Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 07:50:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1818767.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_SRR1818767 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1818767.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 07:50:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1818767.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	245,583
Mapped reads	235,059 / 95.71%
Unmapped reads	10,524 / 4.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,782 / 0.73%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	29,823 / 12.14%
Duplication rate	11.58%
Clipped reads	235,341 / 95.83%

2.2. ACGT Content

Number/percentage of A's	4,621,199 / 28.99%
Number/percentage of C's	3,557,502 / 22.31%
Number/percentage of T's	4,513,146 / 28.31%
Number/percentage of G's	3,249,718 / 20.38%
Number/percentage of N's	1,018 / 0.01%
GC Percentage	42.7%

2.3. Coverage

Mean	0.0052

Standard Deviation	0.093

2.4. Mapping Quality

Mean Mapping Quality	48

2.5. Mismatches and indels

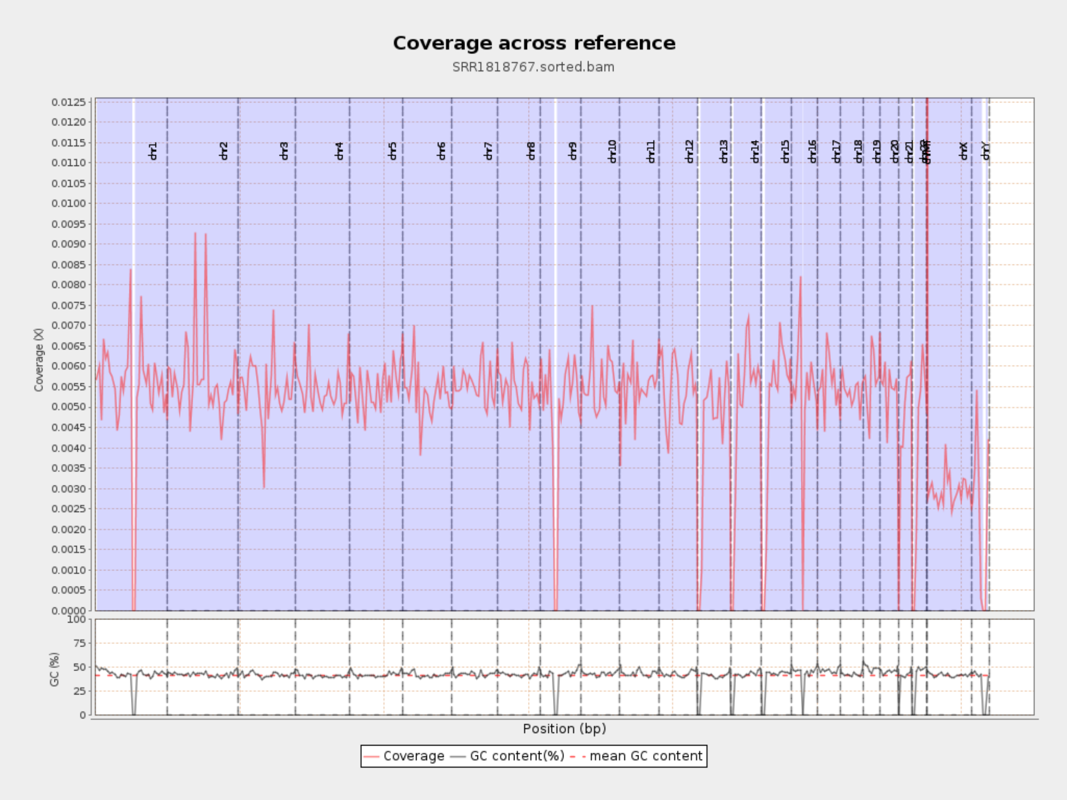
General error rate	0.53%
Mismatches	81,150
Insertions	1,677
Mapped reads with at least one insertion	0.71%
Deletions	4,042
Mapped reads with at least one deletion	1.7%
Homopolymer indels	41%

2.6. Chromosome stats

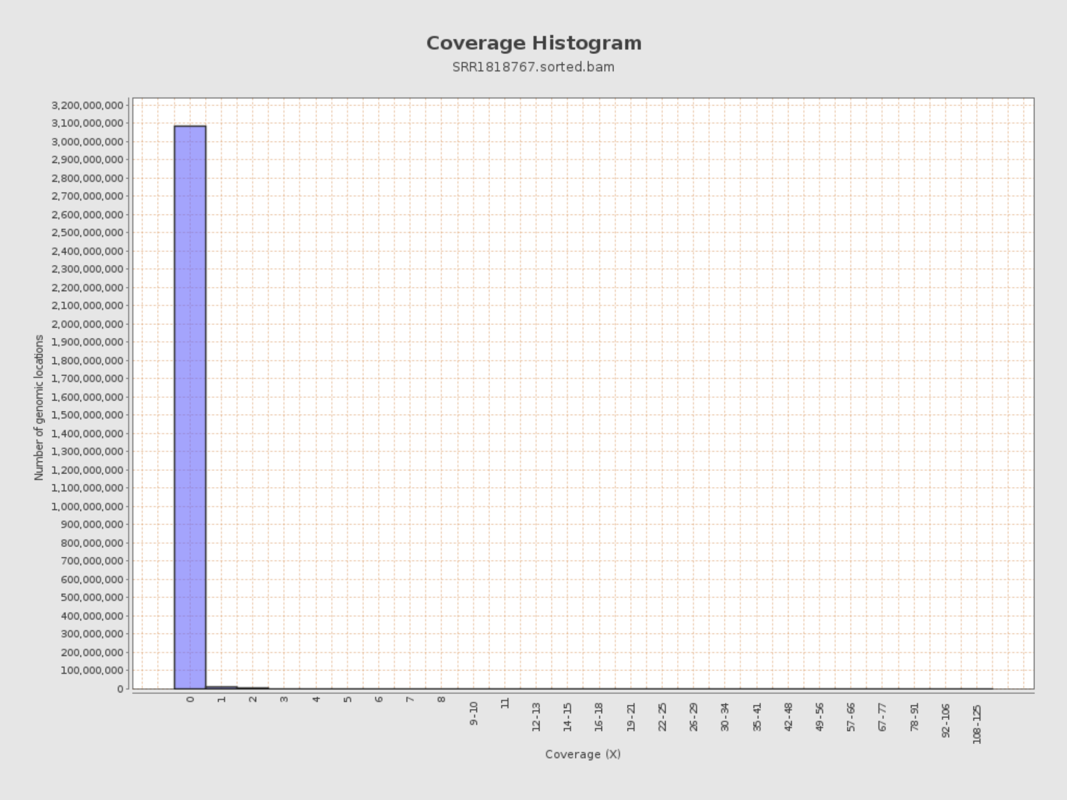
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1342552	0.0054	0.1158
chr2	243199373	1393414	0.0057	0.1176
chr3	198022430	1076220	0.0054	0.0861
chr4	191154276	1041161	0.0054	0.0888
chr5	180915260	992114	0.0055	0.087
chr6	171115067	920296	0.0054	0.0878
chr7	159138663	888445	0.0056	0.0922

chr8	146364022	801899	0.0055	0.0904
chr9	141213431	684988	0.0049	0.0852
chr10	135534747	764139	0.0056	0.0975
chr11	135006516	742842	0.0055	0.0891
chr12	133851895	727753	0.0054	0.0879
chr13	115169878	501478	0.0044	0.0772
chr14	107349540	525867	0.0049	0.0841
chr15	102531392	490422	0.0048	0.0811
chr16	90354753	474303	0.0052	0.1017
chr17	81195210	454804	0.0056	0.0892
chr18	78077248	420243	0.0054	0.0998
chr19	59128983	335122	0.0057	0.1073
chr20	63025520	342415	0.0054	0.088
chr21	48129895	221154	0.0046	0.0806
chr22	51304566	197208	0.0038	0.0755
chrMT	16571	9273	0.5596	0.949
chrX	155270560	459955	0.003	0.065
chrY	59373566	141047	0.0024	0.094

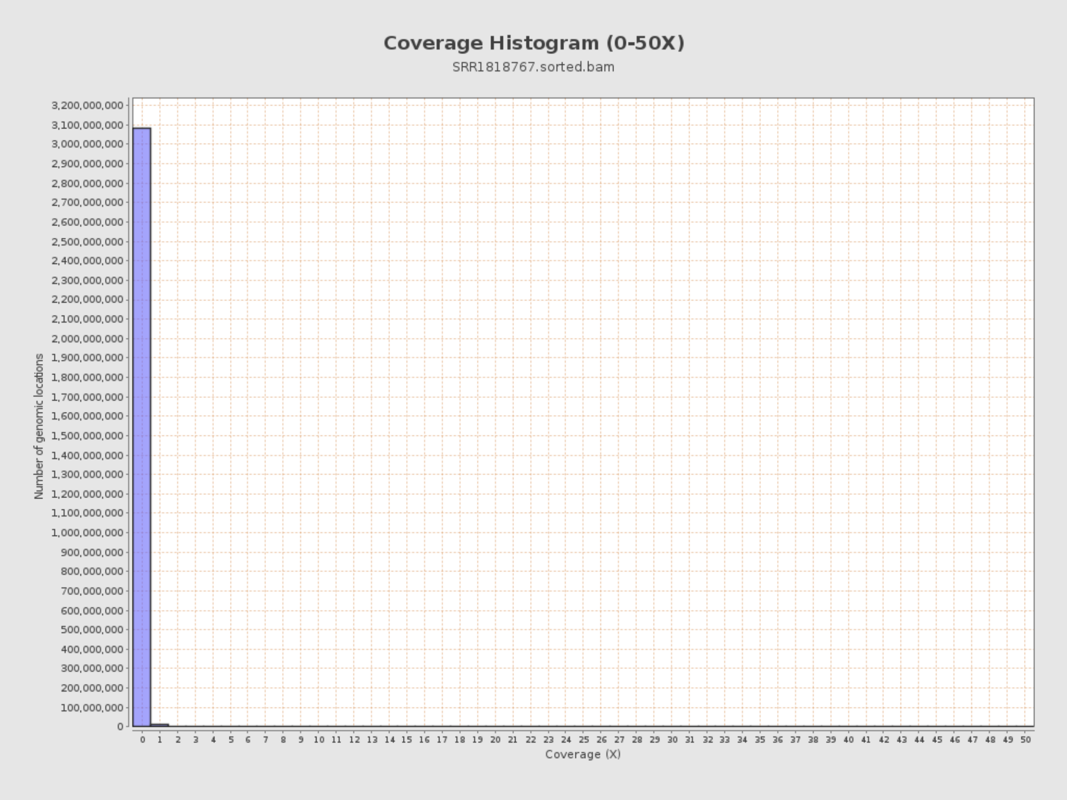
3. Results : Coverage across reference



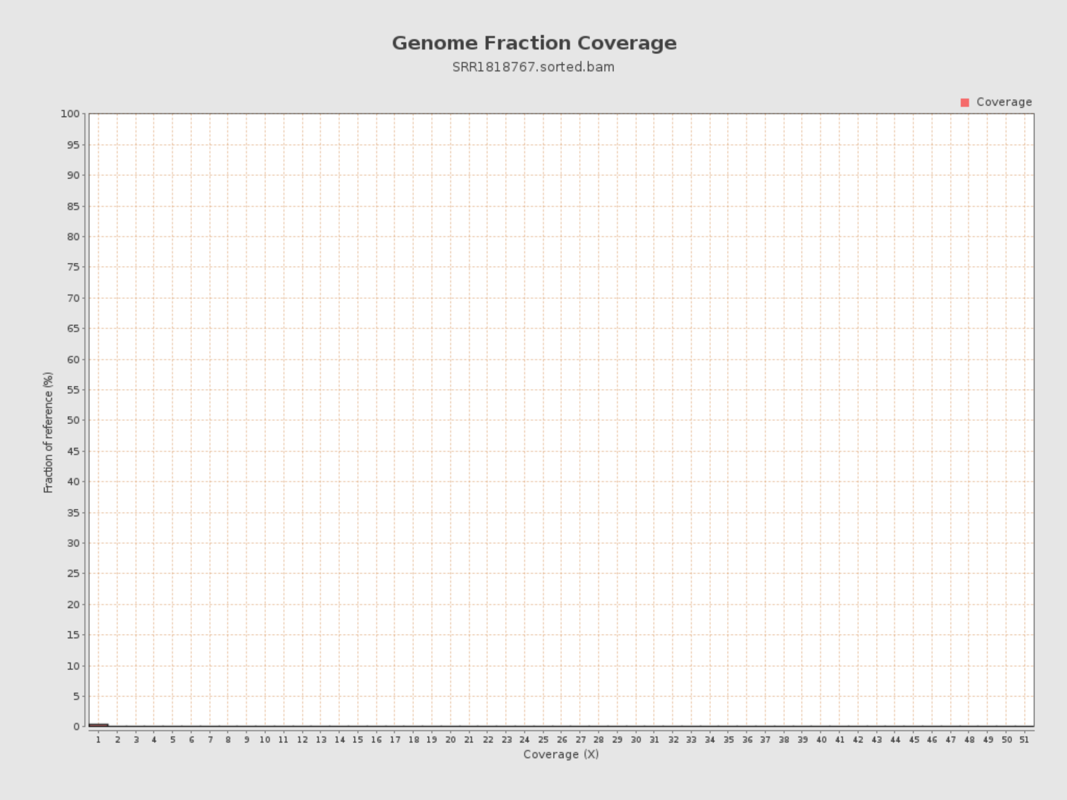
4. Results : Coverage Histogram



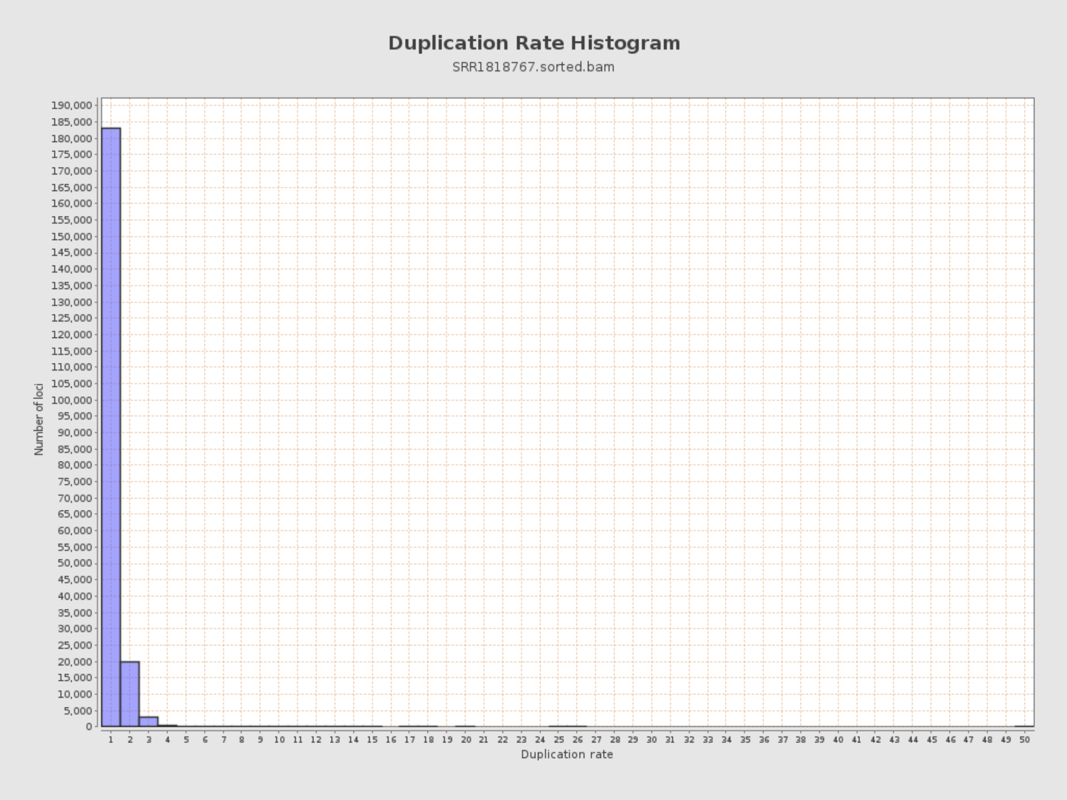
5. Results : Coverage Histogram (0-50X)



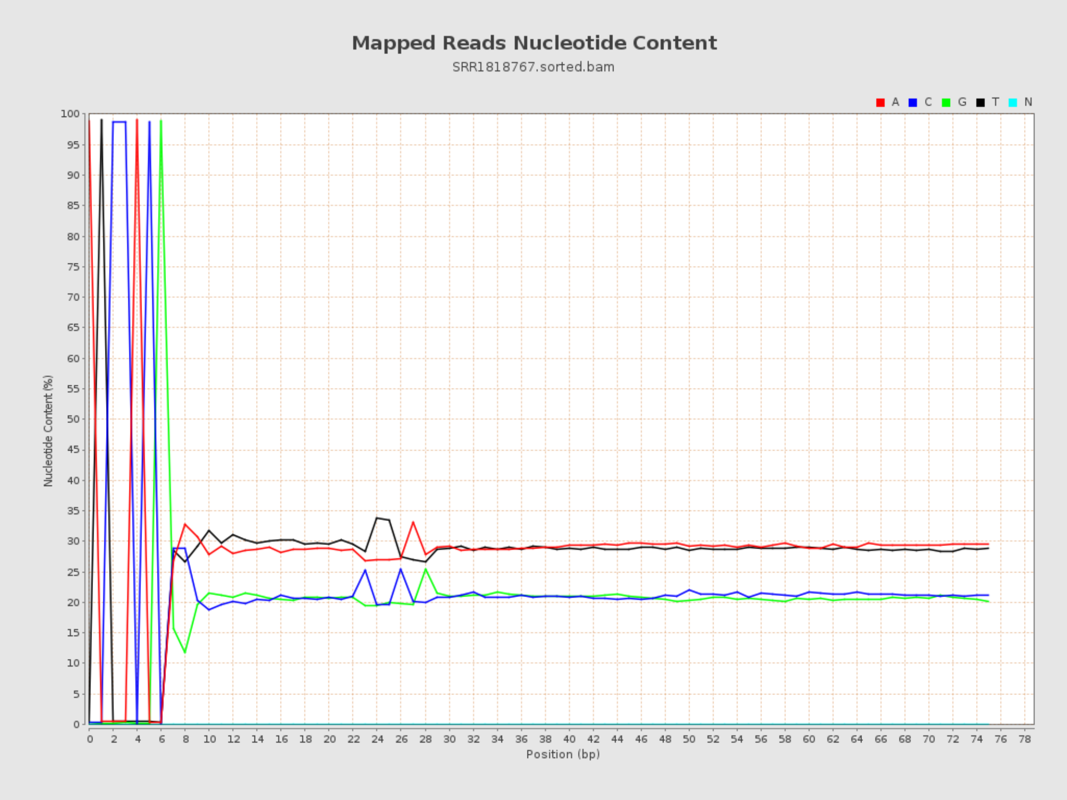
6. Results : Genome Fraction Coverage



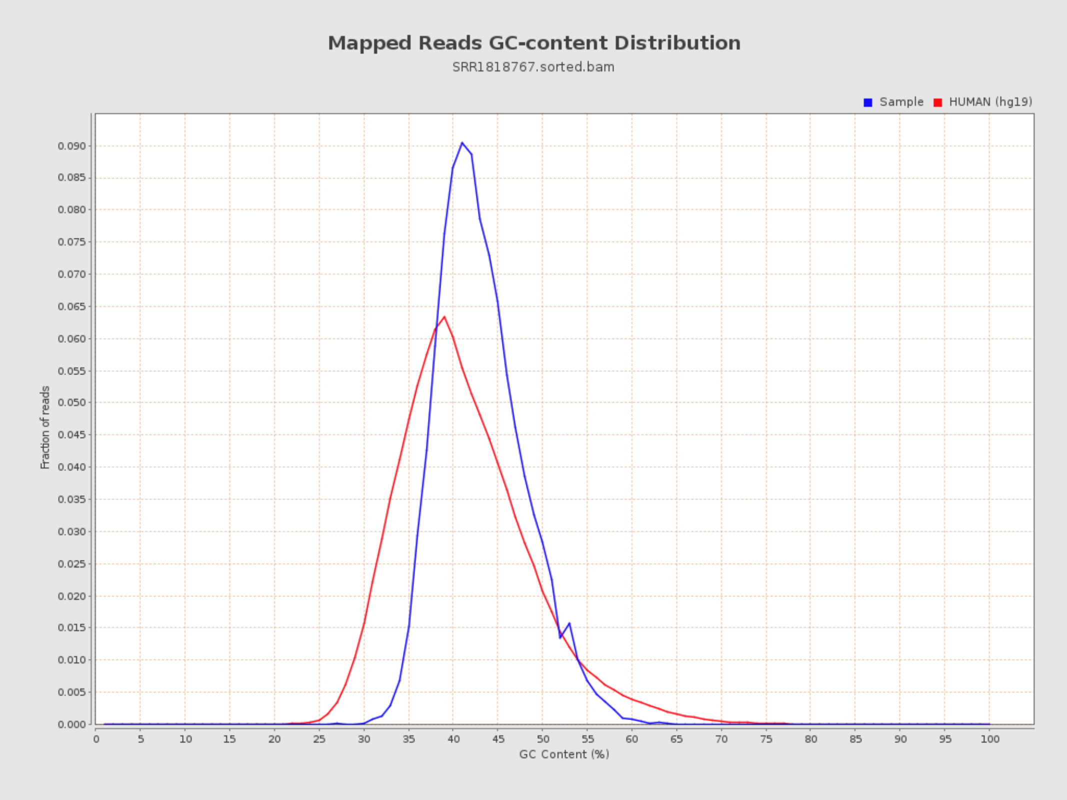
7. Results : Duplication Rate Histogram



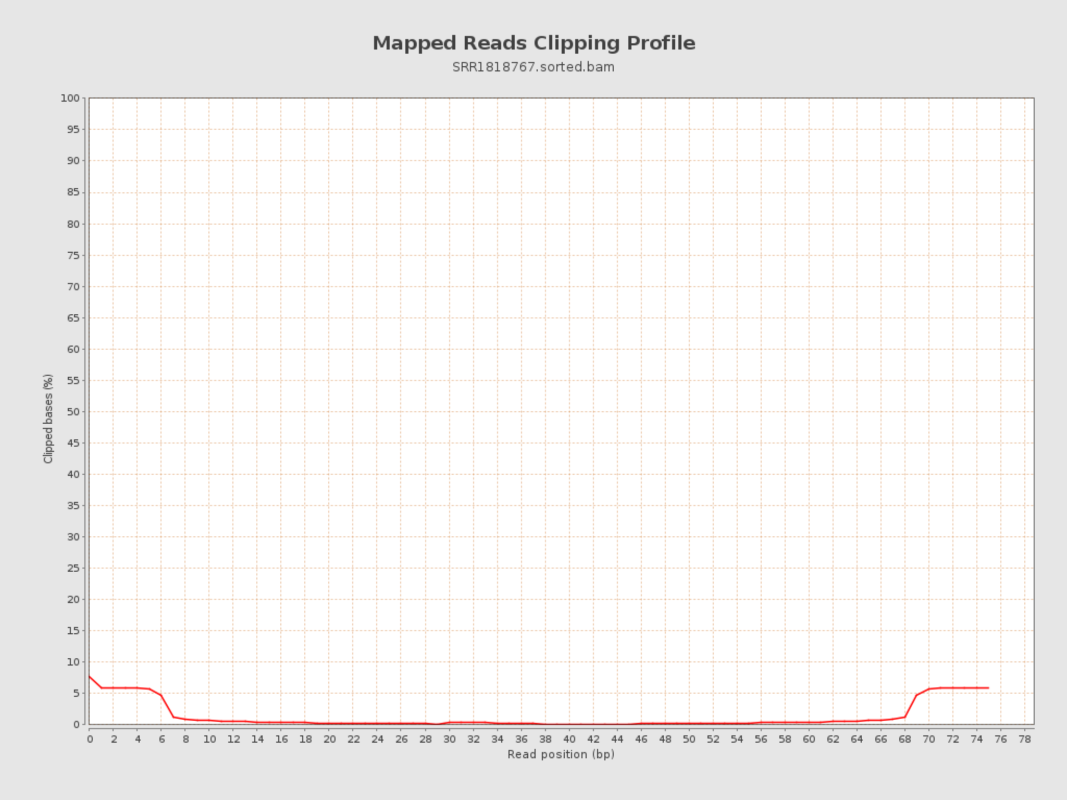
8. Results : Mapped Reads Nucleotide Content



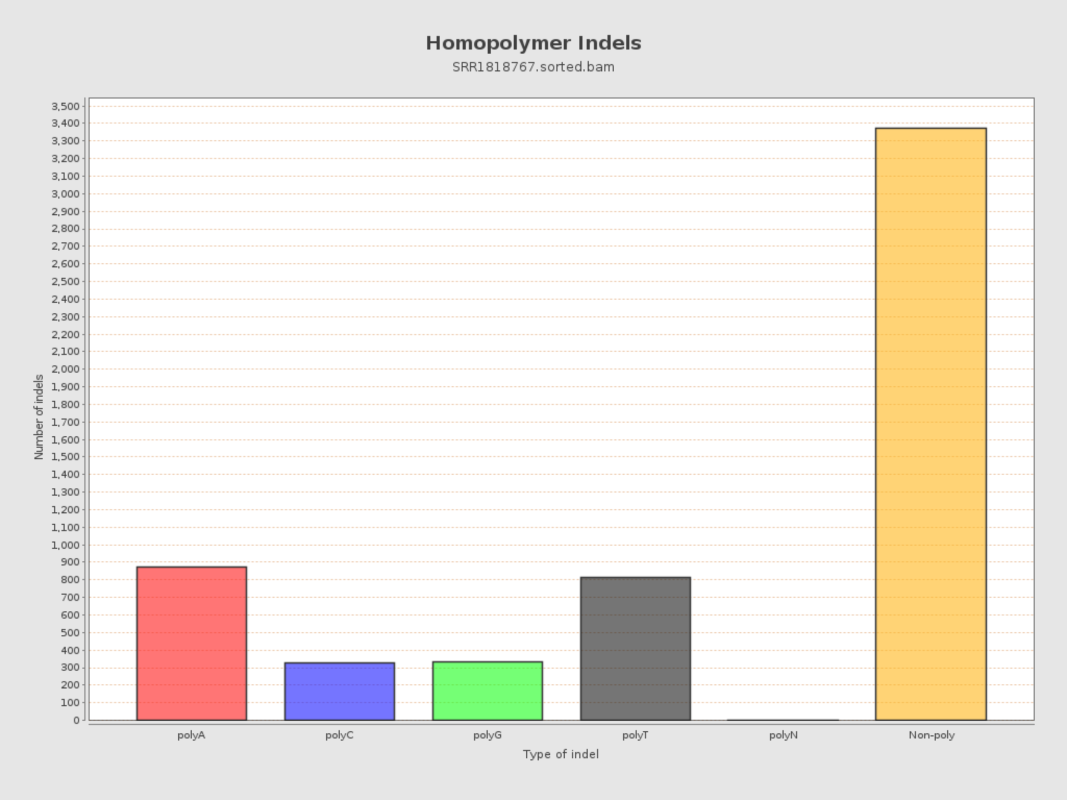
9. Results : Mapped Reads GC-content Distribution



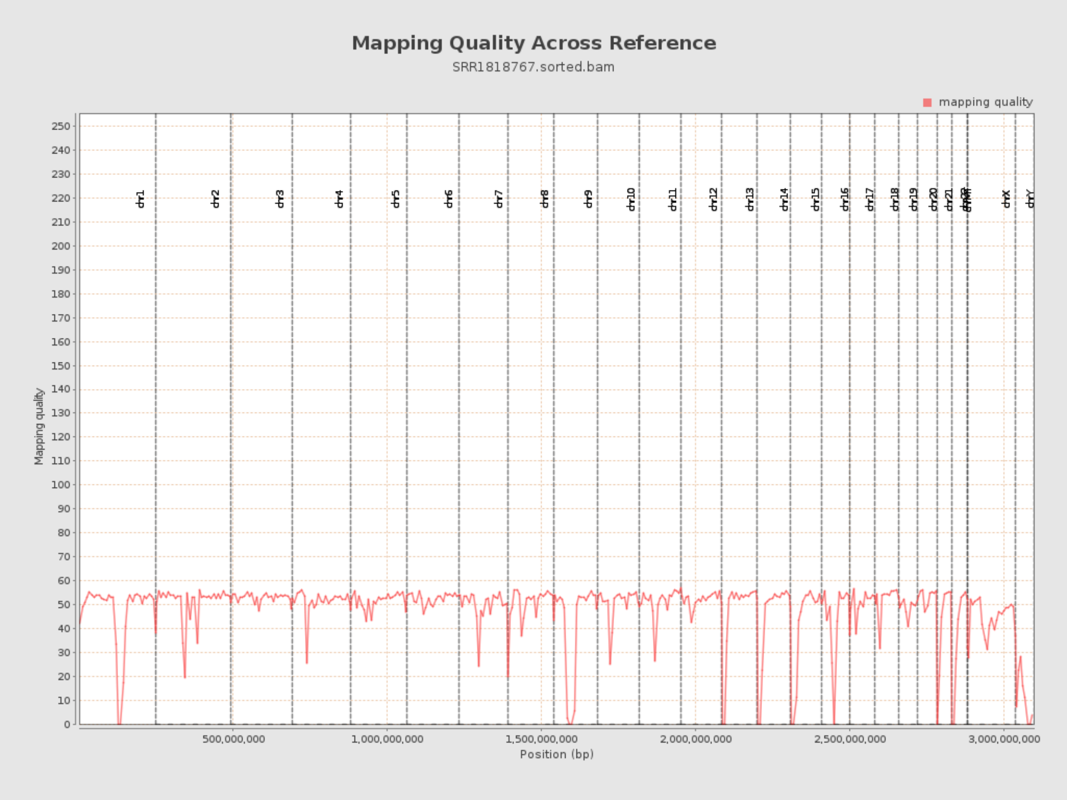
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram