Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 02:27:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818740.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_SRR1818740 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818740.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 02:27:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818740.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	609,774
Mapped reads	593,593 / 97.35%
Unmapped reads	16,181 / 2.65%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,061 / 0.83%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	156,592 / 25.68%
Duplication rate	23.26%
Clipped reads	596,766 / 97.87%

2.2. ACGT Content

Number/percentage of A's	11,273,995 / 27.99%
Number/percentage of C's	8,270,525 / 20.53%
Number/percentage of T's	11,628,883 / 28.87%
Number/percentage of G's	9,100,238 / 22.59%
Number/percentage of N's	2,424 / 0.01%
GC Percentage	43.13%

2.3. Coverage

Mean	0.013

Standard Deviation	0.1901

2.4. Mapping Quality

Mean Mapping Quality	47.57

2.5. Mismatches and indels

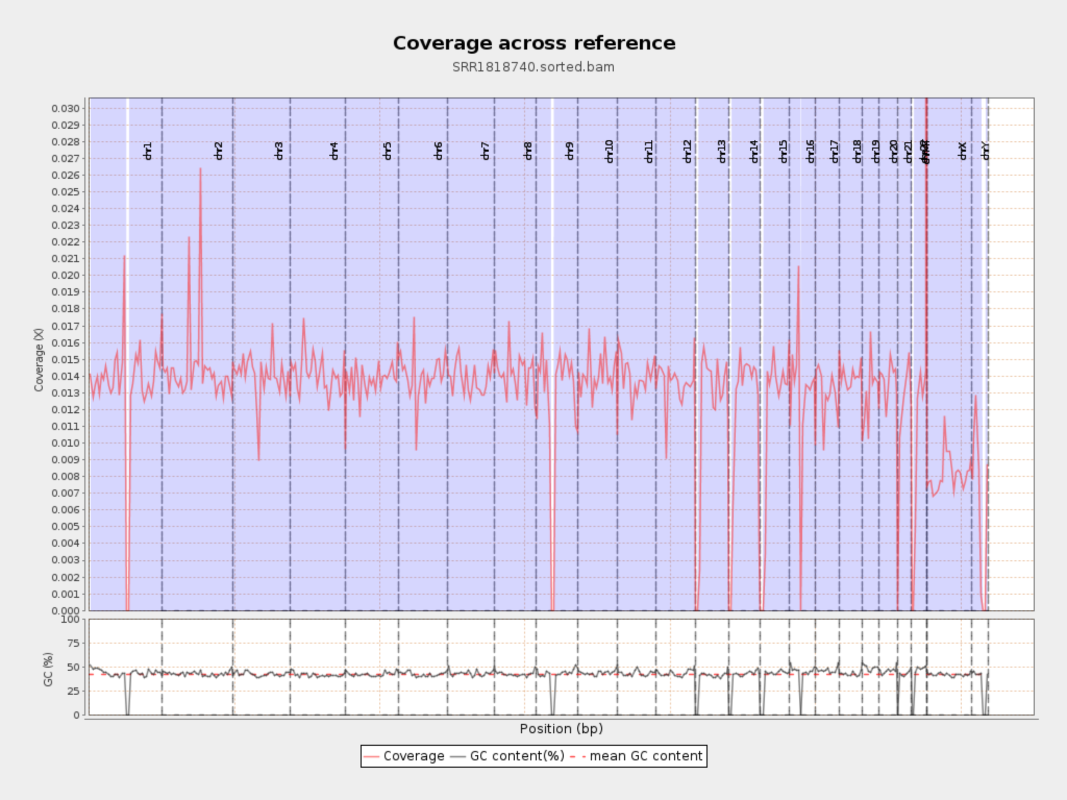
General error rate	0.5%
Mismatches	192,616
Insertions	3,778
Mapped reads with at least one insertion	0.63%
Deletions	10,086
Mapped reads with at least one deletion	1.68%
Homopolymer indels	42.75%

2.6. Chromosome stats

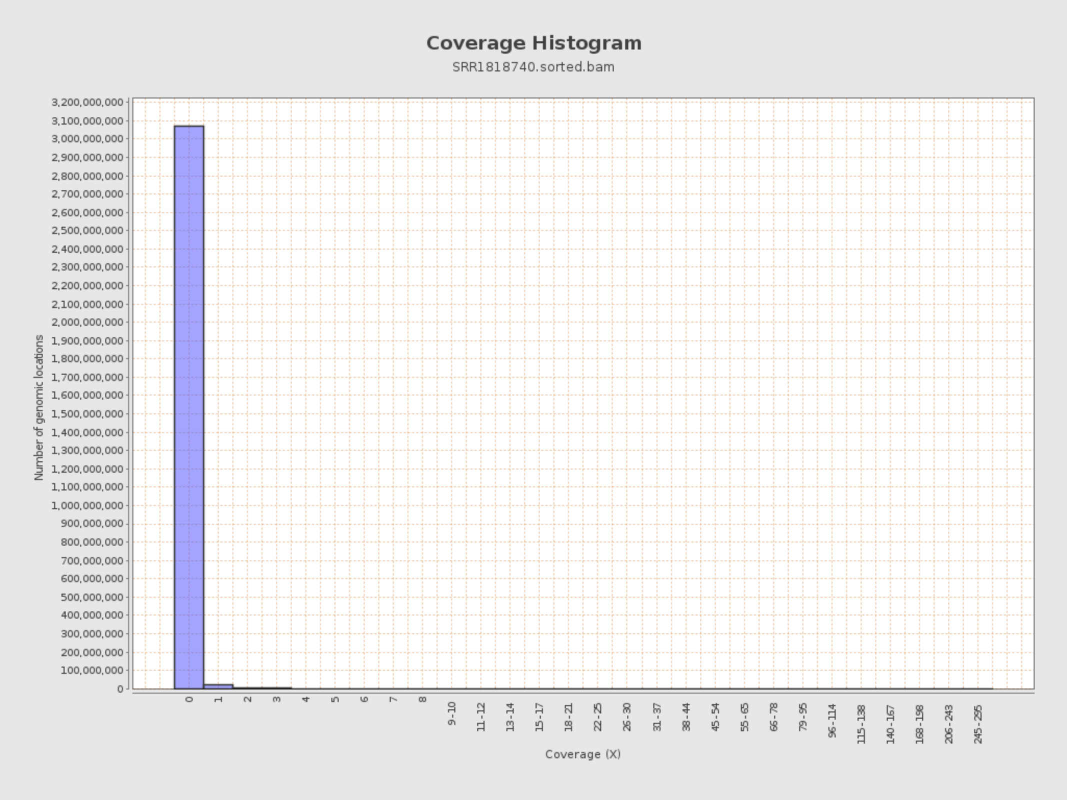
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3314522	0.0133	0.2498
chr2	243199373	3531729	0.0145	0.2593
chr3	198022430	2775151	0.014	0.1682
chr4	191154276	2697391	0.0141	0.1747
chr5	180915260	2494709	0.0138	0.1677
chr6	171115067	2400067	0.014	0.1744
chr7	159138663	2207512	0.0139	0.1754

chr8	146364022	2080450	0.0142	0.1837
chr9	141213431	1771484	0.0125	0.1734
chr10	135534747	1911107	0.0141	0.2048
chr11	135006516	1885884	0.014	0.1752
chr12	133851895	1808127	0.0135	0.1684
chr13	115169878	1335344	0.0116	0.1506
chr14	107349540	1257748	0.0117	0.1615
chr15	102531392	1151885	0.0112	0.1498
chr16	90354753	1162733	0.0129	0.2056
chr17	81195210	1044145	0.0129	0.1644
chr18	78077248	1093550	0.014	0.2234
chr19	59128983	769608	0.013	0.2124
chr20	63025520	870126	0.0138	0.1733
chr21	48129895	558426	0.0116	0.1634
chr22	51304566	480655	0.0094	0.1441
chrMT	16571	67441	4.0698	4.0712
chrX	155270560	1262819	0.0081	0.1333
chrY	59373566	359668	0.0061	0.2118

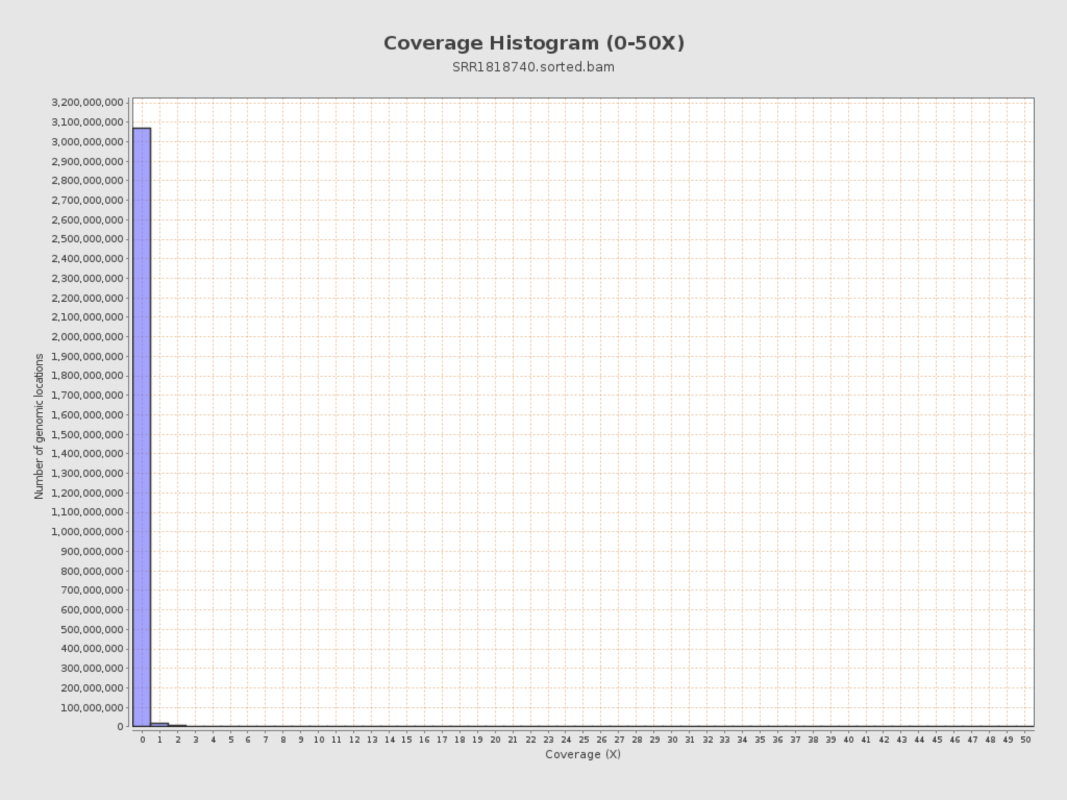
3. Results : Coverage across reference



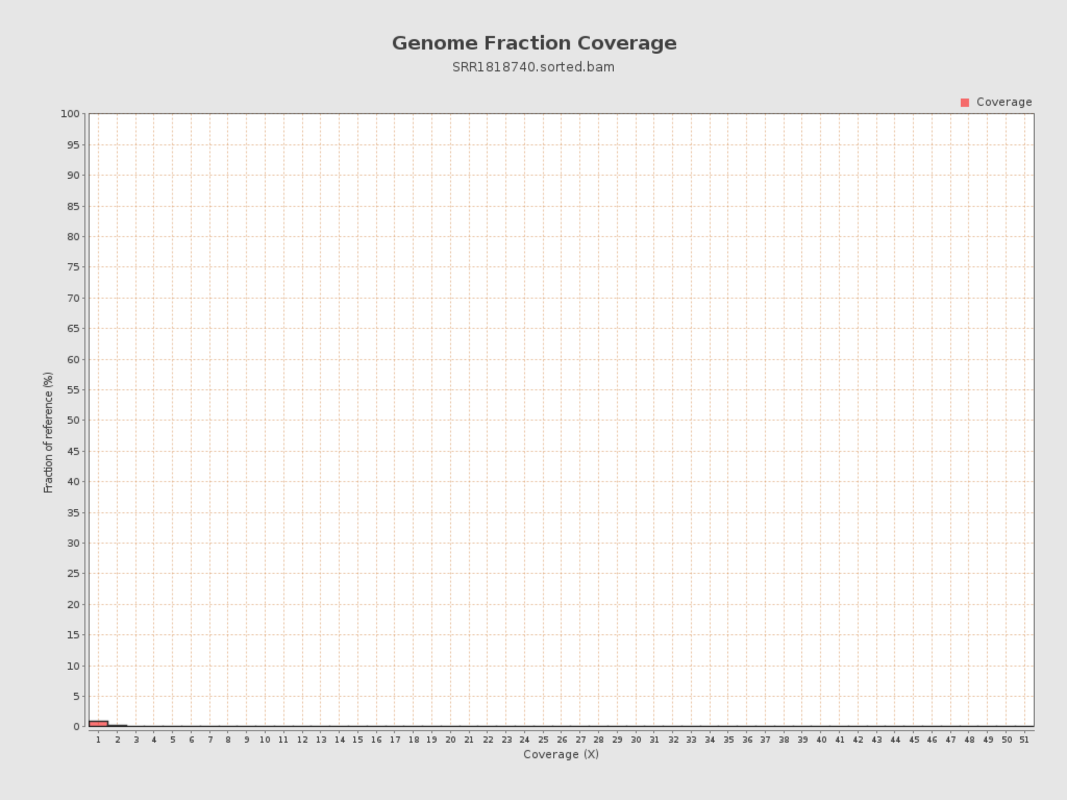
4. Results : Coverage Histogram



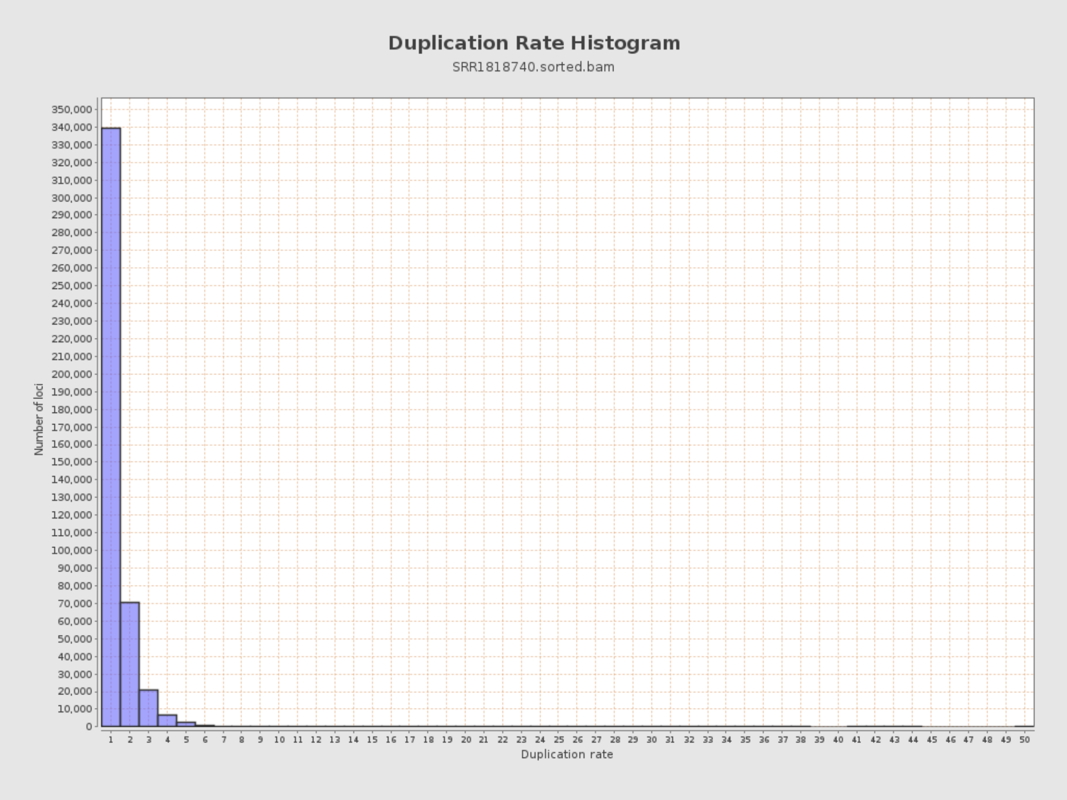
5. Results : Coverage Histogram (0-50X)



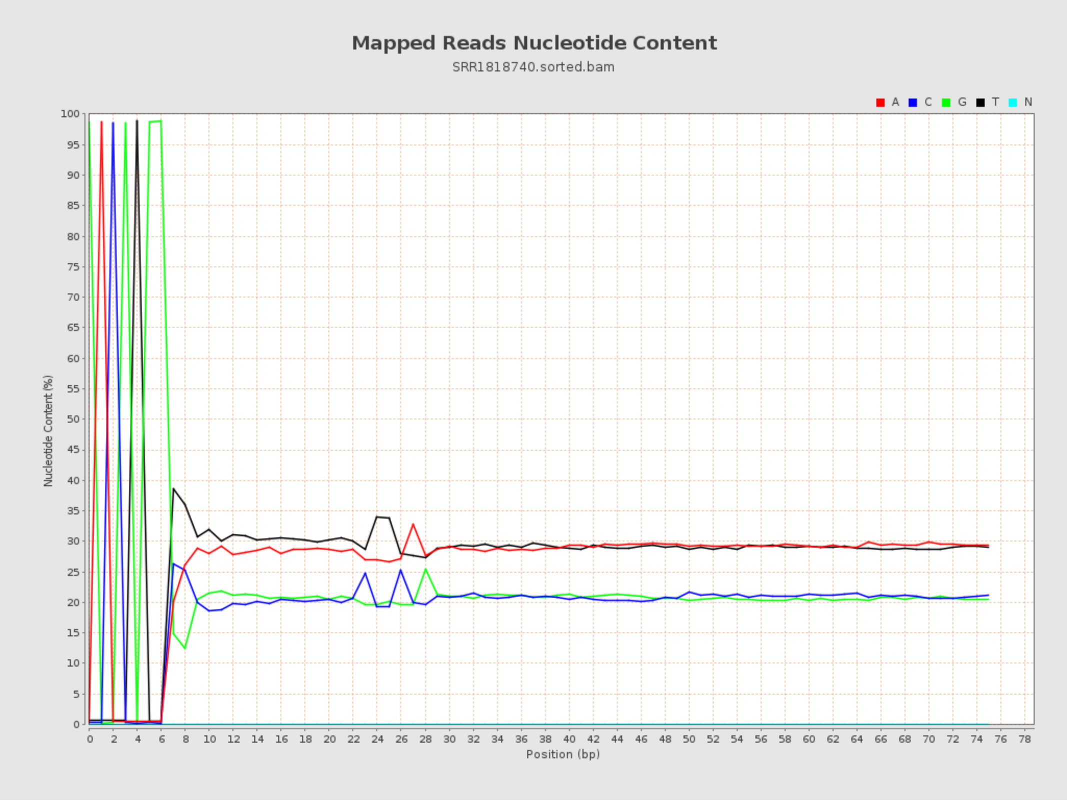
6. Results : Genome Fraction Coverage



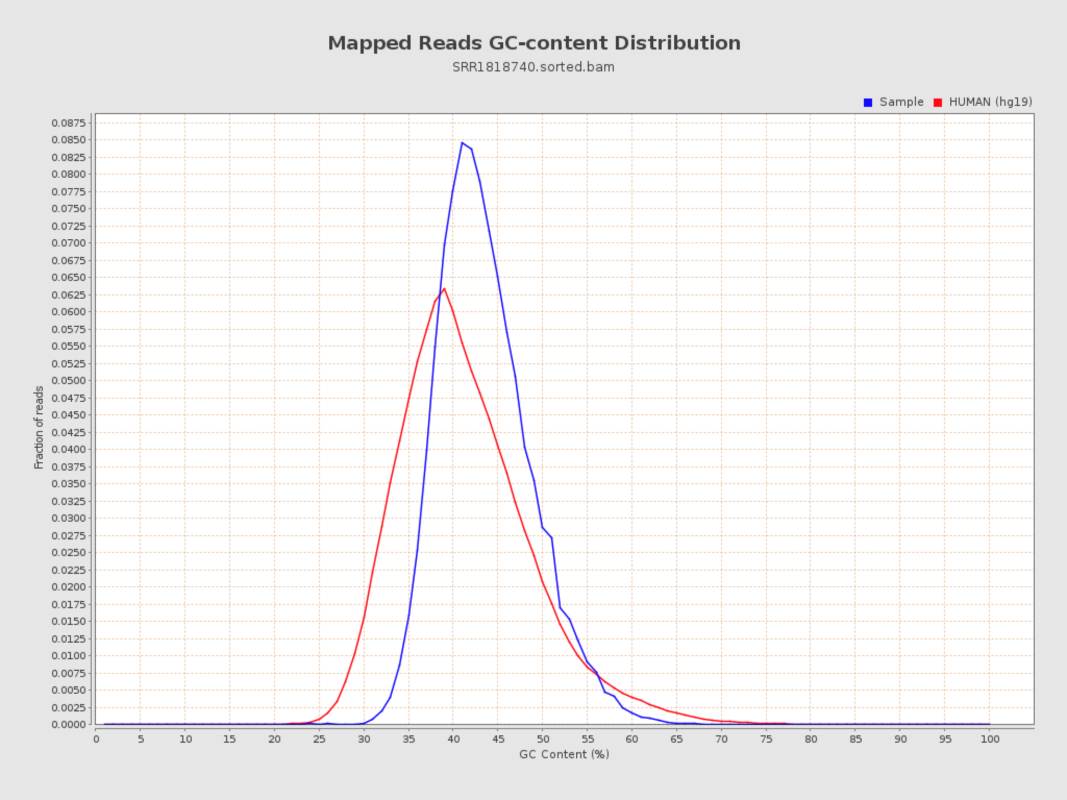
7. Results : Duplication Rate Histogram



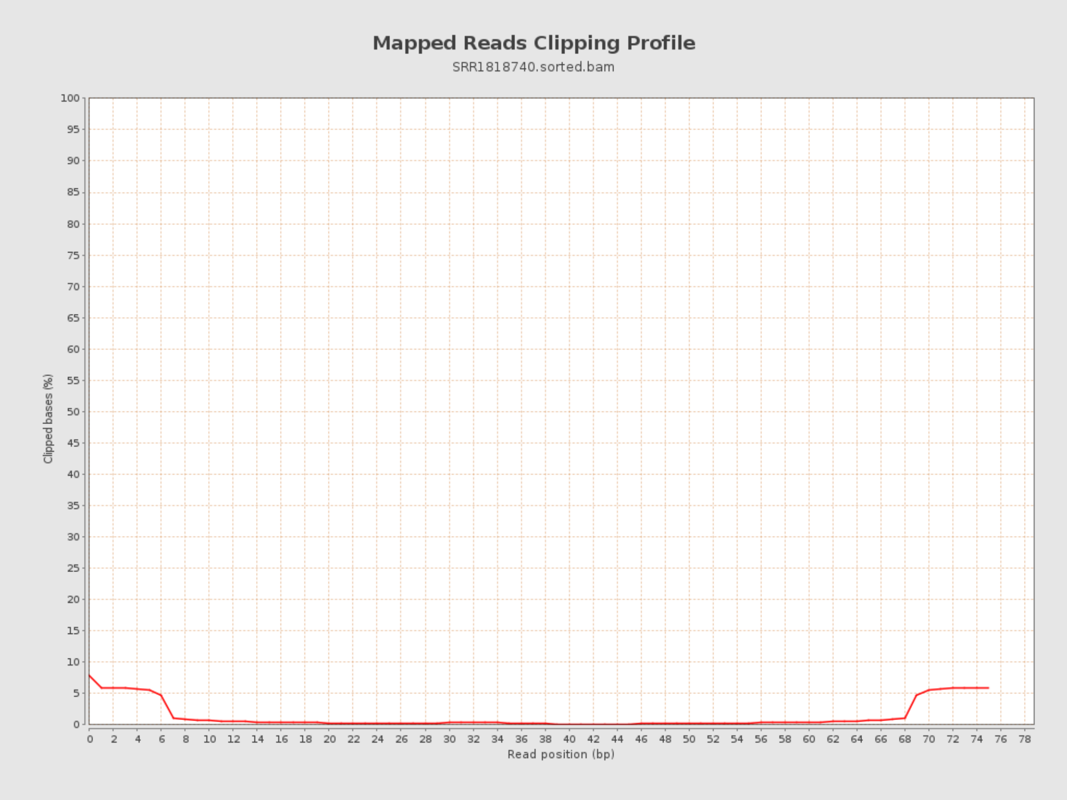
8. Results : Mapped Reads Nucleotide Content



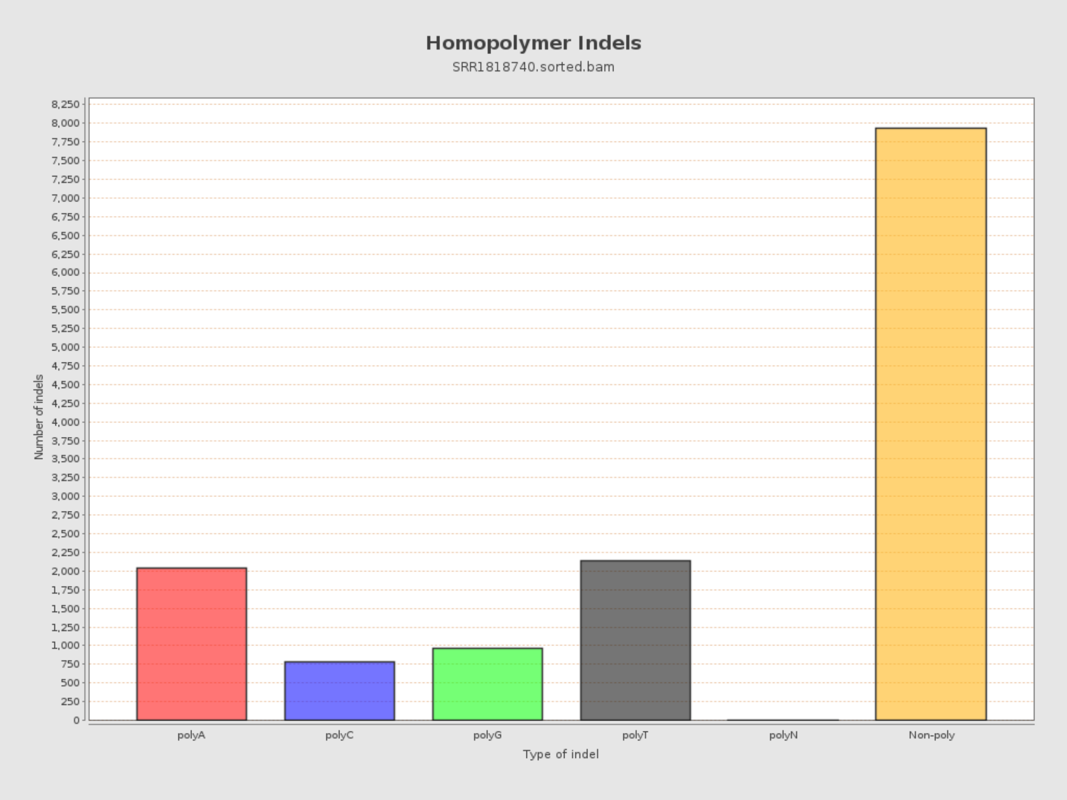
9. Results : Mapped Reads GC-content Distribution



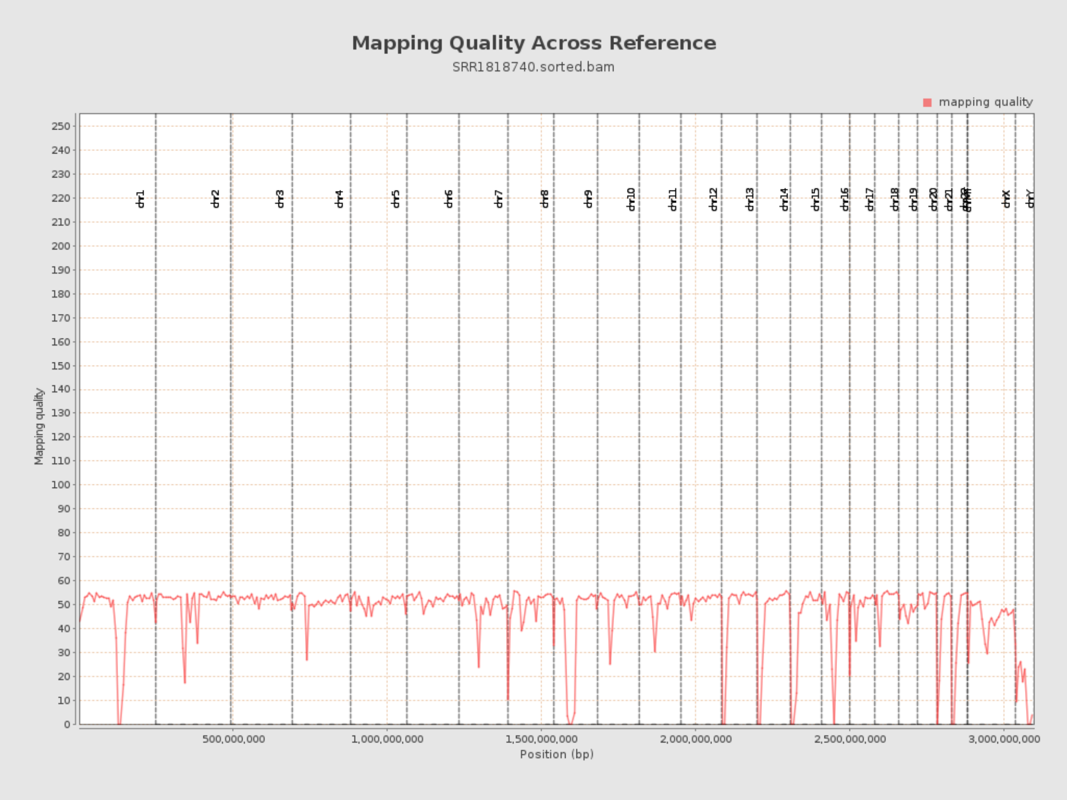
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram