Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 14:21:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819002.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_SRR1819002 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819002.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 14:21:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819002.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,355,235
Mapped reads	1,324,806 / 97.75%
Unmapped reads	30,429 / 2.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,916 / 1.54%
Read min/max/mean length	30 / 101 / 101.6
Duplicated reads (estimated)	534,669 / 39.45%
Duplication rate	33.69%
Clipped reads	1,336,273 / 98.6%

2.2. ACGT Content

Number/percentage of A's	35,391,179 / 28.89%
Number/percentage of C's	25,693,191 / 20.97%
Number/percentage of T's	35,152,570 / 28.7%
Number/percentage of G's	26,254,421 / 21.43%
Number/percentage of N's	6,231 / 0.01%
GC Percentage	42.41%

2.3. Coverage

Mean	0.0396

Standard Deviation	0.5191

2.4. Mapping Quality

Mean Mapping Quality	49.22

2.5. Mismatches and indels

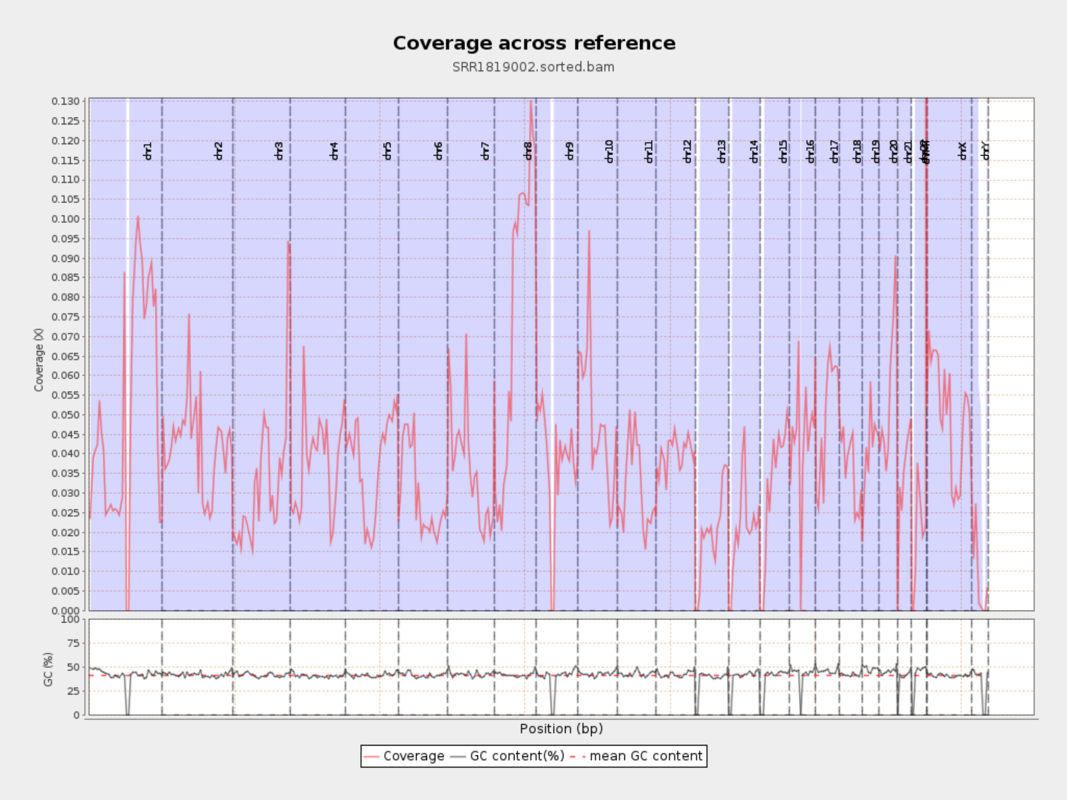
General error rate	0.67%
Mismatches	776,554
Insertions	20,706
Mapped reads with at least one insertion	1.52%
Deletions	38,573
Mapped reads with at least one deletion	2.84%
Homopolymer indels	40.98%

2.6. Chromosome stats

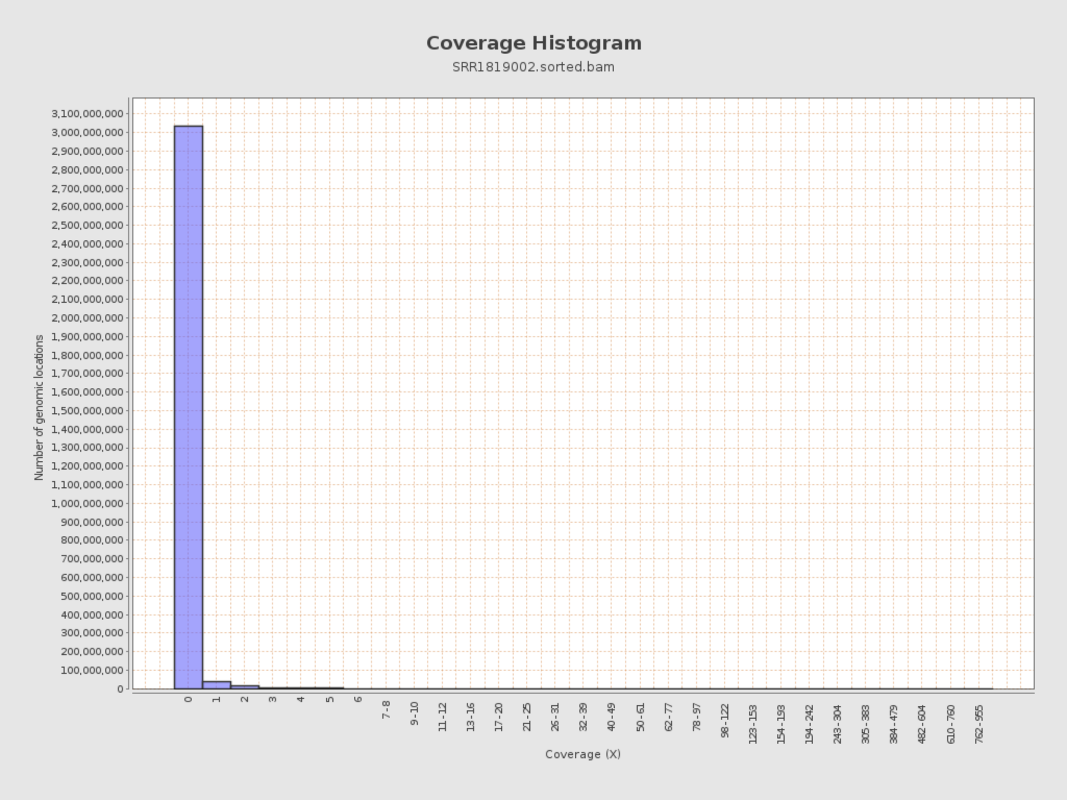
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12714059	0.051	0.956
chr2	243199373	10300965	0.0424	0.6746
chr3	198022430	6423423	0.0324	0.308
chr4	191154276	7194994	0.0376	0.393
chr5	180915260	6862778	0.0379	0.3446
chr6	171115067	5002291	0.0292	0.334
chr7	159138663	5758505	0.0362	0.6285

chr8	146364022	11220431	0.0767	0.5083
chr9	141213431	5336840	0.0378	0.4318
chr10	135534747	6591290	0.0486	0.6641
chr11	135006516	4218545	0.0312	0.3378
chr12	133851895	5370708	0.0401	0.3494
chr13	115169878	2305064	0.02	0.2424
chr14	107349540	2268973	0.0211	0.2673
chr15	102531392	3290401	0.0321	0.3169
chr16	90354753	3928561	0.0435	0.5396
chr17	81195210	4066711	0.0501	0.4272
chr18	78077248	2830410	0.0363	0.4908
chr19	59128983	2466993	0.0417	0.7746
chr20	63025520	3527547	0.056	0.4367
chr21	48129895	1648590	0.0343	0.3703
chr22	51304566	923268	0.018	0.243
chrMT	16571	26118	1.5761	2.3195
chrX	155270560	7801883	0.0502	0.4269
chrY	59373566	489948	0.0083	0.5427

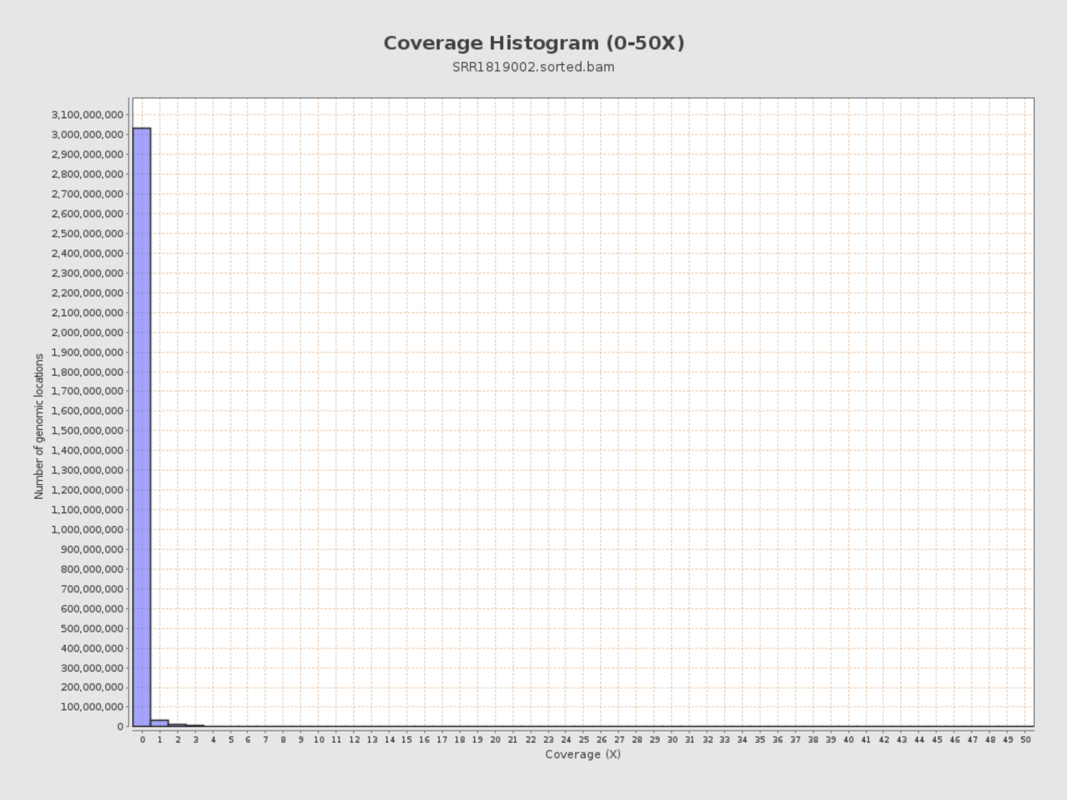
3. Results : Coverage across reference



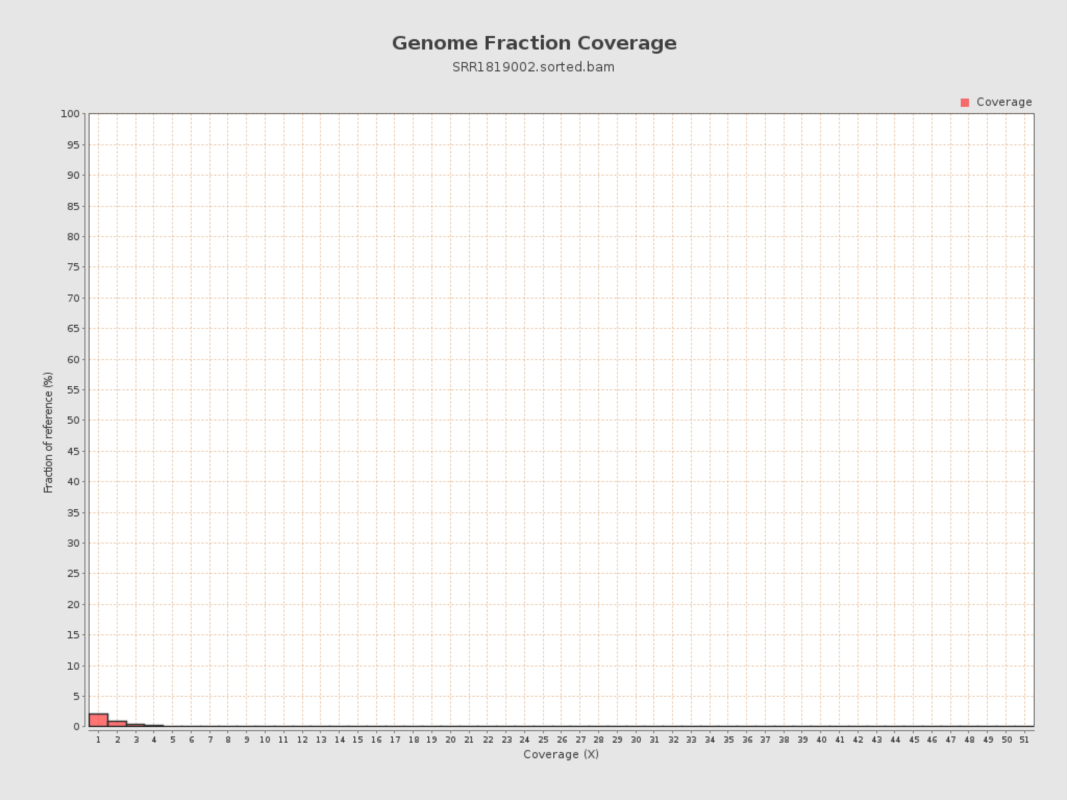
4. Results : Coverage Histogram



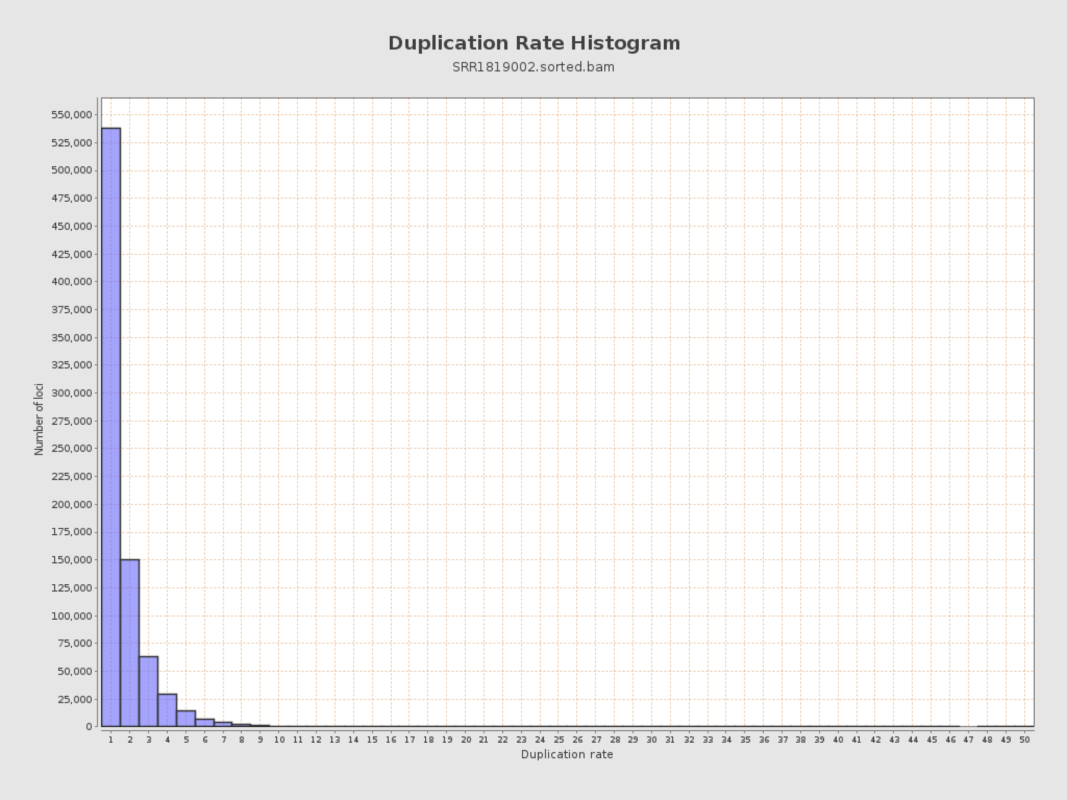
5. Results : Coverage Histogram (0-50X)



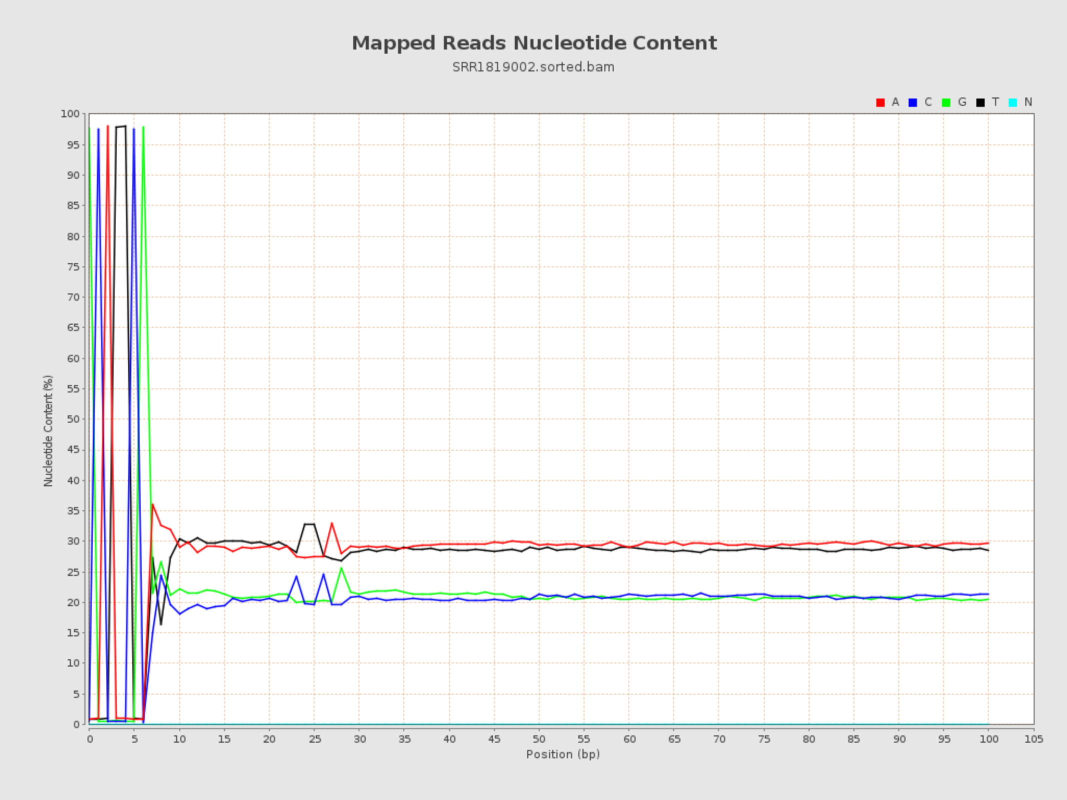
6. Results : Genome Fraction Coverage



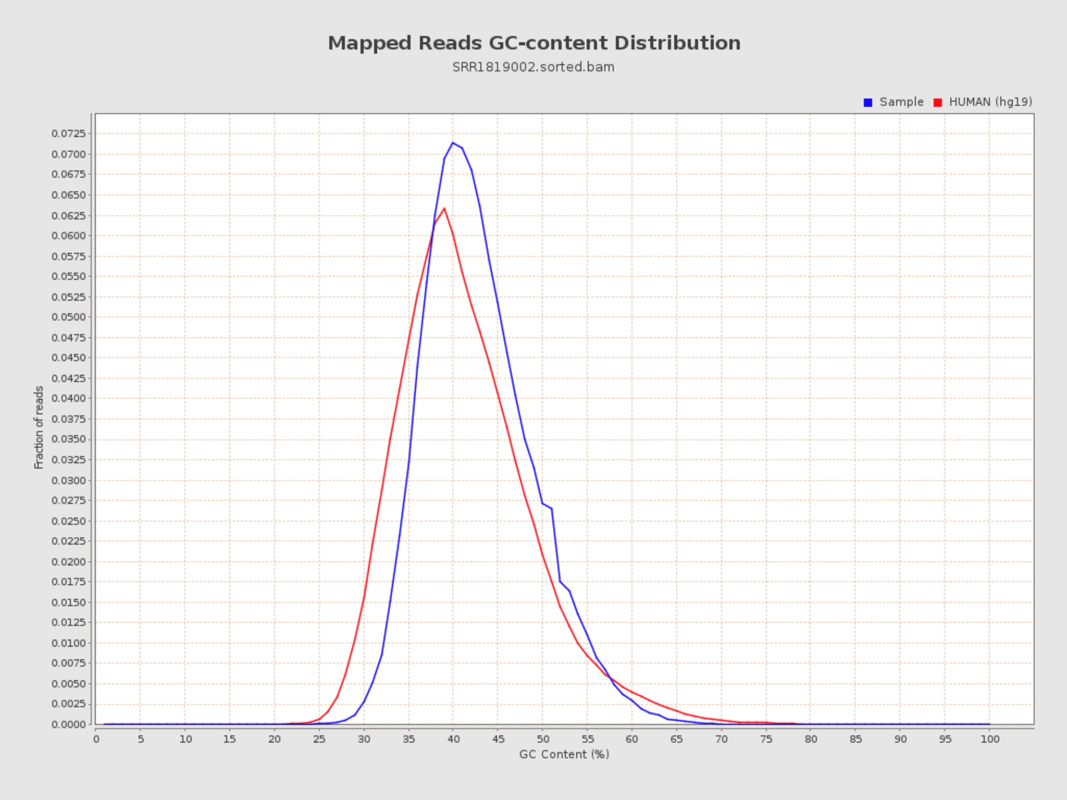
7. Results : Duplication Rate Histogram



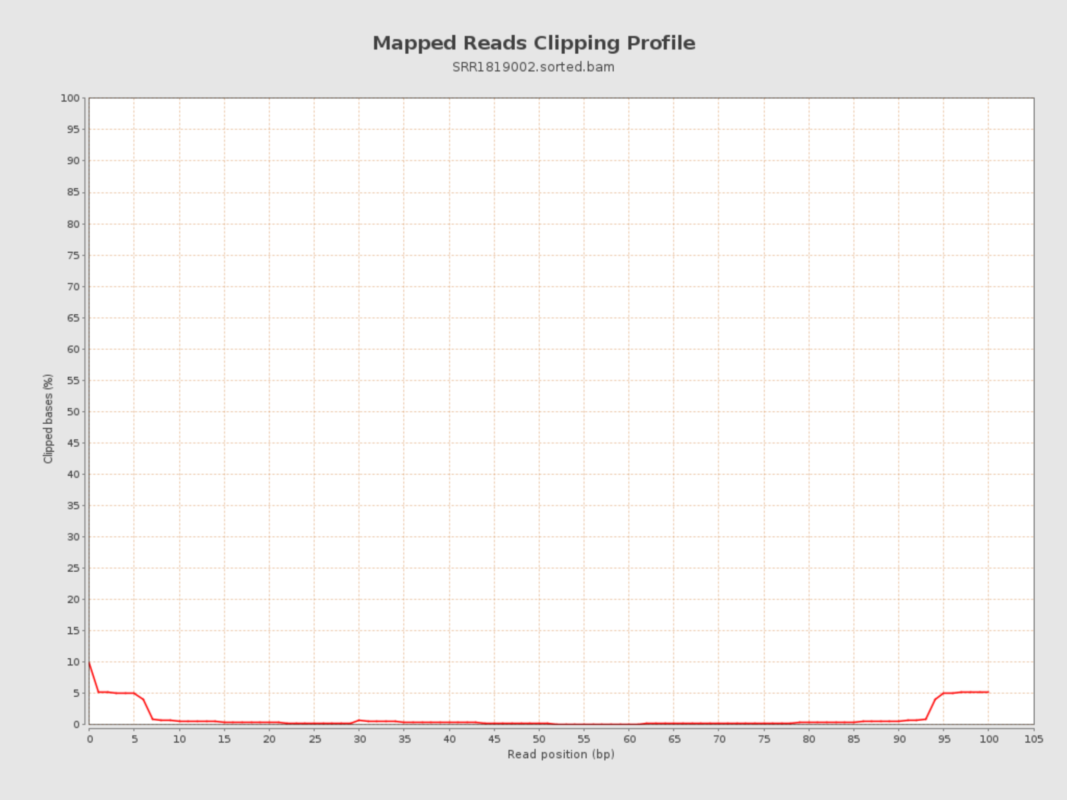
8. Results : Mapped Reads Nucleotide Content



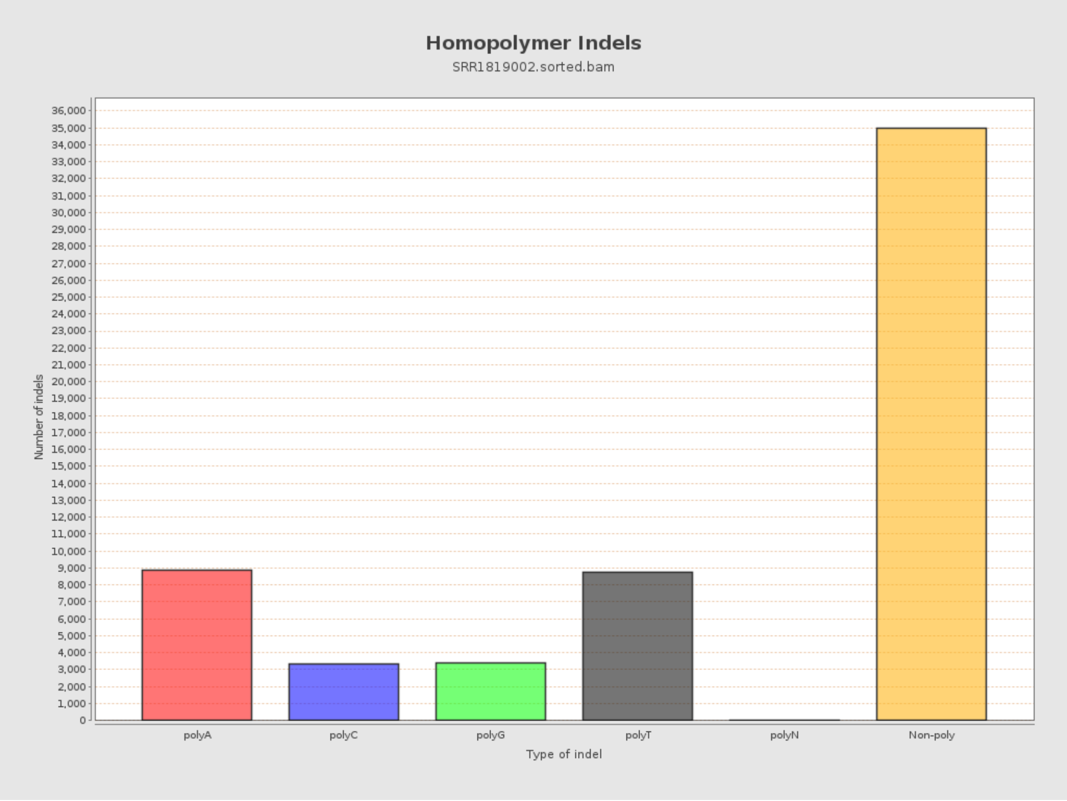
9. Results : Mapped Reads GC-content Distribution



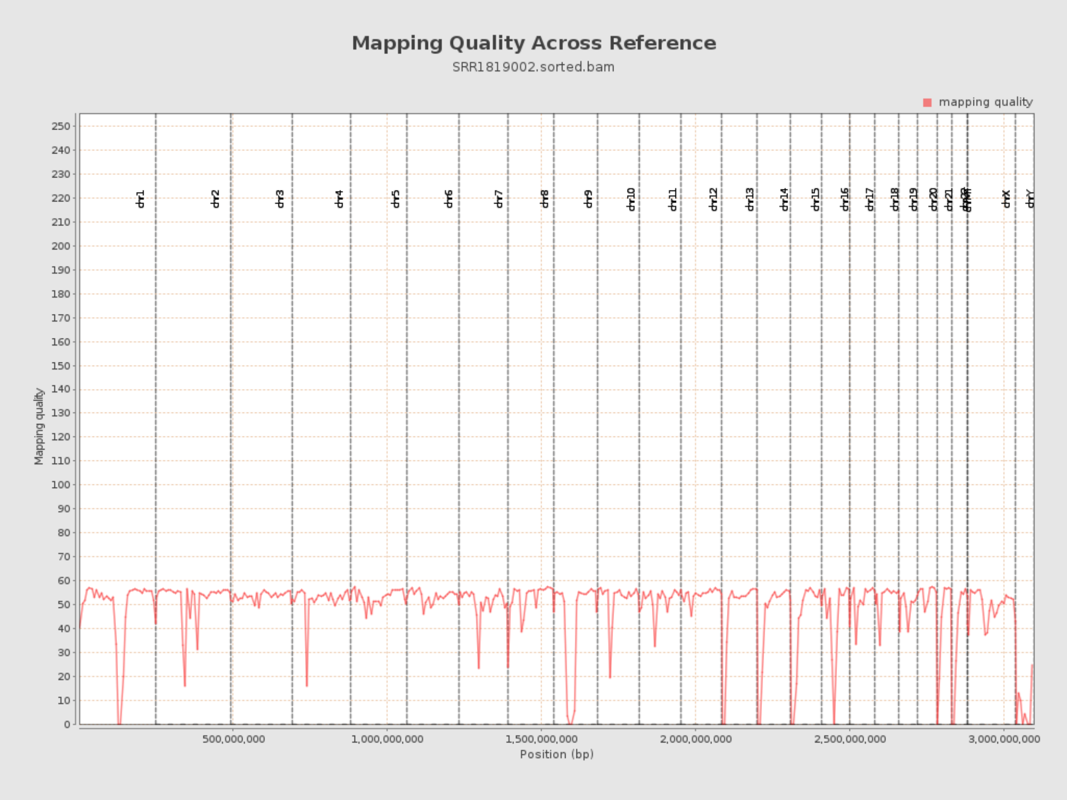
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram