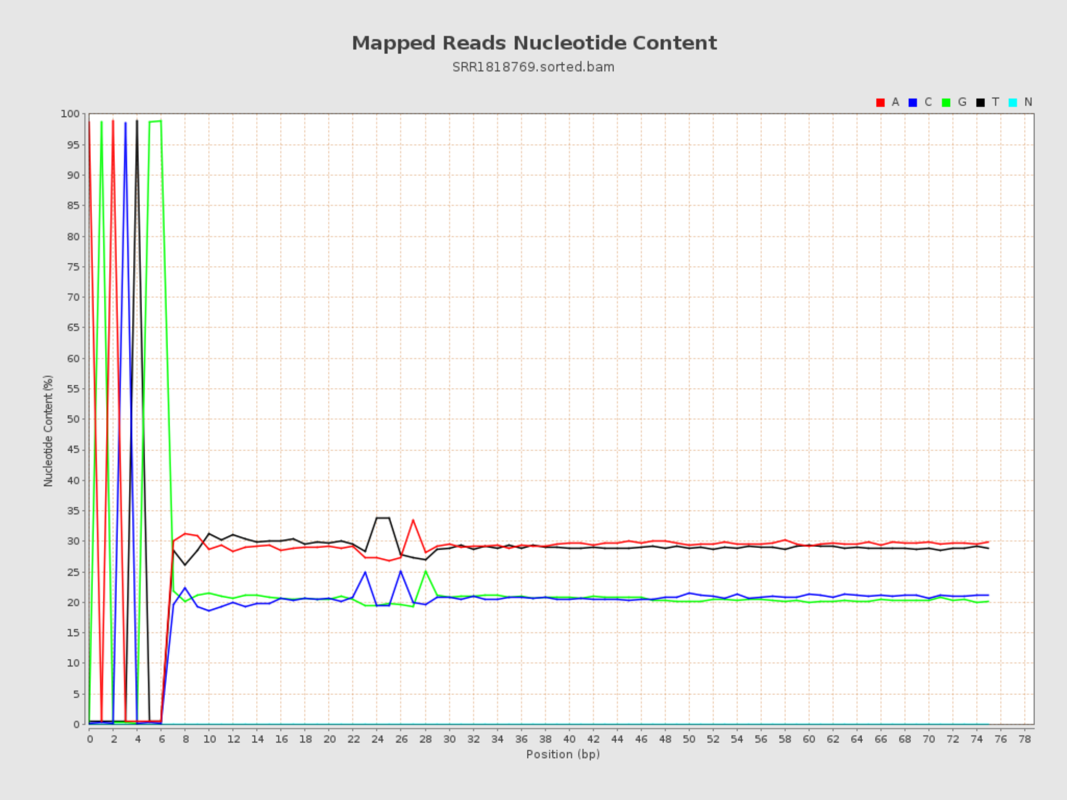
6. Results : Genome Fraction Coverage



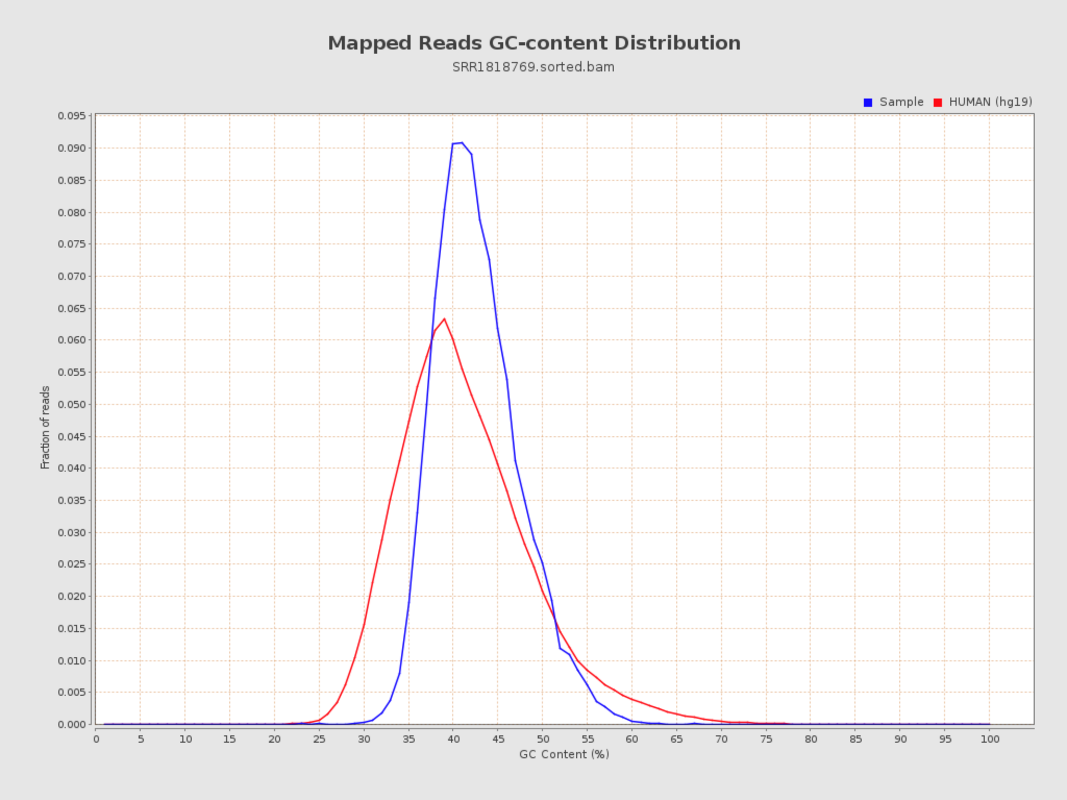
7. Results : Duplication Rate Histogram



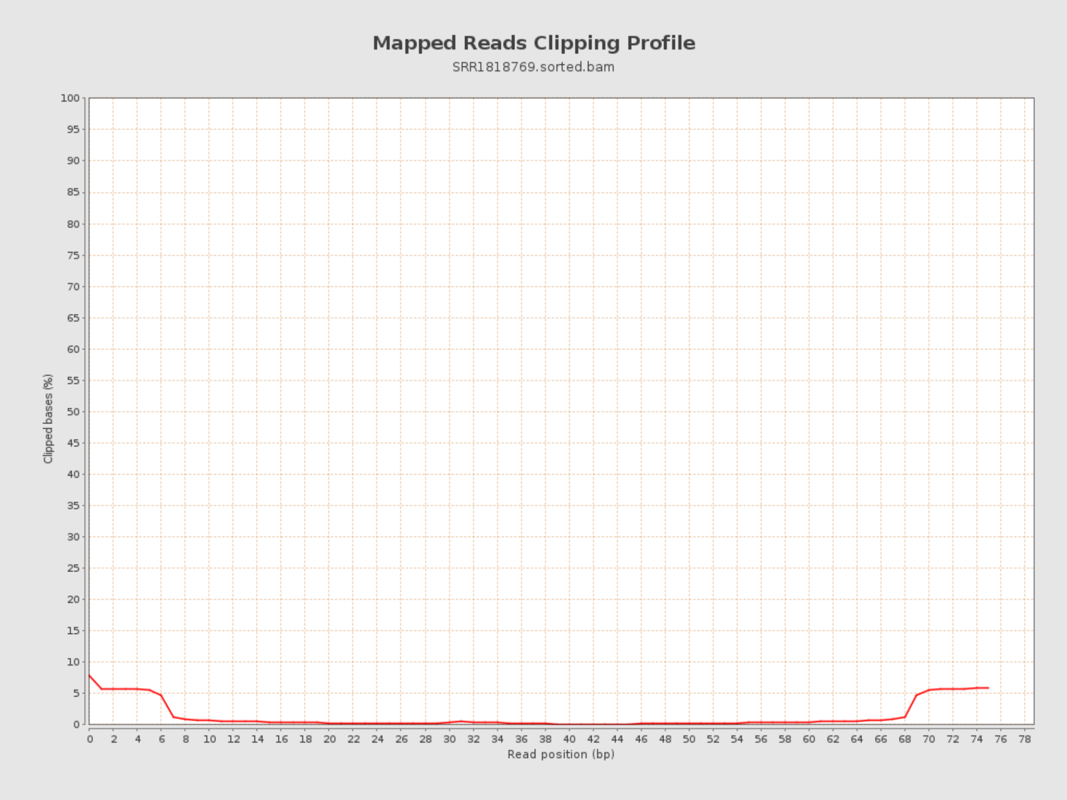
8. Results : Mapped Reads Nucleotide Content



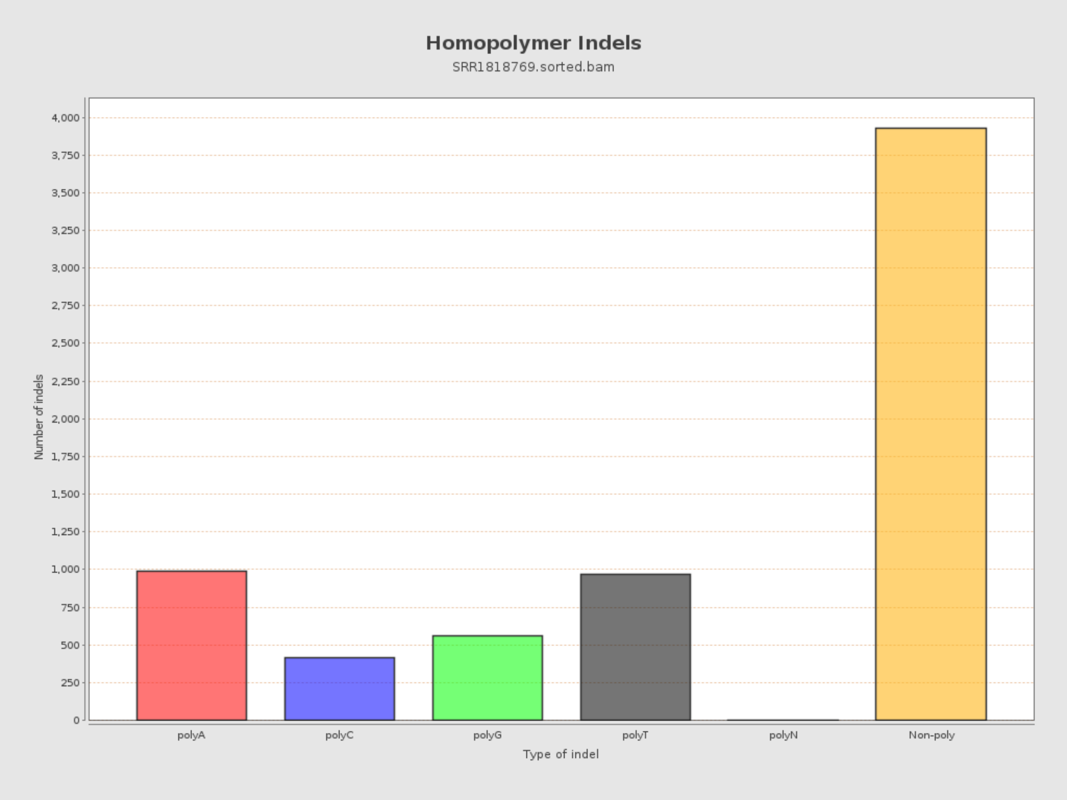
9. Results : Mapped Reads GC-content Distribution



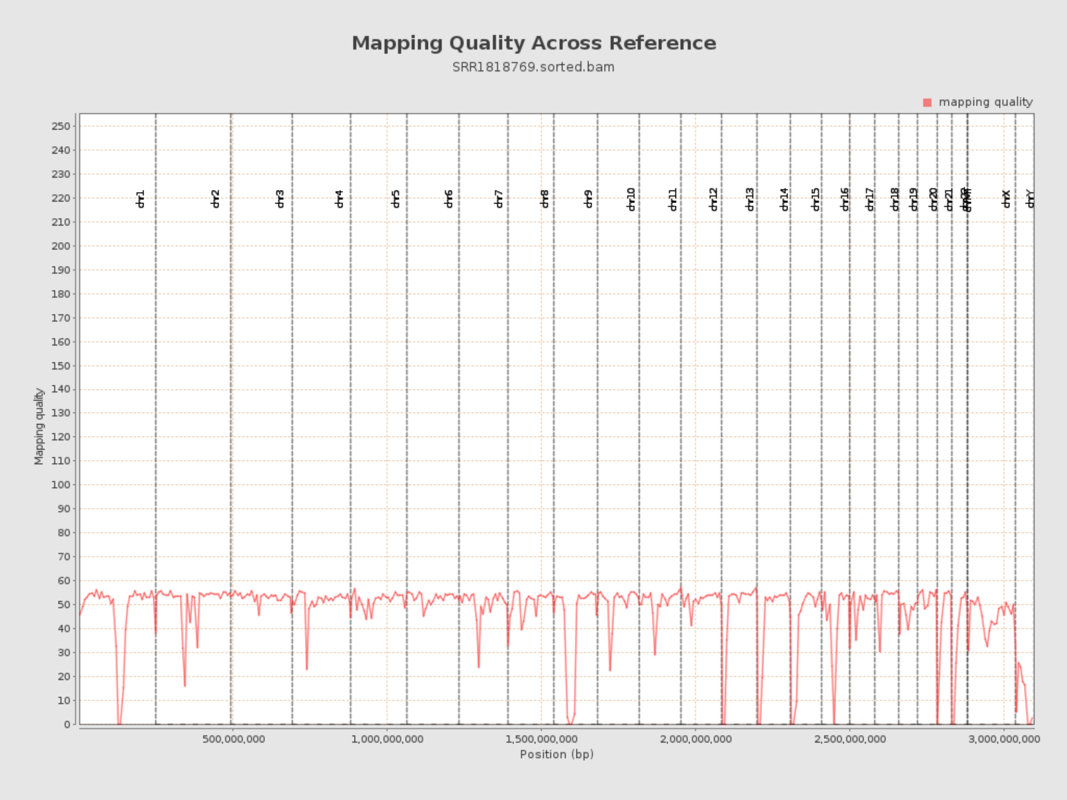
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram