Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 02:30:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819141.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_SRR1819141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 02:30:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,971,334
Mapped reads	4,338,277 / 87.27%
Unmapped reads	633,057 / 12.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	28,220 / 0.57%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	208,344 / 4.19%
Duplication rate	2.22%
Clipped reads	4,355,033 / 87.6%

2.2. ACGT Content

Number/percentage of A's	64,071,571 / 25.92%
Number/percentage of C's	44,978,560 / 18.2%
Number/percentage of T's	76,342,776 / 30.89%
Number/percentage of G's	61,748,940 / 24.98%
Number/percentage of N's	3,433 / 0%
GC Percentage	43.18%

2.3. Coverage

Mean	0.0799

Standard Deviation	0.9782

2.4. Mapping Quality

Mean Mapping Quality	40.28

2.5. Mismatches and indels

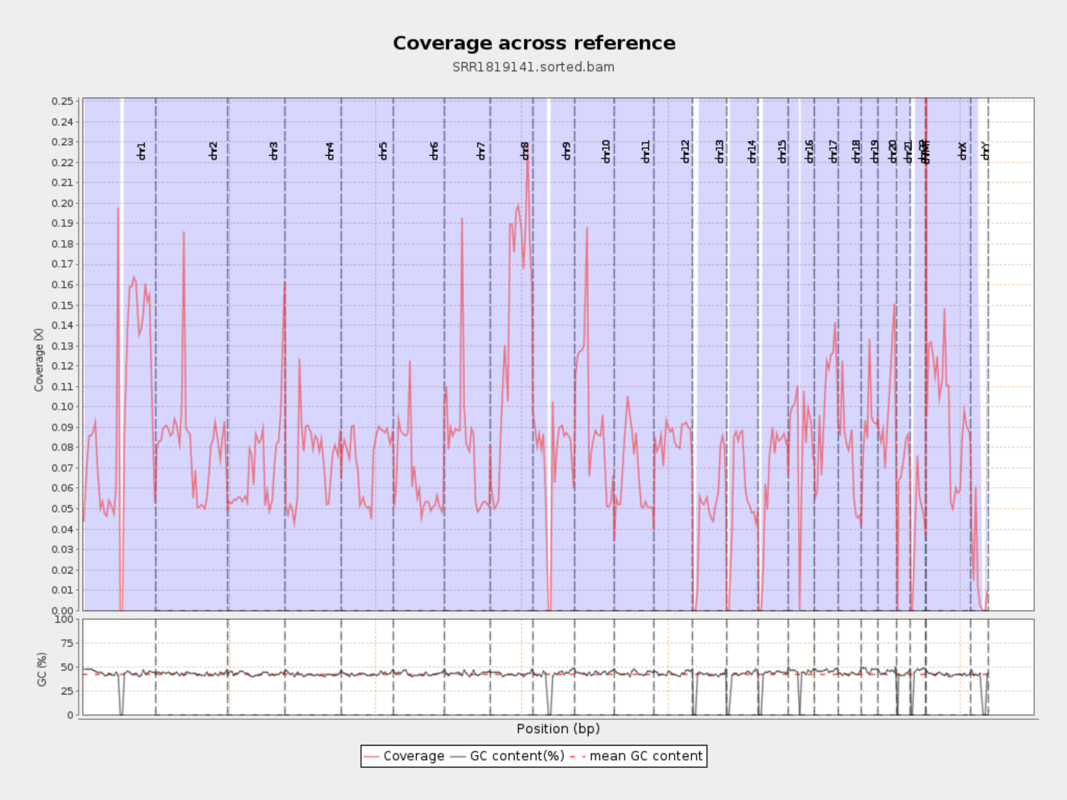
General error rate	0.54%
Mismatches	1,286,840
Insertions	18,981
Mapped reads with at least one insertion	0.44%
Deletions	41,096
Mapped reads with at least one deletion	0.94%
Homopolymer indels	40.8%

2.6. Chromosome stats

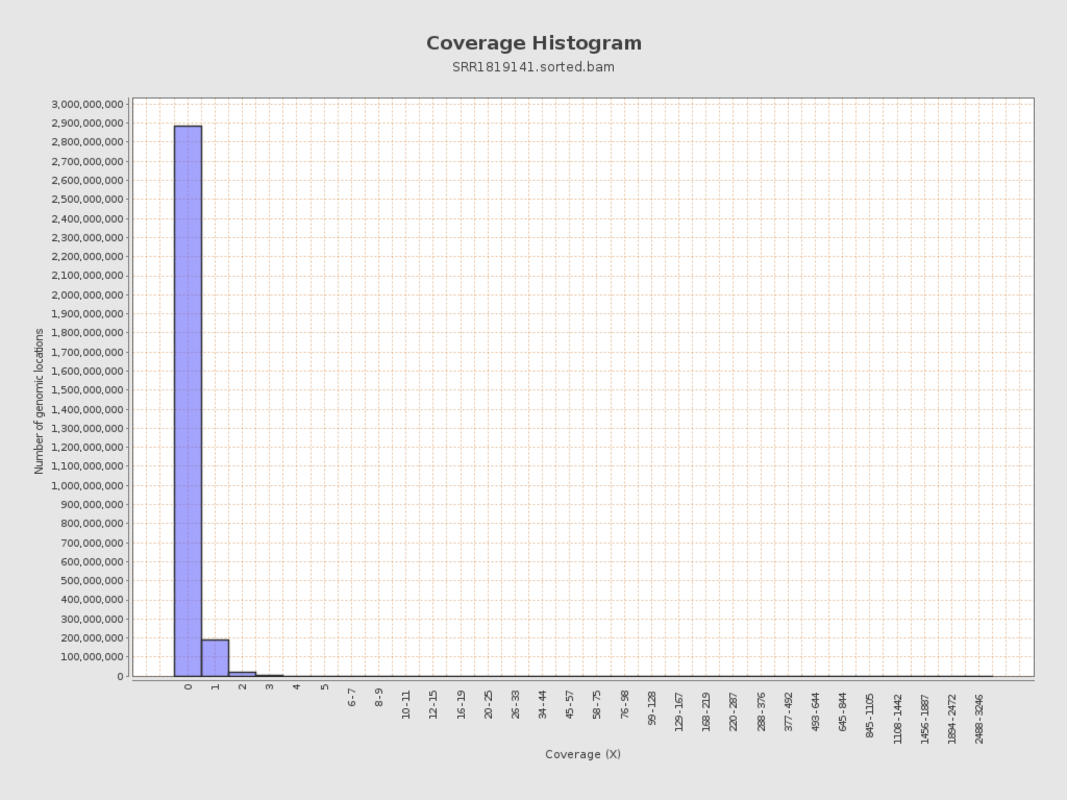
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	23729185	0.0952	2.3835
chr2	243199373	19916629	0.0819	1.022
chr3	198022430	13950903	0.0705	0.3254
chr4	191154276	14054319	0.0735	0.4589
chr5	180915260	13587419	0.0751	0.3471
chr6	171115067	11167445	0.0653	0.5323
chr7	159138663	13011503	0.0818	1.3903

chr8	146364022	20834137	0.1423	0.794
chr9	141213431	10325449	0.0731	0.6736
chr10	135534747	12822509	0.0946	0.8496
chr11	135006516	8918035	0.0661	0.7721
chr12	133851895	11453787	0.0856	0.3629
chr13	115169878	5707769	0.0496	0.2702
chr14	107349540	6038467	0.0563	0.3356
chr15	102531392	6424984	0.0627	0.3622
chr16	90354753	7544943	0.0835	0.4418
chr17	81195210	8309060	0.1023	0.4659
chr18	78077248	5925195	0.0759	1.5927
chr19	59128983	5489121	0.0928	1.5747
chr20	63025520	6474460	0.1027	0.4023
chr21	48129895	3247054	0.0675	0.409
chr22	51304566	2066176	0.0403	0.2302
chrMT	16571	137315	8.2865	5.4634
chrX	155270560	15104630	0.0973	0.5572
chrY	59373566	973598	0.0164	0.4958

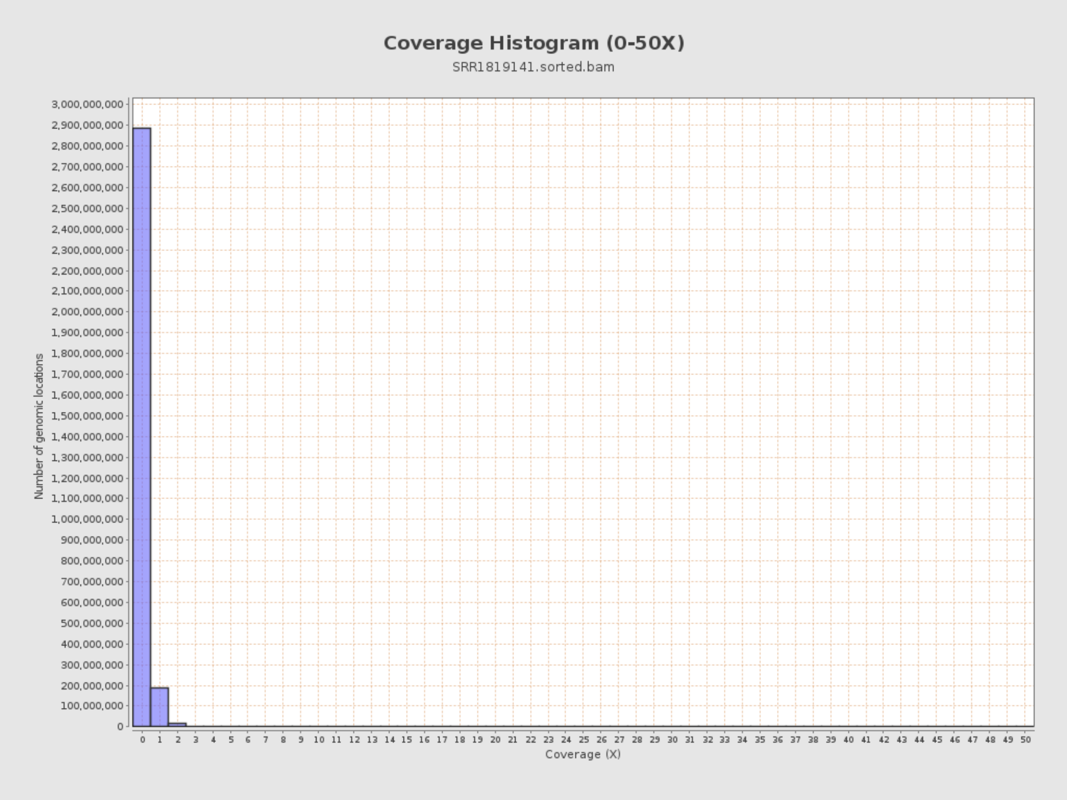
3. Results : Coverage across reference



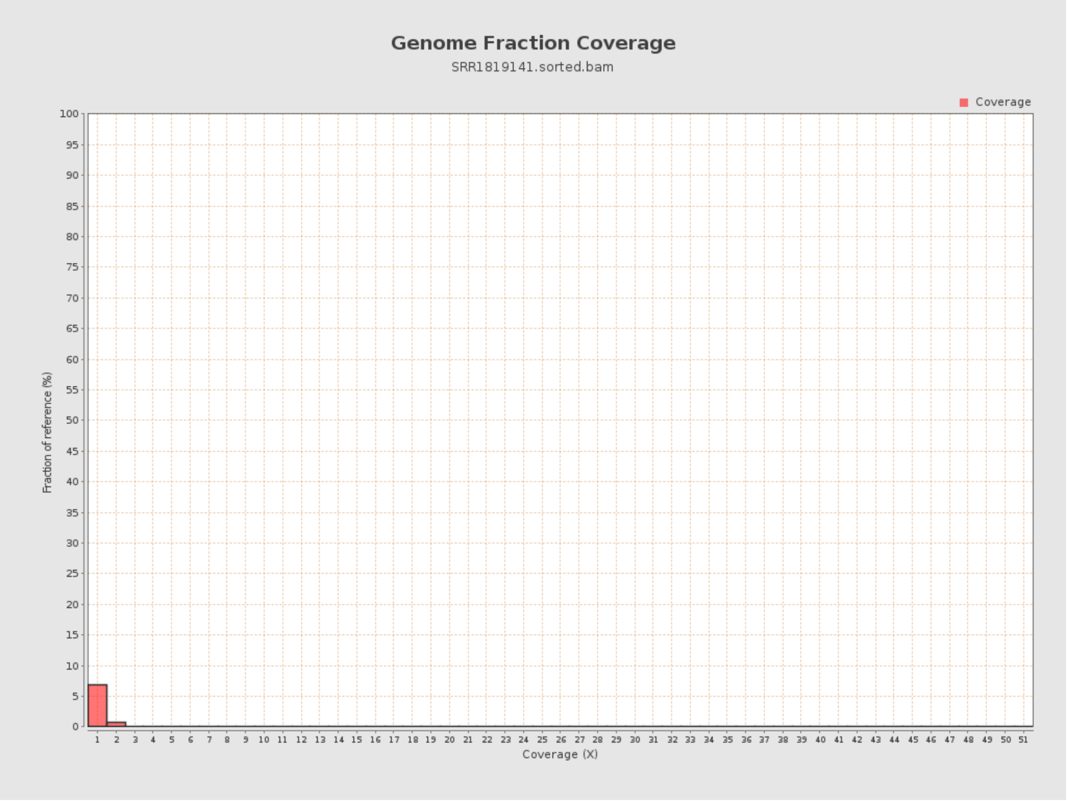
4. Results : Coverage Histogram



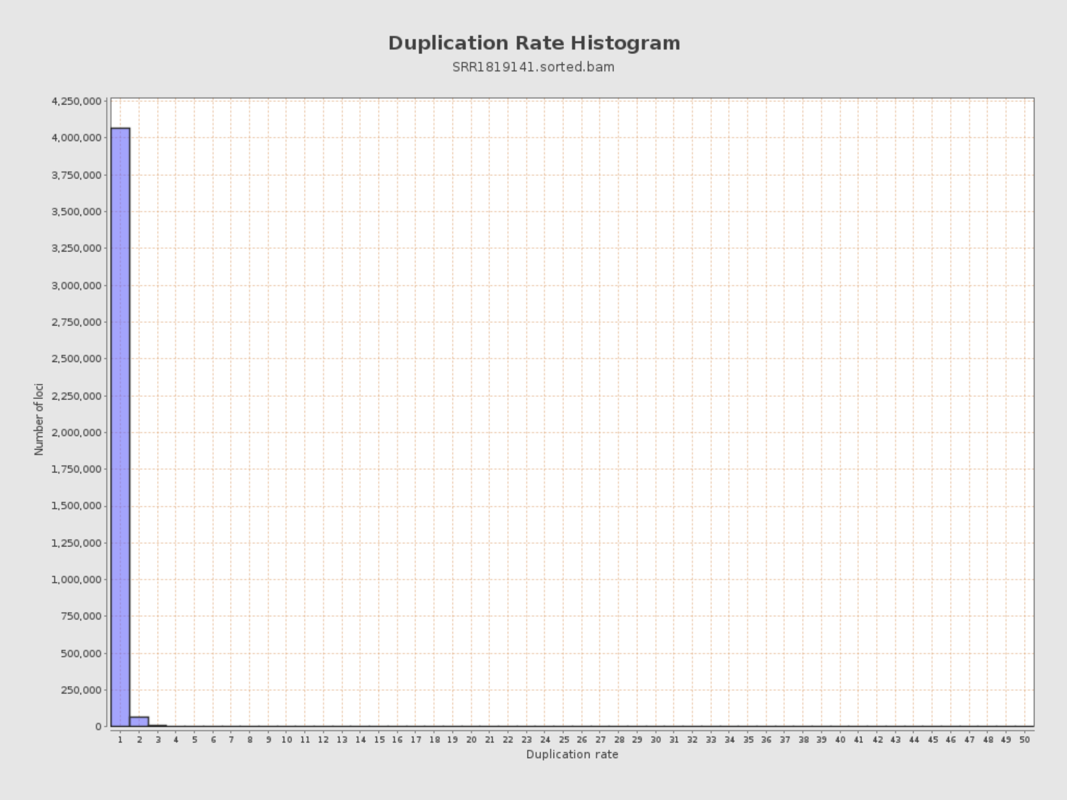
5. Results : Coverage Histogram (0-50X)



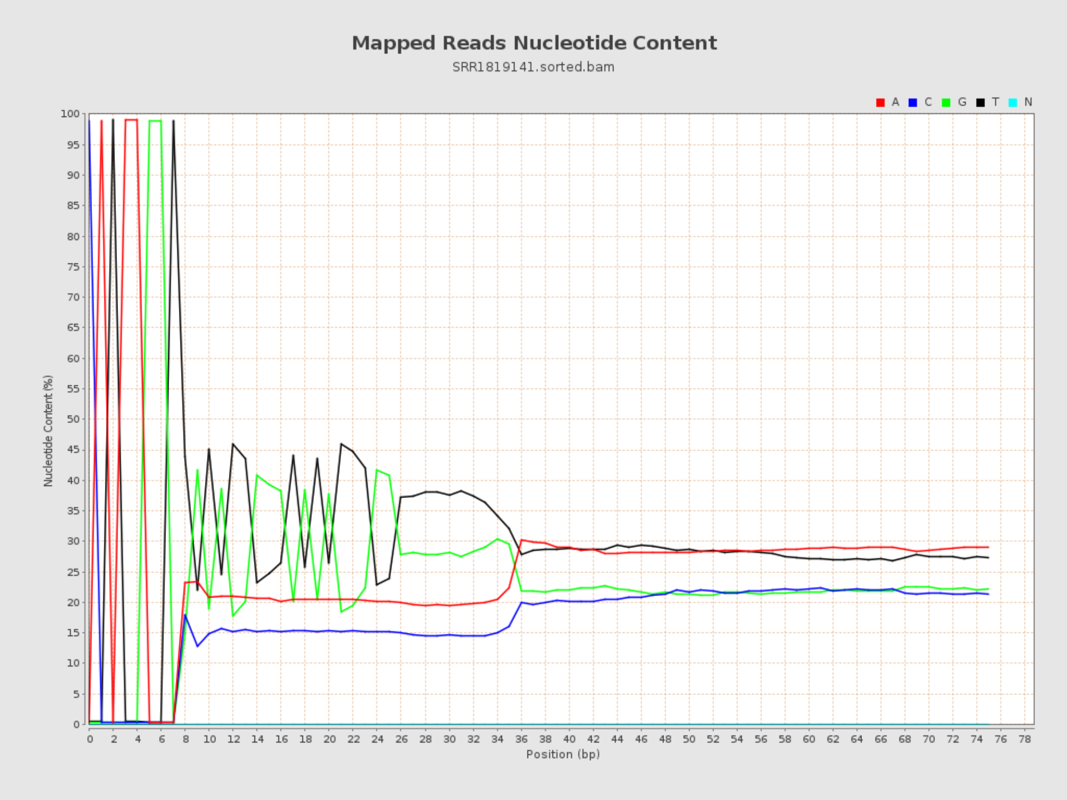
6. Results : Genome Fraction Coverage



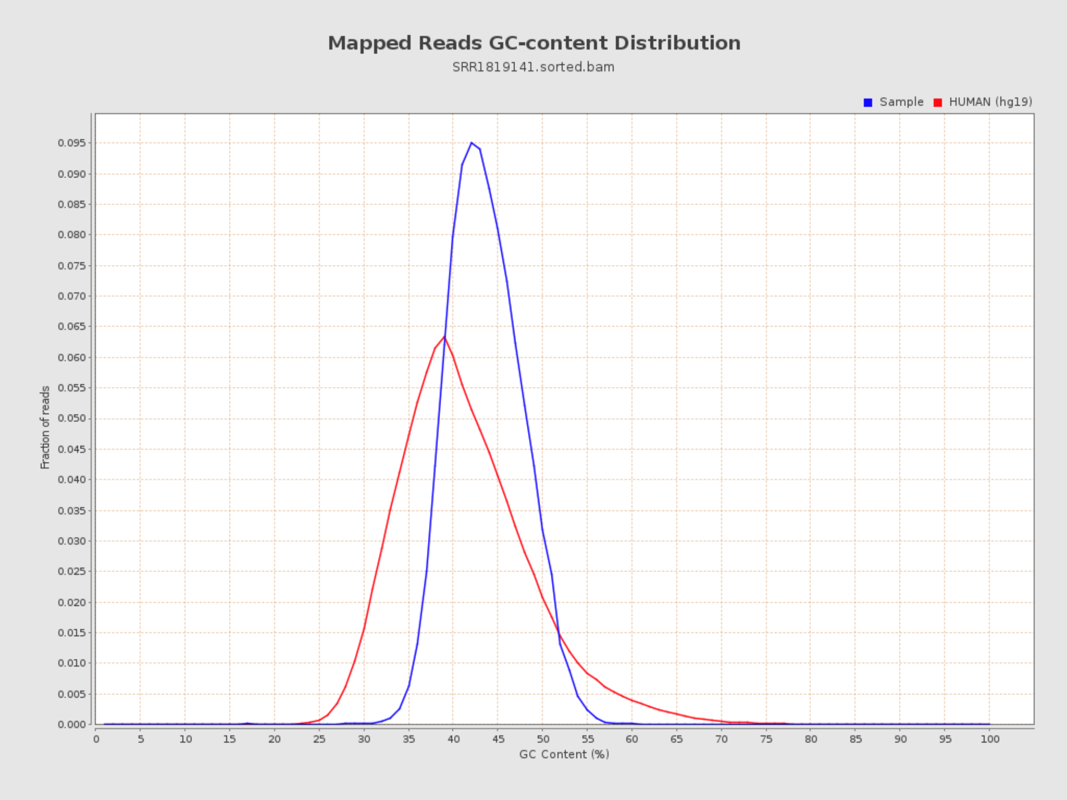
7. Results : Duplication Rate Histogram



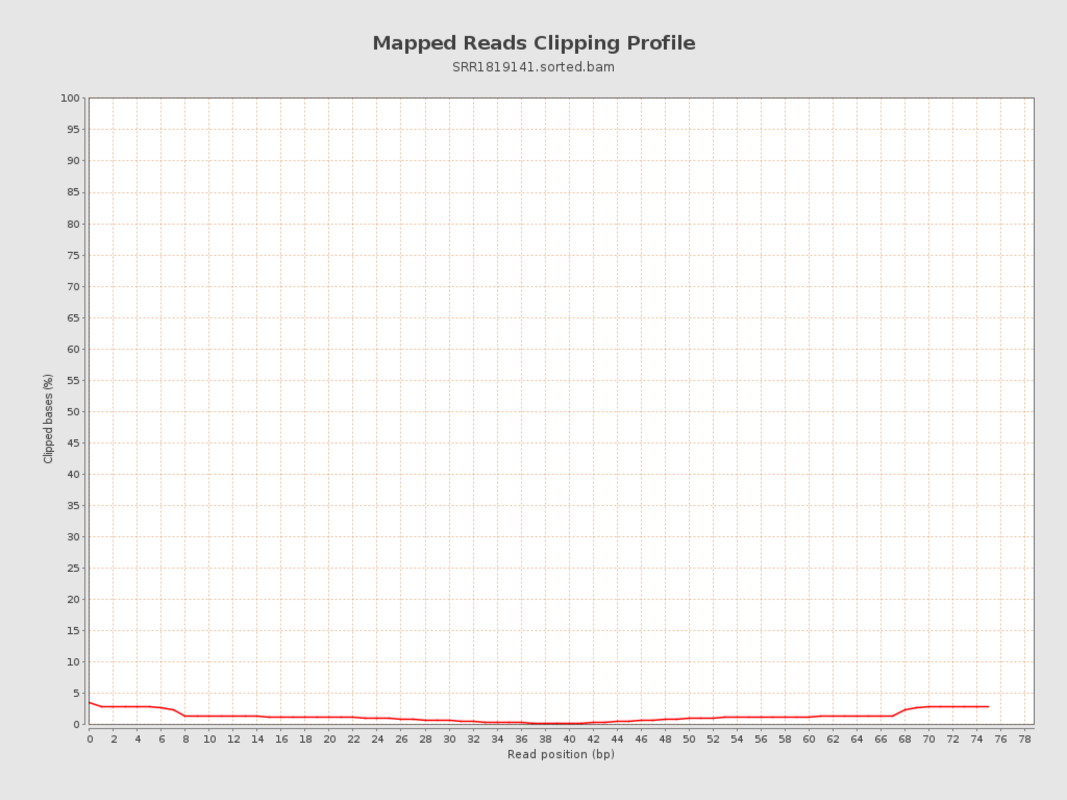
8. Results : Mapped Reads Nucleotide Content



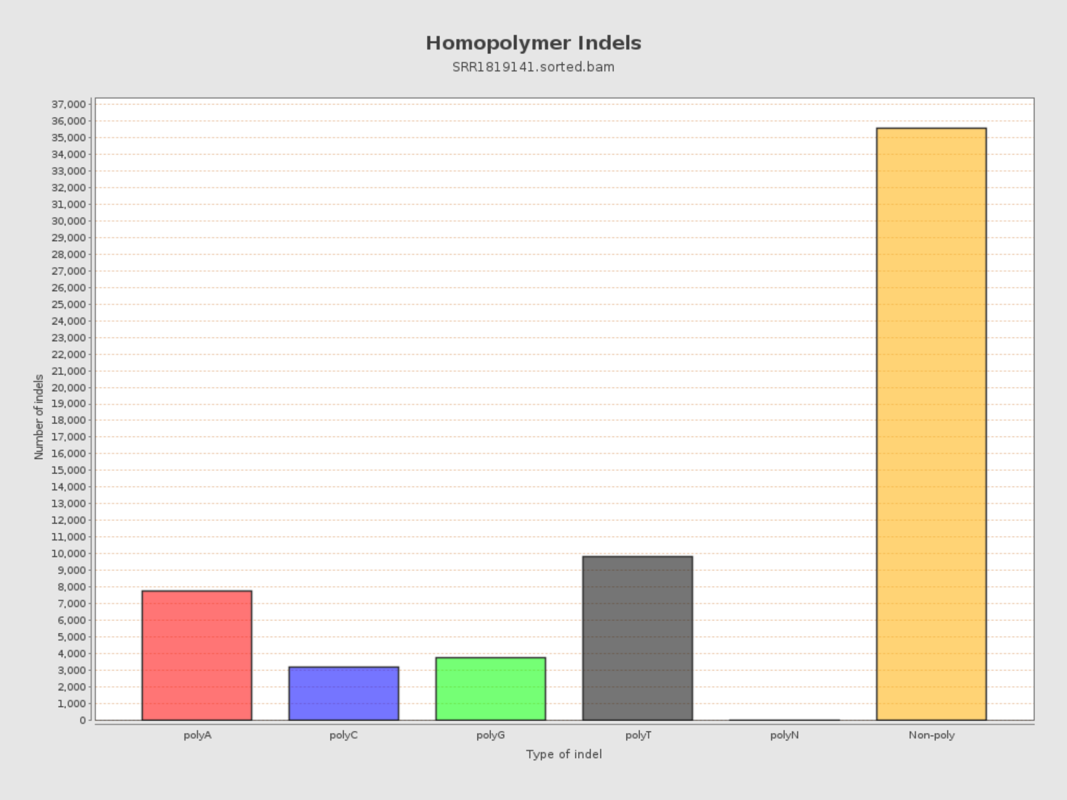
9. Results : Mapped Reads GC-content Distribution



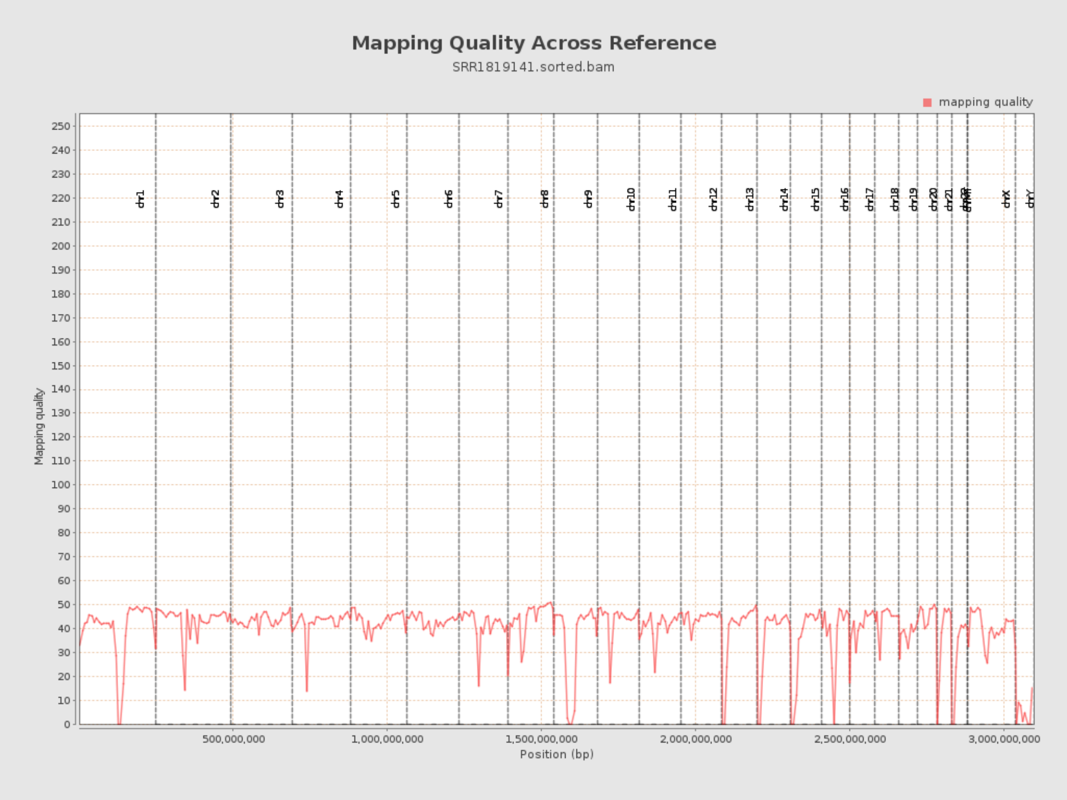
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram