Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:36:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819007.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_SRR1819007 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819007.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:36:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819007.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	617,856
Mapped reads	605,280 / 97.96%
Unmapped reads	12,576 / 2.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,603 / 1.72%
Read min/max/mean length	30 / 101 / 101.66
Duplicated reads (estimated)	199,368 / 32.27%
Duplication rate	28.43%
Clipped reads	611,044 / 98.9%

2.2. ACGT Content

Number/percentage of A's	16,504,537 / 29.6%
Number/percentage of C's	12,149,059 / 21.79%
Number/percentage of T's	15,728,866 / 28.21%
Number/percentage of G's	11,374,455 / 20.4%
Number/percentage of N's	2,744 / 0%
GC Percentage	42.19%

2.3. Coverage

Mean	0.018

Standard Deviation	0.3015

2.4. Mapping Quality

Mean Mapping Quality	48.66

2.5. Mismatches and indels

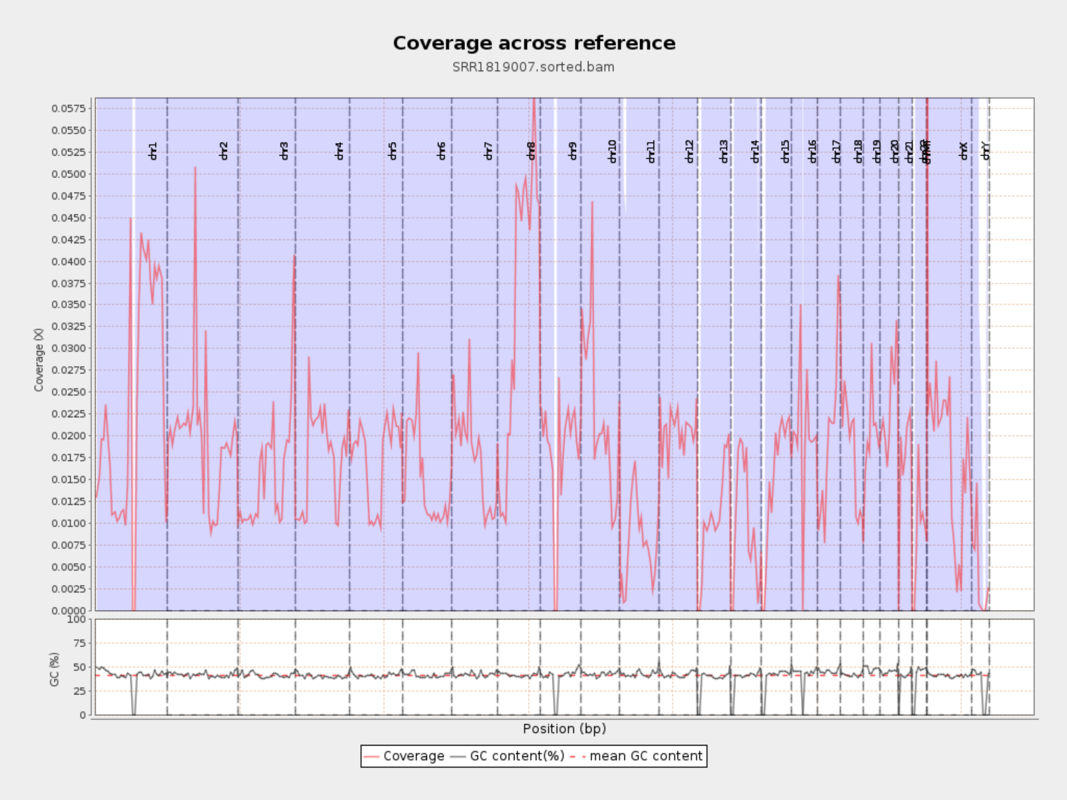
General error rate	0.74%
Mismatches	389,361
Insertions	10,359
Mapped reads with at least one insertion	1.66%
Deletions	19,087
Mapped reads with at least one deletion	3.09%
Homopolymer indels	41.29%

2.6. Chromosome stats

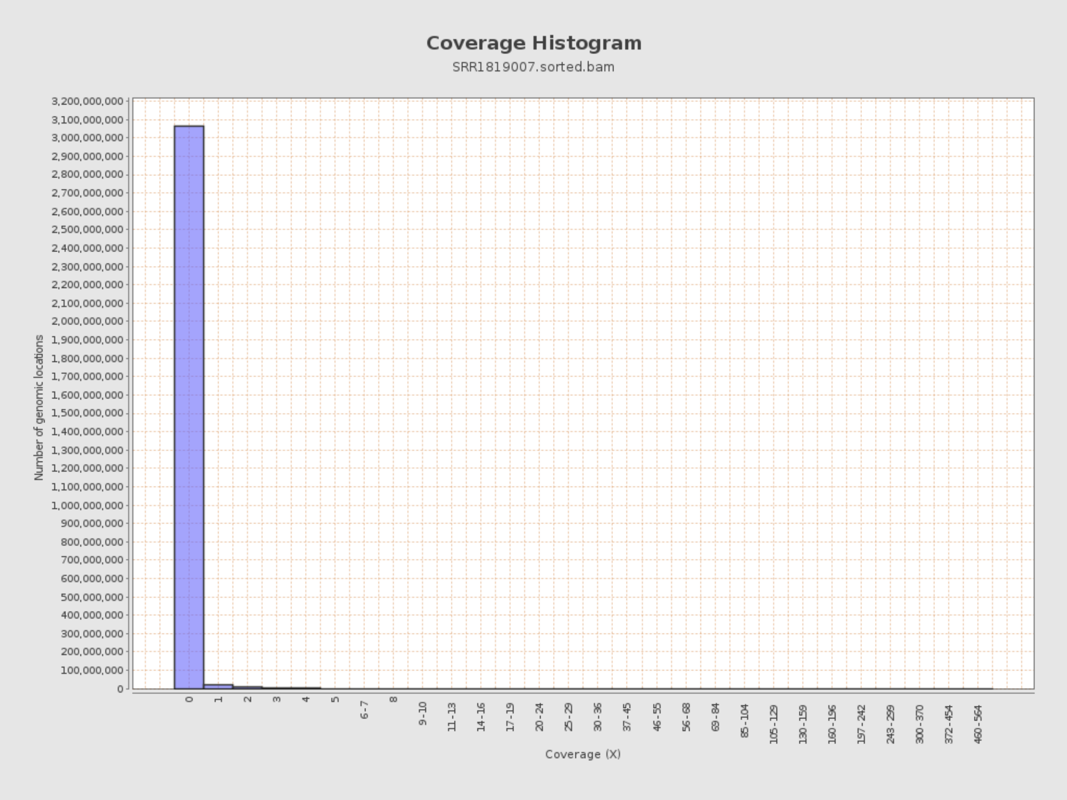
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5804894	0.0233	0.5441
chr2	243199373	4779470	0.0197	0.4609
chr3	198022430	3088887	0.0156	0.1877
chr4	191154276	3341955	0.0175	0.2235
chr5	180915260	3151526	0.0174	0.202
chr6	171115067	2558930	0.015	0.2065
chr7	159138663	2848095	0.0179	0.2786

chr8	146364022	5173122	0.0353	0.3065
chr9	141213431	2550597	0.0181	0.2676
chr10	135534747	3115581	0.023	0.3565
chr11	135006516	1033217	0.0077	0.1588
chr12	133851895	2754884	0.0206	0.2183
chr13	115169878	1226265	0.0106	0.1561
chr14	107349540	1030720	0.0096	0.1531
chr15	102531392	1537397	0.015	0.185
chr16	90354753	1784865	0.0198	0.3309
chr17	81195210	1588391	0.0196	0.2257
chr18	78077248	1428095	0.0183	0.2918
chr19	59128983	1189155	0.0201	0.4455
chr20	63025520	1507627	0.0239	0.242
chr21	48129895	843088	0.0175	0.2158
chr22	51304566	452601	0.0088	0.1457
chrMT	16571	7847	0.4735	1.1593
chrX	155270560	2760858	0.0178	0.2241
chrY	59373566	236853	0.004	0.298

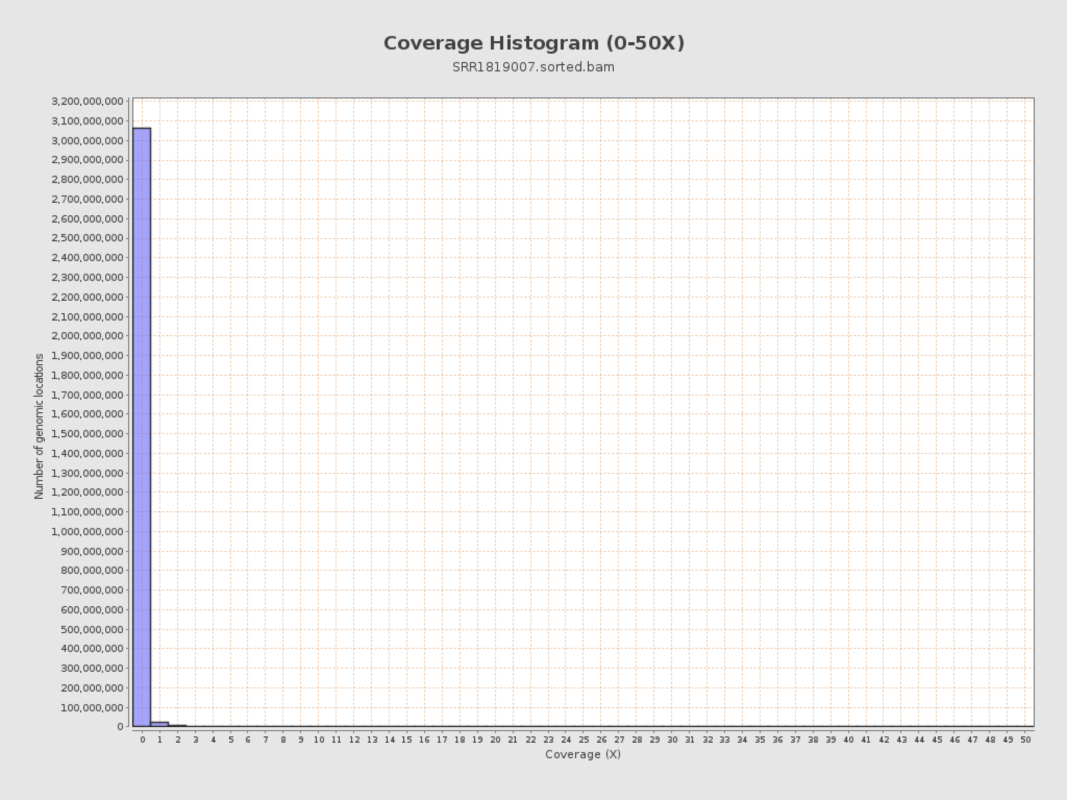
3. Results : Coverage across reference



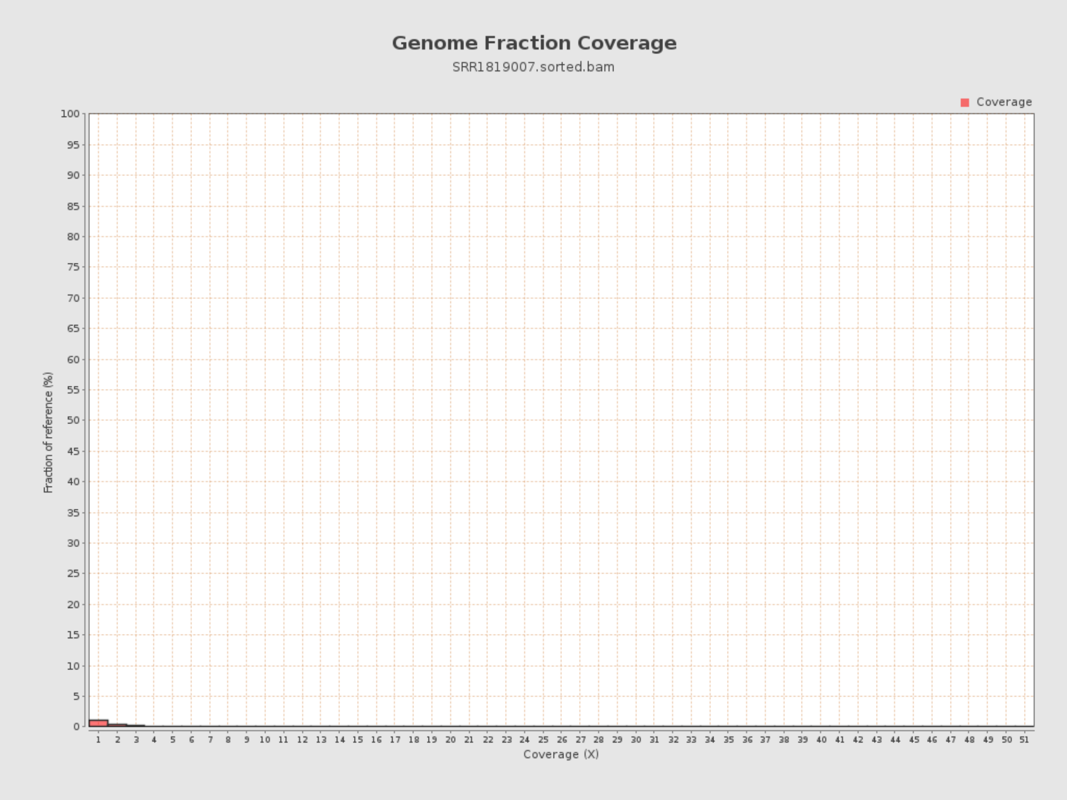
4. Results : Coverage Histogram



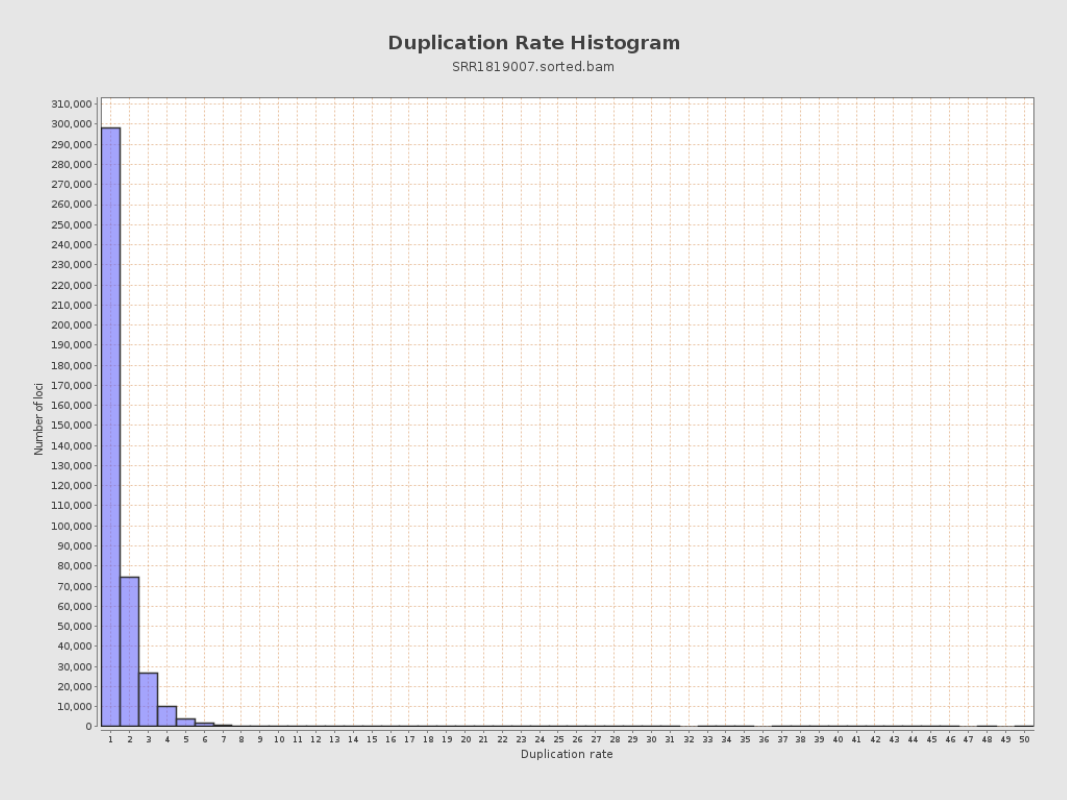
5. Results : Coverage Histogram (0-50X)



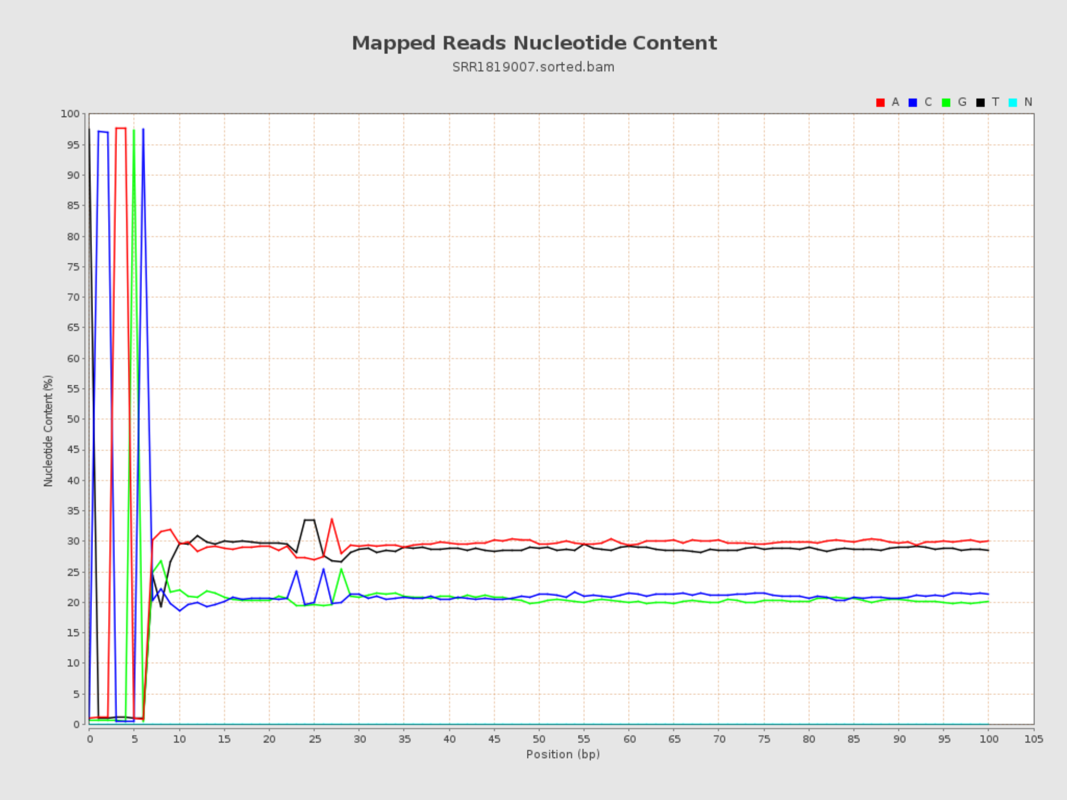
6. Results : Genome Fraction Coverage



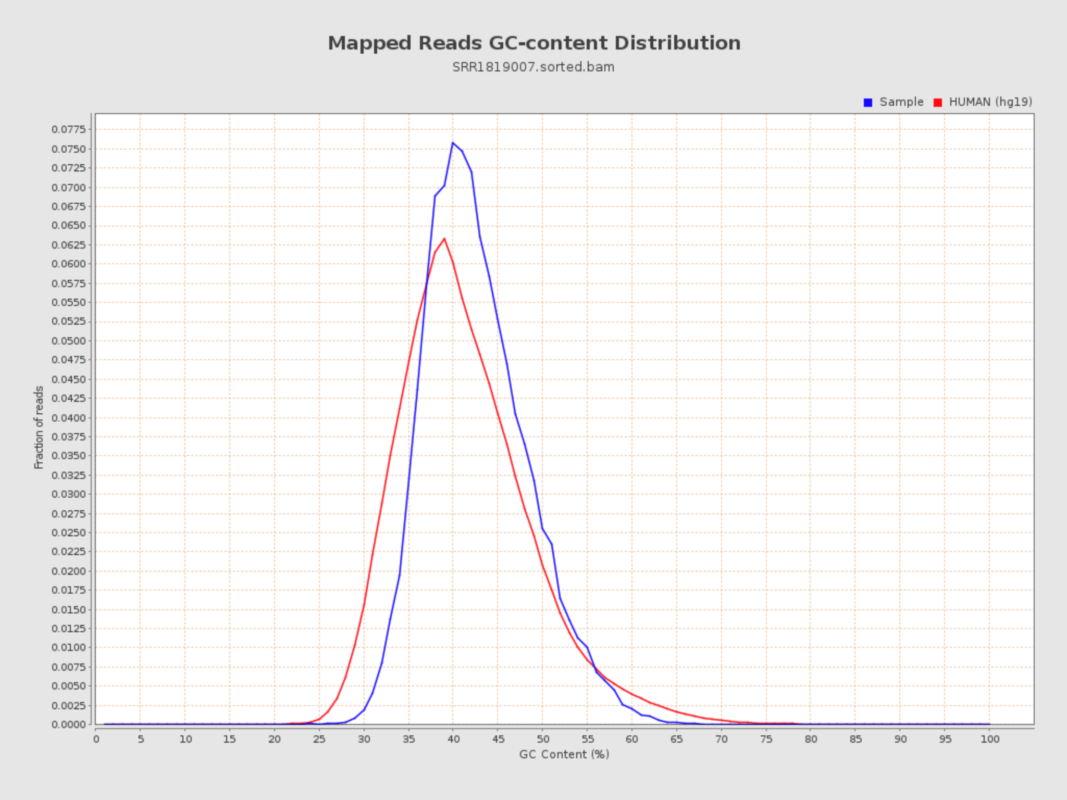
7. Results : Duplication Rate Histogram



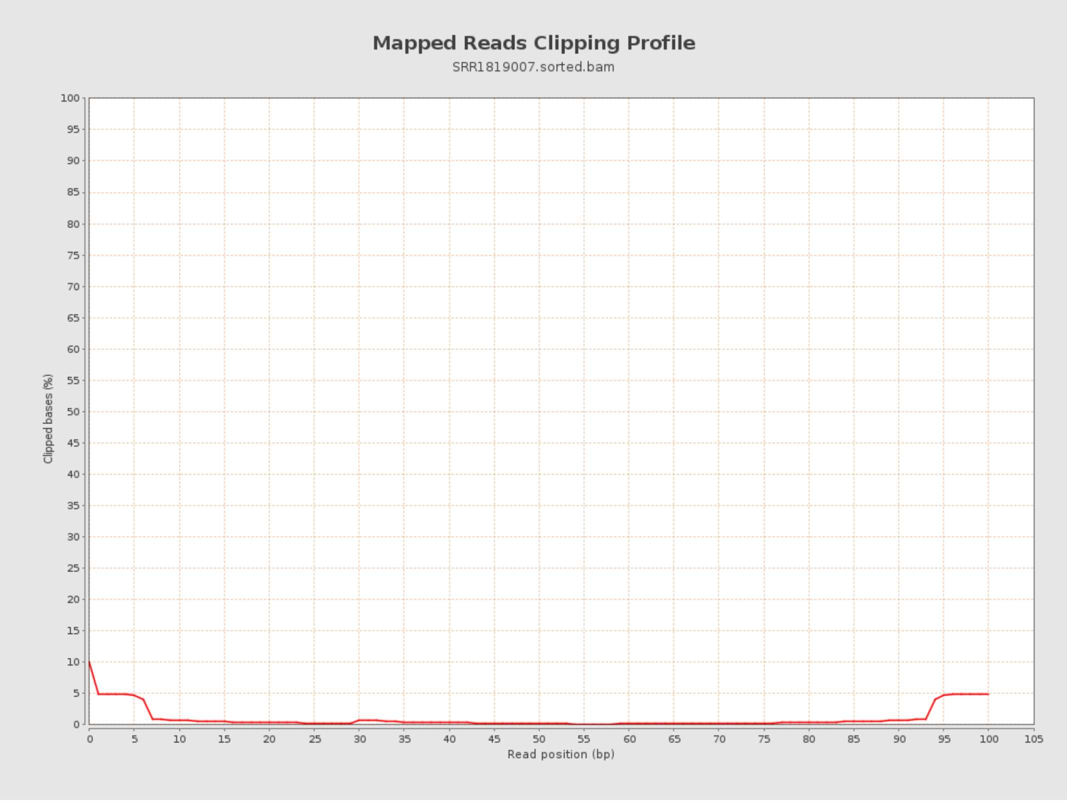
8. Results : Mapped Reads Nucleotide Content



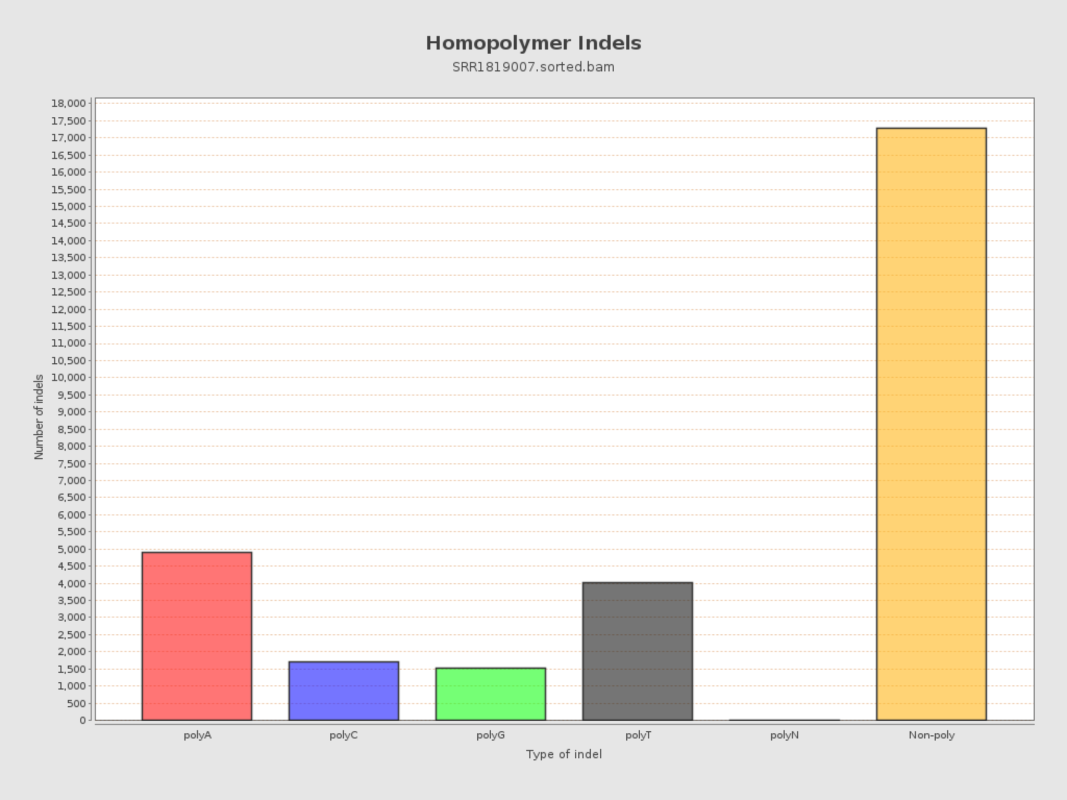
9. Results : Mapped Reads GC-content Distribution



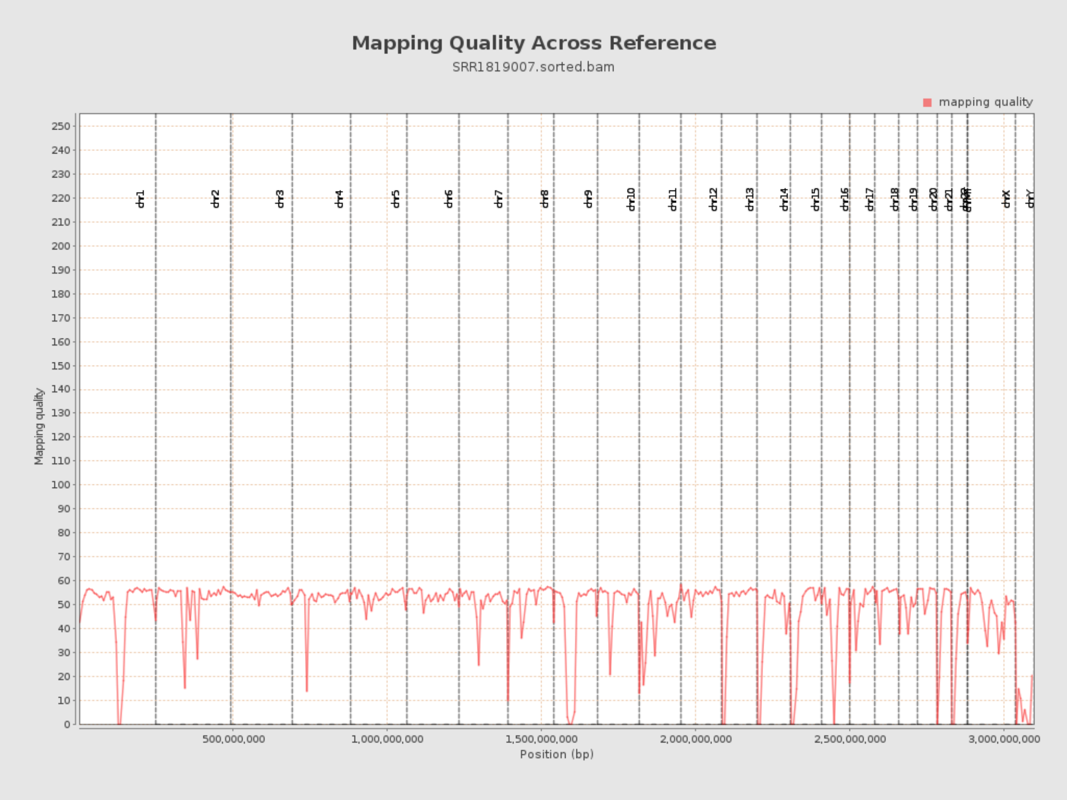
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram