Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:32:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819026.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_SRR1819026 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819026.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:32:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819026.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	590,755
Mapped reads	579,557 / 98.1%
Unmapped reads	11,198 / 1.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,808 / 1.15%
Read min/max/mean length	30 / 101 / 101.44
Duplicated reads (estimated)	103,603 / 17.54%
Duplication rate	15.48%
Clipped reads	585,439 / 99.1%

2.2. ACGT Content

Number/percentage of A's	15,505,860 / 28.92%
Number/percentage of C's	11,810,181 / 22.03%
Number/percentage of T's	14,848,203 / 27.69%
Number/percentage of G's	11,446,855 / 21.35%
Number/percentage of N's	2,424 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.2796

2.4. Mapping Quality

Mean Mapping Quality	49.05

2.5. Mismatches and indels

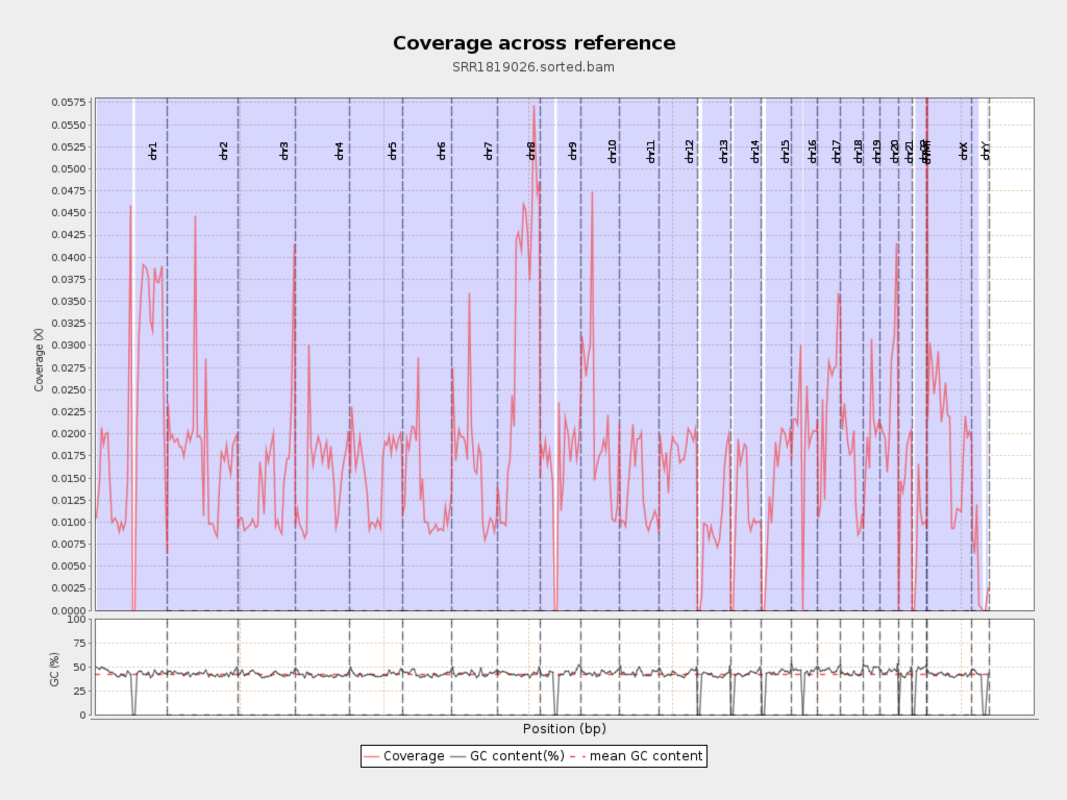
General error rate	0.7%
Mismatches	357,997
Insertions	7,923
Mapped reads with at least one insertion	1.33%
Deletions	16,184
Mapped reads with at least one deletion	2.74%
Homopolymer indels	40.9%

2.6. Chromosome stats

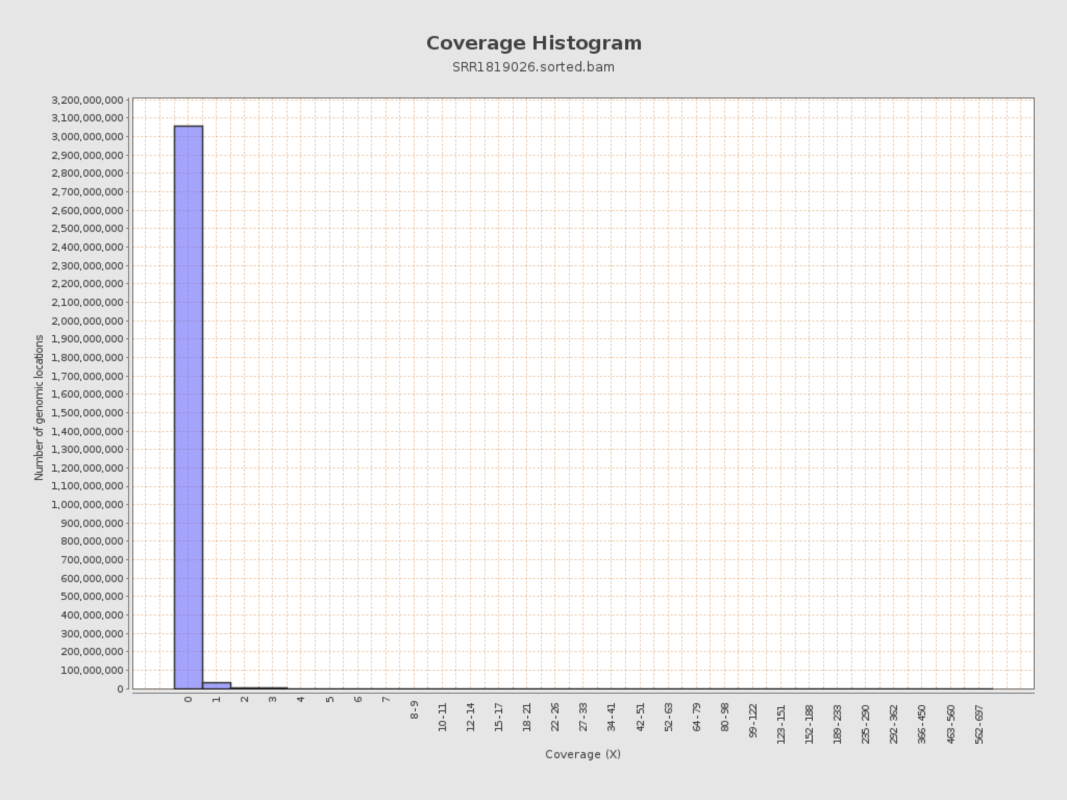
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5429876	0.0218	0.5708
chr2	243199373	4402764	0.0181	0.3466
chr3	198022430	2797789	0.0141	0.1483
chr4	191154276	2965998	0.0155	0.1807
chr5	180915260	2919239	0.0161	0.1636
chr6	171115067	2296781	0.0134	0.1713
chr7	159138663	2657985	0.0167	0.3371

chr8	146364022	4723698	0.0323	0.2475
chr9	141213431	2268145	0.0161	0.2551
chr10	135534747	2907569	0.0215	0.3389
chr11	135006516	1818704	0.0135	0.177
chr12	133851895	2438121	0.0182	0.1693
chr13	115169878	1097713	0.0095	0.1208
chr14	107349540	1234866	0.0115	0.1427
chr15	102531392	1411720	0.0138	0.1459
chr16	90354753	1771073	0.0196	0.2767
chr17	81195210	1902611	0.0234	0.212
chr18	78077248	1283203	0.0164	0.298
chr19	59128983	1189420	0.0201	0.4726
chr20	63025520	1592646	0.0253	0.2082
chr21	48129895	734722	0.0153	0.1651
chr22	51304566	429254	0.0084	0.122
chrMT	16571	3583	0.2162	0.5741
chrX	155270560	3154884	0.0203	0.2038
chrY	59373566	212403	0.0036	0.2331

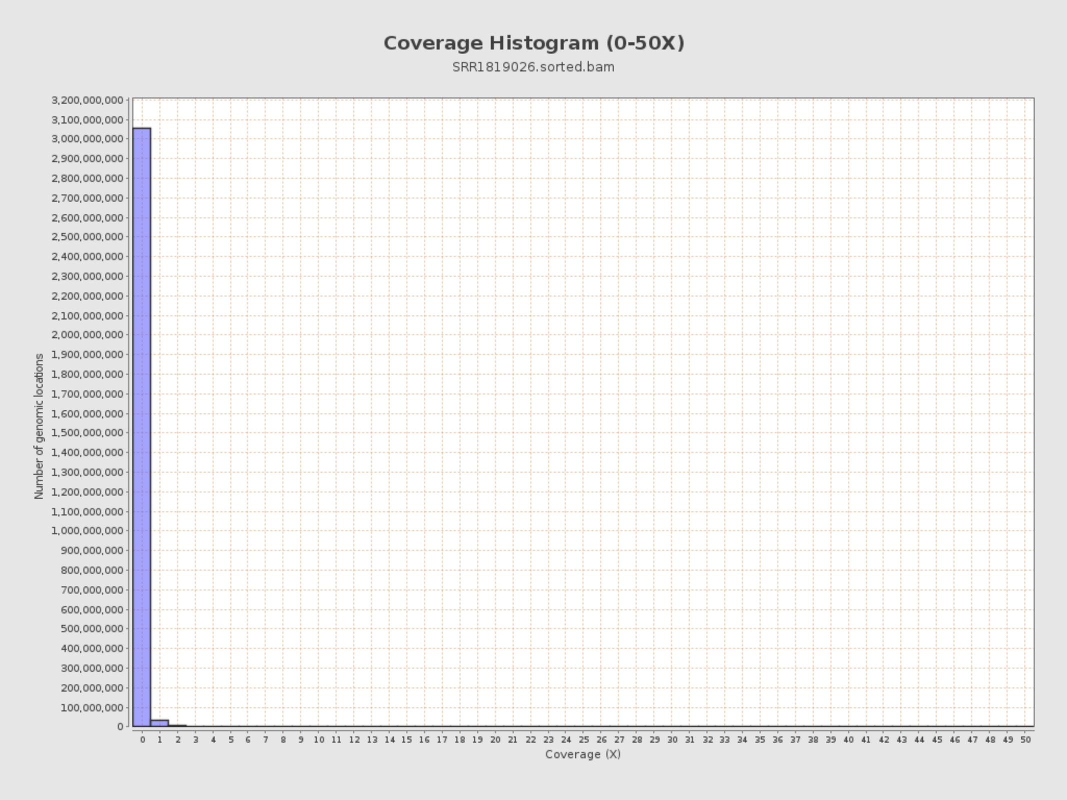
3. Results : Coverage across reference



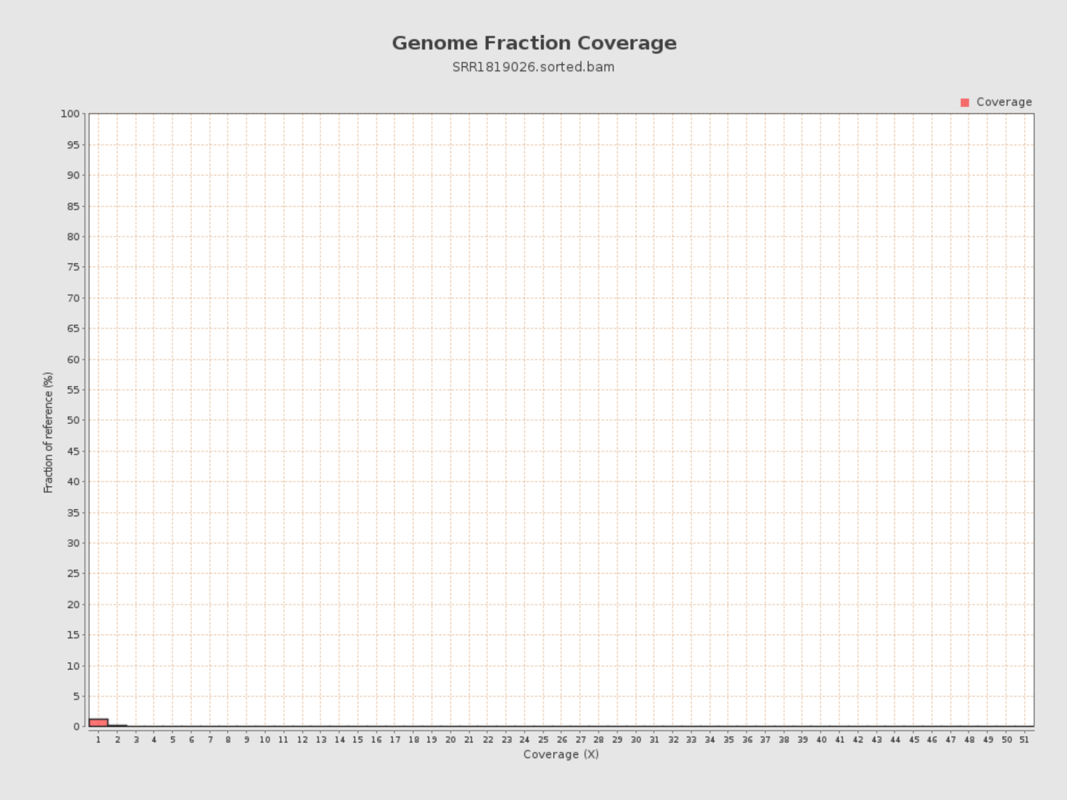
4. Results : Coverage Histogram



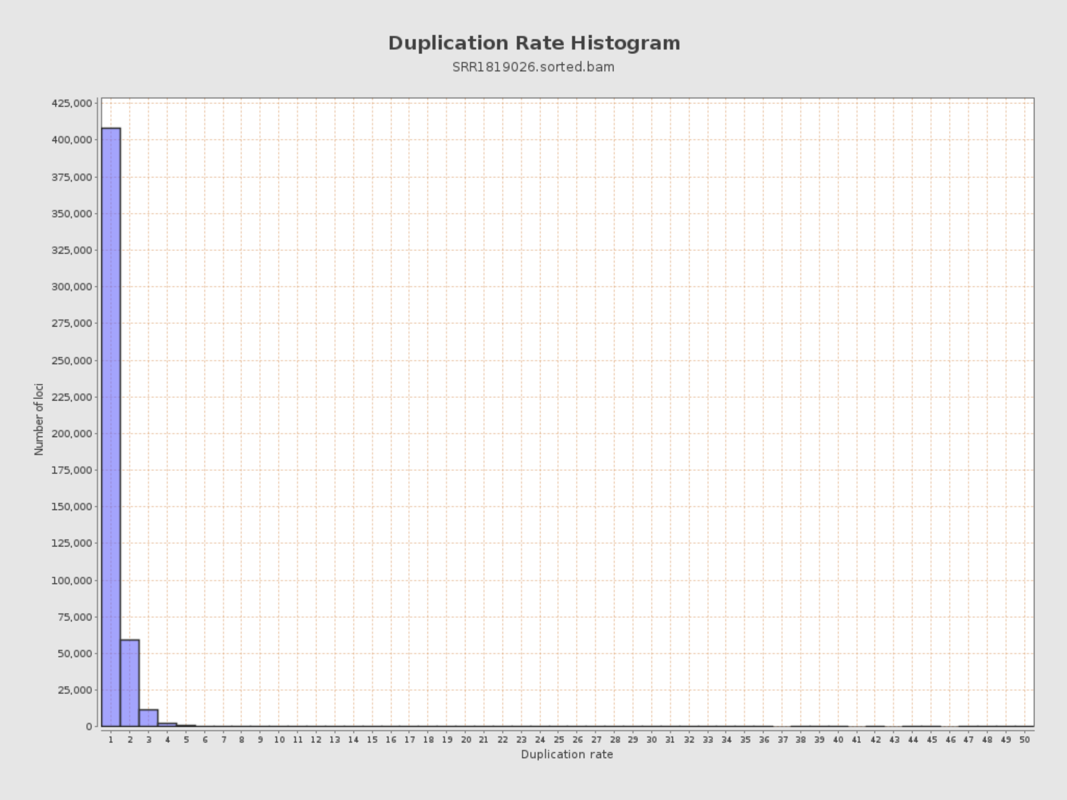
5. Results : Coverage Histogram (0-50X)



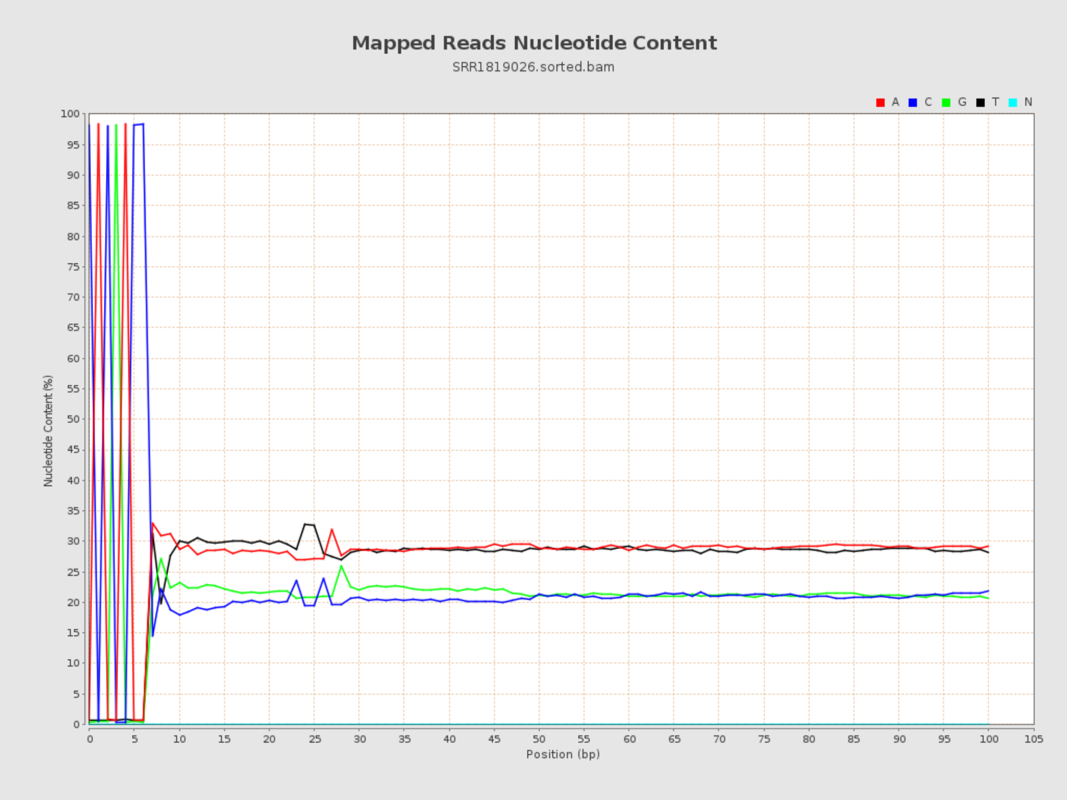
6. Results : Genome Fraction Coverage



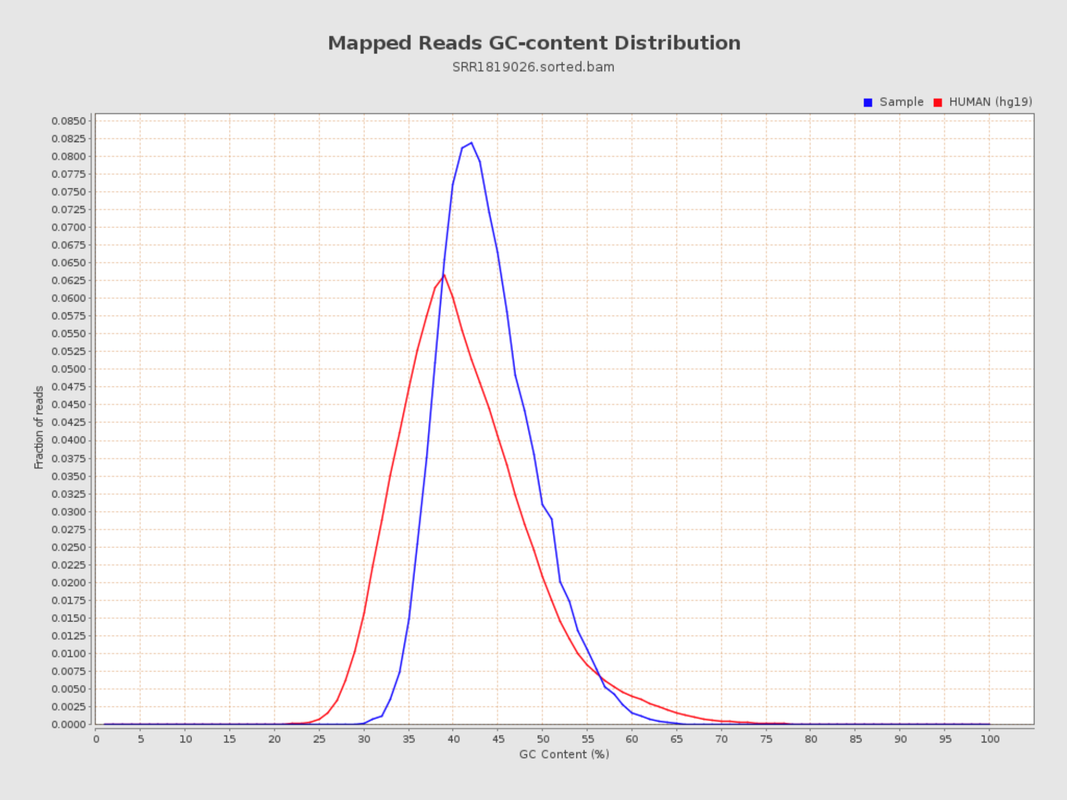
7. Results : Duplication Rate Histogram



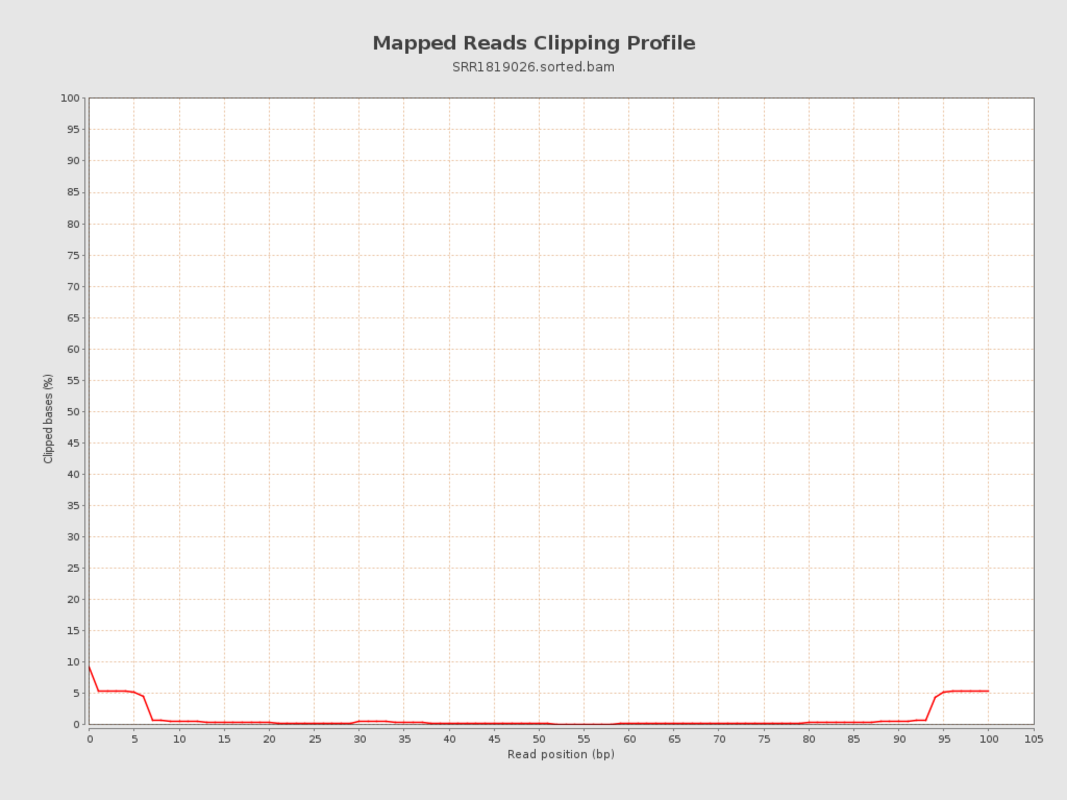
8. Results : Mapped Reads Nucleotide Content



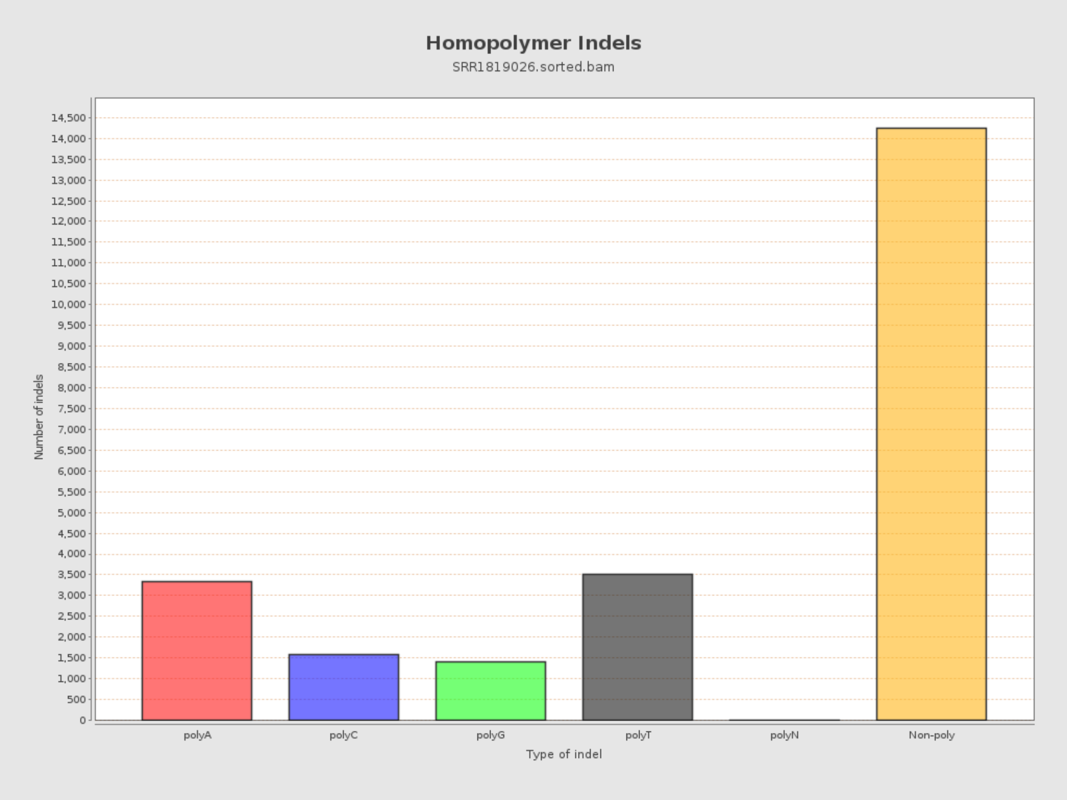
9. Results : Mapped Reads GC-content Distribution



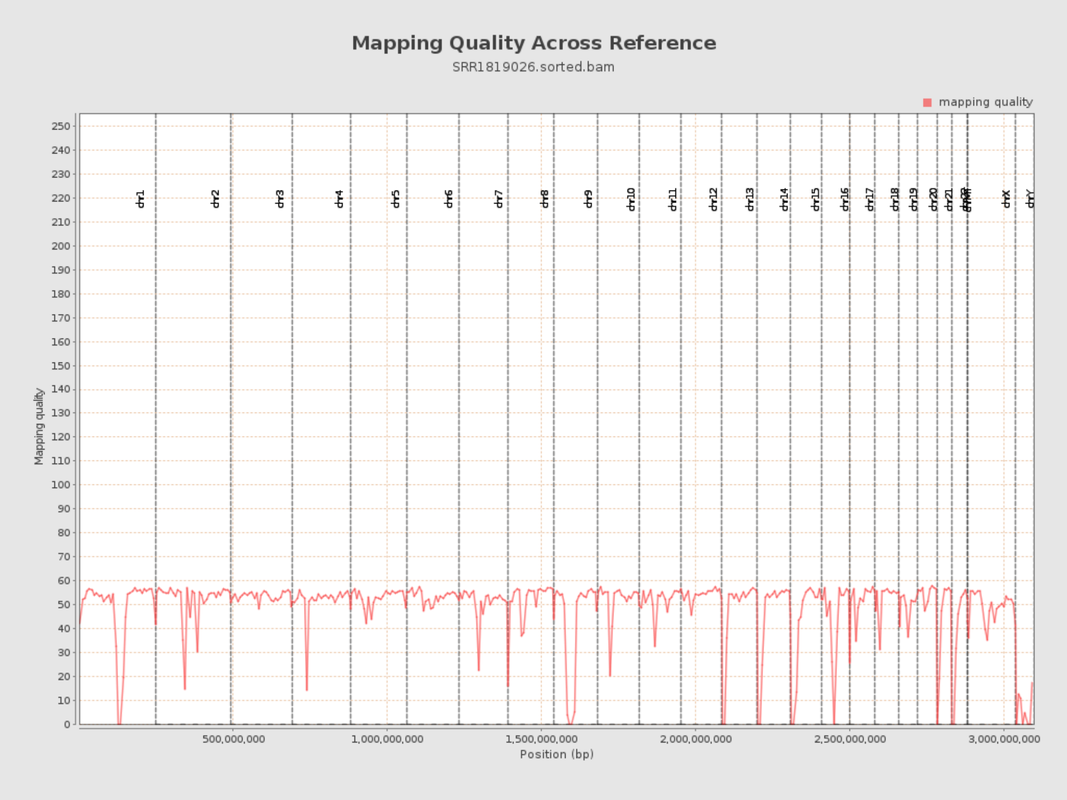
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram