Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 09:23:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818776.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_SRR1818776 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818776.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 09:23:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818776.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	556,665
Mapped reads	541,878 / 97.34%
Unmapped reads	14,787 / 2.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,654 / 0.84%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	156,072 / 28.04%
Duplication rate	24.87%
Clipped reads	542,752 / 97.5%

2.2. ACGT Content

Number/percentage of A's	10,735,163 / 29.2%
Number/percentage of C's	7,827,988 / 21.29%
Number/percentage of T's	10,318,495 / 28.07%
Number/percentage of G's	7,879,355 / 21.43%
Number/percentage of N's	2,027 / 0.01%
GC Percentage	42.73%

2.3. Coverage

Mean	0.0119

Standard Deviation	0.1836

2.4. Mapping Quality

Mean Mapping Quality	47.95

2.5. Mismatches and indels

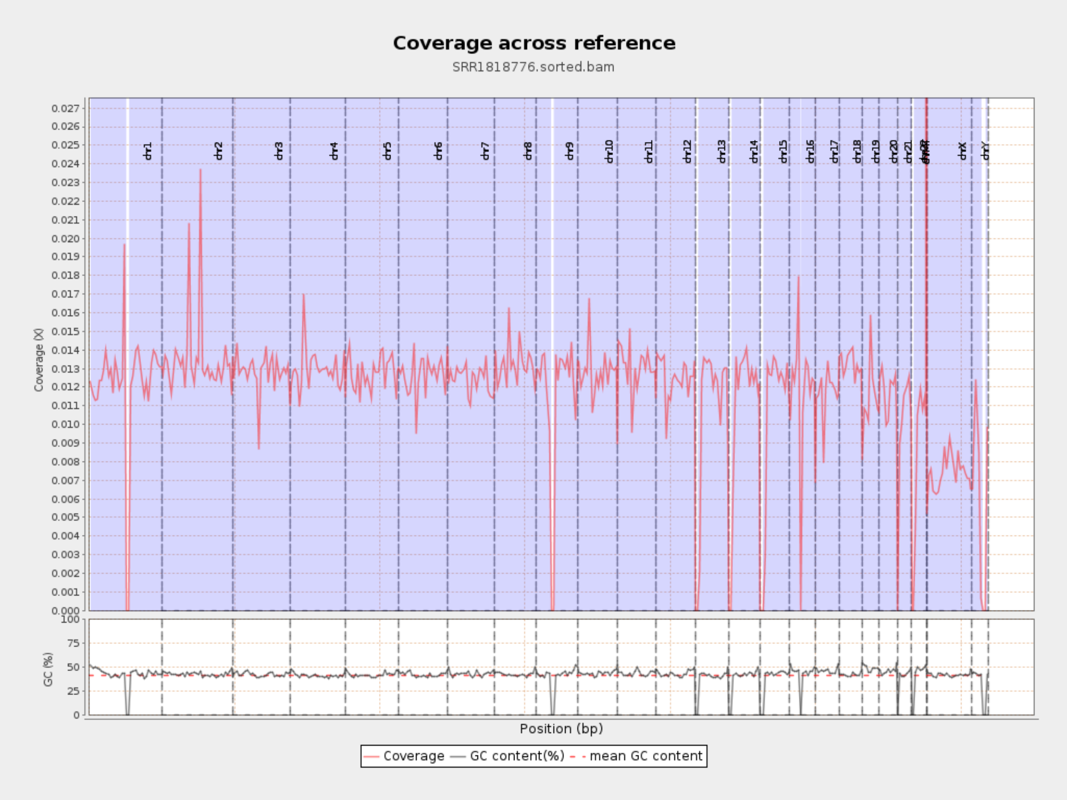
General error rate	0.52%
Mismatches	183,483
Insertions	3,822
Mapped reads with at least one insertion	0.7%
Deletions	9,197
Mapped reads with at least one deletion	1.68%
Homopolymer indels	40.63%

2.6. Chromosome stats

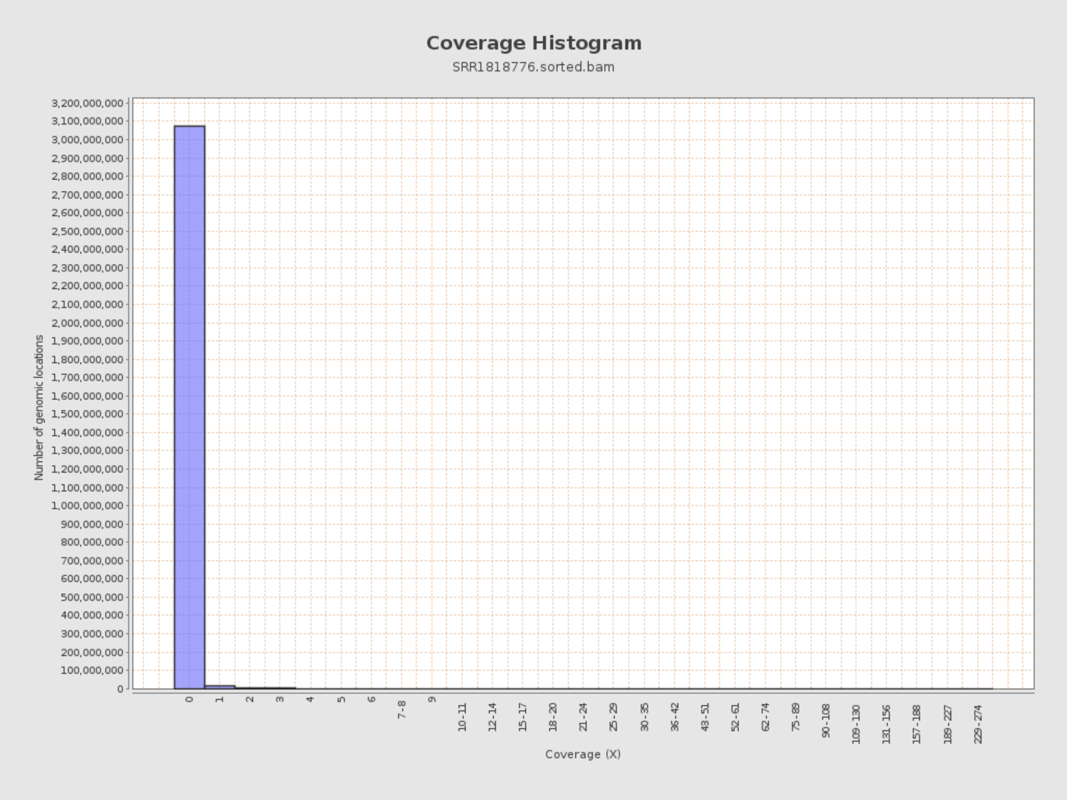
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3014840	0.0121	0.2388
chr2	243199373	3300779	0.0136	0.2481
chr3	198022430	2541531	0.0128	0.1666
chr4	191154276	2478123	0.013	0.1722
chr5	180915260	2305063	0.0127	0.1651
chr6	171115067	2164285	0.0126	0.1695
chr7	159138663	1981809	0.0125	0.177

chr8	146364022	1937108	0.0132	0.1779
chr9	141213431	1601406	0.0113	0.1714
chr10	135534747	1735668	0.0128	0.1898
chr11	135006516	1756001	0.013	0.1752
chr12	133851895	1666199	0.0124	0.1673
chr13	115169878	1209943	0.0105	0.1516
chr14	107349540	1156890	0.0108	0.1575
chr15	102531392	1050809	0.0102	0.1454
chr16	90354753	1062842	0.0118	0.1954
chr17	81195210	945930	0.0117	0.1623
chr18	78077248	1035705	0.0133	0.2054
chr19	59128983	684105	0.0116	0.1995
chr20	63025520	742491	0.0118	0.1647
chr21	48129895	478199	0.0099	0.1489
chr22	51304566	400000	0.0078	0.135
chrMT	16571	31783	1.918	2.5328
chrX	155270560	1150276	0.0074	0.1314
chrY	59373566	345677	0.0058	0.1967

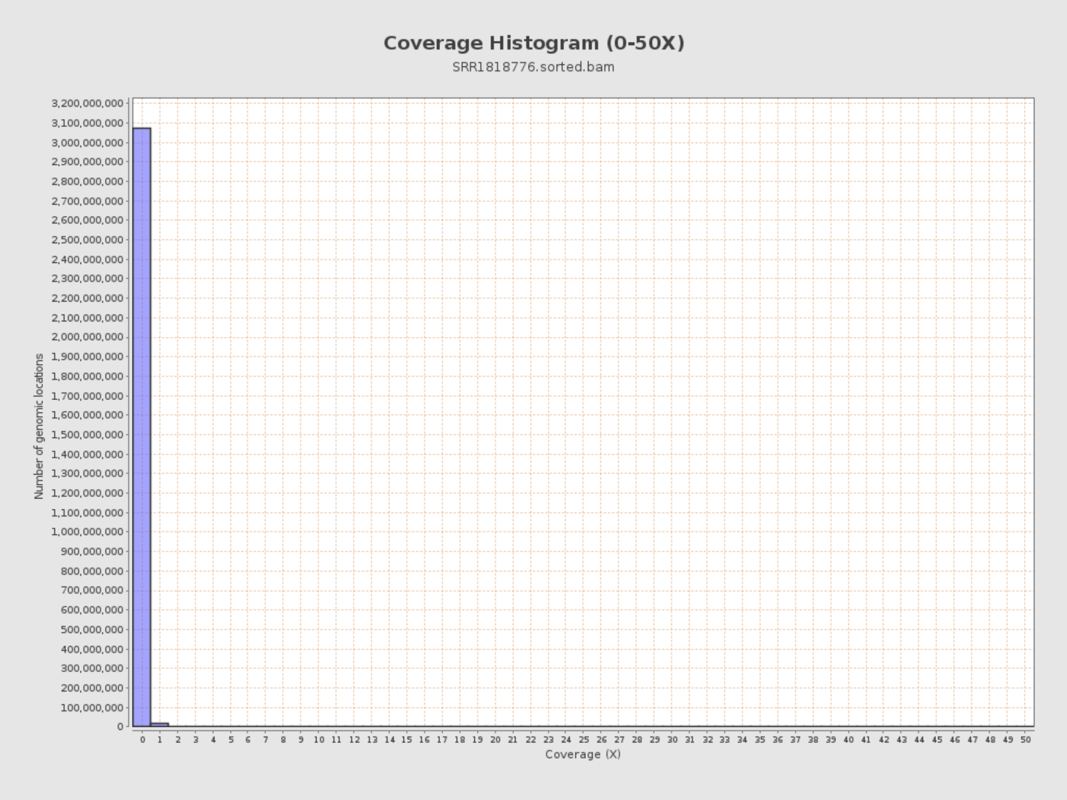
3. Results : Coverage across reference



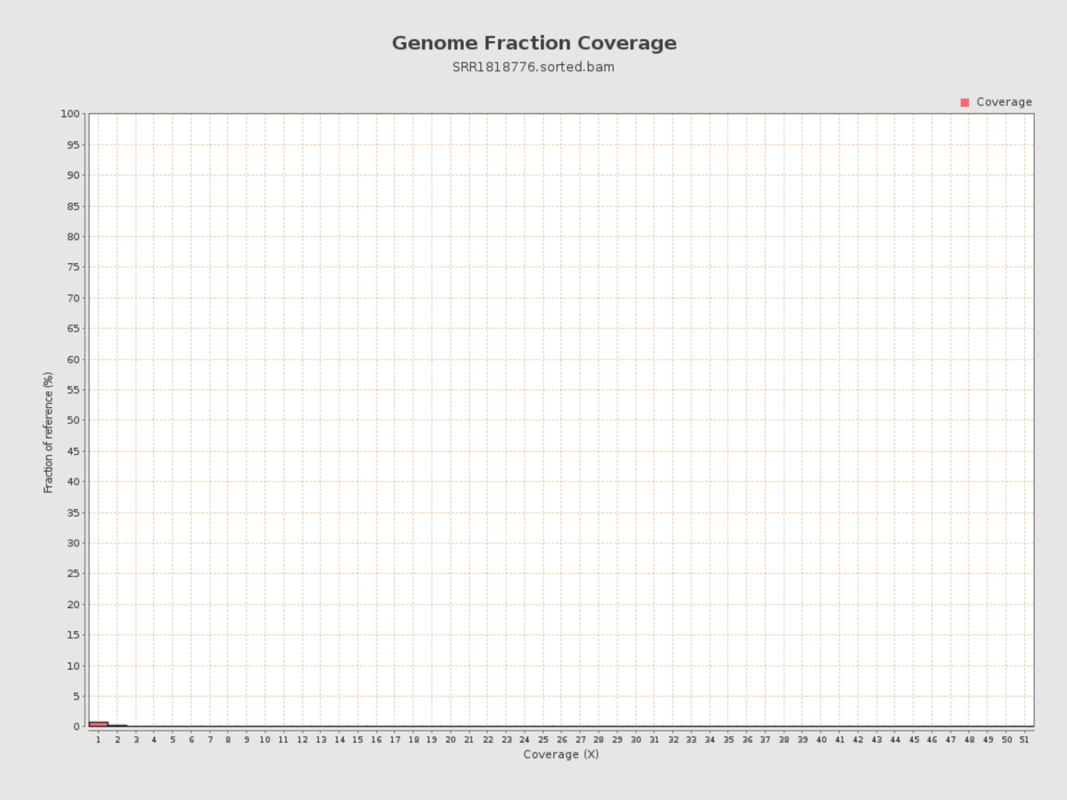
4. Results : Coverage Histogram



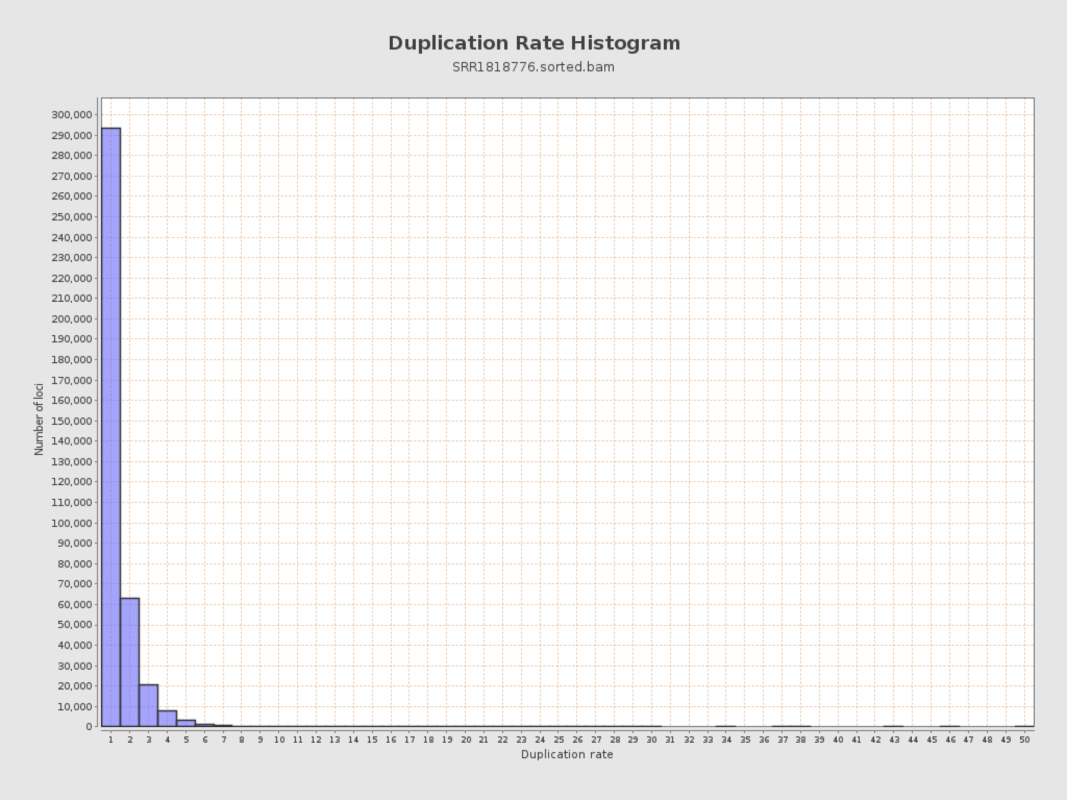
5. Results : Coverage Histogram (0-50X)



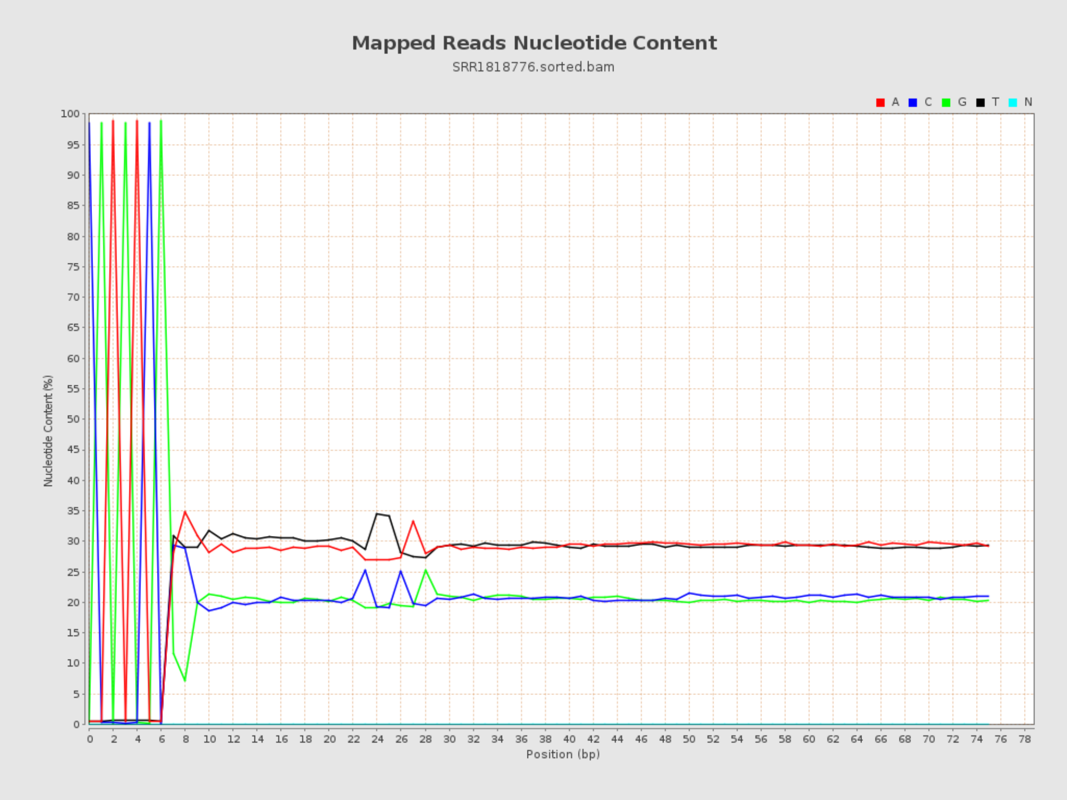
6. Results : Genome Fraction Coverage



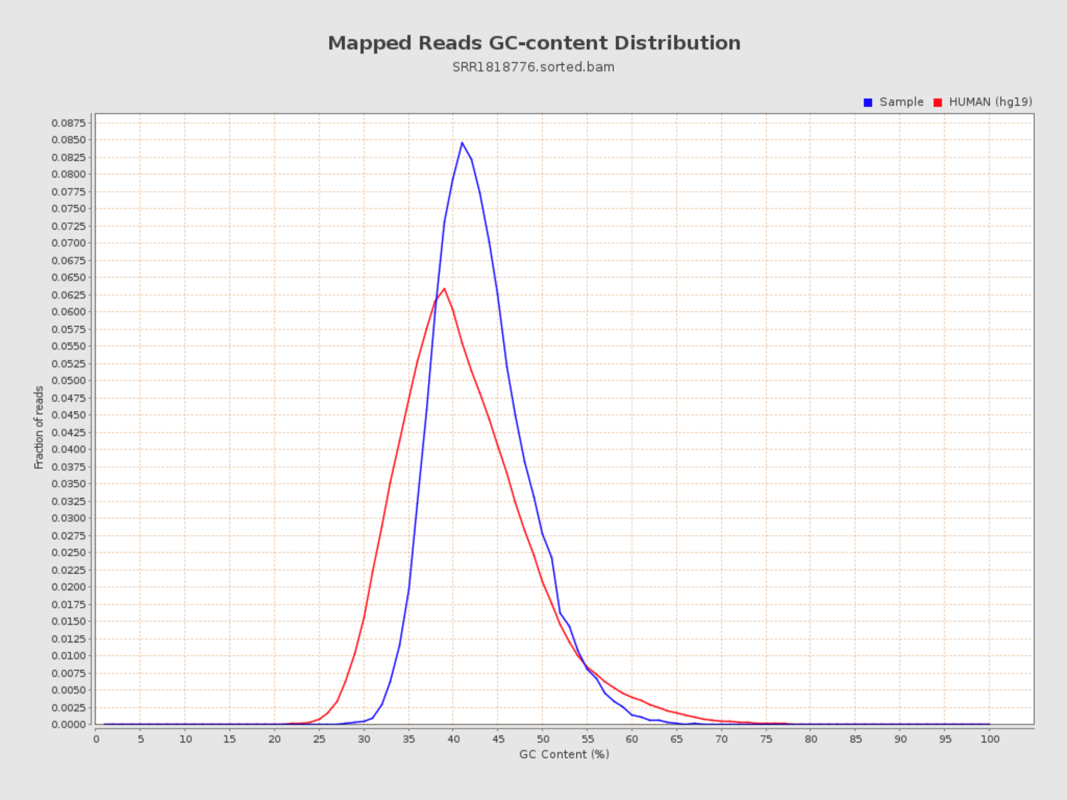
7. Results : Duplication Rate Histogram



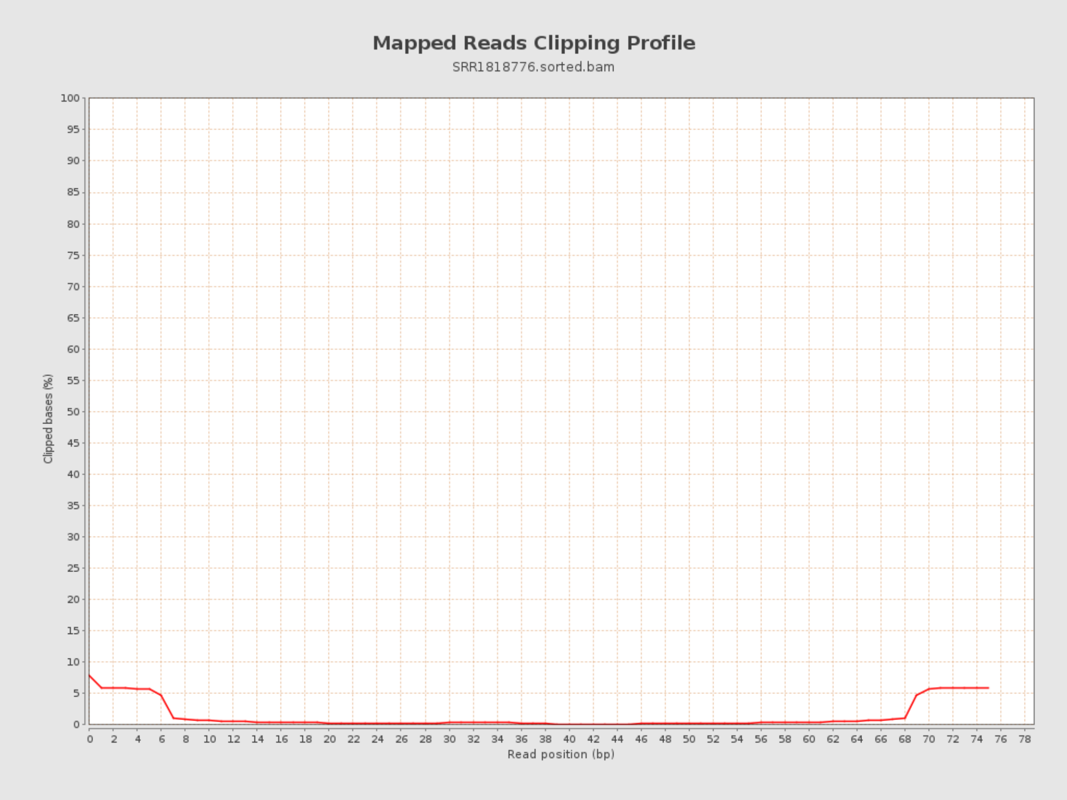
8. Results : Mapped Reads Nucleotide Content



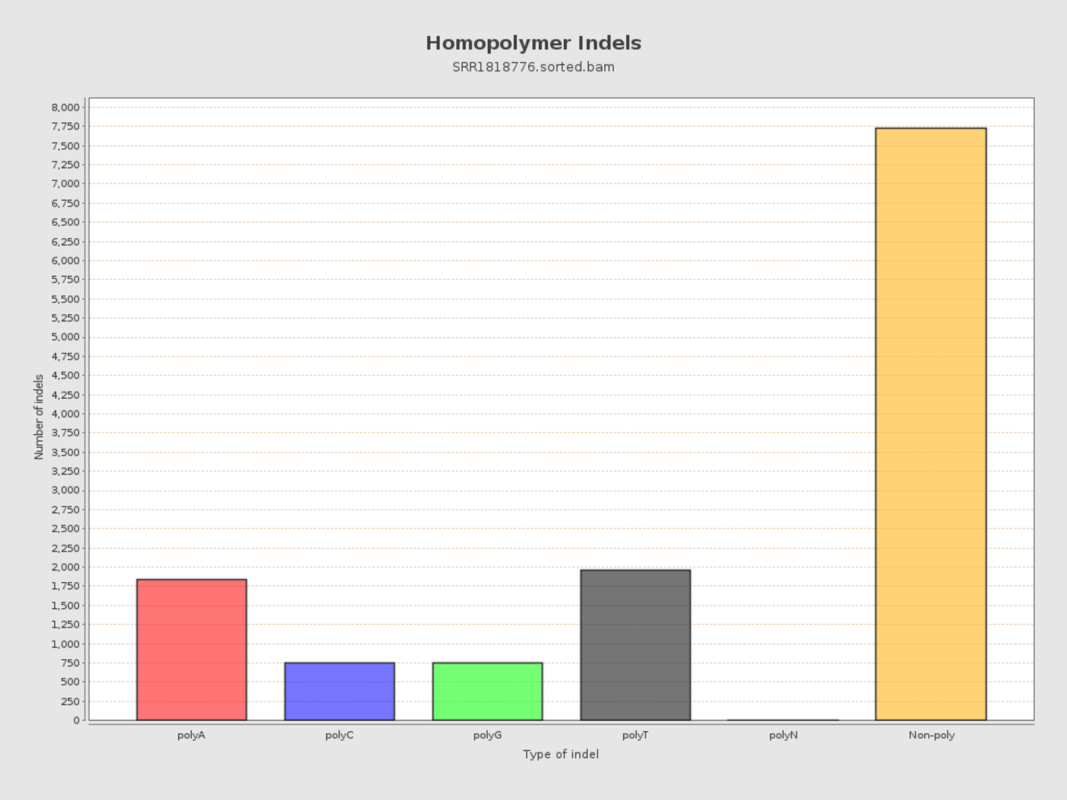
9. Results : Mapped Reads GC-content Distribution



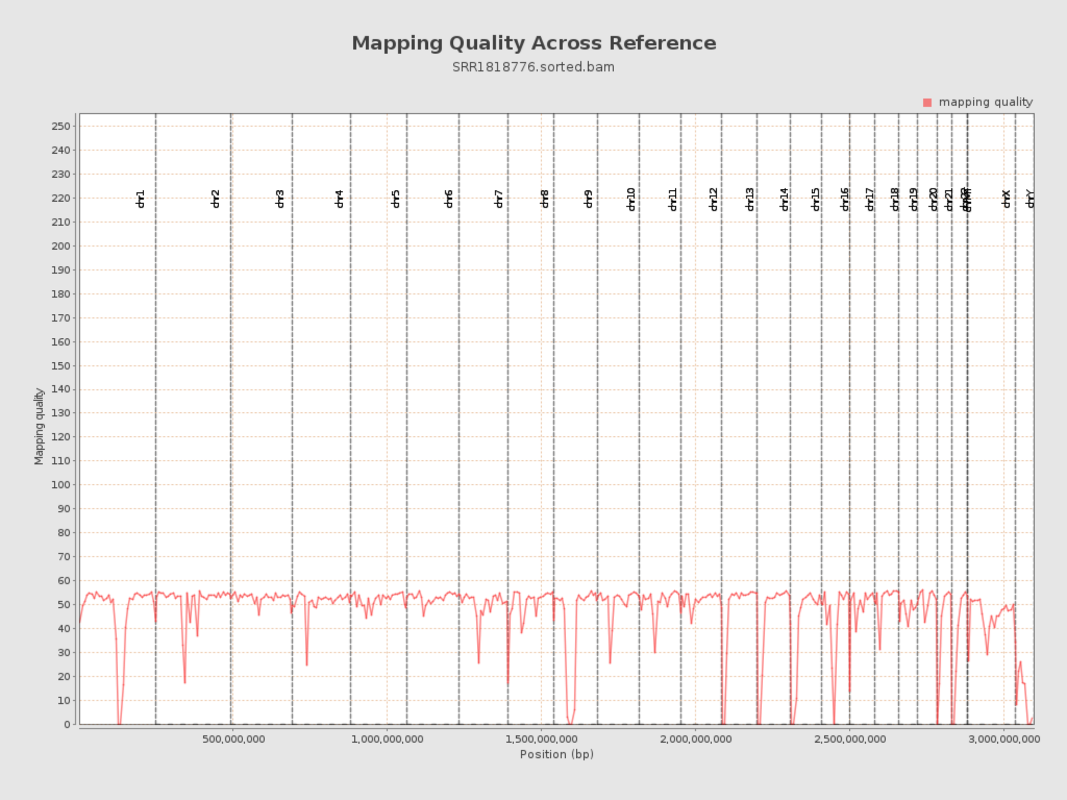
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram