Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:57:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819069.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_SRR1819069 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819069.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:57:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819069.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,130,384
Mapped reads	1,967,683 / 92.36%
Unmapped reads	162,701 / 7.64%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,989 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	108,060 / 5.07%
Duplication rate	4.42%
Clipped reads	1,972,078 / 92.57%

2.2. ACGT Content

Number/percentage of A's	28,979,569 / 25.42%
Number/percentage of C's	22,705,875 / 19.92%
Number/percentage of T's	35,111,110 / 30.8%
Number/percentage of G's	27,185,755 / 23.85%
Number/percentage of N's	2,369 / 0%
GC Percentage	43.77%

2.3. Coverage

Mean	0.0368

Standard Deviation	0.3035

2.4. Mapping Quality

Mean Mapping Quality	45.46

2.5. Mismatches and indels

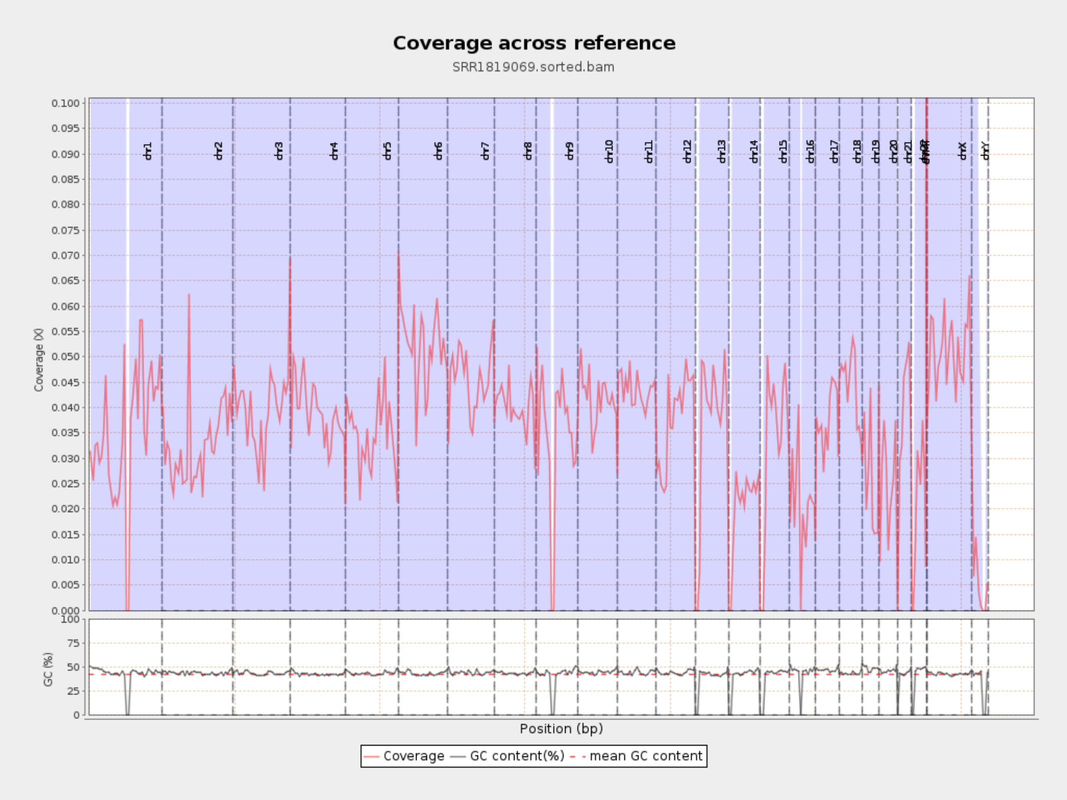
General error rate	0.48%
Mismatches	540,583
Insertions	6,302
Mapped reads with at least one insertion	0.32%
Deletions	16,649
Mapped reads with at least one deletion	0.84%
Homopolymer indels	42.91%

2.6. Chromosome stats

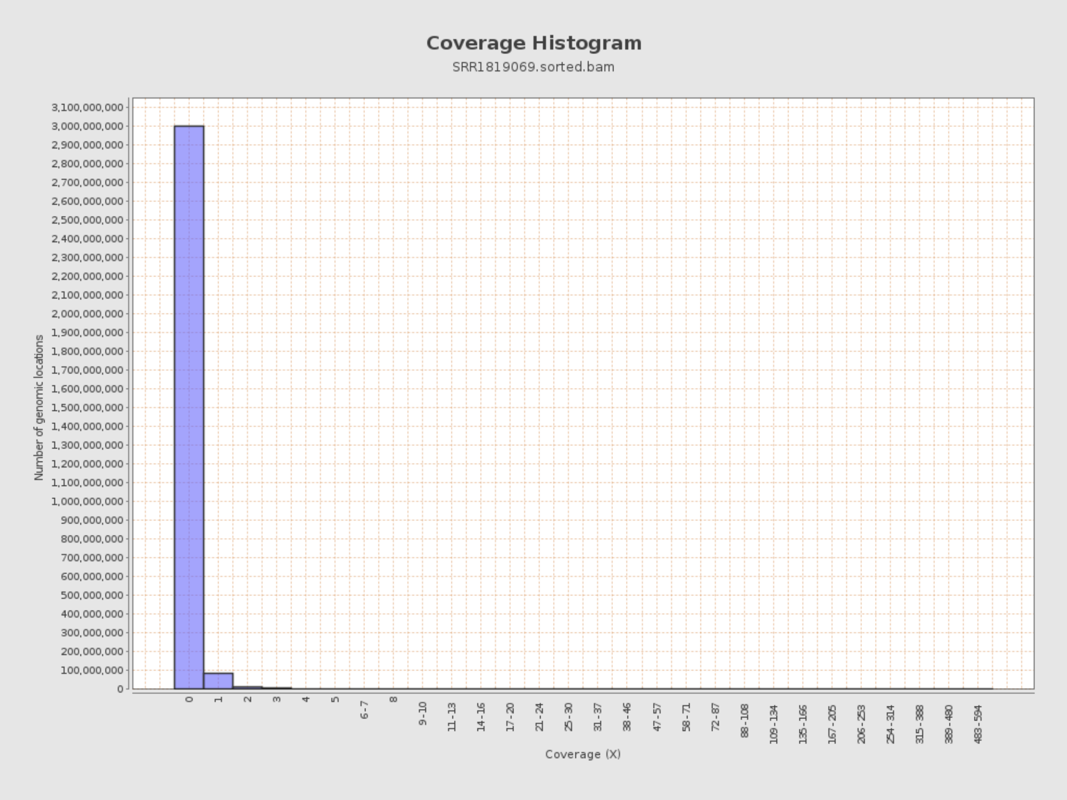
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8628029	0.0346	0.5084
chr2	243199373	7928106	0.0326	0.3541
chr3	198022430	7824396	0.0395	0.2304
chr4	191154276	7469133	0.0391	0.2415
chr5	180915260	6273432	0.0347	0.2185
chr6	171115067	8948050	0.0523	0.2805
chr7	159138663	7244805	0.0455	0.3166

chr8	146364022	5847997	0.04	0.2977
chr9	141213431	4759259	0.0337	0.3119
chr10	135534747	5687324	0.042	0.2657
chr11	135006516	5837415	0.0432	0.3287
chr12	133851895	5057403	0.0378	0.2291
chr13	115169878	4157053	0.0361	0.2199
chr14	107349540	2157026	0.0201	0.1847
chr15	102531392	3431746	0.0335	0.2139
chr16	90354753	1913451	0.0212	0.1879
chr17	81195210	3063047	0.0377	0.2404
chr18	78077248	3514870	0.045	0.5301
chr19	59128983	1546711	0.0262	0.3473
chr20	63025520	1596100	0.0253	0.199
chr21	48129895	1791192	0.0372	0.2424
chr22	51304566	1043954	0.0203	0.165
chrMT	16571	5486	0.3311	0.6065
chrX	155270560	7934951	0.0511	0.3016
chrY	59373566	351201	0.0059	0.1079

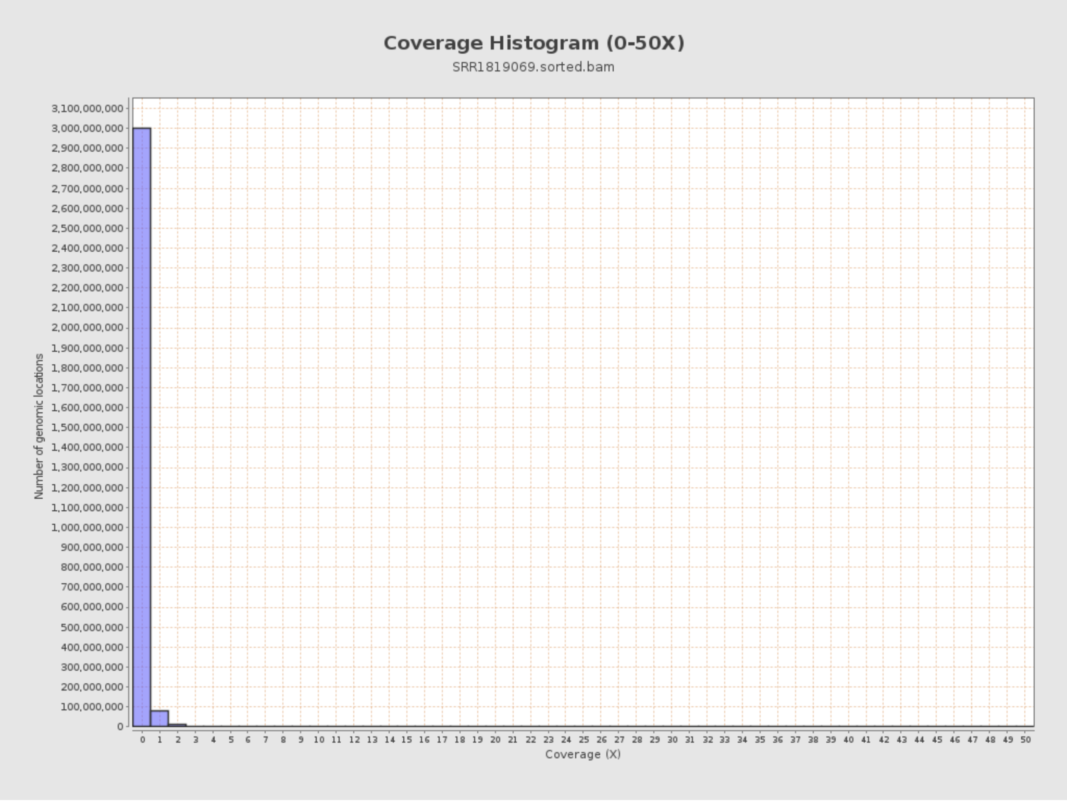
3. Results : Coverage across reference



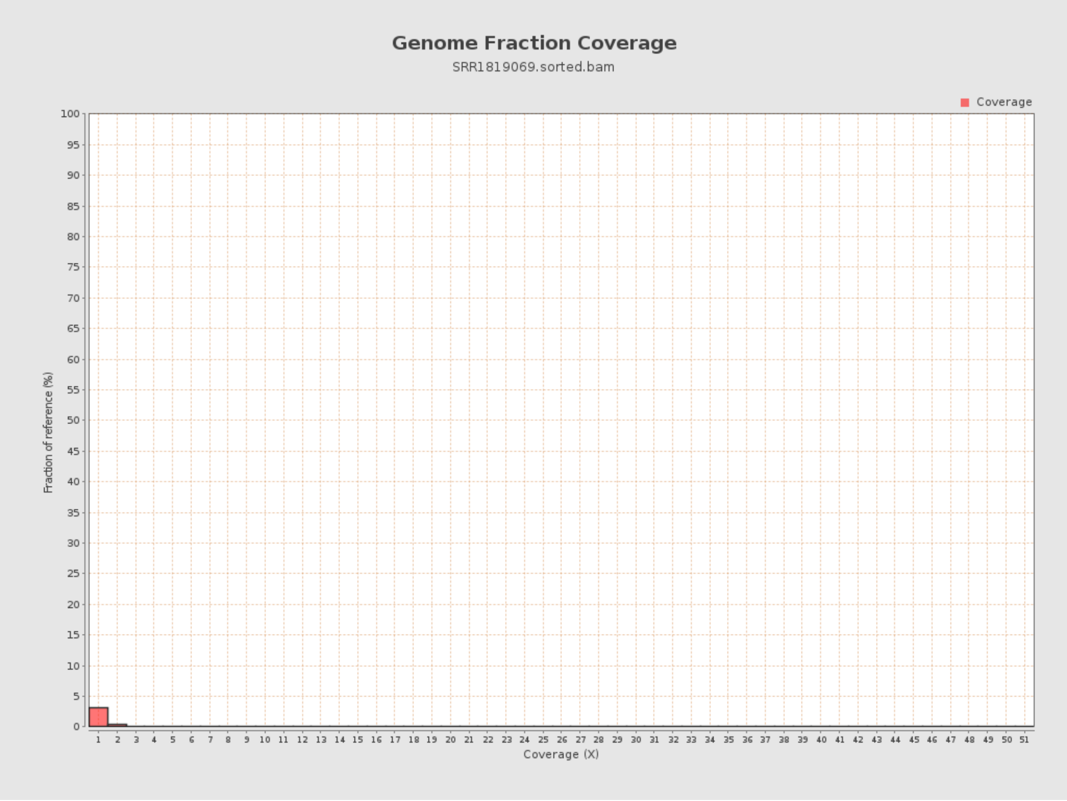
4. Results : Coverage Histogram



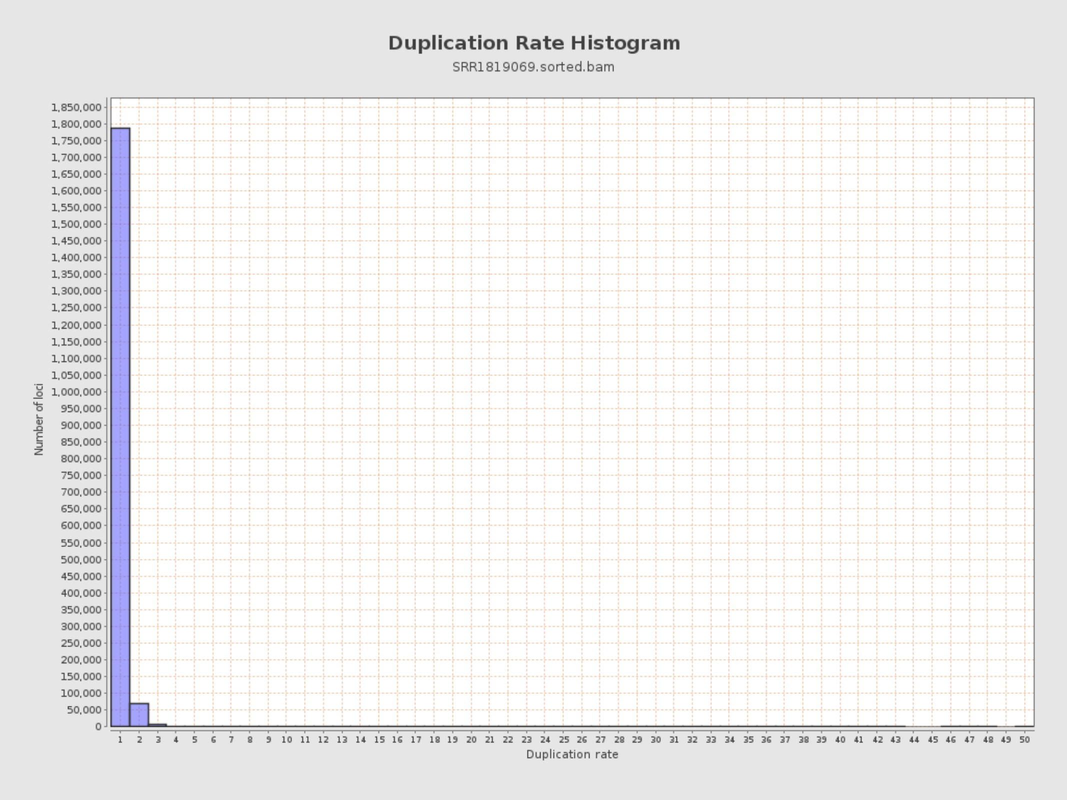
5. Results : Coverage Histogram (0-50X)



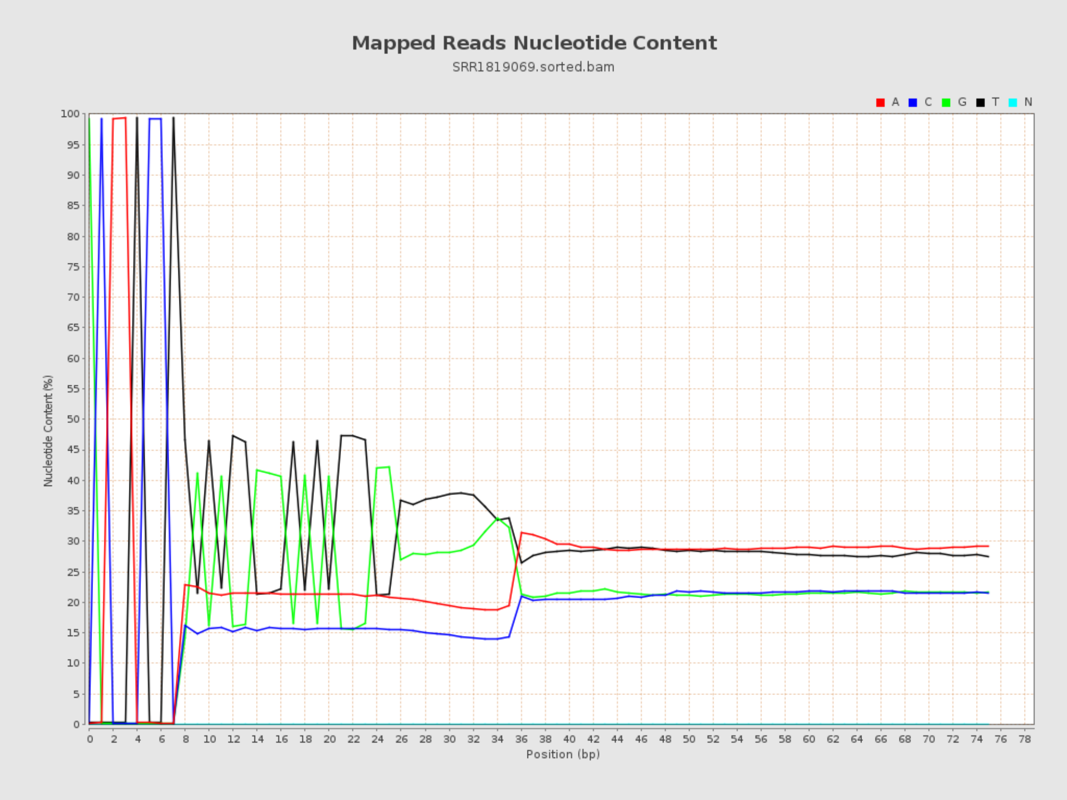
6. Results : Genome Fraction Coverage



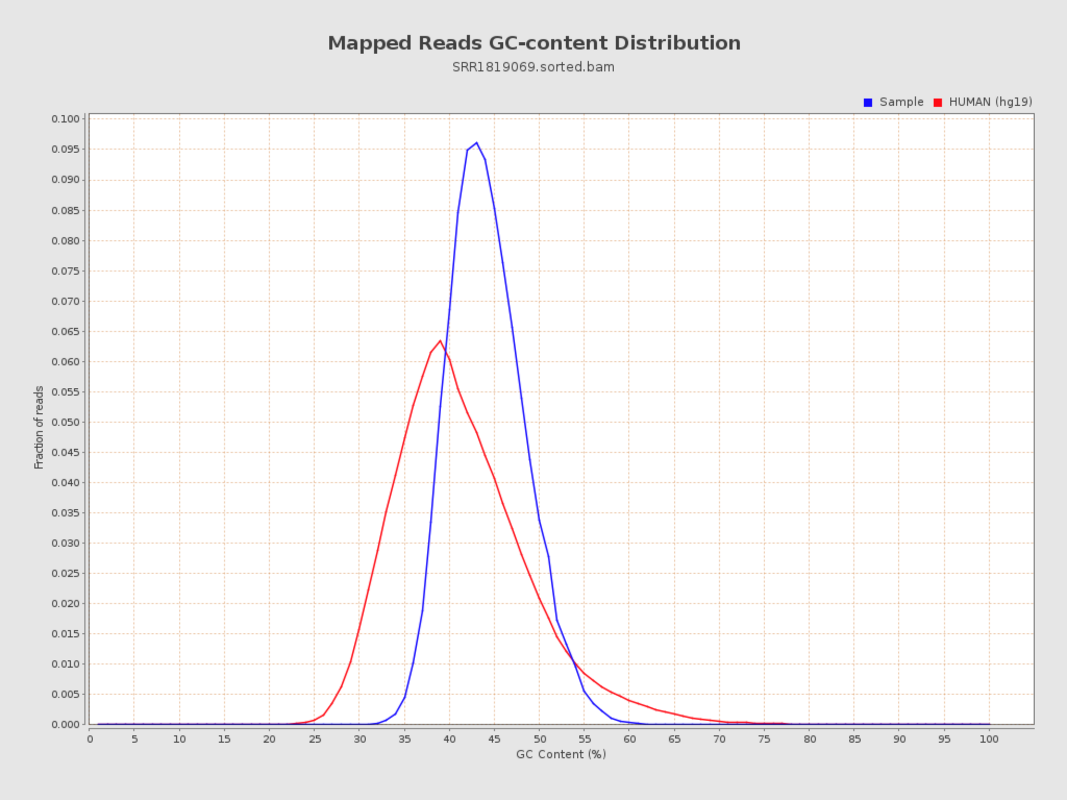
7. Results : Duplication Rate Histogram



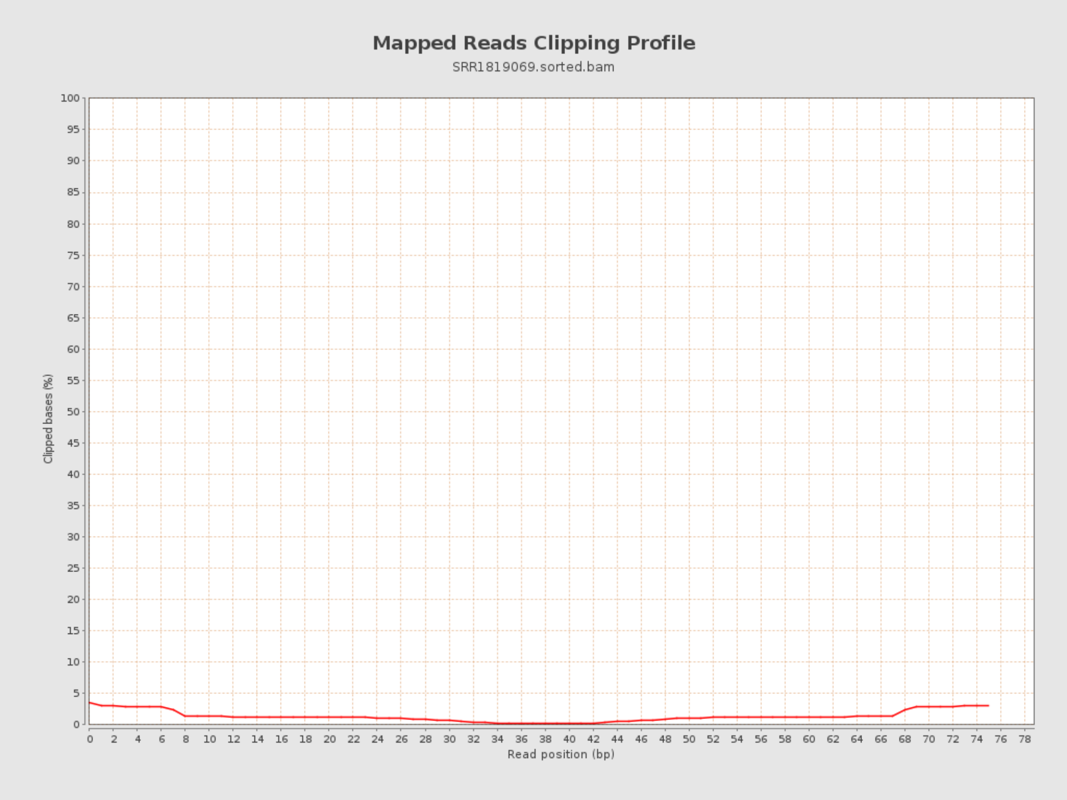
8. Results : Mapped Reads Nucleotide Content



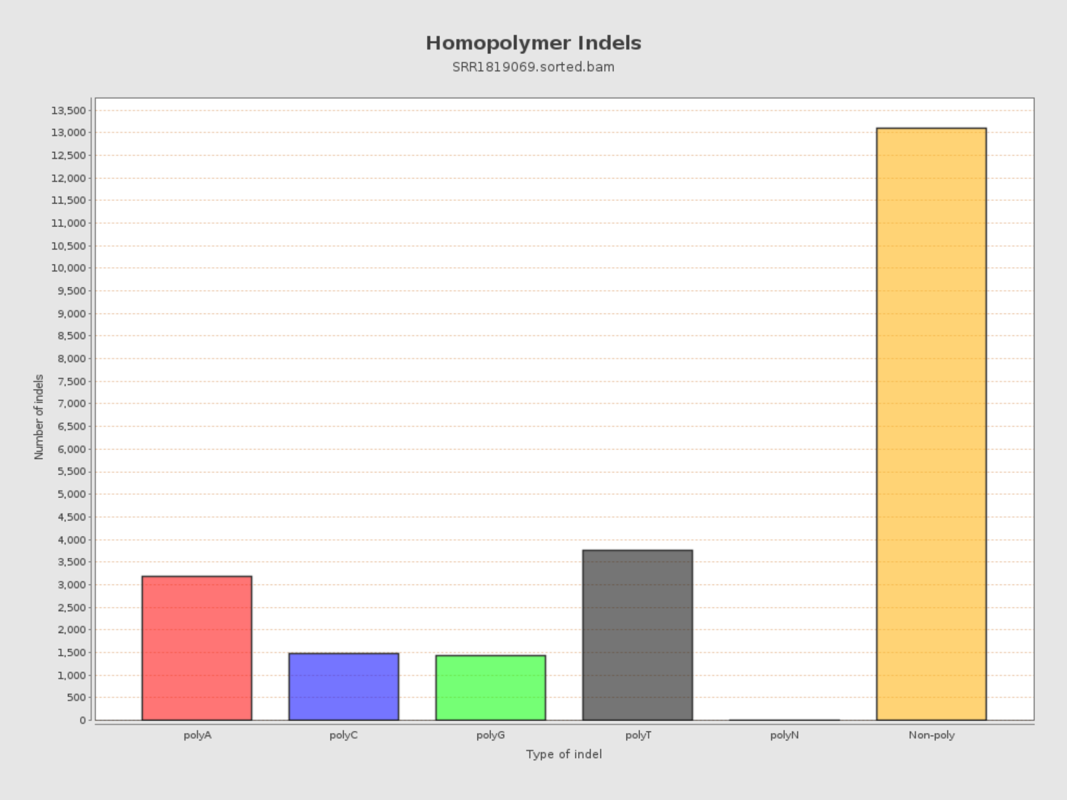
9. Results : Mapped Reads GC-content Distribution



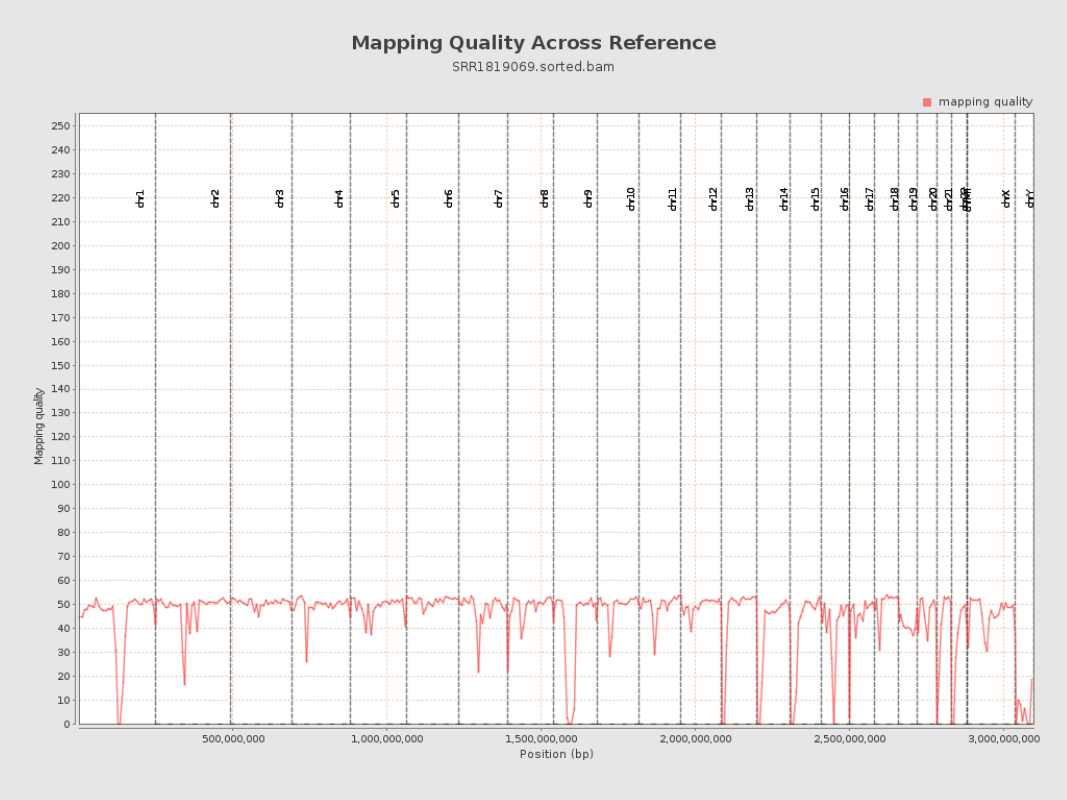
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram