Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:11:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818762.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_SRR1818762 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818762.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:11:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818762.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	812,319
Mapped reads	778,829 / 95.88%
Unmapped reads	33,490 / 4.12%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,269 / 0.77%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	279,087 / 34.36%
Duplication rate	31.43%
Clipped reads	783,631 / 96.47%

2.2. ACGT Content

Number/percentage of A's	14,936,574 / 28.29%
Number/percentage of C's	11,661,464 / 22.09%
Number/percentage of T's	14,976,310 / 28.36%
Number/percentage of G's	11,221,689 / 21.25%
Number/percentage of N's	3,203 / 0.01%
GC Percentage	43.34%

2.3. Coverage

Mean	0.0171

Standard Deviation	0.2526

2.4. Mapping Quality

Mean Mapping Quality	47.76

2.5. Mismatches and indels

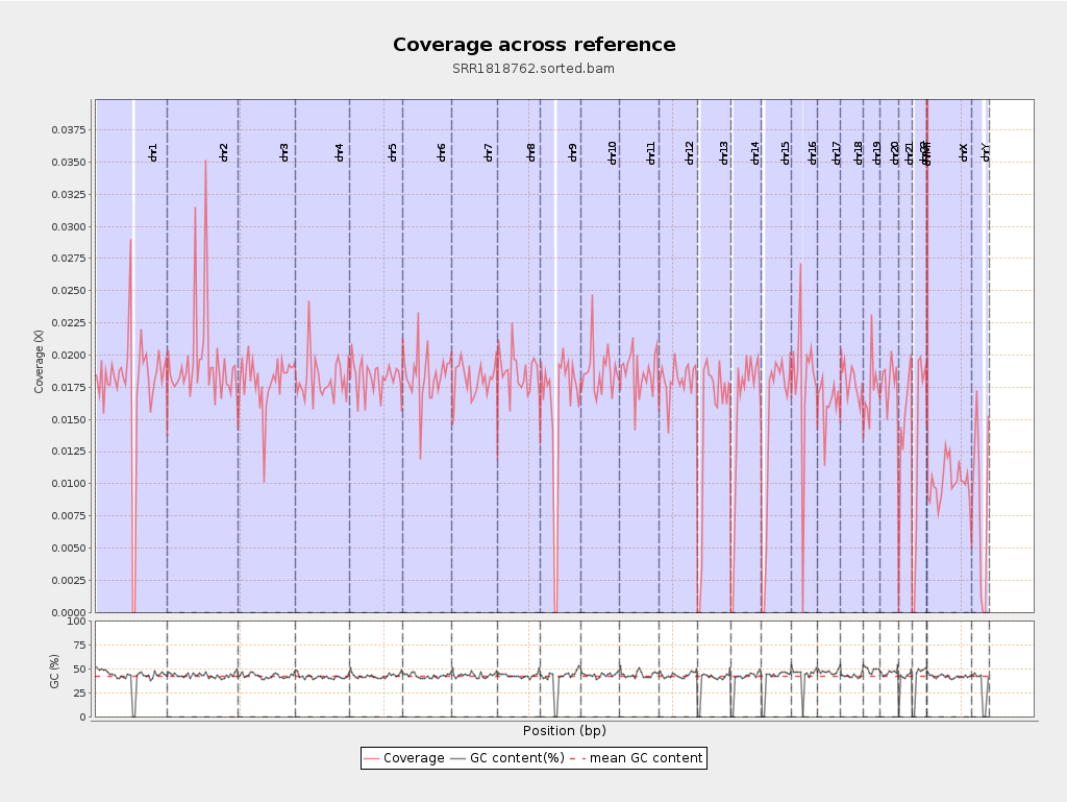
General error rate	0.51%
Mismatches	261,462
Insertions	4,937
Mapped reads with at least one insertion	0.63%
Deletions	13,117
Mapped reads with at least one deletion	1.67%
Homopolymer indels	42.52%

2.6. Chromosome stats

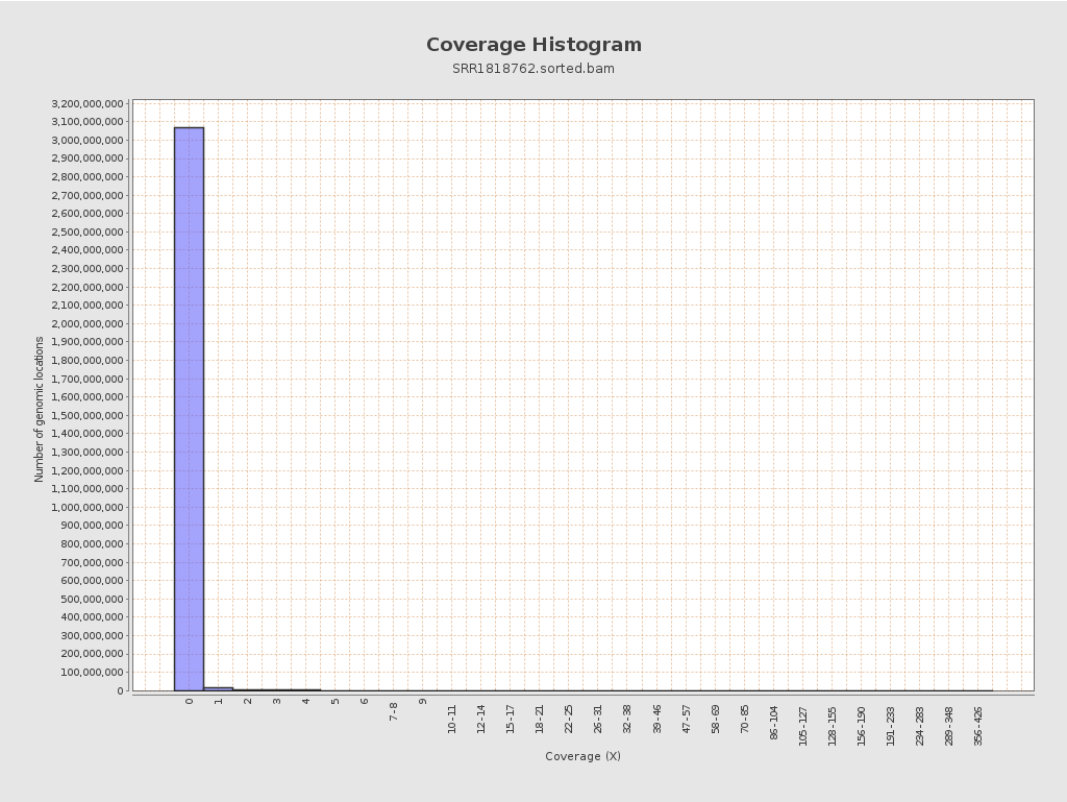
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4386993	0.0176	0.3344
chr2	243199373	4731667	0.0195	0.374
chr3	198022430	3556118	0.018	0.2136
chr4	191154276	3478389	0.0182	0.2293
chr5	180915260	3314751	0.0183	0.2168
chr6	171115067	3150750	0.0184	0.229
chr7	159138663	2882793	0.0181	0.2408

chr8	146364022	2741120	0.0187	0.2346
chr9	141213431	2262749	0.016	0.2186
chr10	135534747	2544110	0.0188	0.2524
chr11	135006516	2517517	0.0186	0.2319
chr12	133851895	2418745	0.0181	0.2211
chr13	115169878	1710596	0.0149	0.1928
chr14	107349540	1647128	0.0153	0.2102
chr15	102531392	1519130	0.0148	0.1942
chr16	90354753	1598270	0.0177	0.2781
chr17	81195210	1323395	0.0163	0.2103
chr18	78077248	1403119	0.018	0.2663
chr19	59128983	1021112	0.0173	0.2888
chr20	63025520	1131687	0.018	0.2241
chr21	48129895	706980	0.0147	0.1993
chr22	51304566	672018	0.0131	0.1974
chrMT	16571	23935	1.4444	2.1715
chrX	155270560	1574849	0.0101	0.1638
chrY	59373566	501989	0.0085	0.3496

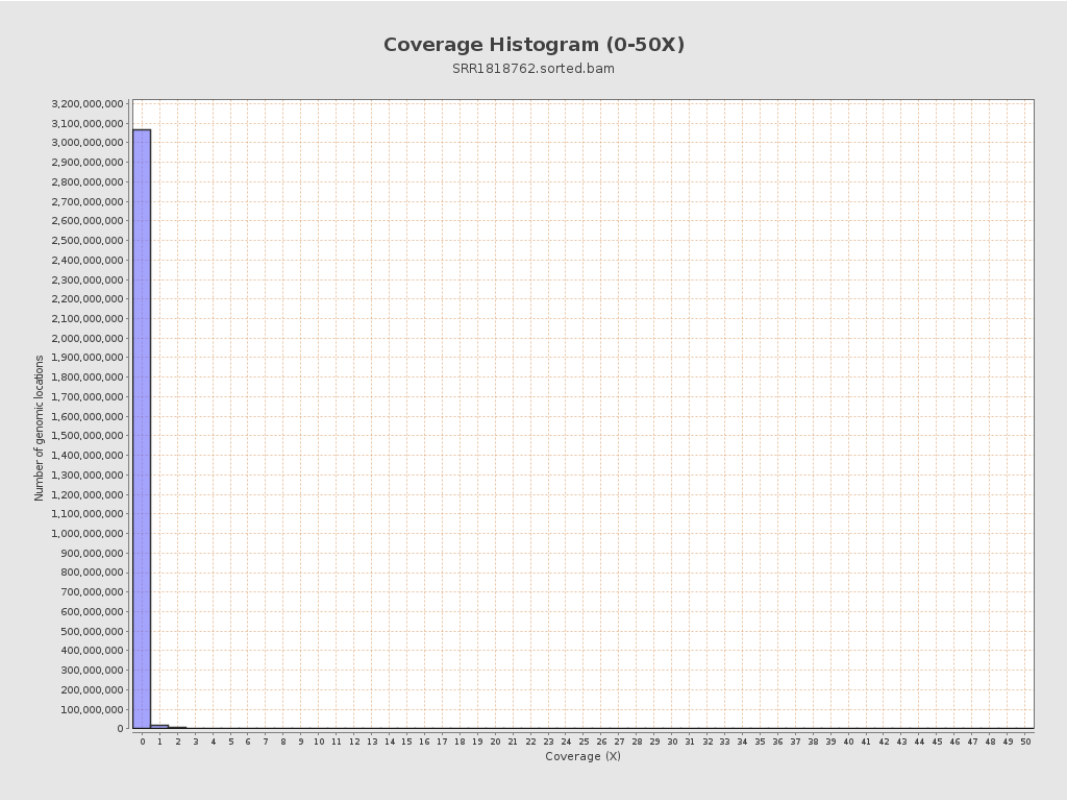
3. Results : Coverage across reference



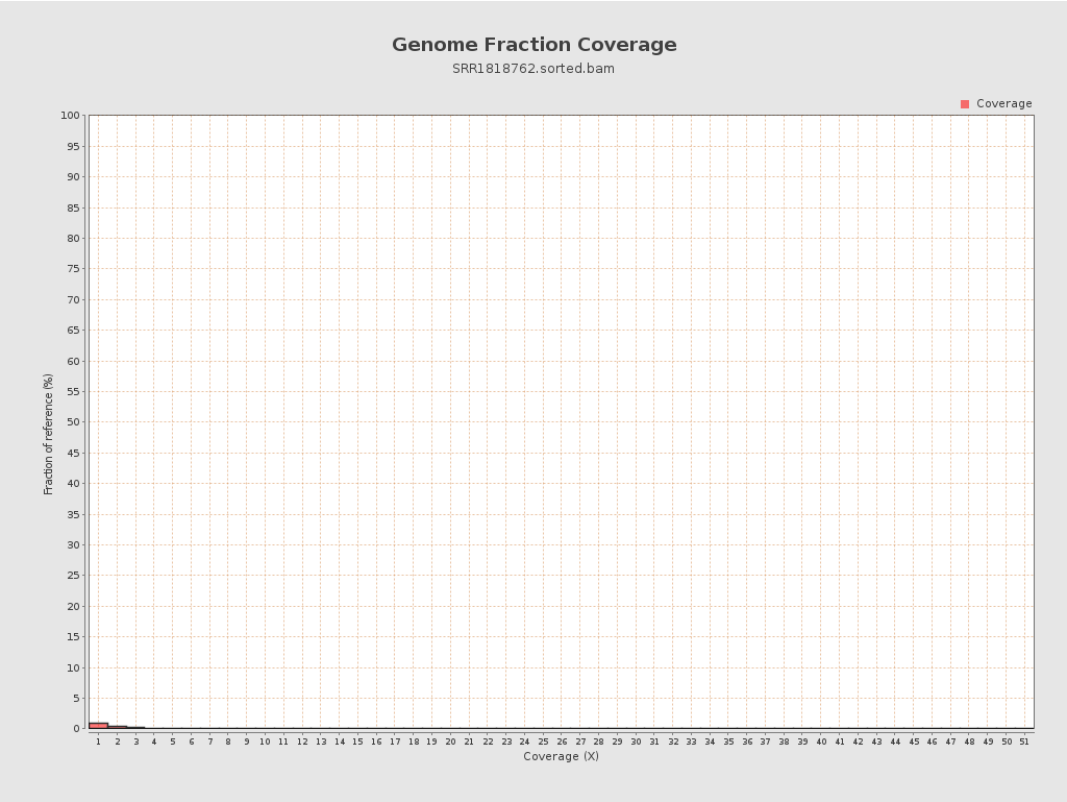
4. Results : Coverage Histogram



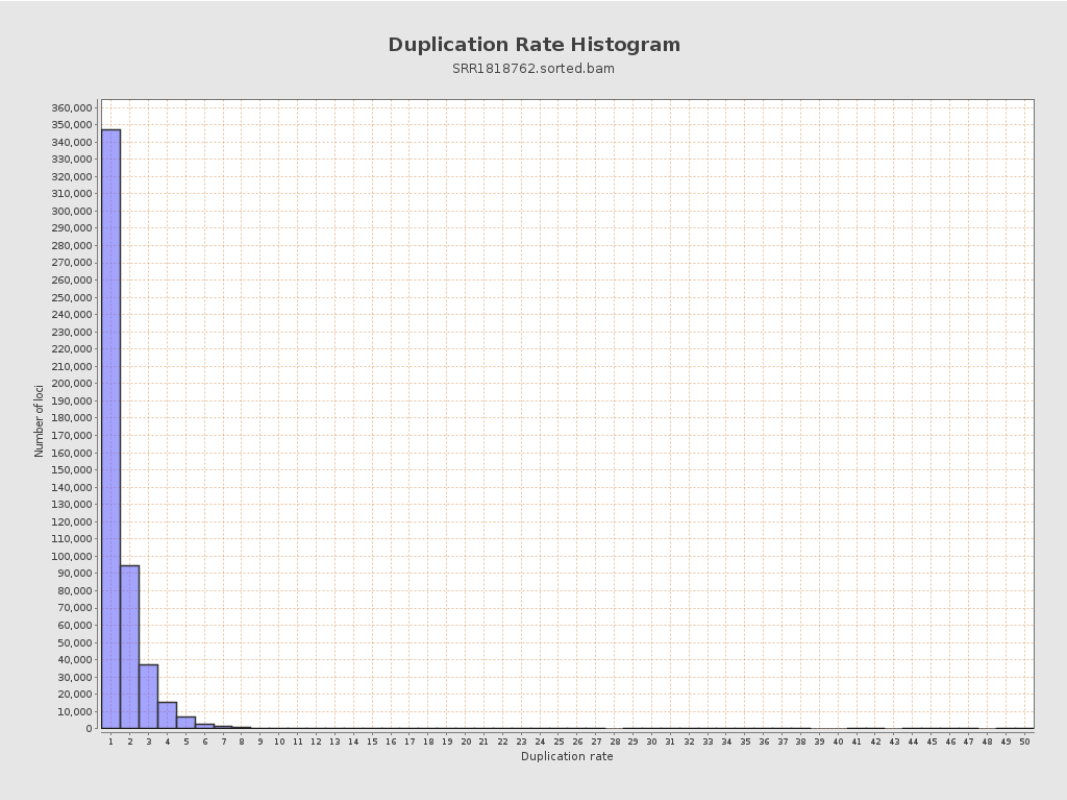
5. Results : Coverage Histogram (0-50X)



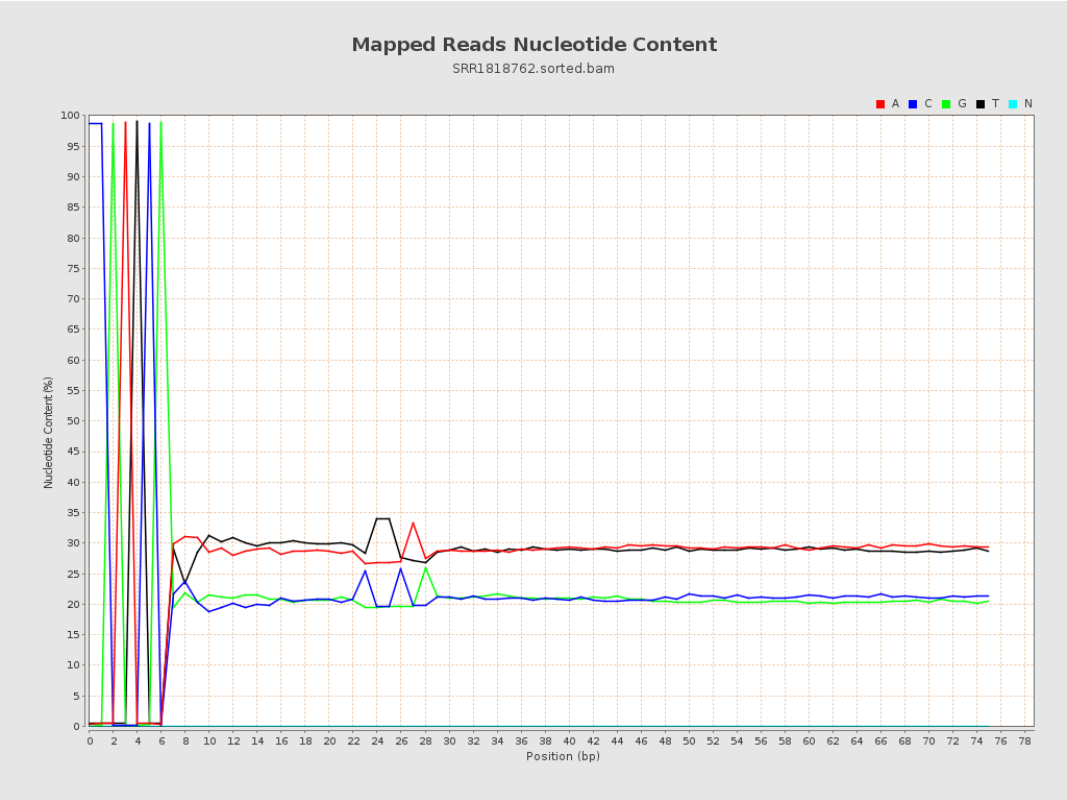
6. Results : Genome Fraction Coverage



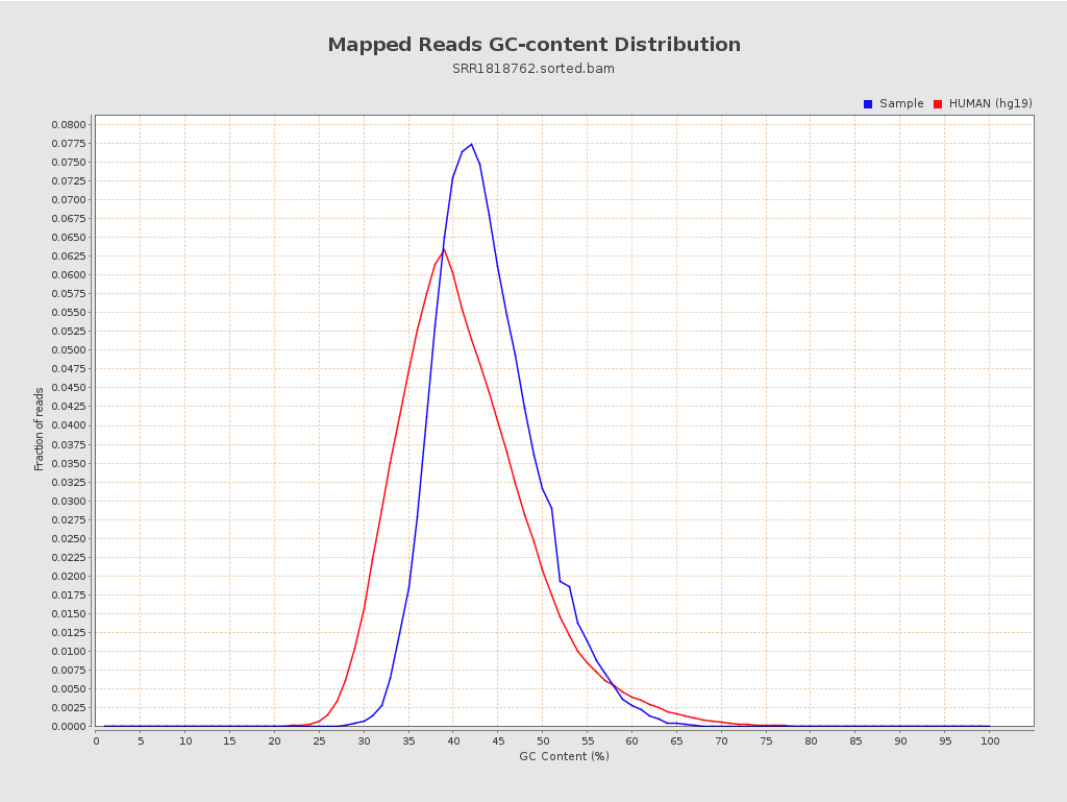
7. Results : Duplication Rate Histogram



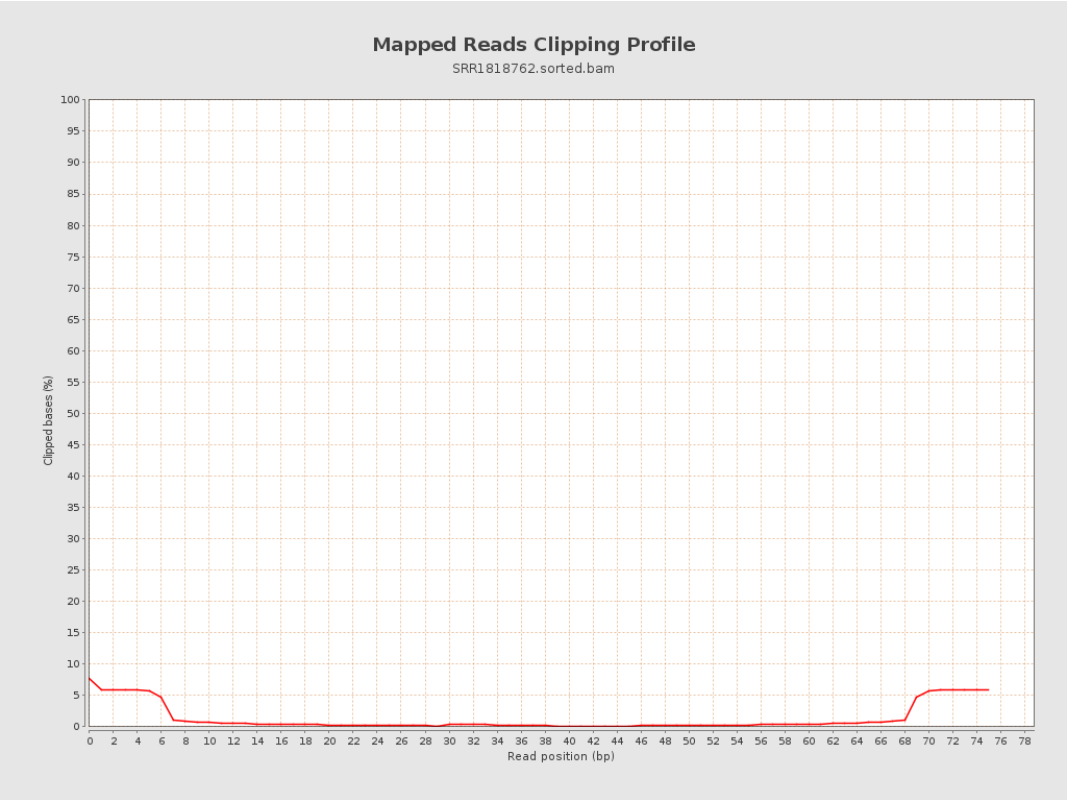
8. Results : Mapped Reads Nucleotide Content



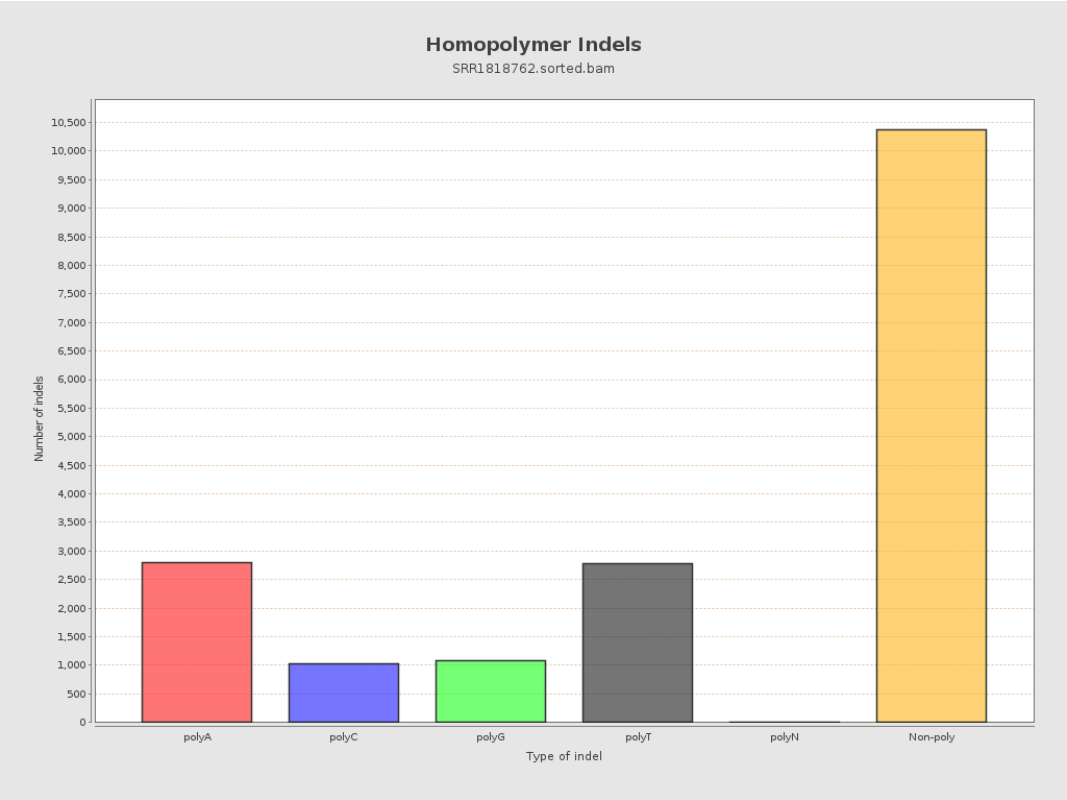
9. Results : Mapped Reads GC-content Distribution



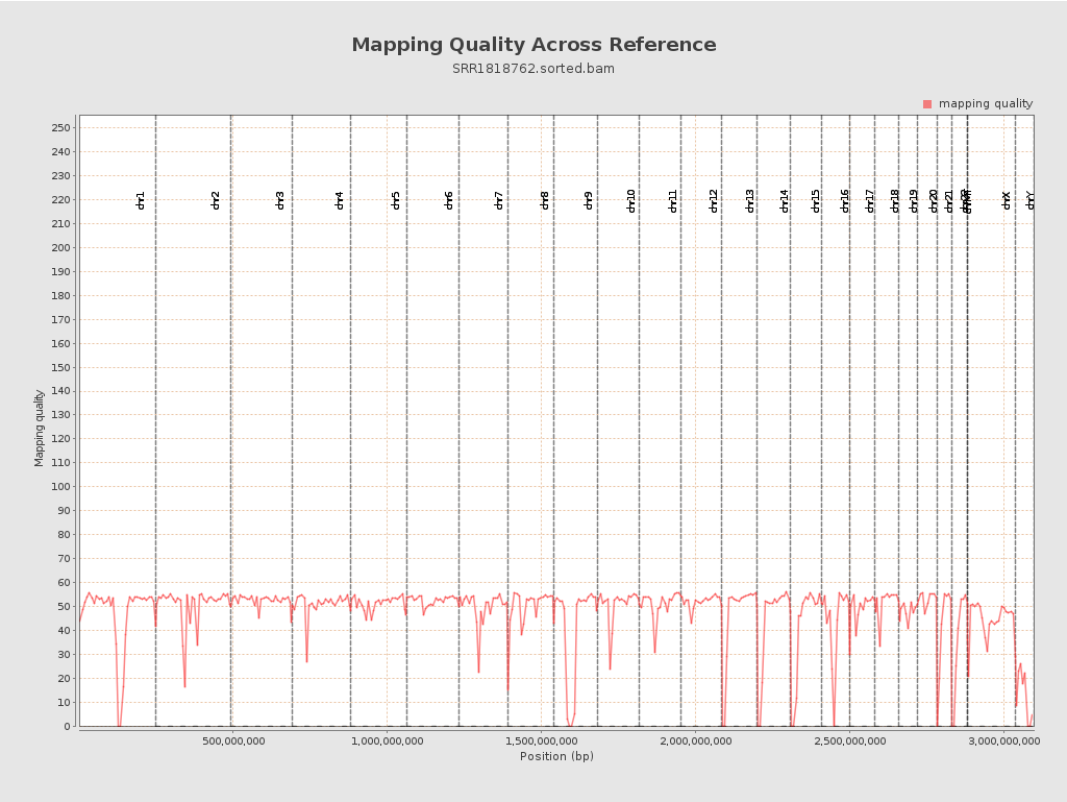
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram