Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 18:30:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819060.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_SRR1819060 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819060.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 18:30:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819060.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,325,019
Mapped reads	3,001,248 / 90.26%
Unmapped reads	323,771 / 9.74%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	13,246 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	140,169 / 4.22%
Duplication rate	3.64%
Clipped reads	3,008,159 / 90.47%

2.2. ACGT Content

Number/percentage of A's	44,292,532 / 25.54%
Number/percentage of C's	33,350,330 / 19.23%
Number/percentage of T's	54,568,215 / 31.47%
Number/percentage of G's	41,184,495 / 23.75%
Number/percentage of N's	4,055 / 0%
GC Percentage	42.98%

2.3. Coverage

Mean	0.056

Standard Deviation	0.3797

2.4. Mapping Quality

Mean Mapping Quality	44.88

2.5. Mismatches and indels

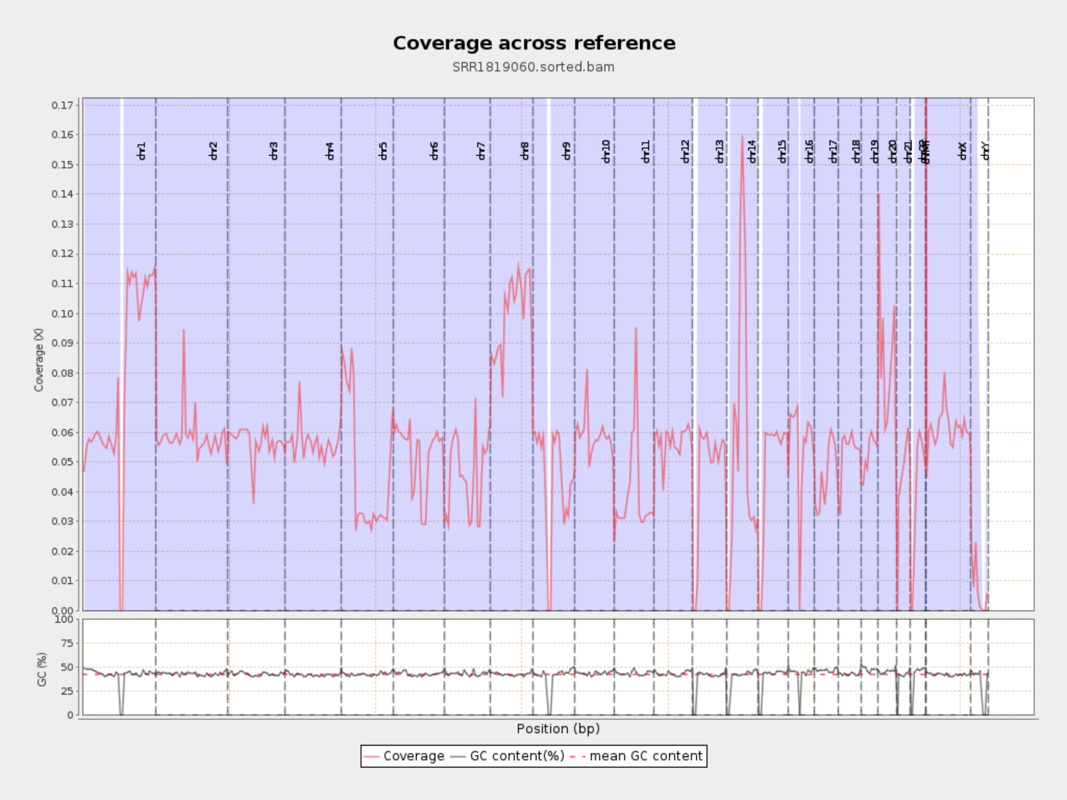
General error rate	0.49%
Mismatches	825,019
Insertions	9,830
Mapped reads with at least one insertion	0.33%
Deletions	26,392
Mapped reads with at least one deletion	0.87%
Homopolymer indels	41.71%

2.6. Chromosome stats

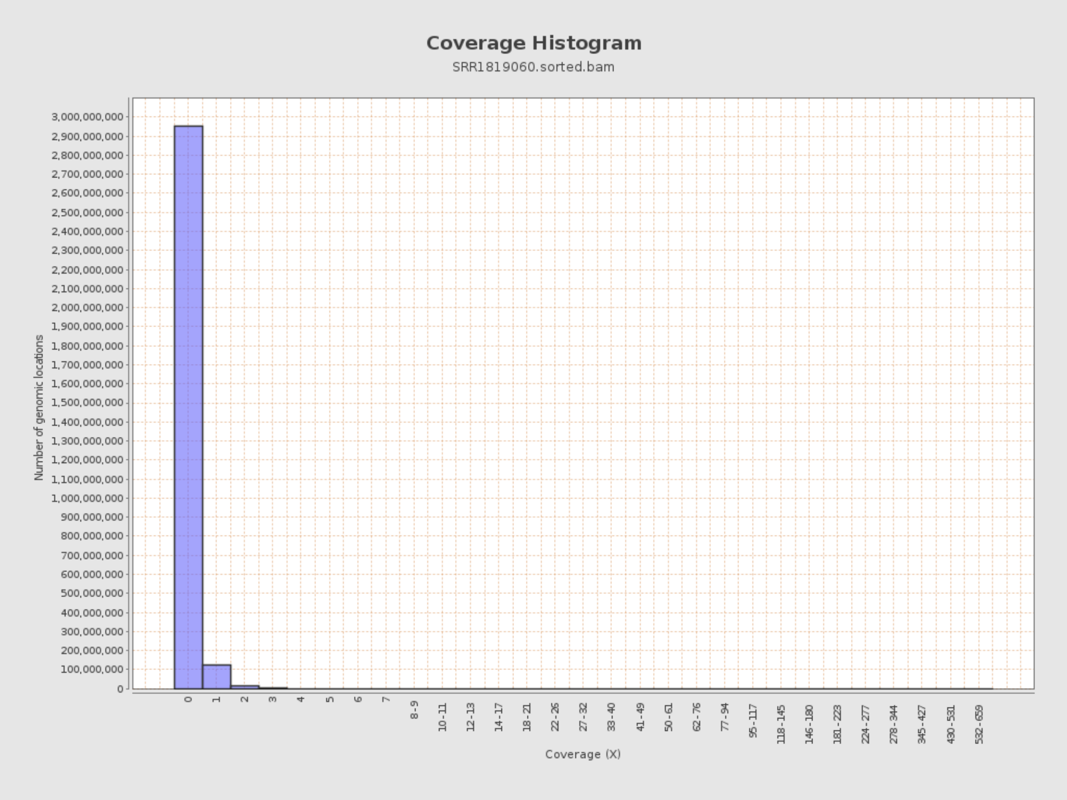
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	18959016	0.0761	0.6083
chr2	243199373	14237281	0.0585	0.4429
chr3	198022430	11226700	0.0567	0.2759
chr4	191154276	10804996	0.0565	0.3034
chr5	180915260	8440968	0.0467	0.258
chr6	171115067	8995792	0.0526	0.2938
chr7	159138663	7264319	0.0456	0.3263

chr8	146364022	14634039	0.1	0.4598
chr9	141213431	6206461	0.044	0.3896
chr10	135534747	7981582	0.0589	0.3716
chr11	135006516	5322744	0.0394	0.3591
chr12	133851895	7660889	0.0572	0.287
chr13	115169878	5314011	0.0461	0.2474
chr14	107349540	6014910	0.056	0.3065
chr15	102531392	4877823	0.0476	0.2546
chr16	90354753	4904780	0.0543	0.302
chr17	81195210	3720029	0.0458	0.2663
chr18	78077248	4163130	0.0533	0.7622
chr19	59128983	3130419	0.0529	0.4641
chr20	63025520	5421661	0.086	0.356
chr21	48129895	2168508	0.0451	0.2764
chr22	51304566	2000268	0.039	0.2269
chrMT	16571	8492	0.5125	0.8855
chrX	155270560	9534189	0.0614	0.3403
chrY	59373566	450621	0.0076	0.1557

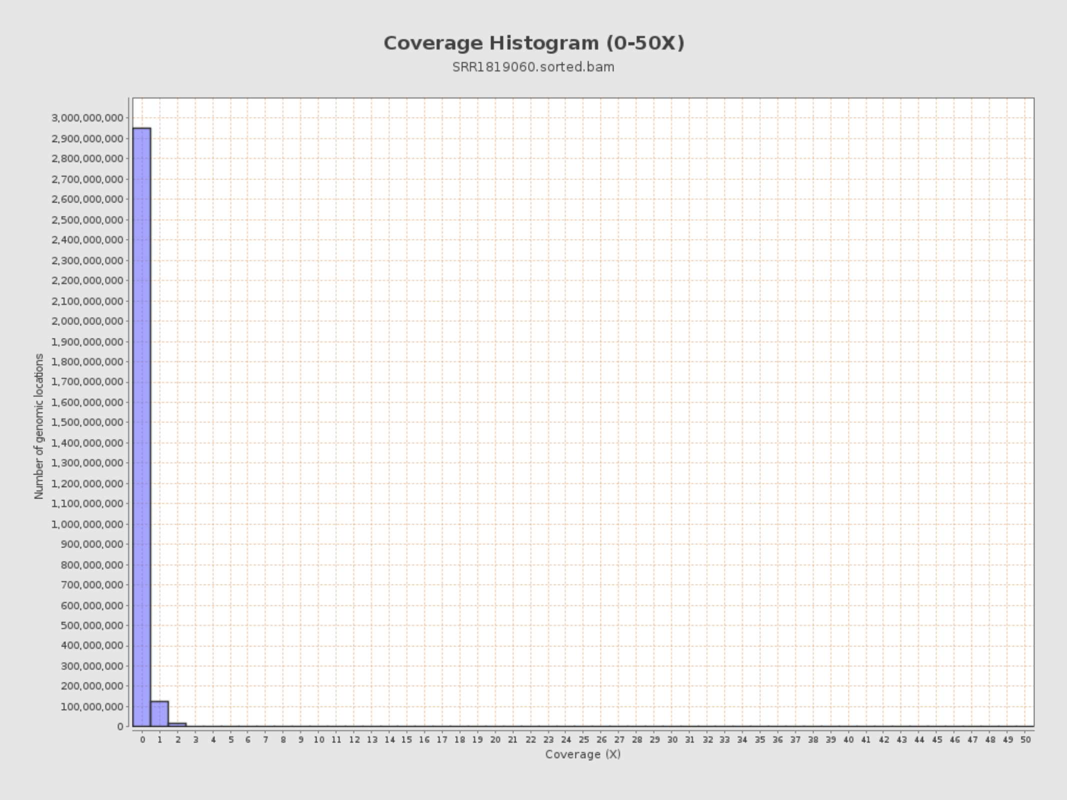
3. Results : Coverage across reference



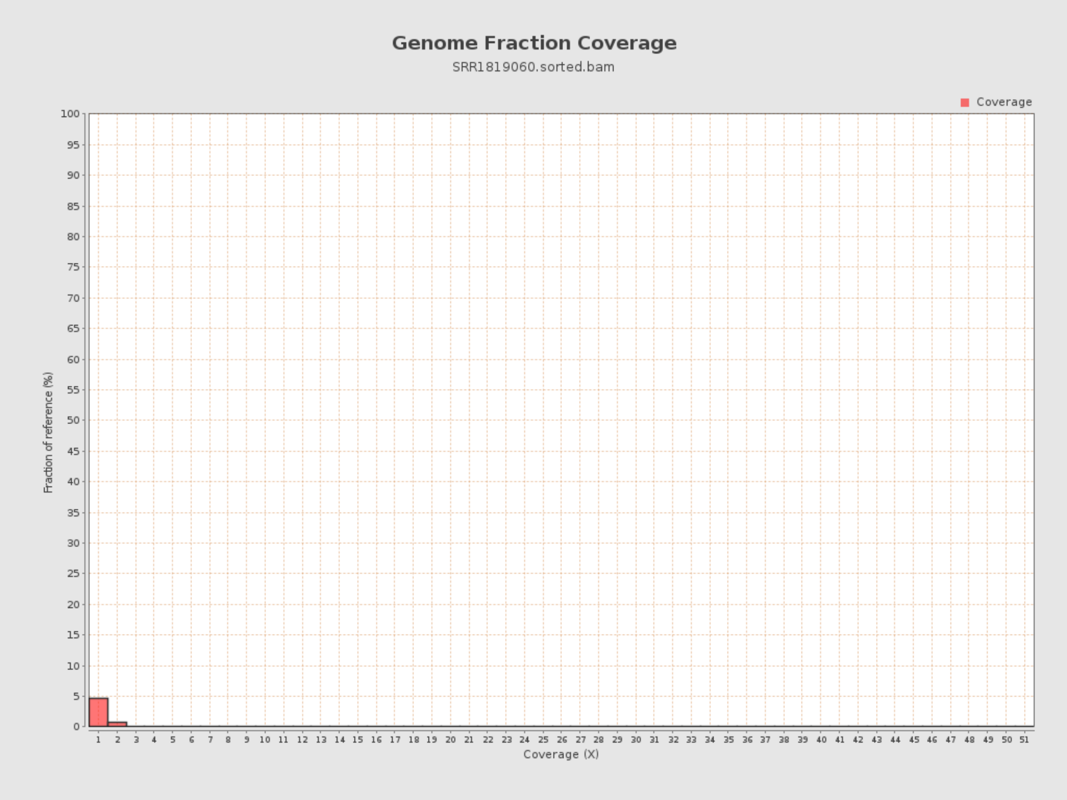
4. Results : Coverage Histogram



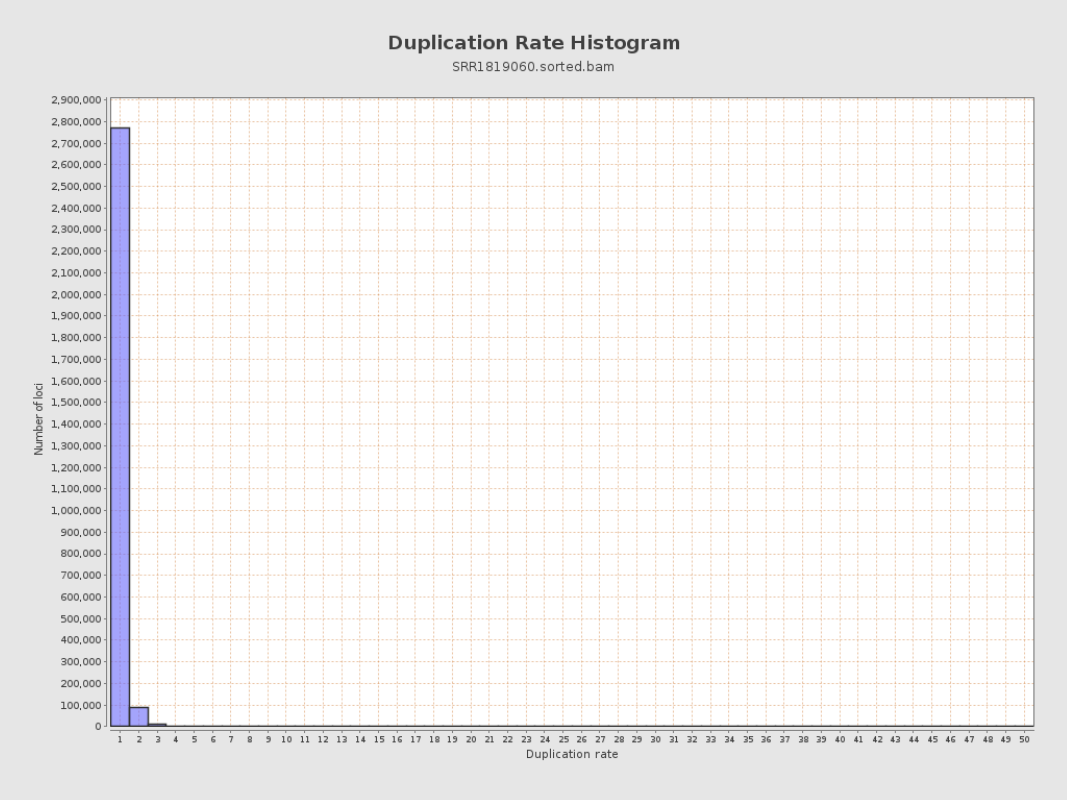
5. Results : Coverage Histogram (0-50X)



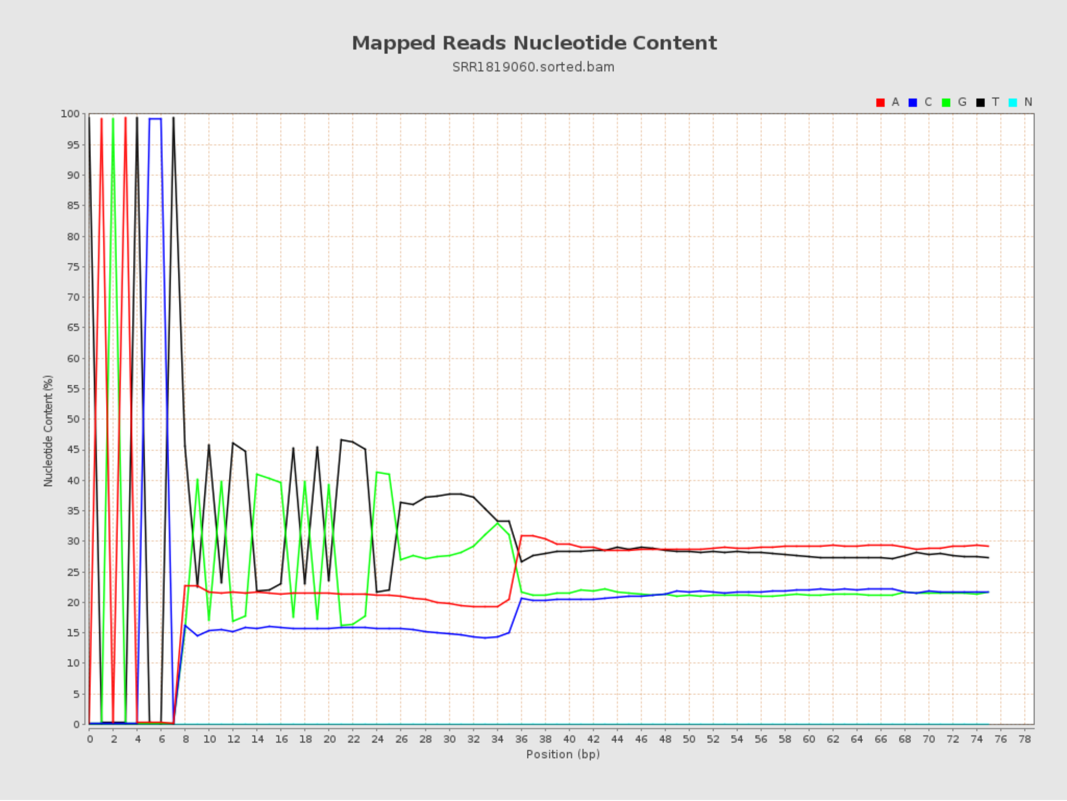
6. Results : Genome Fraction Coverage



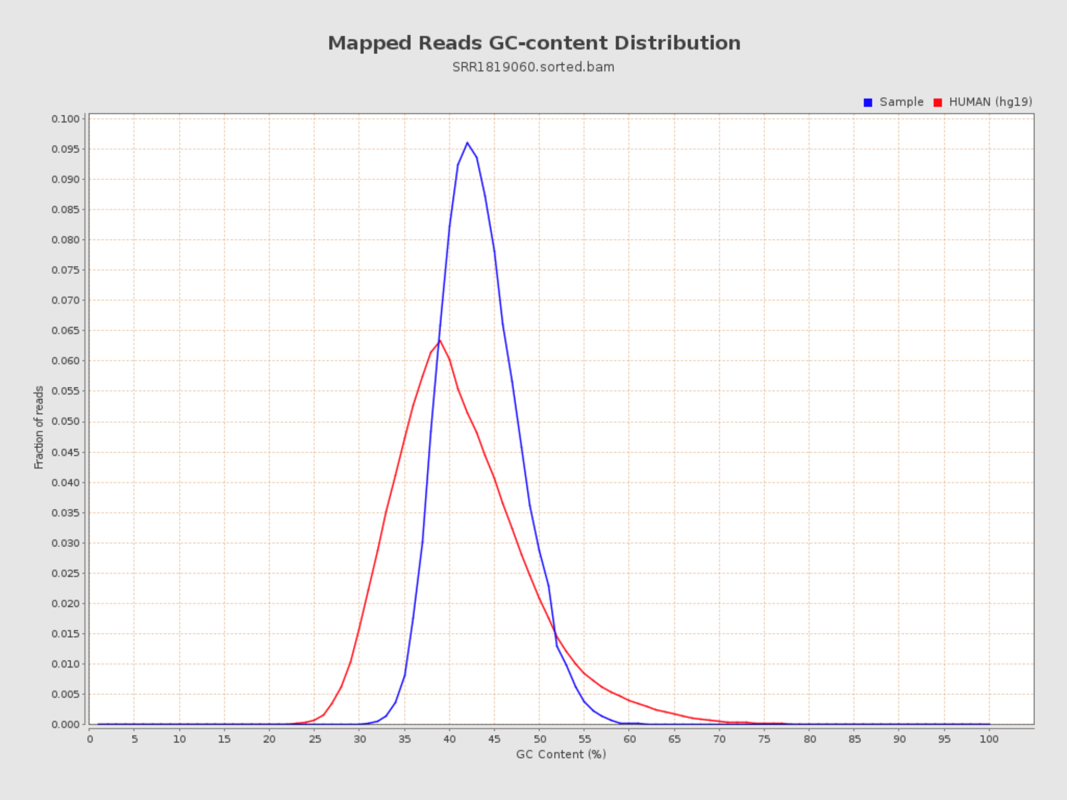
7. Results : Duplication Rate Histogram



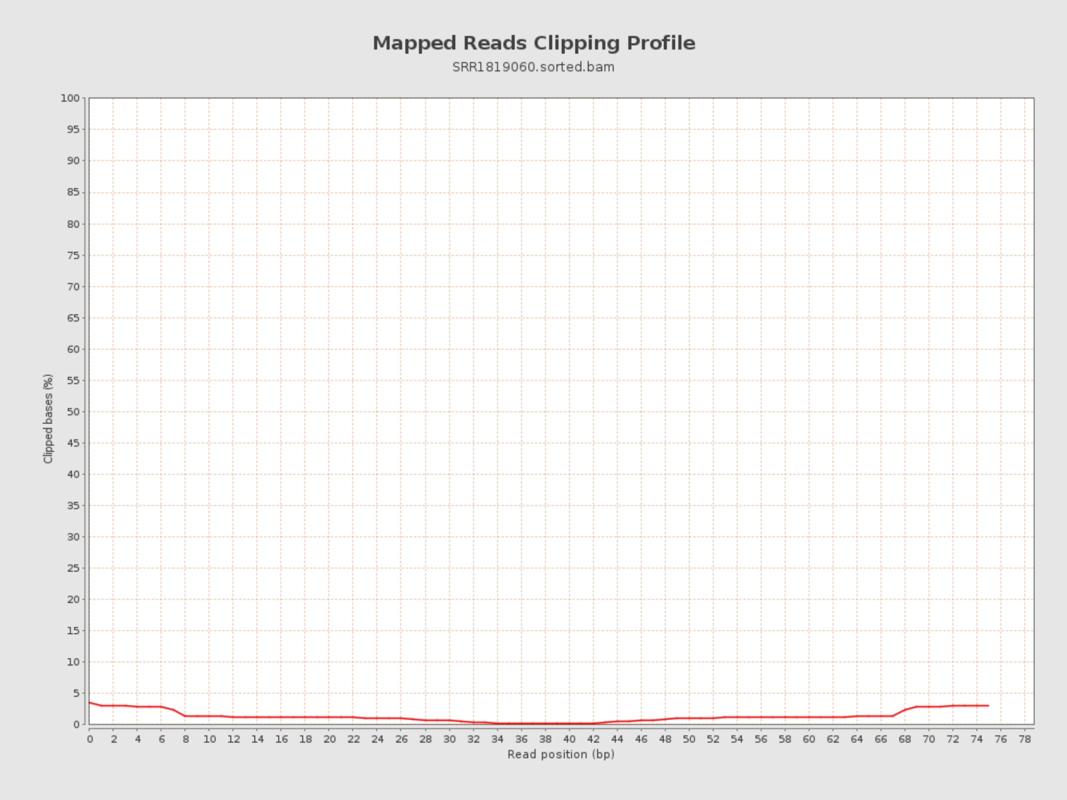
8. Results : Mapped Reads Nucleotide Content



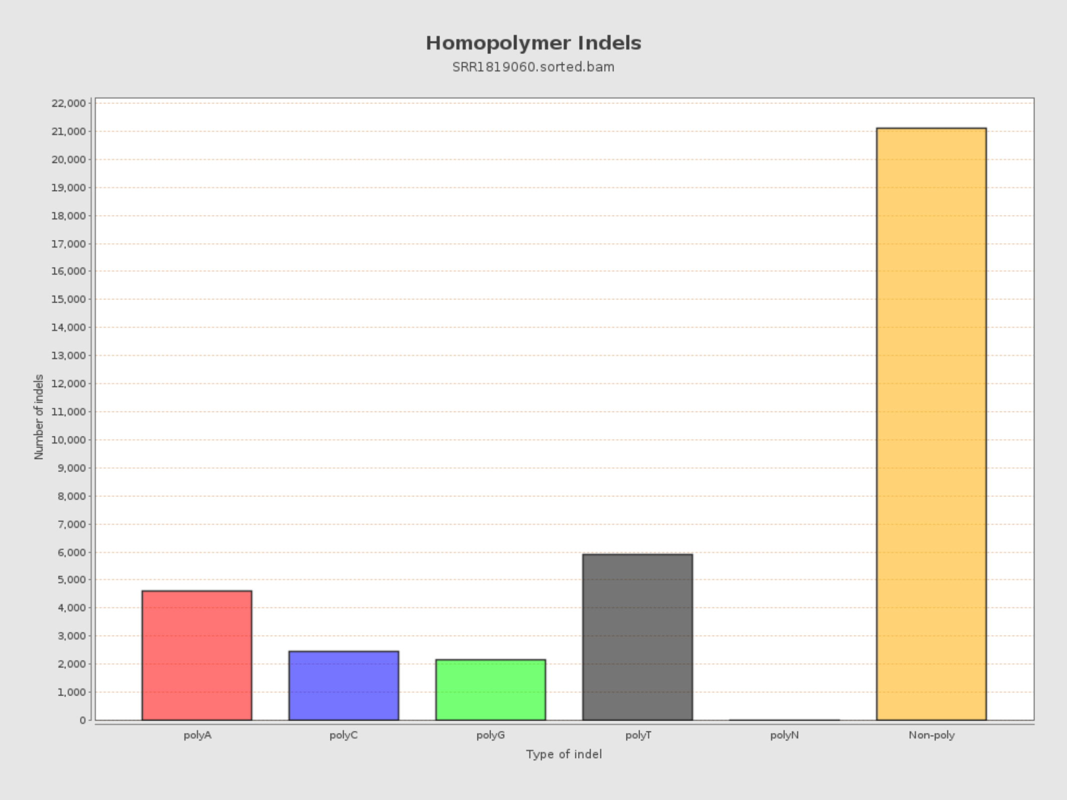
9. Results : Mapped Reads GC-content Distribution



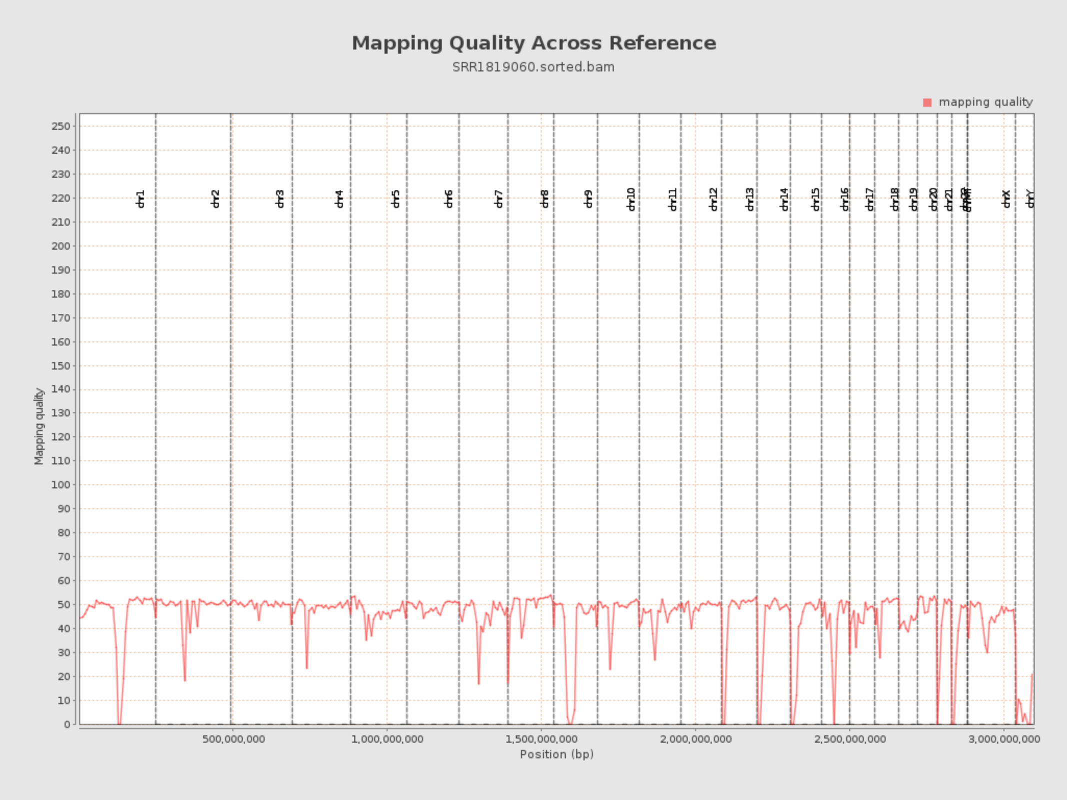
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram