Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:15:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819036.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_SRR1819036 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819036.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:15:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819036.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	659,251
Mapped reads	592,913 / 89.94%
Unmapped reads	66,338 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,853 / 0.58%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	9,205 / 1.4%
Duplication rate	1.18%
Clipped reads	595,215 / 90.29%

2.2. ACGT Content

Number/percentage of A's	8,566,826 / 25.22%
Number/percentage of C's	6,650,179 / 19.58%
Number/percentage of T's	10,061,934 / 29.62%
Number/percentage of G's	8,691,324 / 25.58%
Number/percentage of N's	769 / 0%
GC Percentage	45.16%

2.3. Coverage

Mean	0.011

Standard Deviation	0.1207

2.4. Mapping Quality

Mean Mapping Quality	43.6

2.5. Mismatches and indels

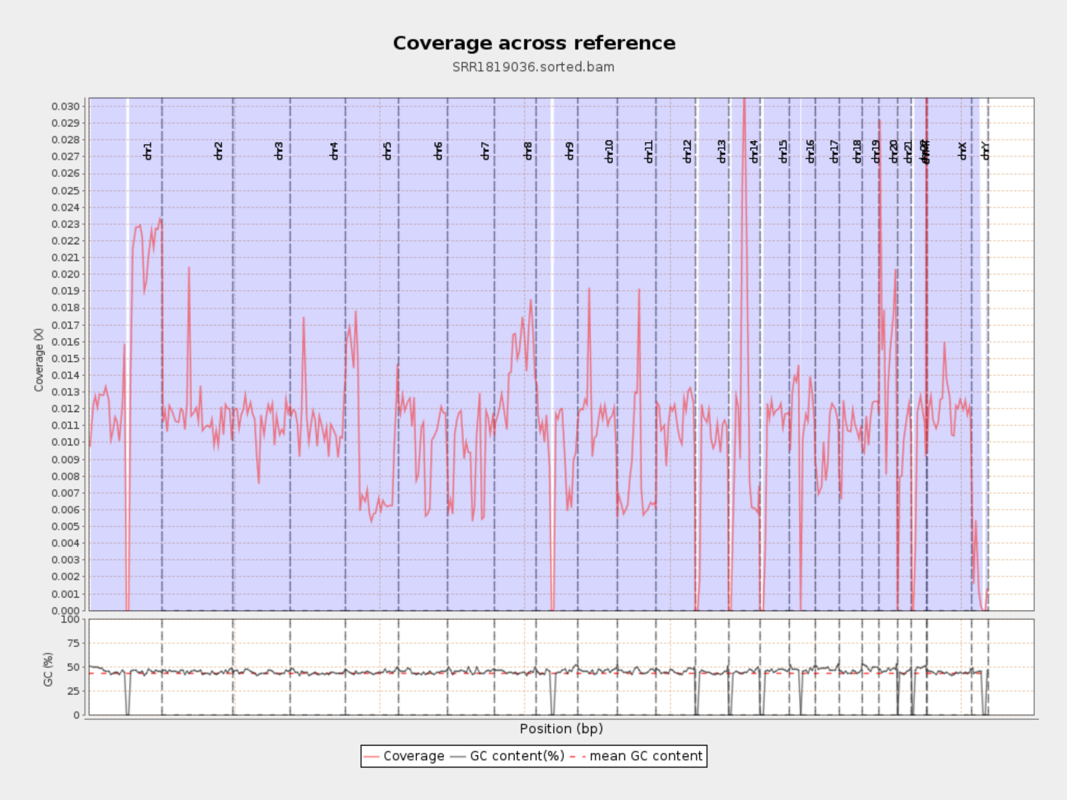
General error rate	0.51%
Mismatches	168,392
Insertions	2,320
Mapped reads with at least one insertion	0.39%
Deletions	5,357
Mapped reads with at least one deletion	0.9%
Homopolymer indels	39.17%

2.6. Chromosome stats

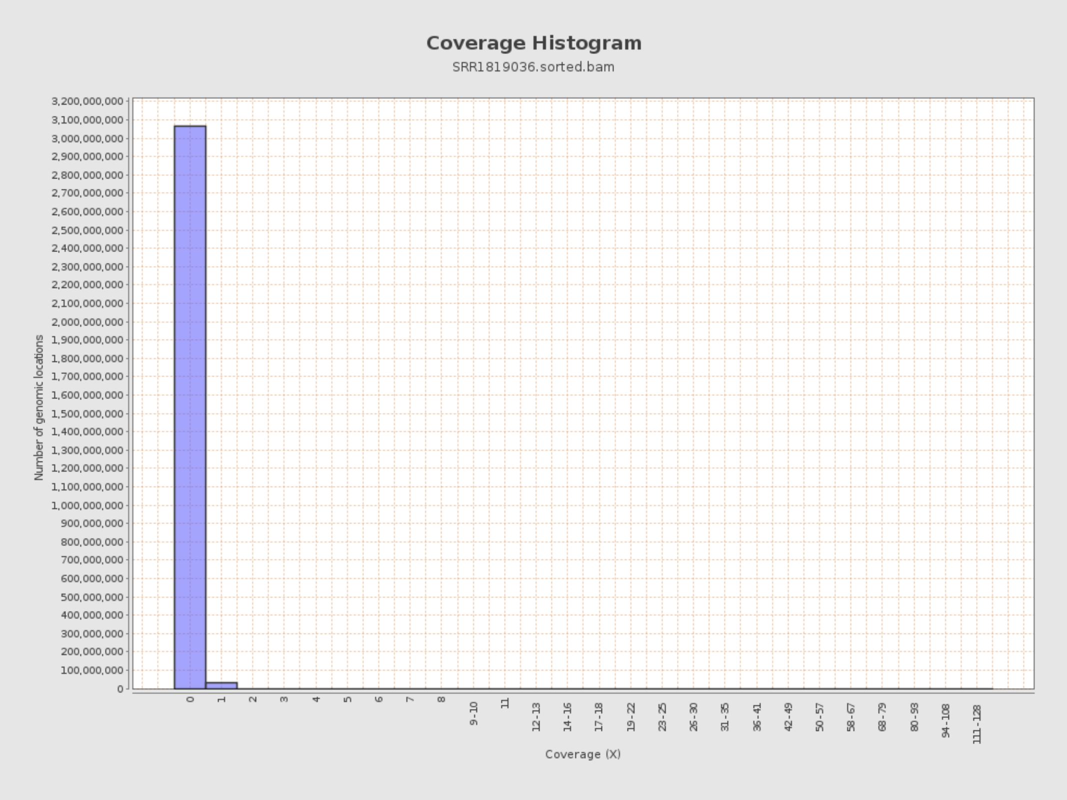
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3847044	0.0154	0.1589
chr2	243199373	2847499	0.0117	0.1347
chr3	198022430	2239841	0.0113	0.1103
chr4	191154276	2124938	0.0111	0.1128
chr5	180915260	1680015	0.0093	0.1005
chr6	171115067	1788684	0.0105	0.1088
chr7	159138663	1473501	0.0093	0.1114

chr8	146364022	2127405	0.0145	0.1316
chr9	141213431	1239103	0.0088	0.1145
chr10	135534747	1605317	0.0118	0.1304
chr11	135006516	1080904	0.008	0.1118
chr12	133851895	1542081	0.0115	0.1117
chr13	115169878	1042590	0.0091	0.098
chr14	107349540	1173793	0.0109	0.1125
chr15	102531392	979214	0.0096	0.1013
chr16	90354753	1029756	0.0114	0.115
chr17	81195210	792593	0.0098	0.104
chr18	78077248	822986	0.0105	0.1821
chr19	59128983	667782	0.0113	0.1275
chr20	63025520	1044820	0.0166	0.1358
chr21	48129895	439560	0.0091	0.1026
chr22	51304566	415347	0.0081	0.0927
chrMT	16571	964	0.0582	0.2341
chrX	155270560	1876370	0.0121	0.1198
chrY	59373566	97955	0.0016	0.0513

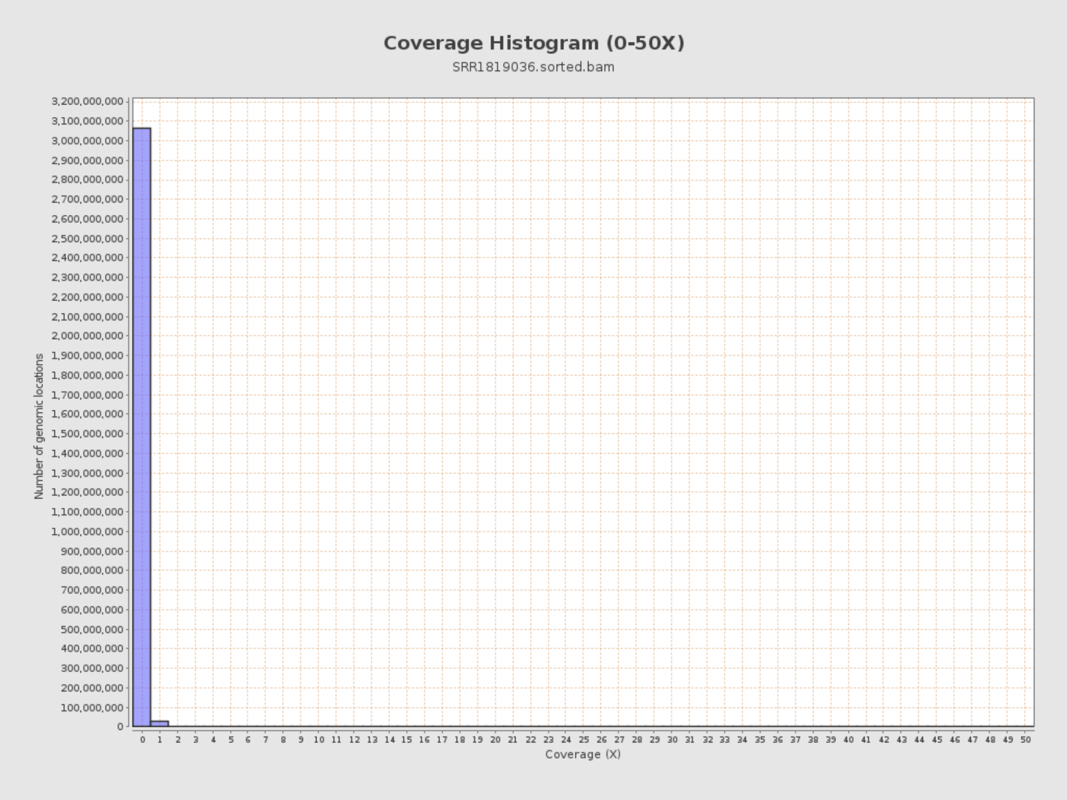
3. Results : Coverage across reference



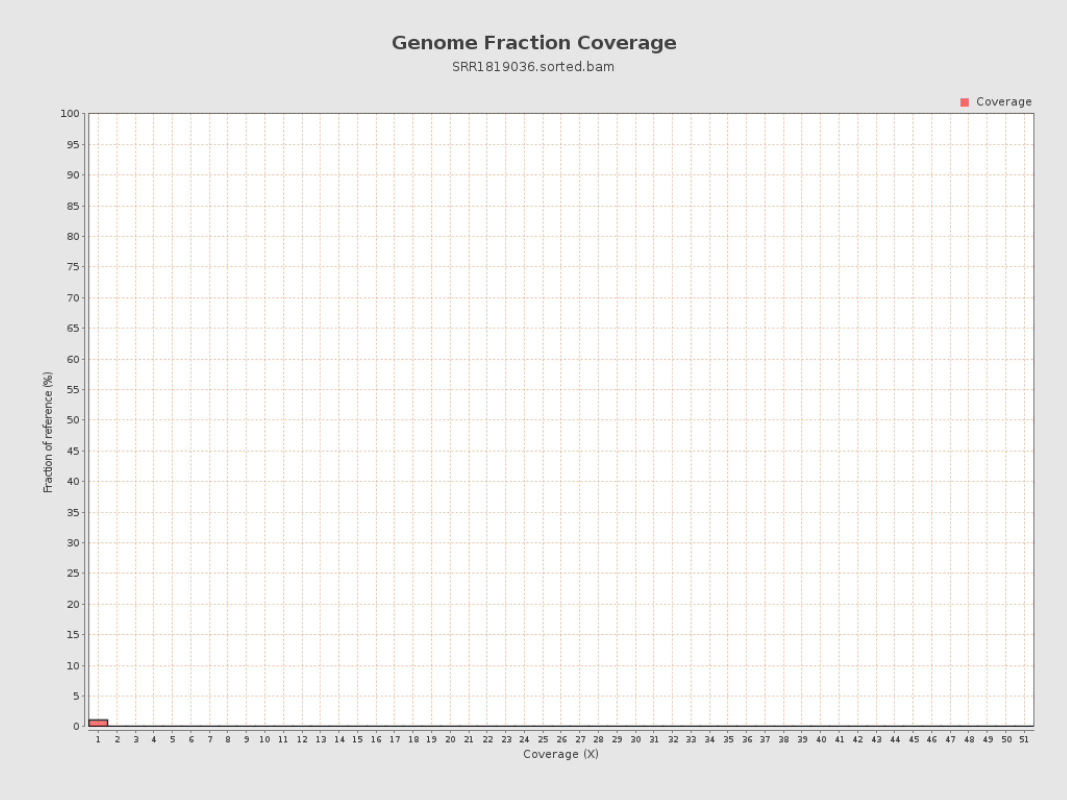
4. Results : Coverage Histogram



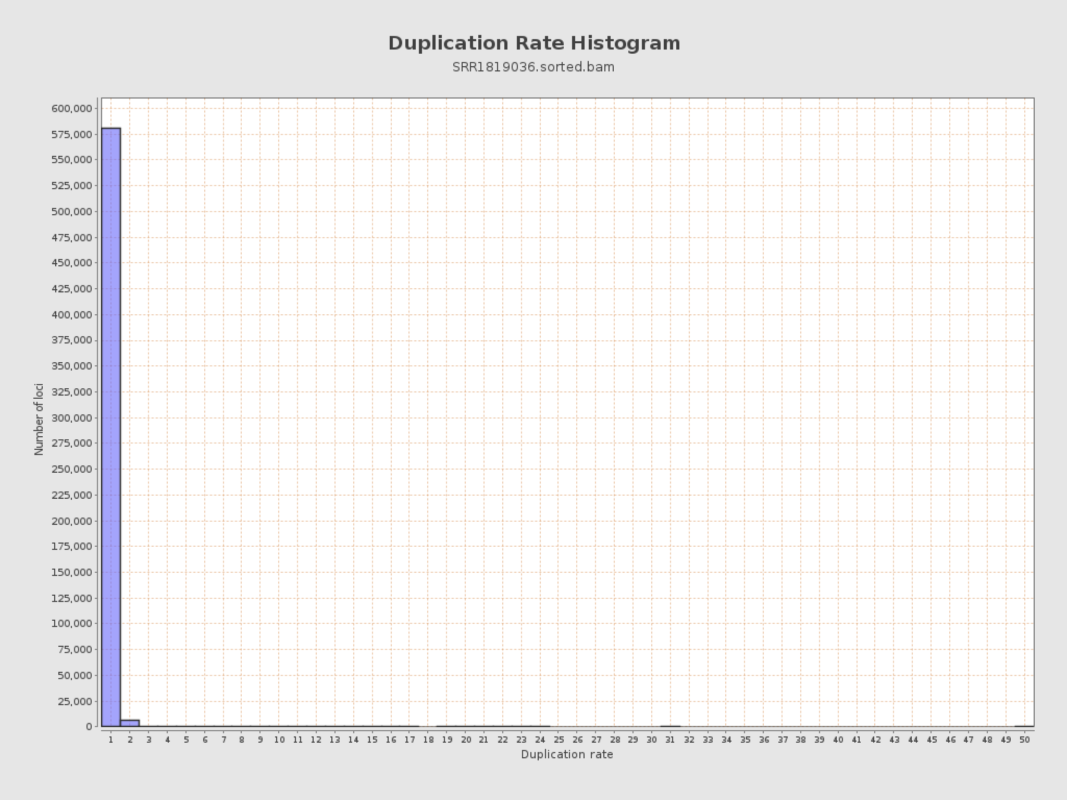
5. Results : Coverage Histogram (0-50X)



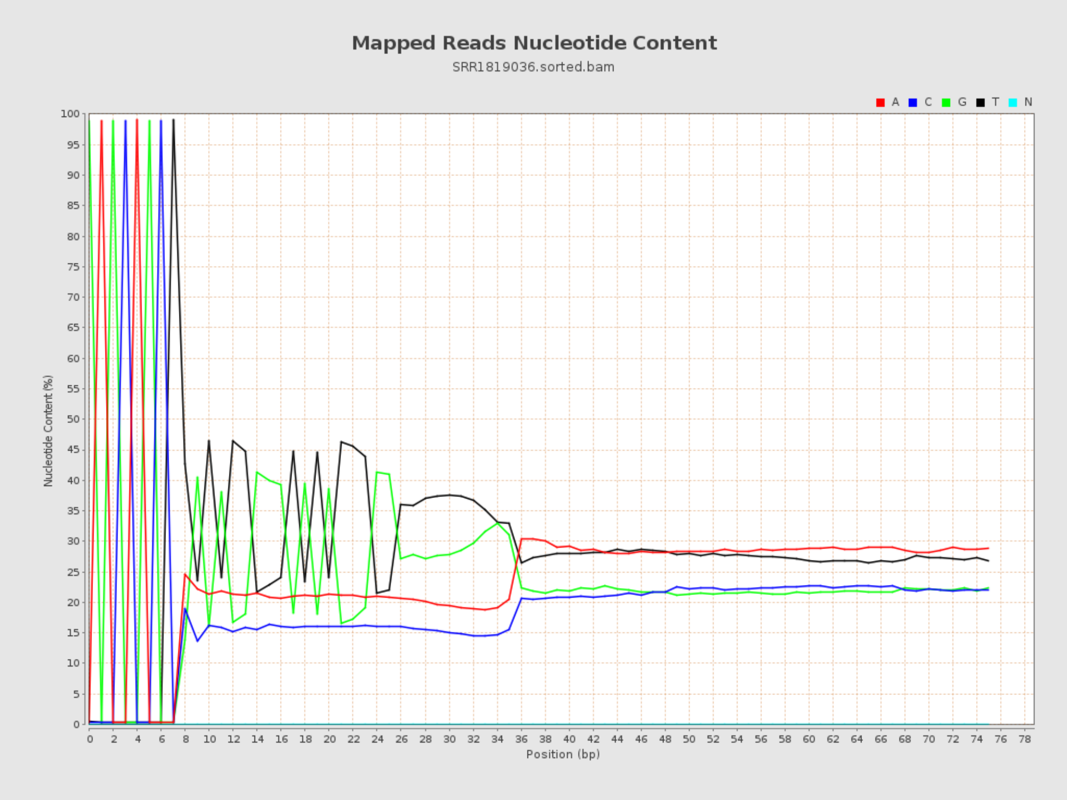
6. Results : Genome Fraction Coverage



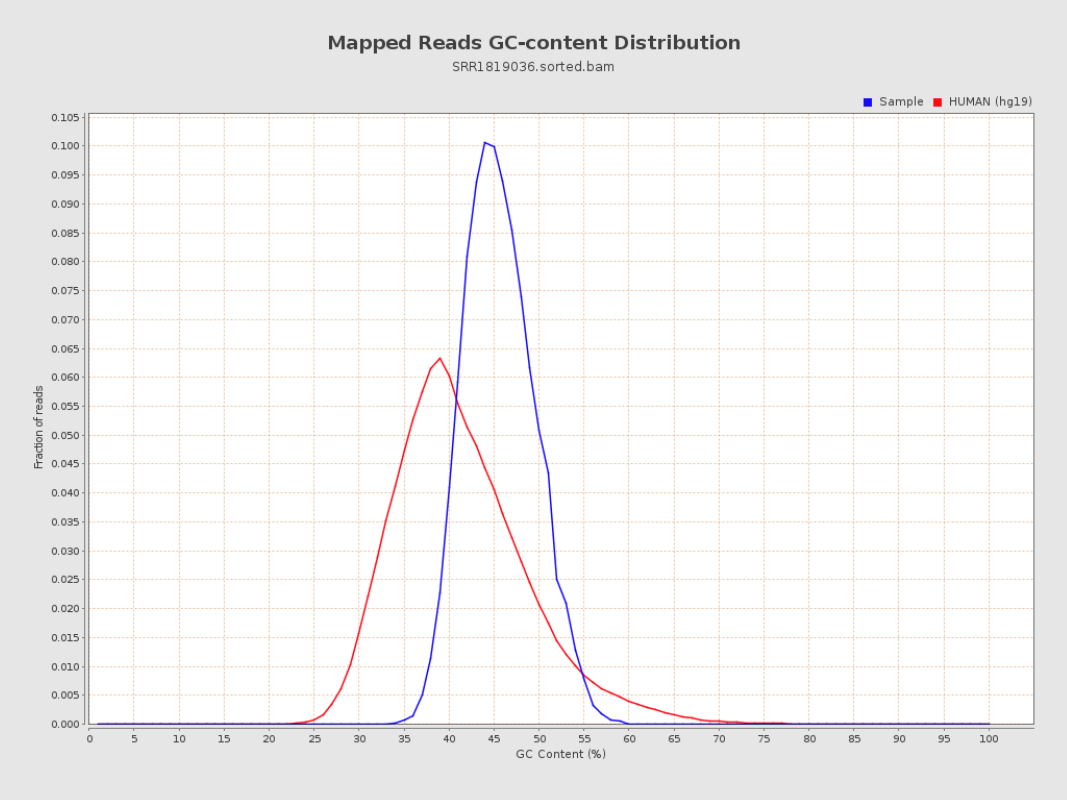
7. Results : Duplication Rate Histogram



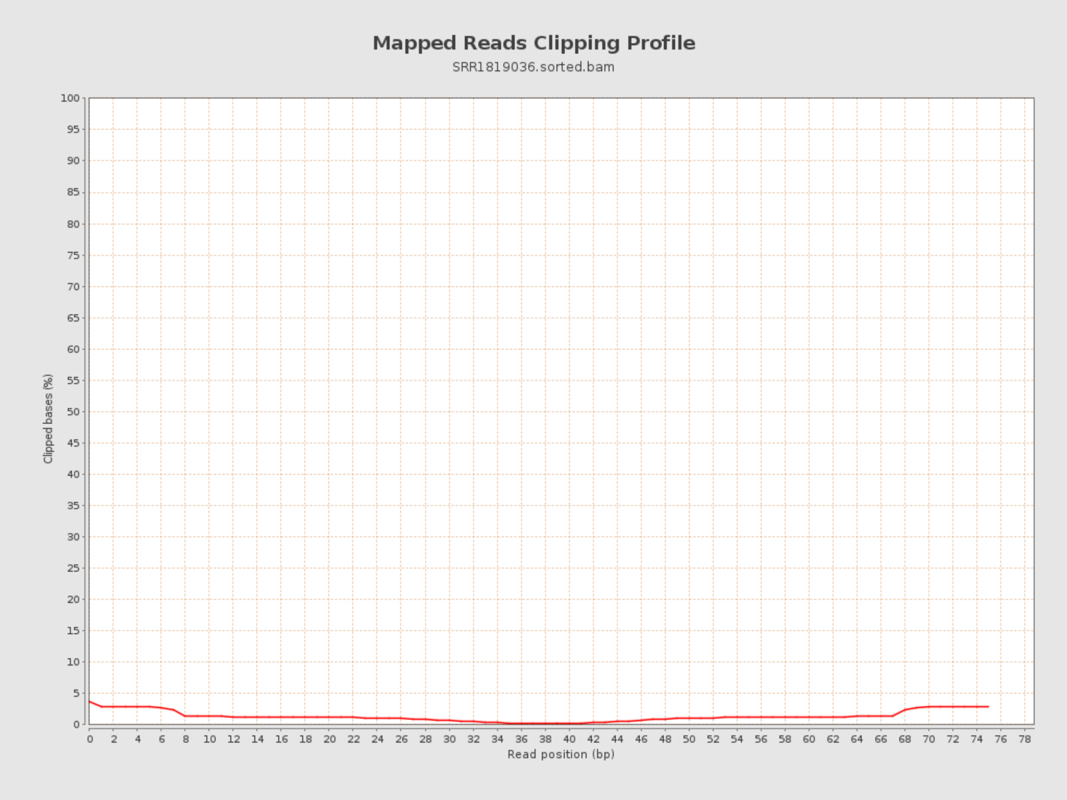
8. Results : Mapped Reads Nucleotide Content



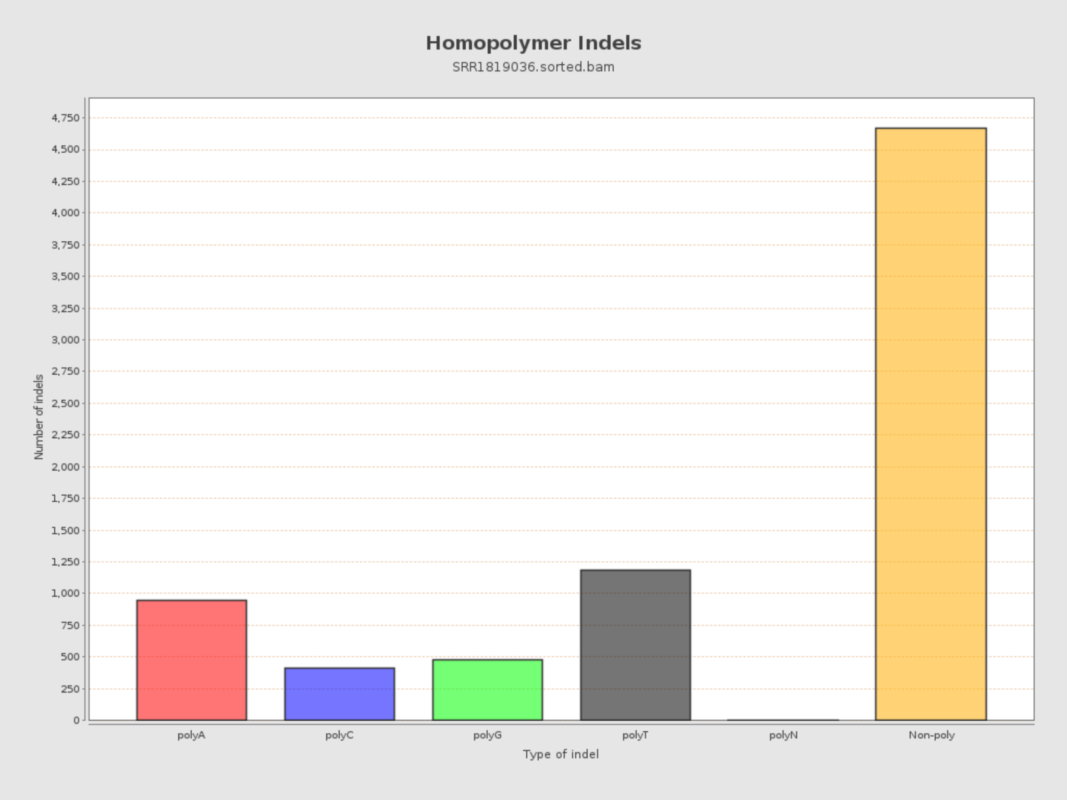
9. Results : Mapped Reads GC-content Distribution



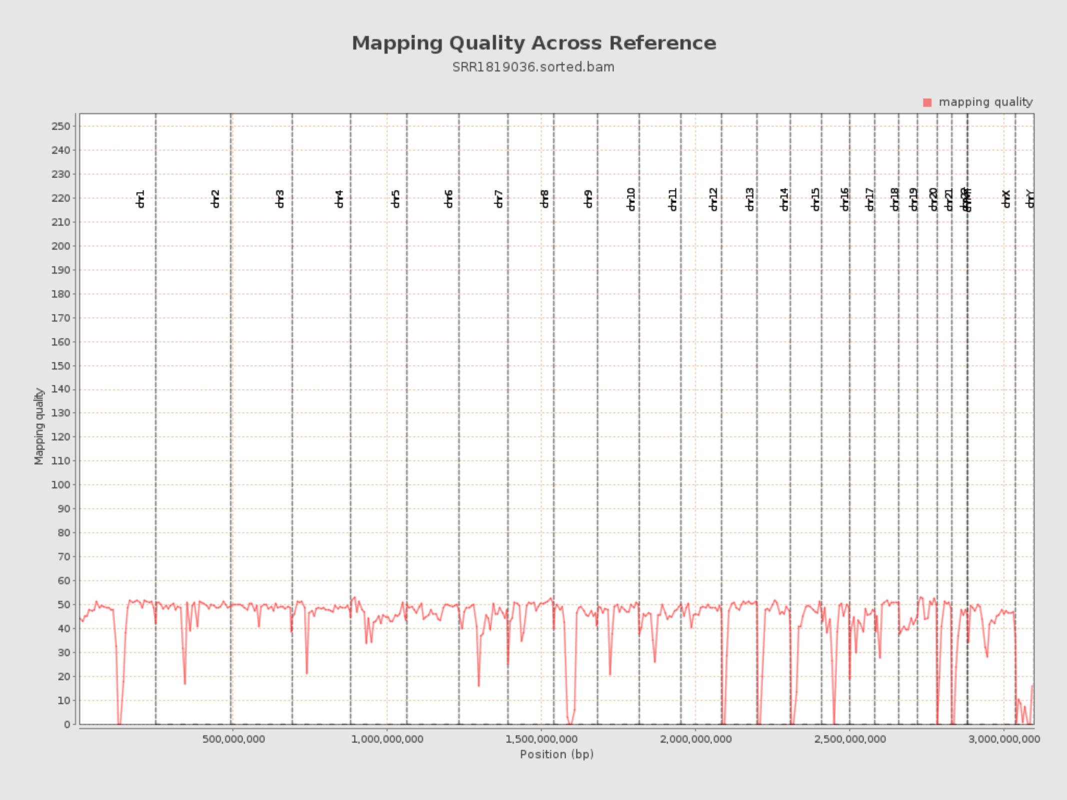
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram