Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:06:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819084.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_SRR1819084 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819084.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:06:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819084.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	820,411
Mapped reads	751,488 / 91.6%
Unmapped reads	68,923 / 8.4%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,319 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	16,045 / 1.96%
Duplication rate	1.56%
Clipped reads	752,896 / 91.77%

2.2. ACGT Content

Number/percentage of A's	11,177,917 / 25.59%
Number/percentage of C's	8,574,239 / 19.63%
Number/percentage of T's	13,615,733 / 31.17%
Number/percentage of G's	10,320,001 / 23.62%
Number/percentage of N's	732 / 0%
GC Percentage	43.25%

2.3. Coverage

Mean	0.0141

Standard Deviation	0.1543

2.4. Mapping Quality

Mean Mapping Quality	44.68

2.5. Mismatches and indels

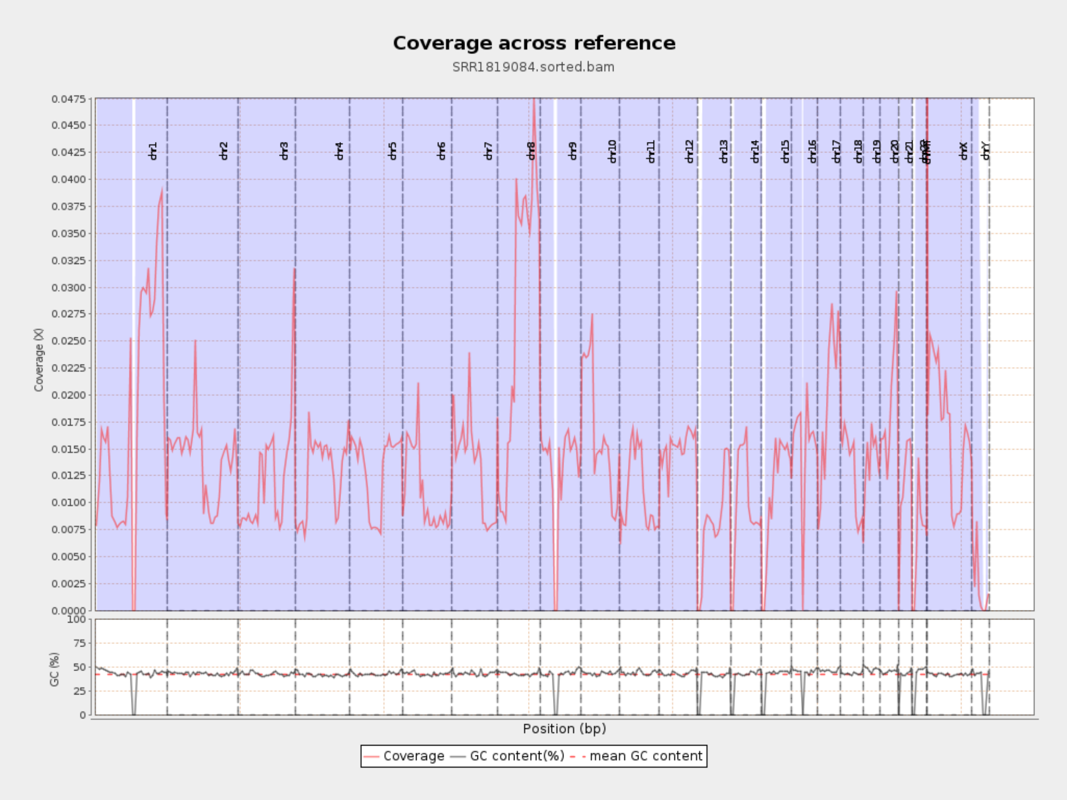
General error rate	0.51%
Mismatches	218,219
Insertions	2,975
Mapped reads with at least one insertion	0.39%
Deletions	8,320
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.41%

2.6. Chromosome stats

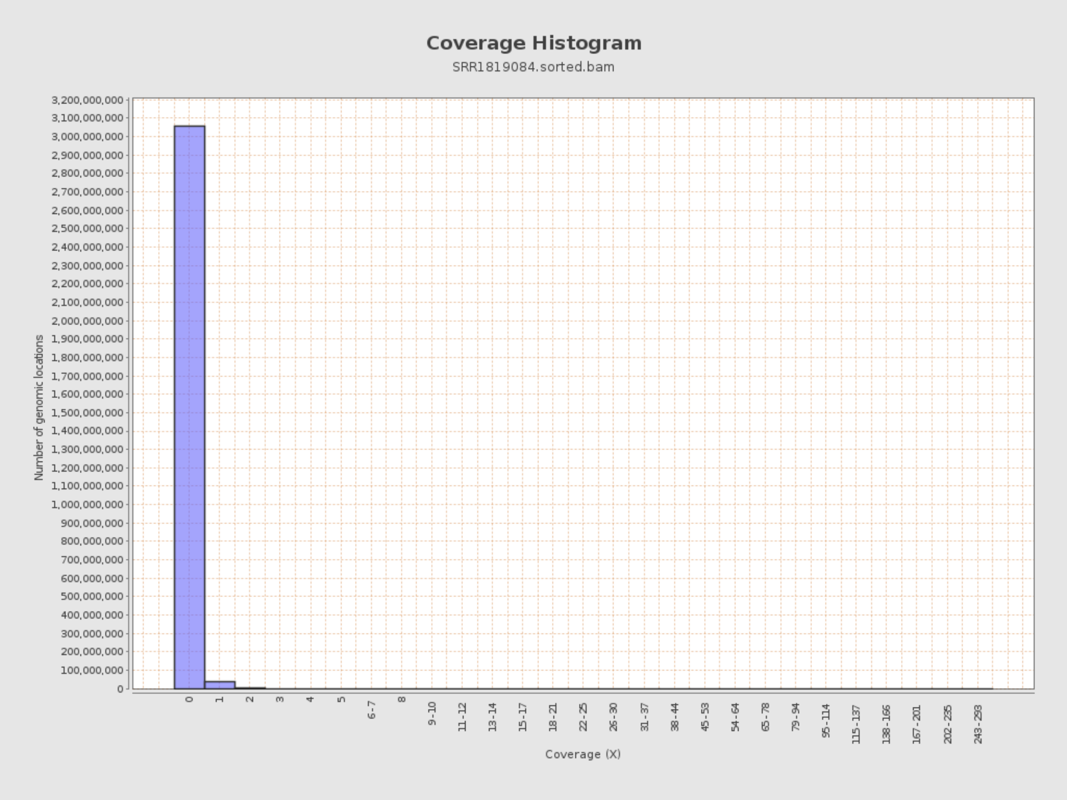
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4477680	0.018	0.2512
chr2	243199373	3432177	0.0141	0.1631
chr3	198022430	2400141	0.0121	0.1158
chr4	191154276	2428152	0.0127	0.1243
chr5	180915260	2369581	0.0131	0.1198
chr6	171115067	1876891	0.011	0.1266
chr7	159138663	2154434	0.0135	0.1821

chr8	146364022	4082675	0.0279	0.1869
chr9	141213431	1835203	0.013	0.14
chr10	135534747	2289074	0.0169	0.1651
chr11	135006516	1486435	0.011	0.1413
chr12	133851895	2030996	0.0152	0.1288
chr13	115169878	948064	0.0082	0.0946
chr14	107349540	1051228	0.0098	0.1044
chr15	102531392	1124166	0.011	0.1119
chr16	90354753	1363629	0.0151	0.1334
chr17	81195210	1580961	0.0195	0.1489
chr18	78077248	1009981	0.0129	0.2213
chr19	59128983	832668	0.0141	0.1877
chr20	63025520	1207889	0.0192	0.1455
chr21	48129895	575653	0.012	0.1185
chr22	51304566	352945	0.0069	0.0867
chrMT	16571	3186	0.1923	0.4332
chrX	155270560	2648983	0.0171	0.1441
chrY	59373566	139570	0.0024	0.0754

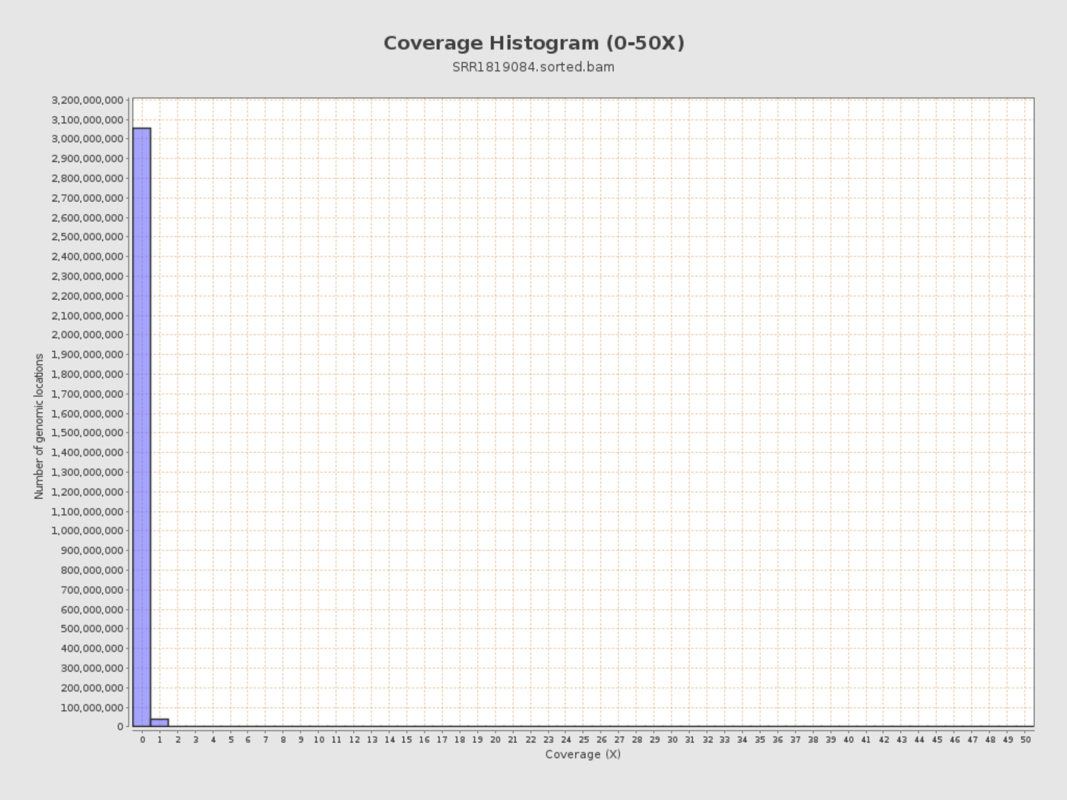
3. Results : Coverage across reference



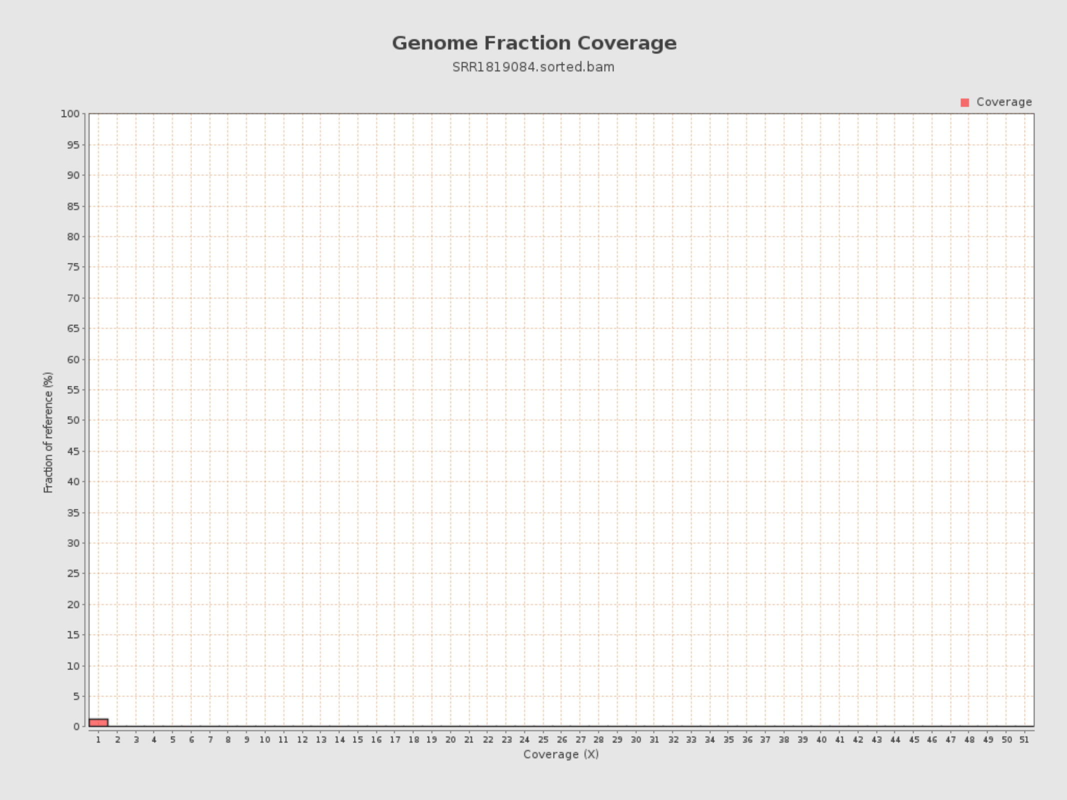
4. Results : Coverage Histogram



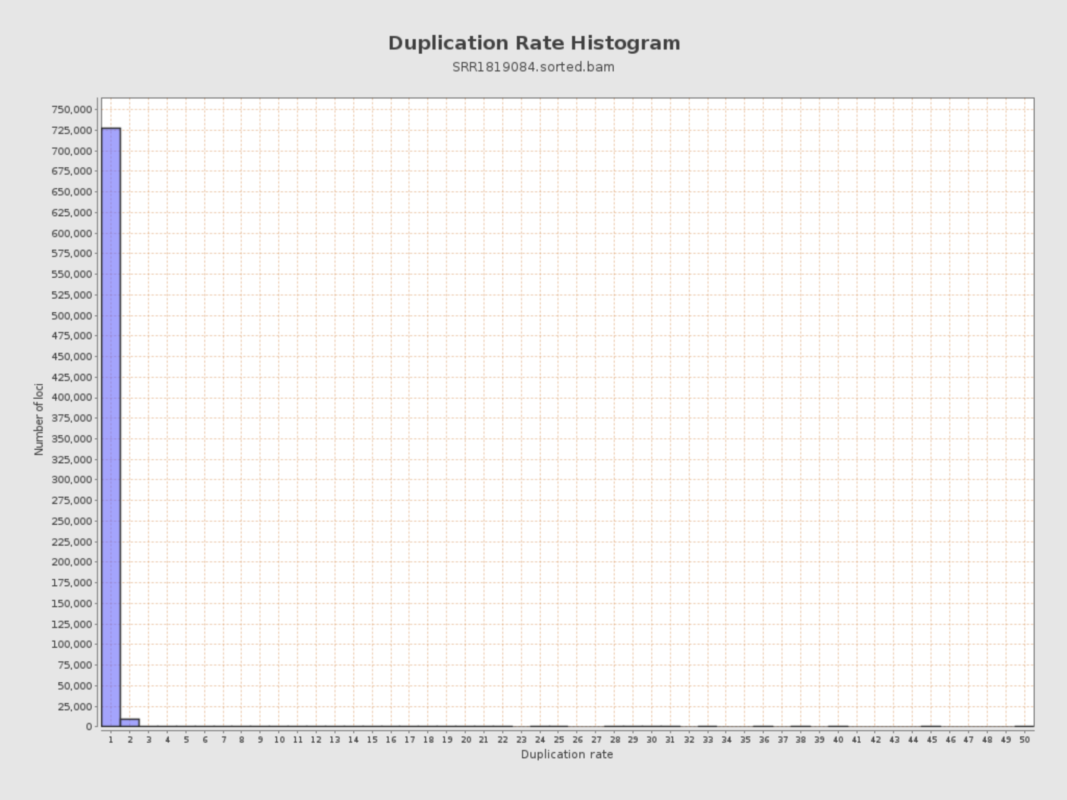
5. Results : Coverage Histogram (0-50X)



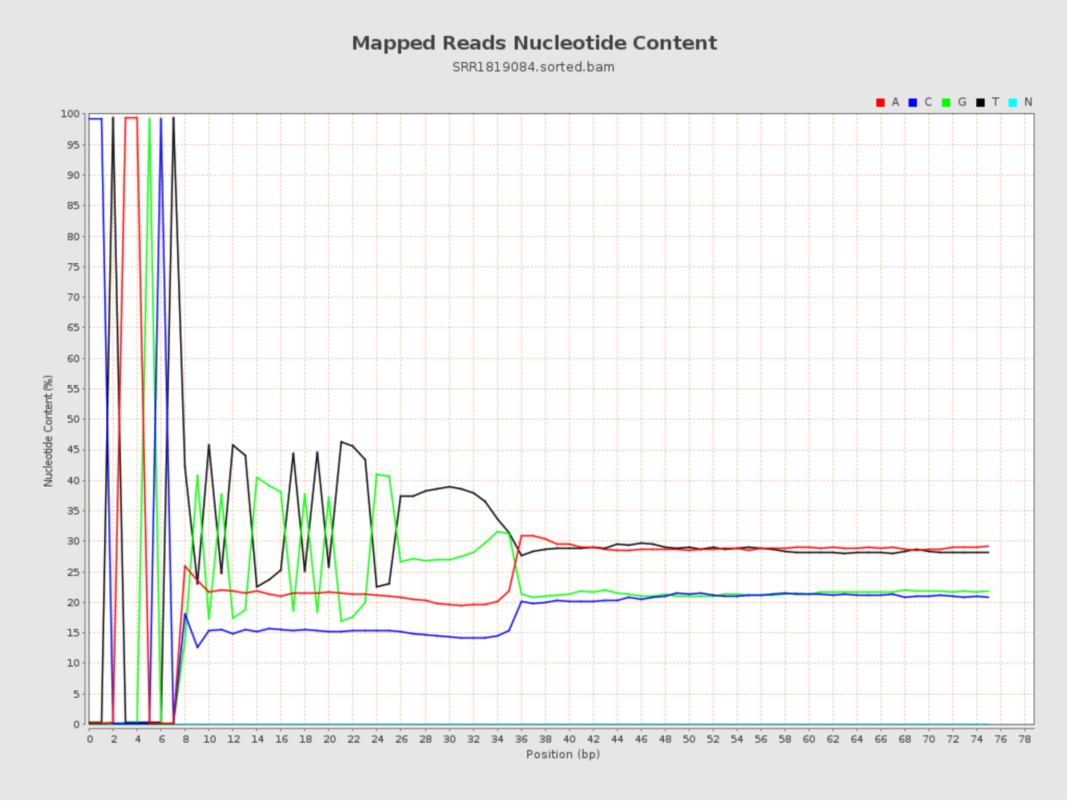
6. Results : Genome Fraction Coverage



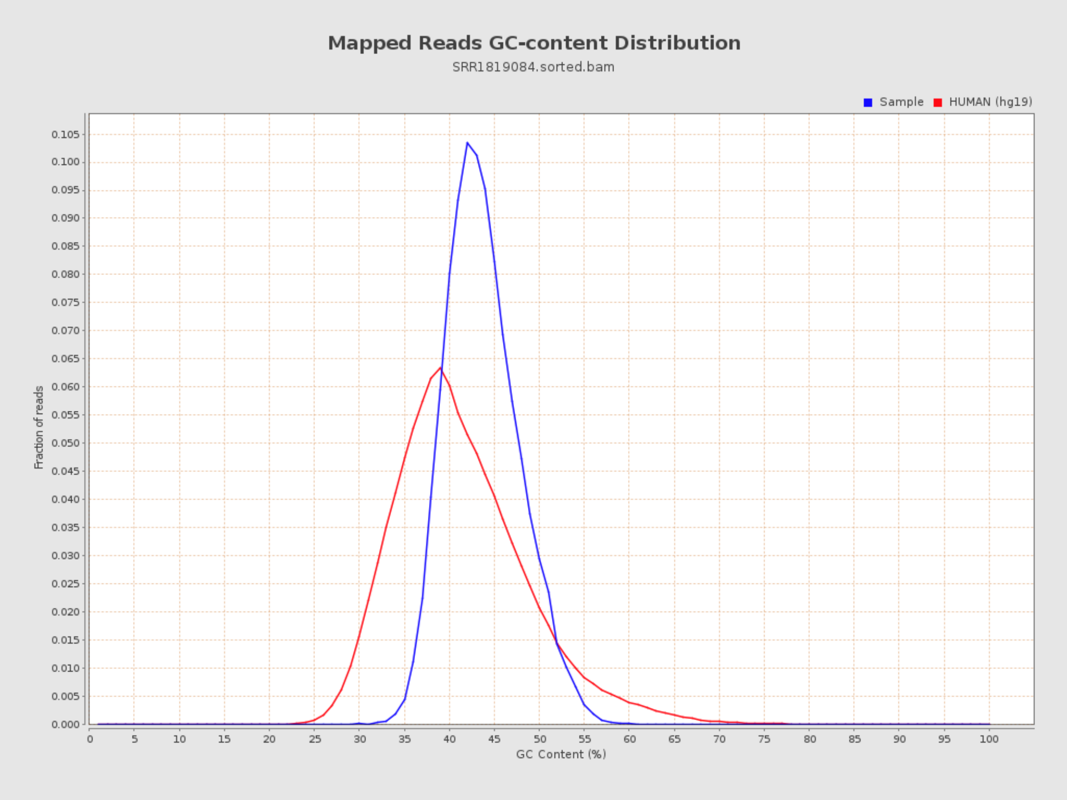
7. Results : Duplication Rate Histogram



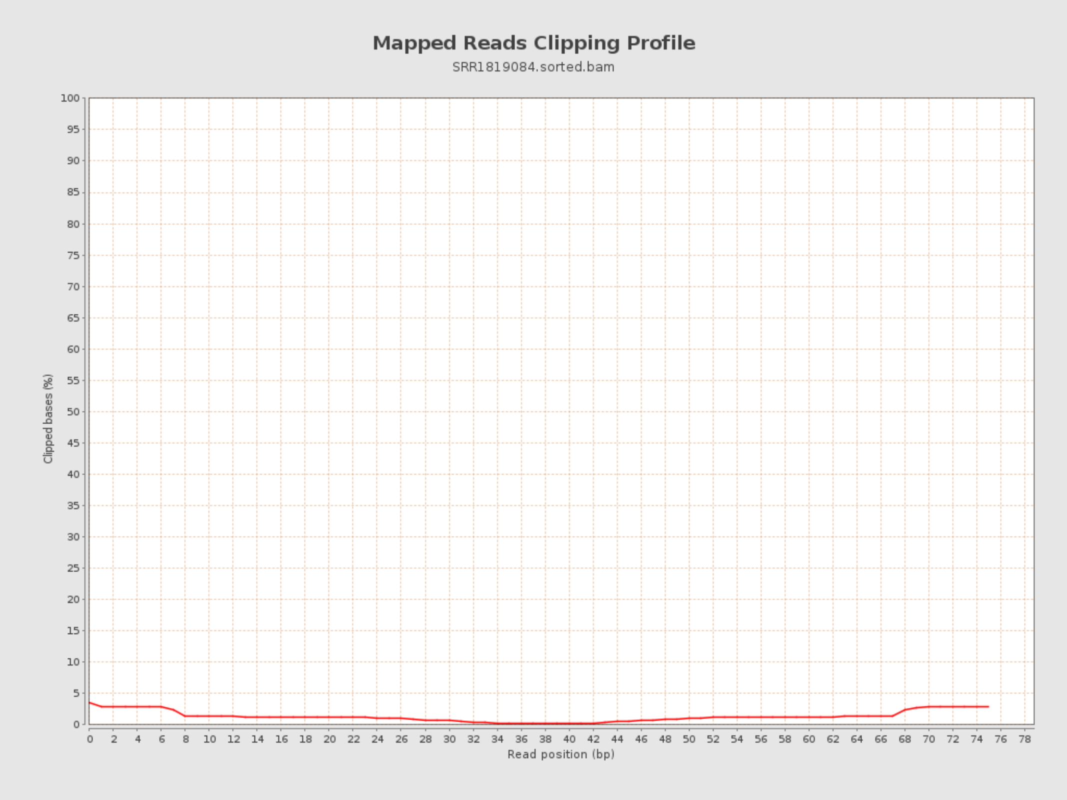
8. Results : Mapped Reads Nucleotide Content



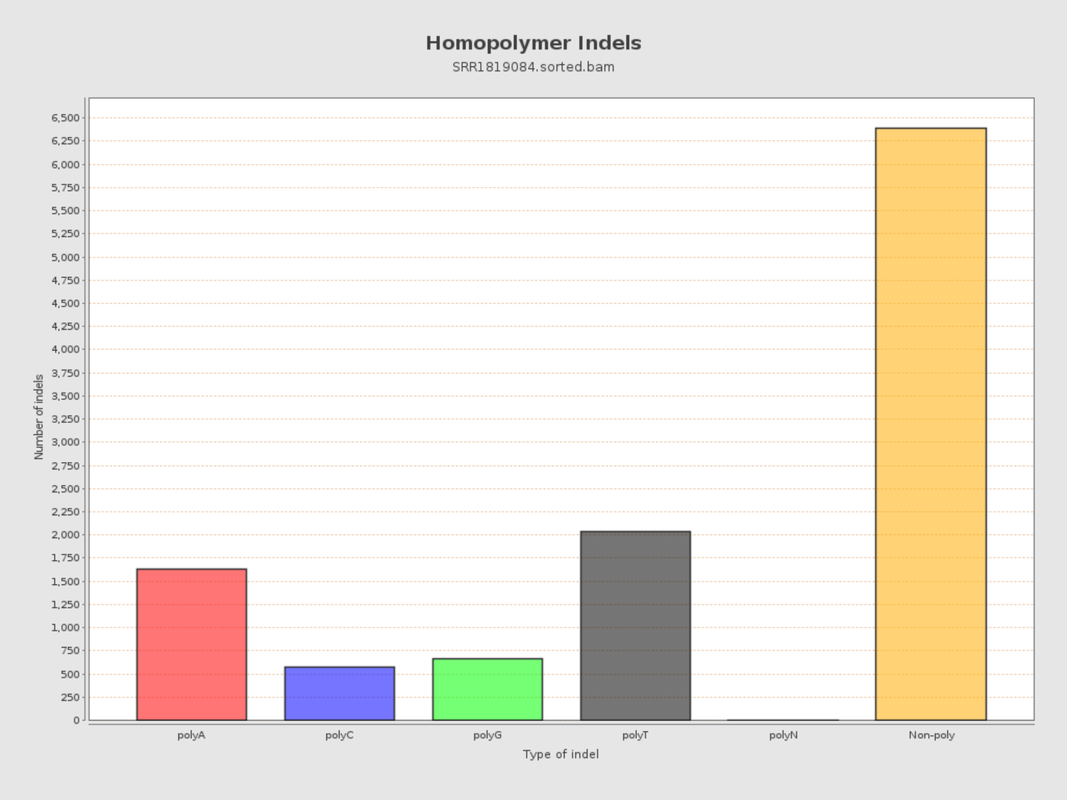
9. Results : Mapped Reads GC-content Distribution



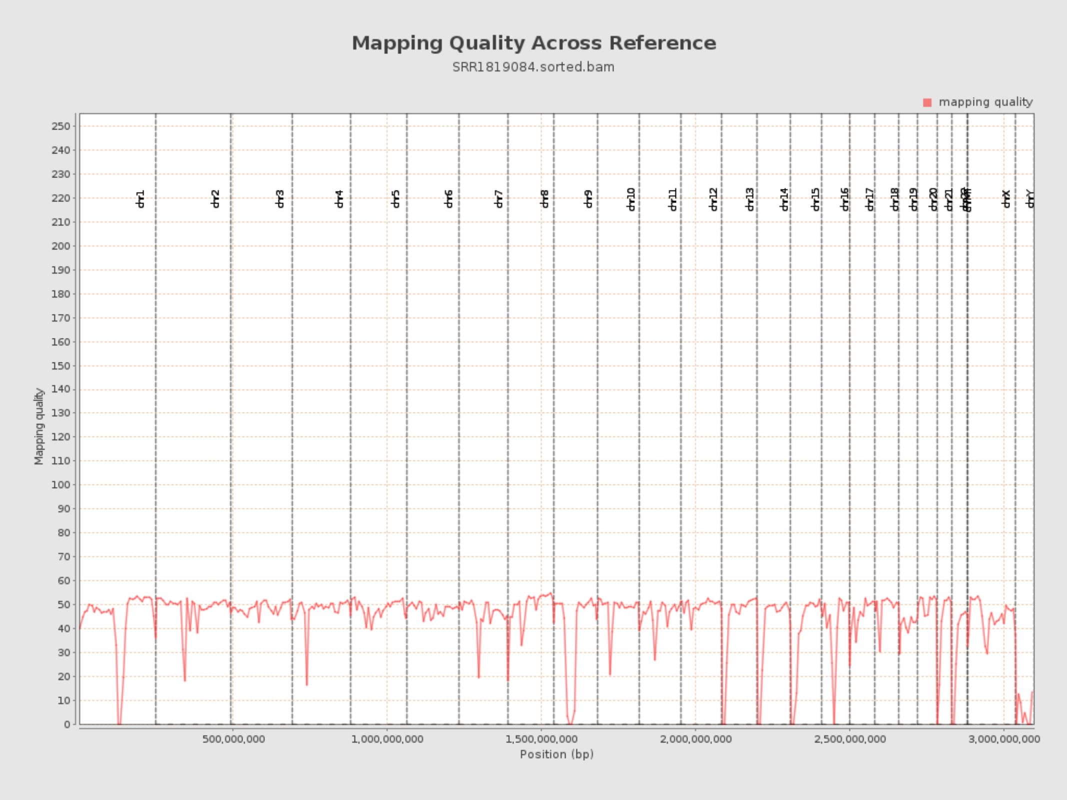
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram