Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 23:33:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819097.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_SRR1819097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819097.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 23:33:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,206,067
Mapped reads	4,775,836 / 91.74%
Unmapped reads	430,231 / 8.26%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,762 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	386,862 / 7.43%
Duplication rate	5.87%
Clipped reads	4,789,034 / 91.99%

2.2. ACGT Content

Number/percentage of A's	66,854,802 / 23.97%
Number/percentage of C's	50,019,898 / 17.94%
Number/percentage of T's	91,575,584 / 32.84%
Number/percentage of G's	70,399,254 / 25.25%
Number/percentage of N's	3,851 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0901

Standard Deviation	0.7387

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

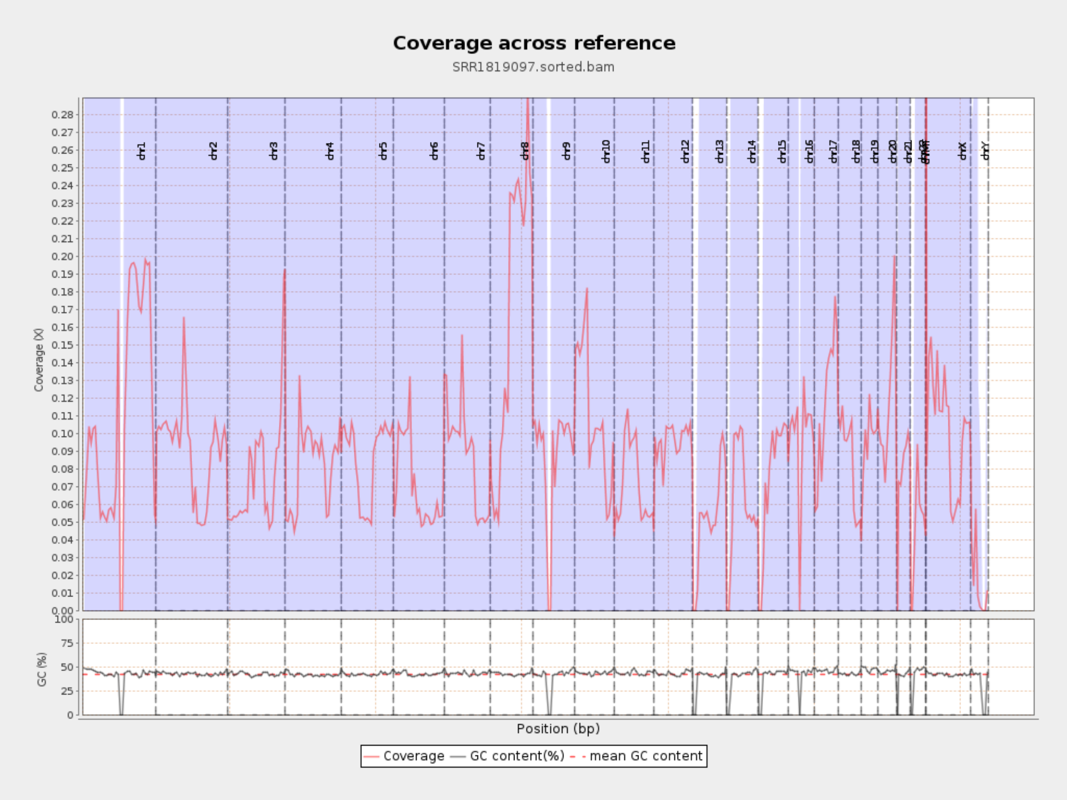
General error rate	0.51%
Mismatches	1,393,243
Insertions	15,127
Mapped reads with at least one insertion	0.32%
Deletions	50,620
Mapped reads with at least one deletion	1.05%
Homopolymer indels	45.77%

2.6. Chromosome stats

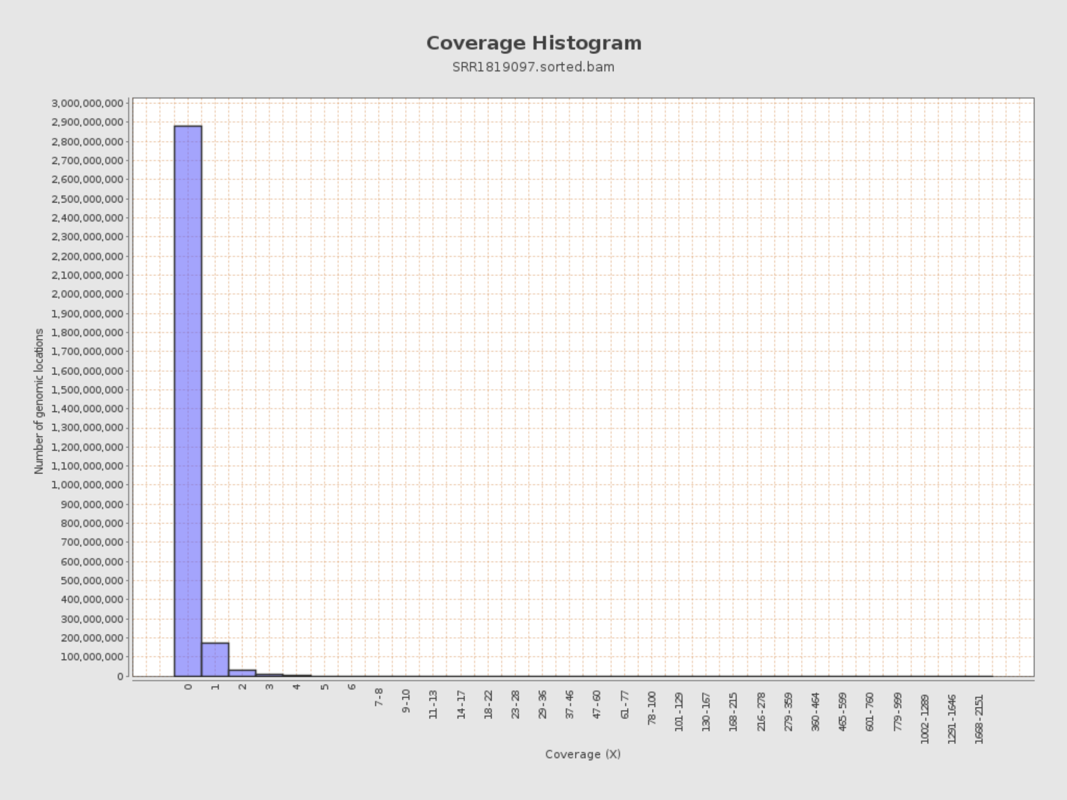
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	27658013	0.111	1.5626
chr2	243199373	22344182	0.0919	0.8386
chr3	198022430	15085276	0.0762	0.3557
chr4	191154276	15699458	0.0821	0.4693
chr5	180915260	15551428	0.086	0.3751
chr6	171115067	12010113	0.0702	0.5202
chr7	159138663	14001383	0.088	0.9768

chr8	146364022	25374814	0.1734	0.7277
chr9	141213431	12210058	0.0865	0.5897
chr10	135534747	14803032	0.1092	0.7623
chr11	135006516	9633700	0.0714	0.6747
chr12	133851895	12943452	0.0967	0.3986
chr13	115169878	6118377	0.0531	0.2886
chr14	107349540	6698686	0.0624	0.331
chr15	102531392	7488733	0.073	0.3586
chr16	90354753	8663385	0.0959	0.4625
chr17	81195210	9571130	0.1179	0.4958
chr18	78077248	6613821	0.0847	1.2306
chr19	59128983	5717758	0.0967	1.0196
chr20	63025520	7634962	0.1211	0.4511
chr21	48129895	3746527	0.0778	0.4324
chr22	51304566	2380850	0.0464	0.2689
chrMT	16571	19709	1.1894	1.5222
chrX	155270560	16046374	0.1033	0.5014
chrY	59373566	922897	0.0155	0.4225

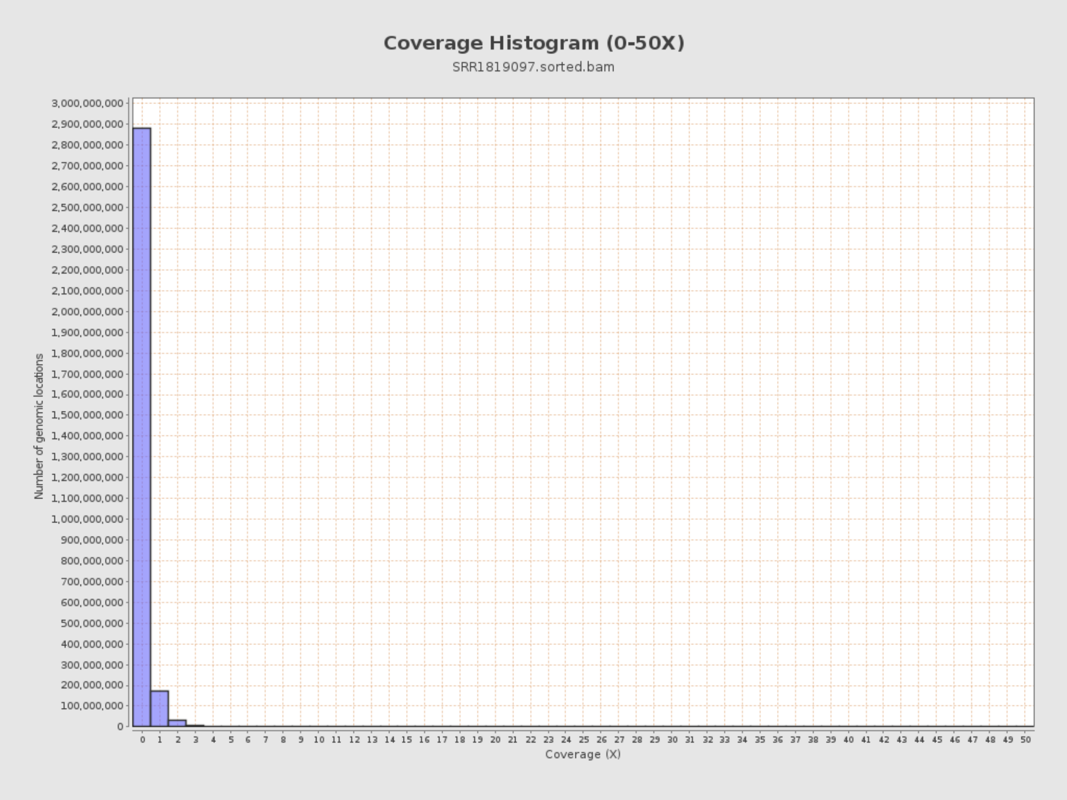
3. Results : Coverage across reference



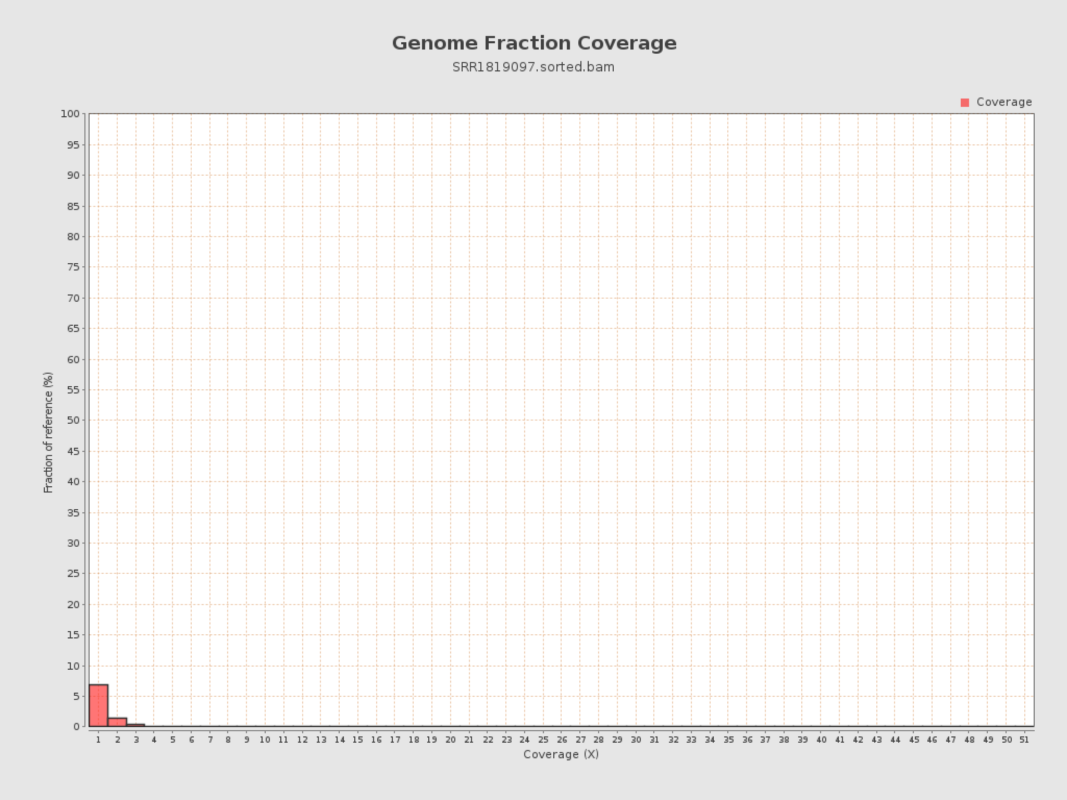
4. Results : Coverage Histogram



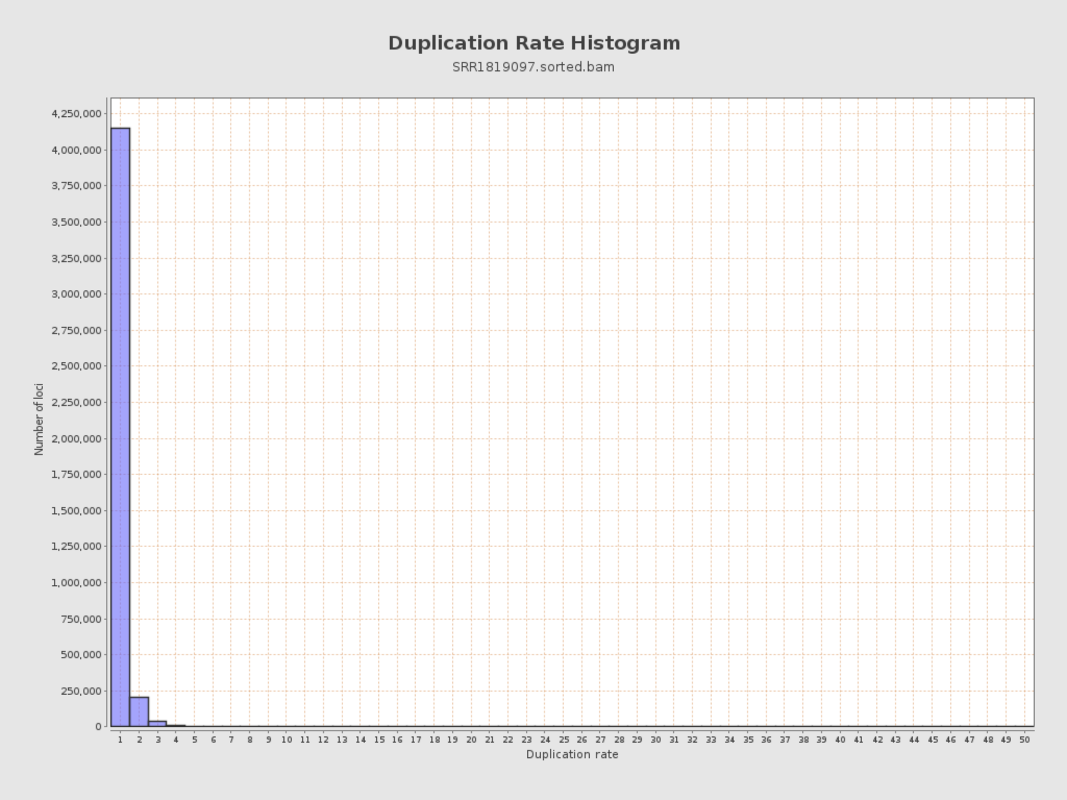
5. Results : Coverage Histogram (0-50X)



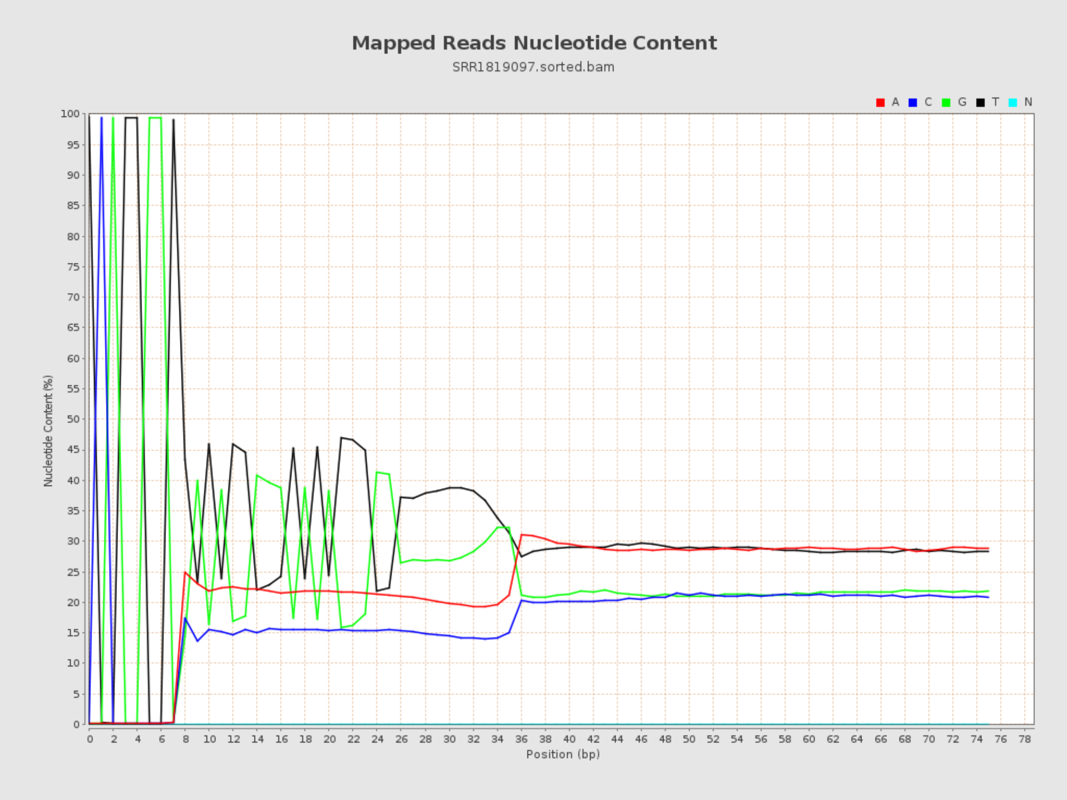
6. Results : Genome Fraction Coverage



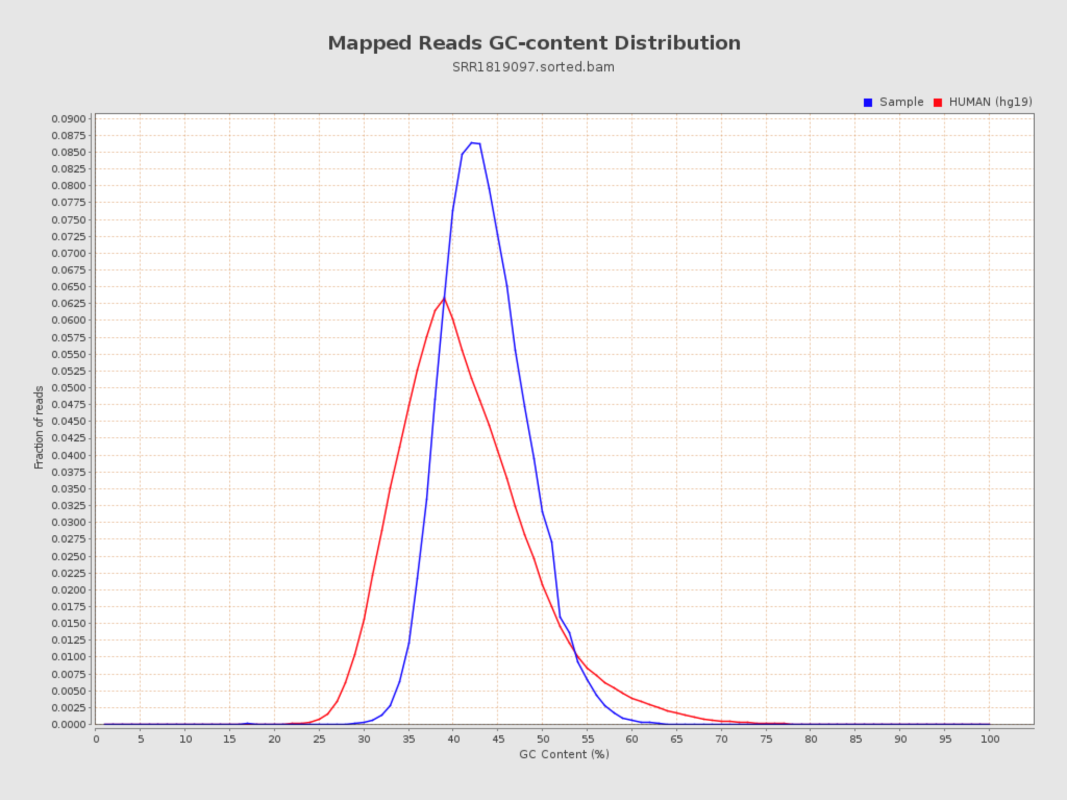
7. Results : Duplication Rate Histogram



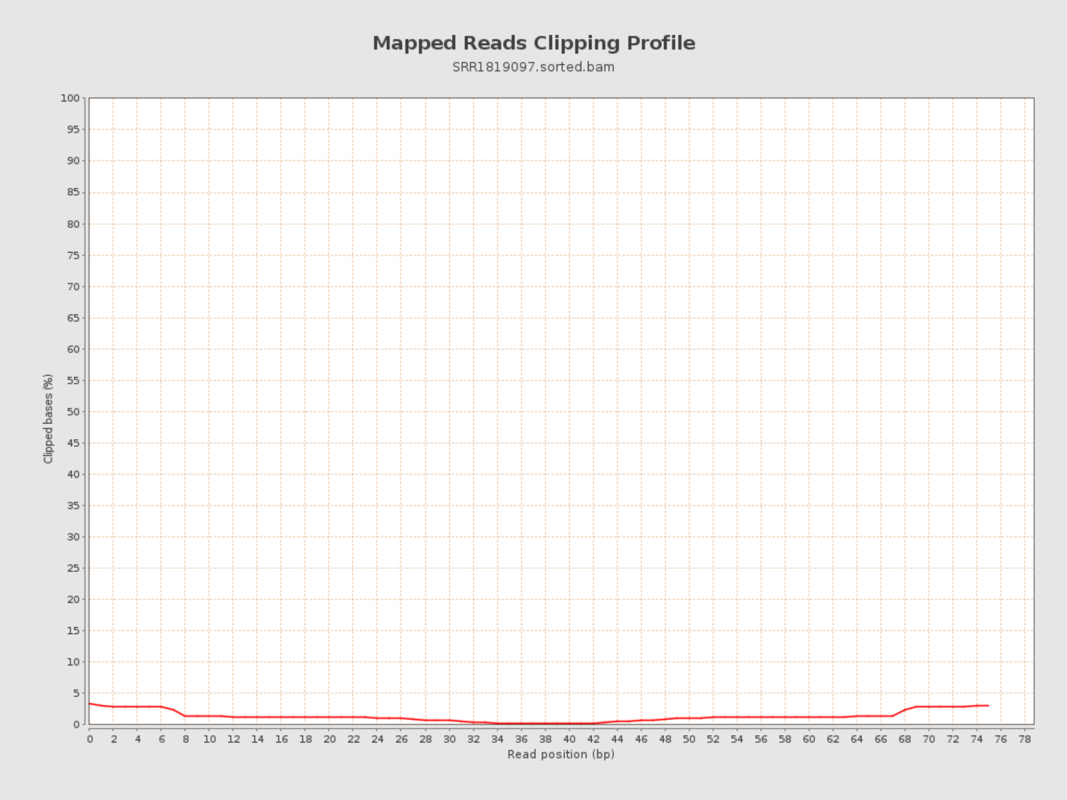
8. Results : Mapped Reads Nucleotide Content



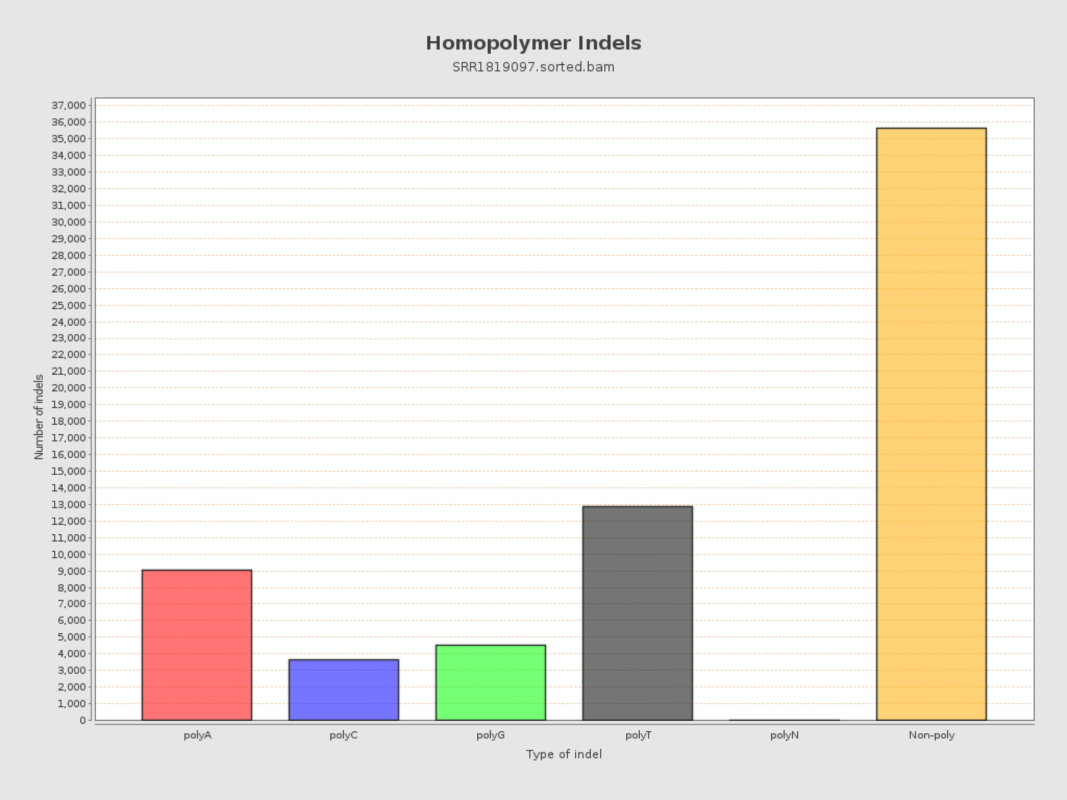
9. Results : Mapped Reads GC-content Distribution



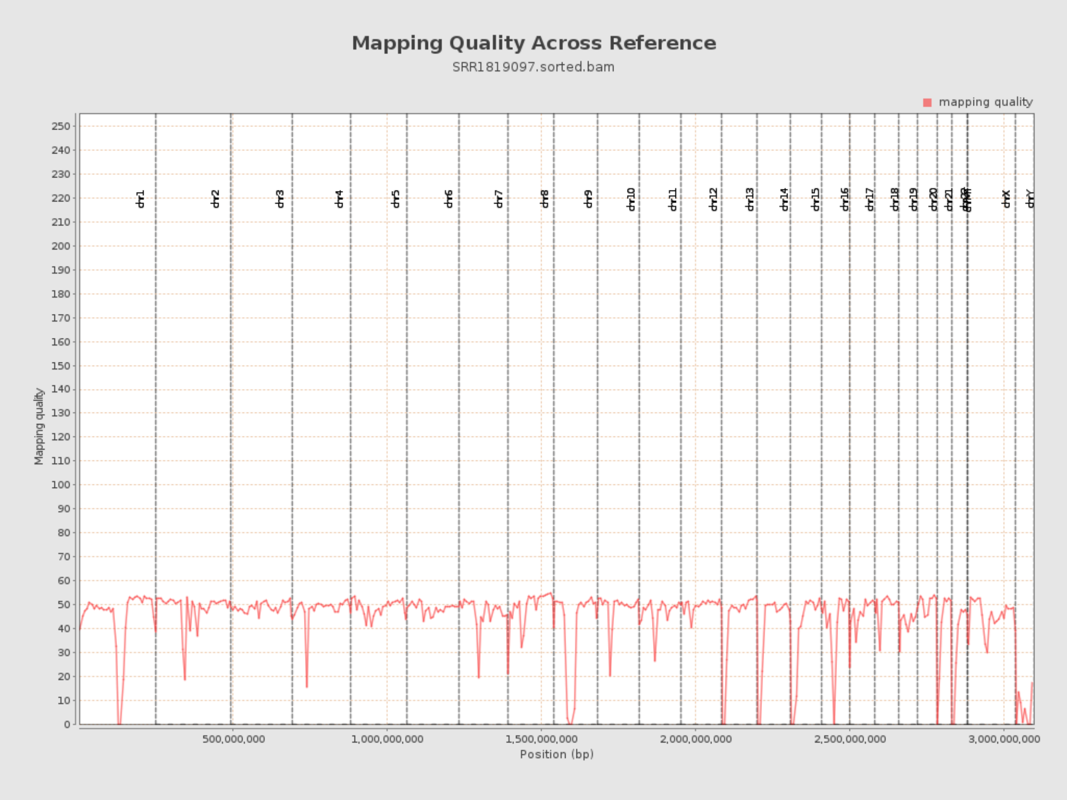
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram