Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 06:43:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818759.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_SRR1818759 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818759.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 06:43:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818759.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	369,515
Mapped reads	343,645 / 93%
Unmapped reads	25,870 / 7%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,586 / 0.7%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	51,337 / 13.89%
Duplication rate	13.32%
Clipped reads	342,107 / 92.58%

2.2. ACGT Content

Number/percentage of A's	6,281,561 / 26.94%
Number/percentage of C's	4,832,281 / 20.72%
Number/percentage of T's	6,973,817 / 29.91%
Number/percentage of G's	5,228,349 / 22.42%
Number/percentage of N's	1,378 / 0.01%
GC Percentage	43.15%

2.3. Coverage

Mean	0.0075

Standard Deviation	0.124

2.4. Mapping Quality

Mean Mapping Quality	47.41

2.5. Mismatches and indels

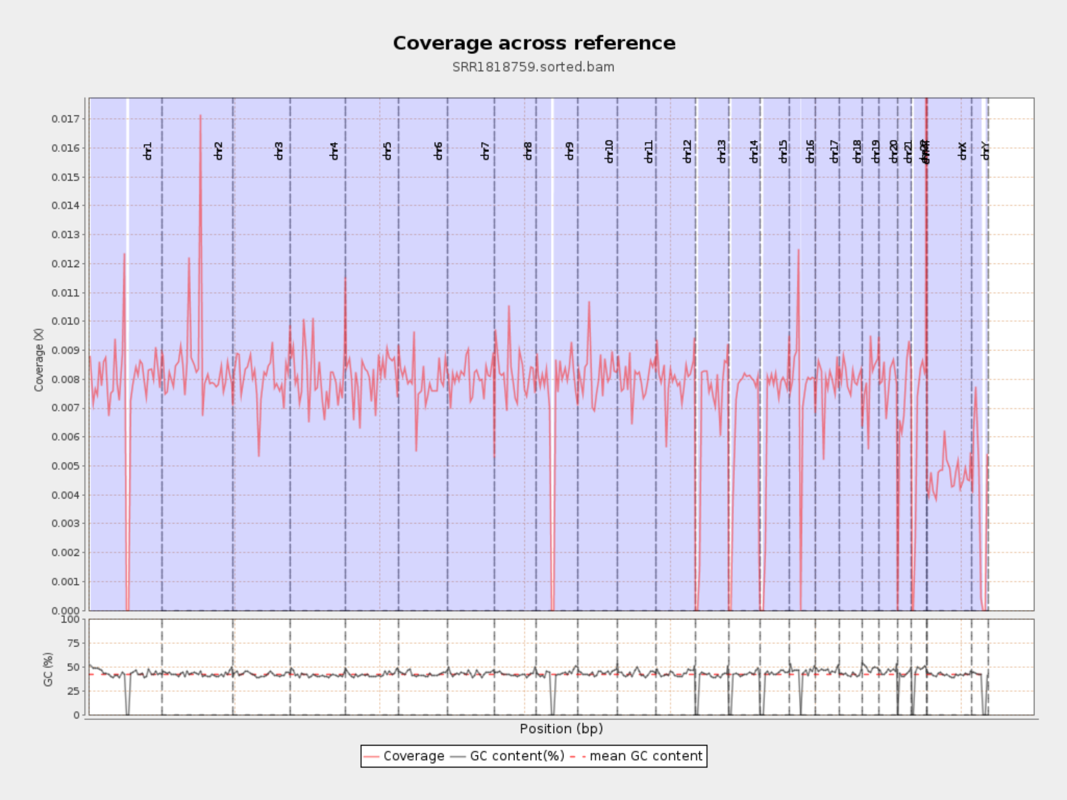
General error rate	0.54%
Mismatches	119,592
Insertions	2,978
Mapped reads with at least one insertion	0.85%
Deletions	6,119
Mapped reads with at least one deletion	1.77%
Homopolymer indels	42.52%

2.6. Chromosome stats

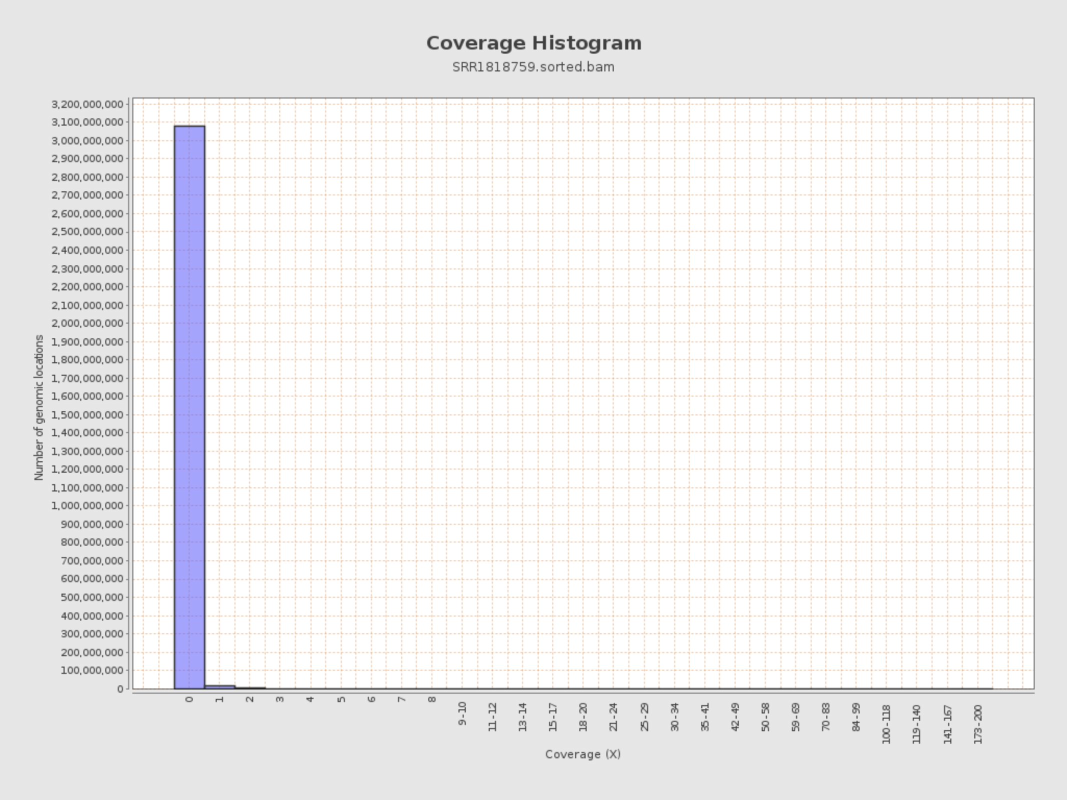
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1921120	0.0077	0.154
chr2	243199373	2071015	0.0085	0.1793
chr3	198022430	1590623	0.008	0.1079
chr4	191154276	1527037	0.008	0.1122
chr5	180915260	1467566	0.0081	0.1104
chr6	171115067	1357202	0.0079	0.1116
chr7	159138663	1286070	0.0081	0.1163

chr8	146364022	1204071	0.0082	0.116
chr9	141213431	1021696	0.0072	0.1132
chr10	135534747	1107749	0.0082	0.1308
chr11	135006516	1084830	0.008	0.1125
chr12	133851895	1070961	0.008	0.1106
chr13	115169878	756629	0.0066	0.0974
chr14	107349540	708173	0.0066	0.1037
chr15	102531392	655091	0.0064	0.0955
chr16	90354753	698680	0.0077	0.1395
chr17	81195210	634739	0.0078	0.1087
chr18	78077248	631955	0.0081	0.1359
chr19	59128983	470219	0.008	0.1386
chr20	63025520	501540	0.008	0.111
chr21	48129895	331283	0.0069	0.1042
chr22	51304566	289169	0.0056	0.0955
chrMT	16571	1933	0.1166	0.3733
chrX	155270560	725475	0.0047	0.086
chrY	59373566	212547	0.0036	0.1753

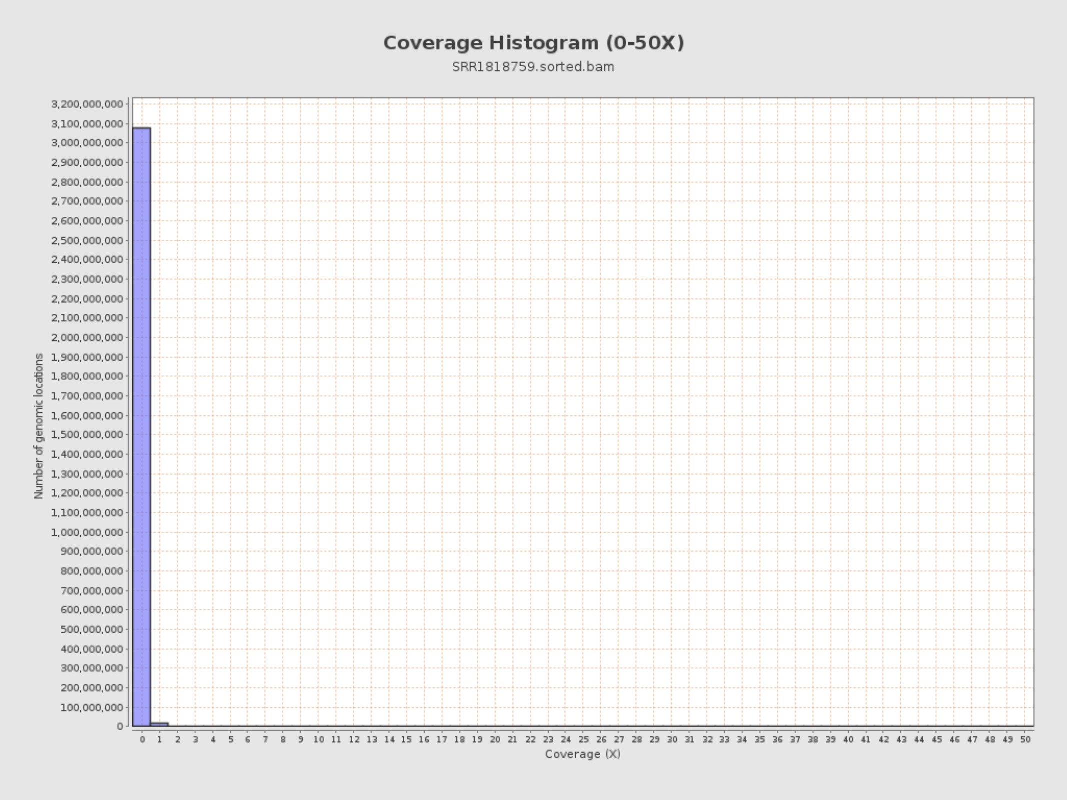
3. Results : Coverage across reference



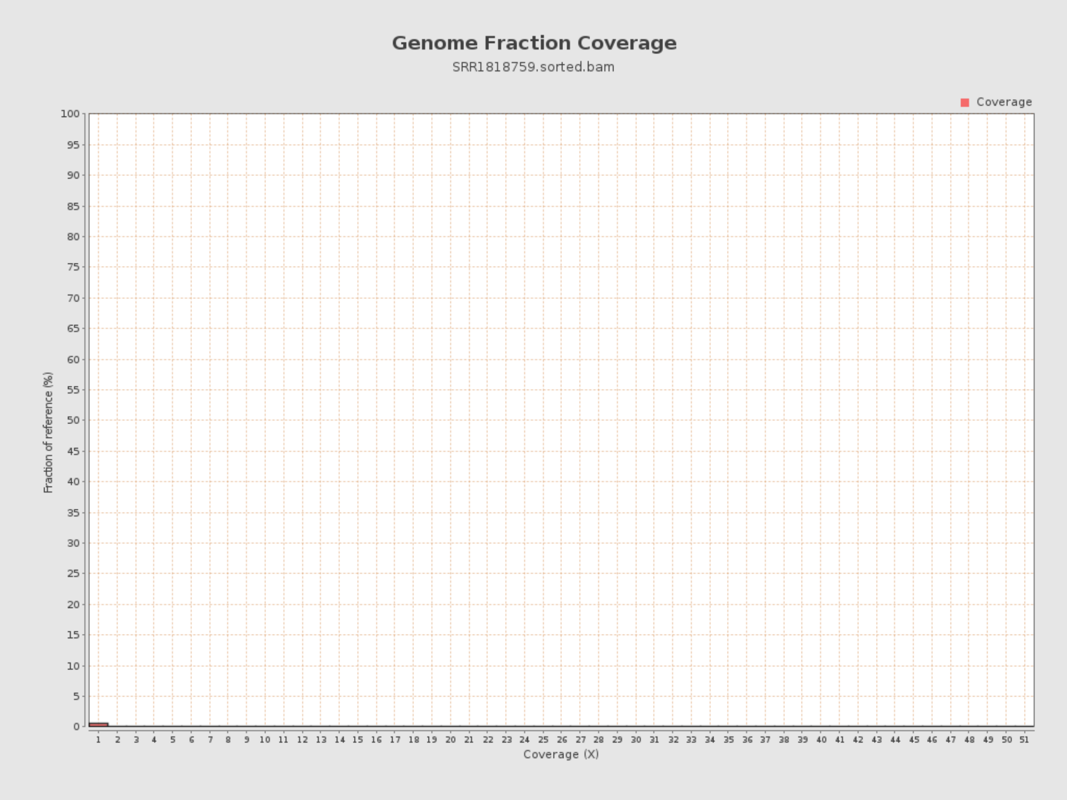
4. Results : Coverage Histogram



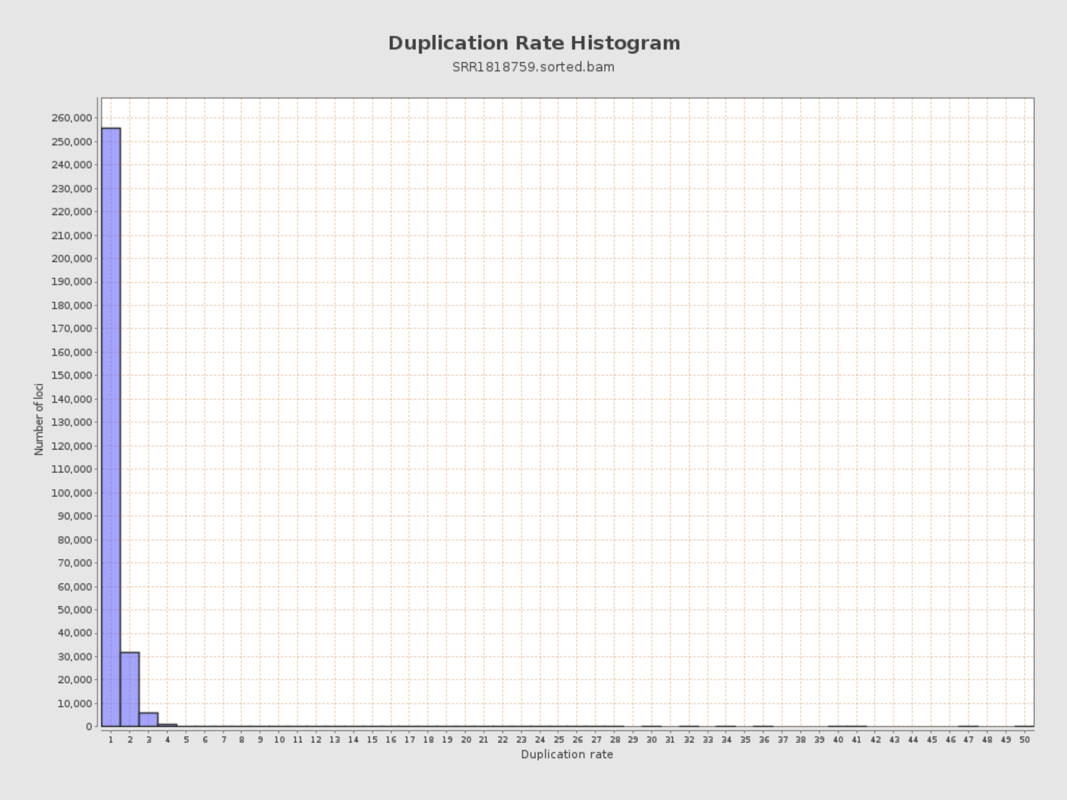
5. Results : Coverage Histogram (0-50X)



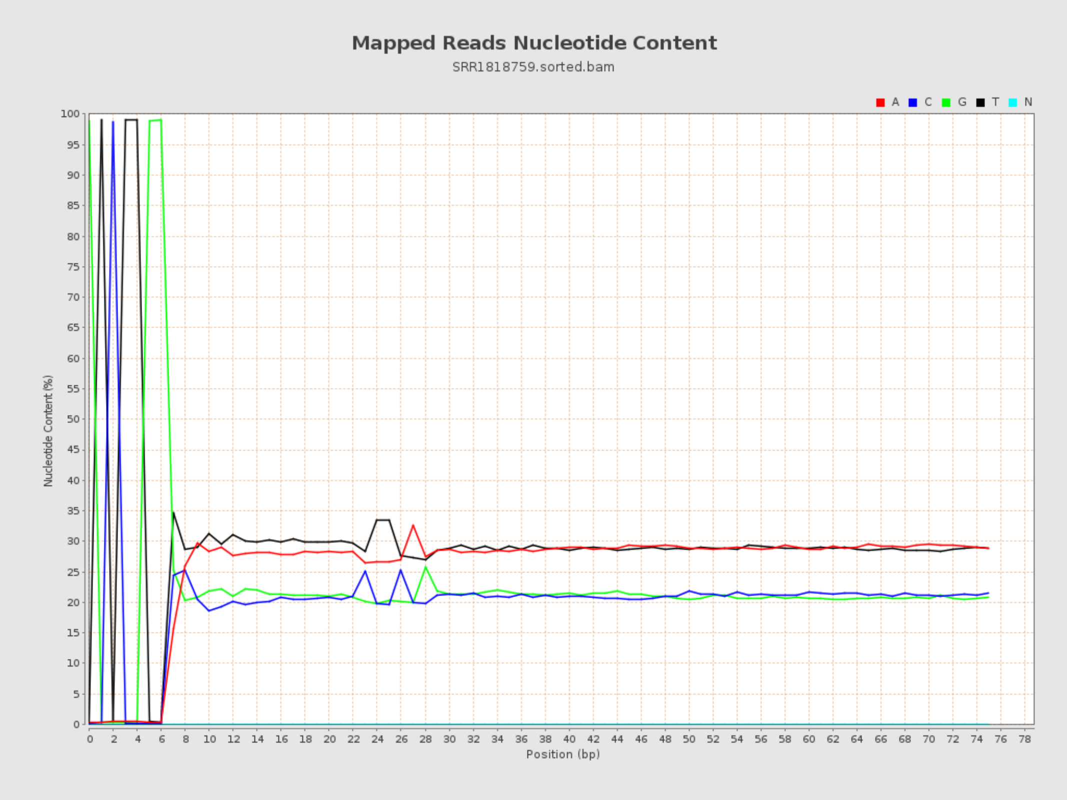
6. Results : Genome Fraction Coverage



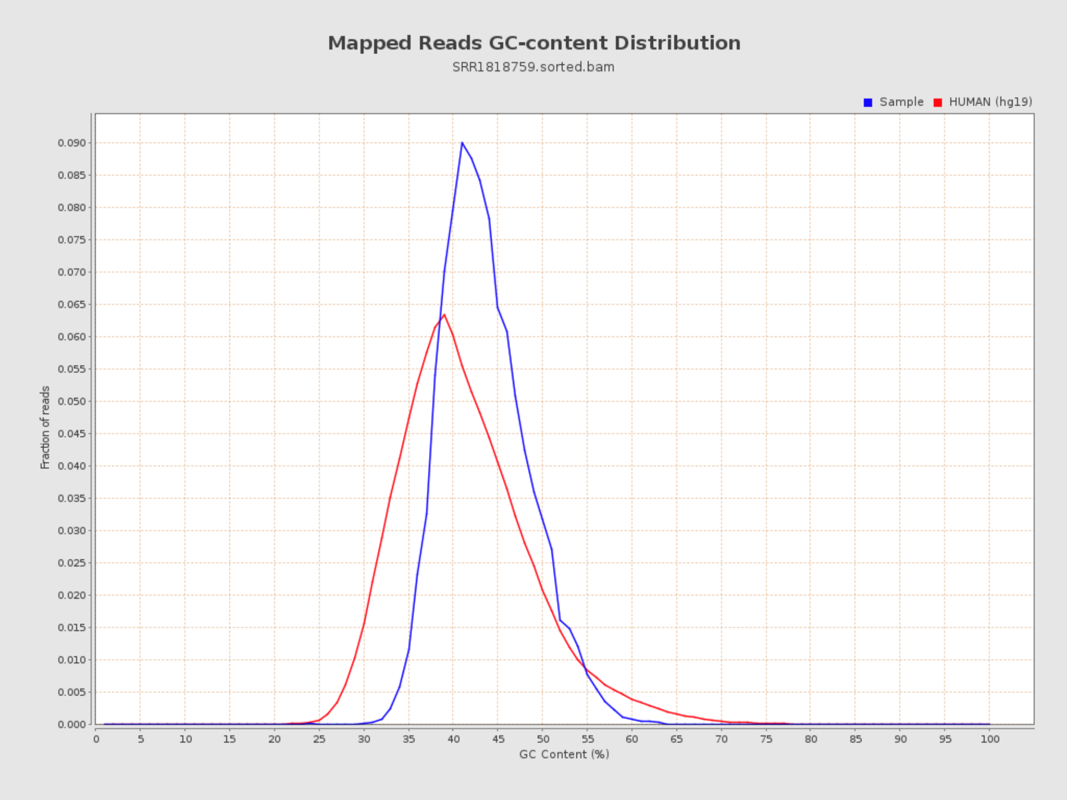
7. Results : Duplication Rate Histogram



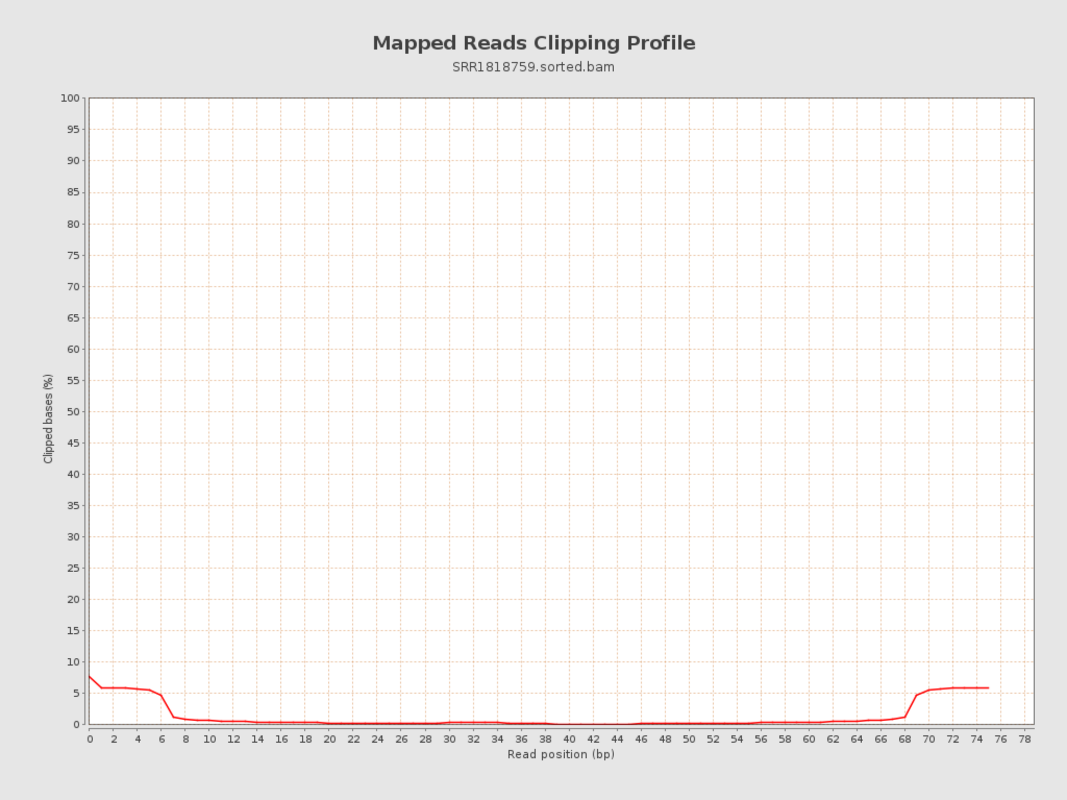
8. Results : Mapped Reads Nucleotide Content



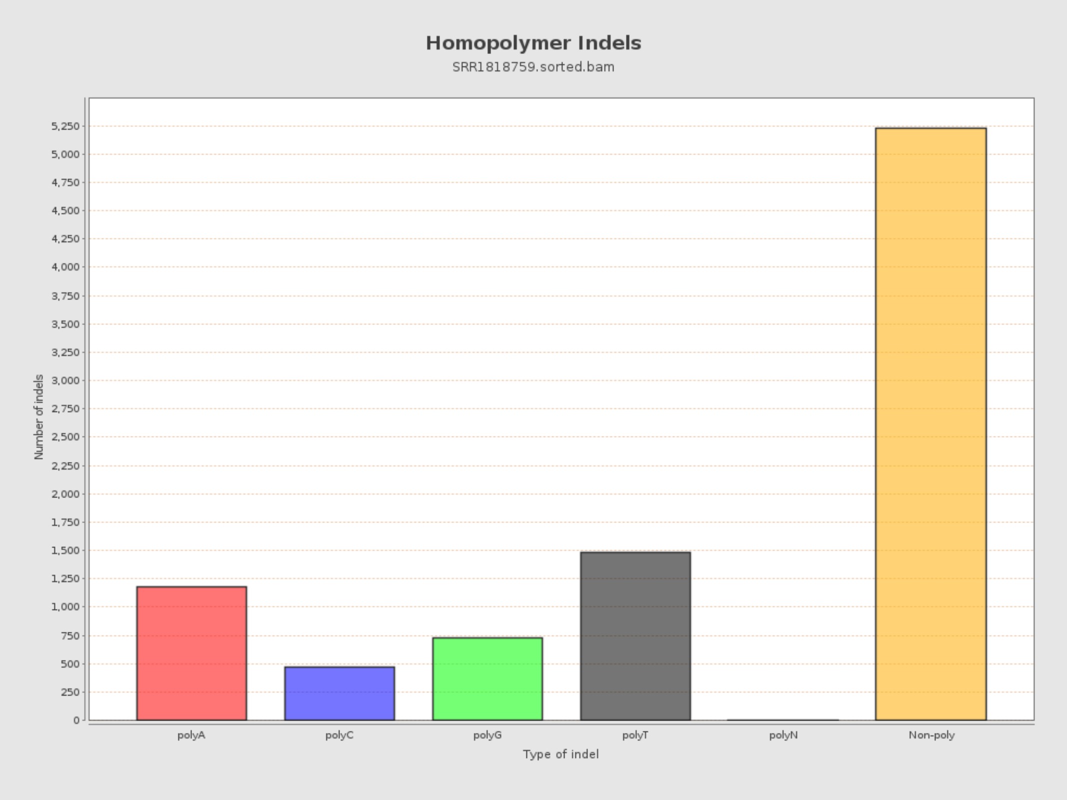
9. Results : Mapped Reads GC-content Distribution



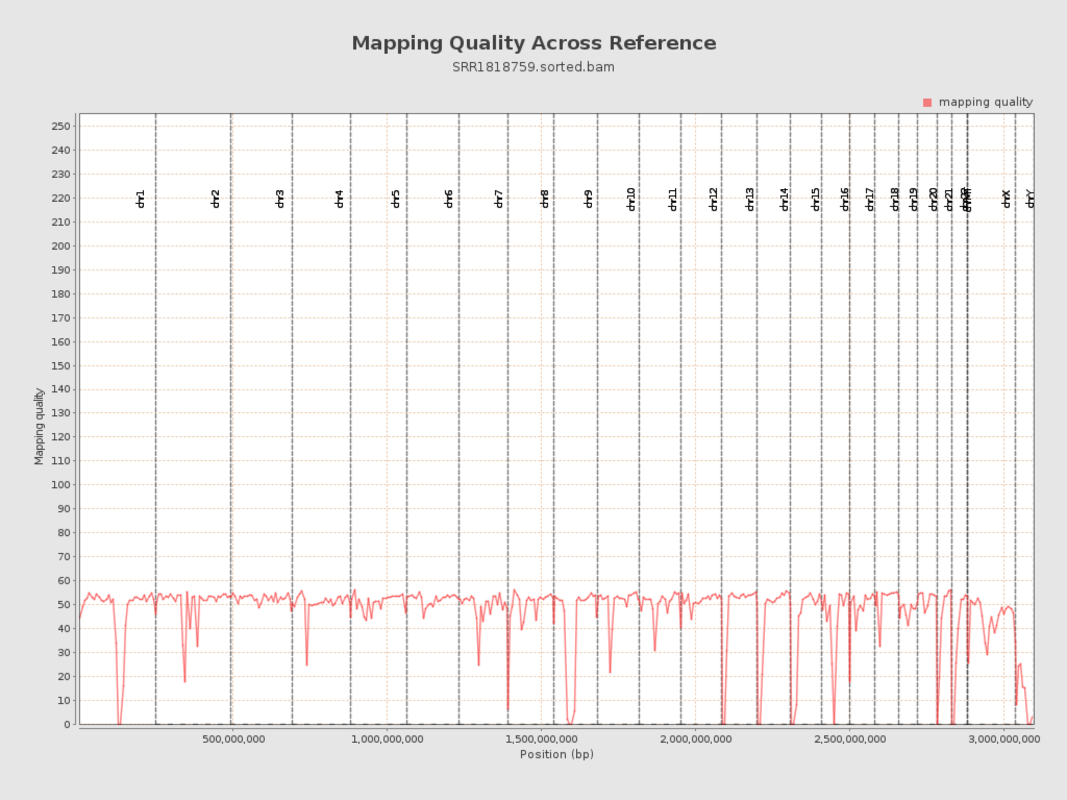
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram