Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:10:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819105.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_SRR1819105 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819105.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:10:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819105.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,021,607
Mapped reads	2,803,932 / 92.8%
Unmapped reads	217,675 / 7.2%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,079 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	205,033 / 6.79%
Duplication rate	5.45%
Clipped reads	2,807,807 / 92.92%

2.2. ACGT Content

Number/percentage of A's	42,591,910 / 25.67%
Number/percentage of C's	32,995,716 / 19.89%
Number/percentage of T's	51,332,667 / 30.94%
Number/percentage of G's	38,966,634 / 23.49%
Number/percentage of N's	2,531 / 0%
GC Percentage	43.38%

2.3. Coverage

Mean	0.0536

Standard Deviation	0.4771

2.4. Mapping Quality

Mean Mapping Quality	45.81

2.5. Mismatches and indels

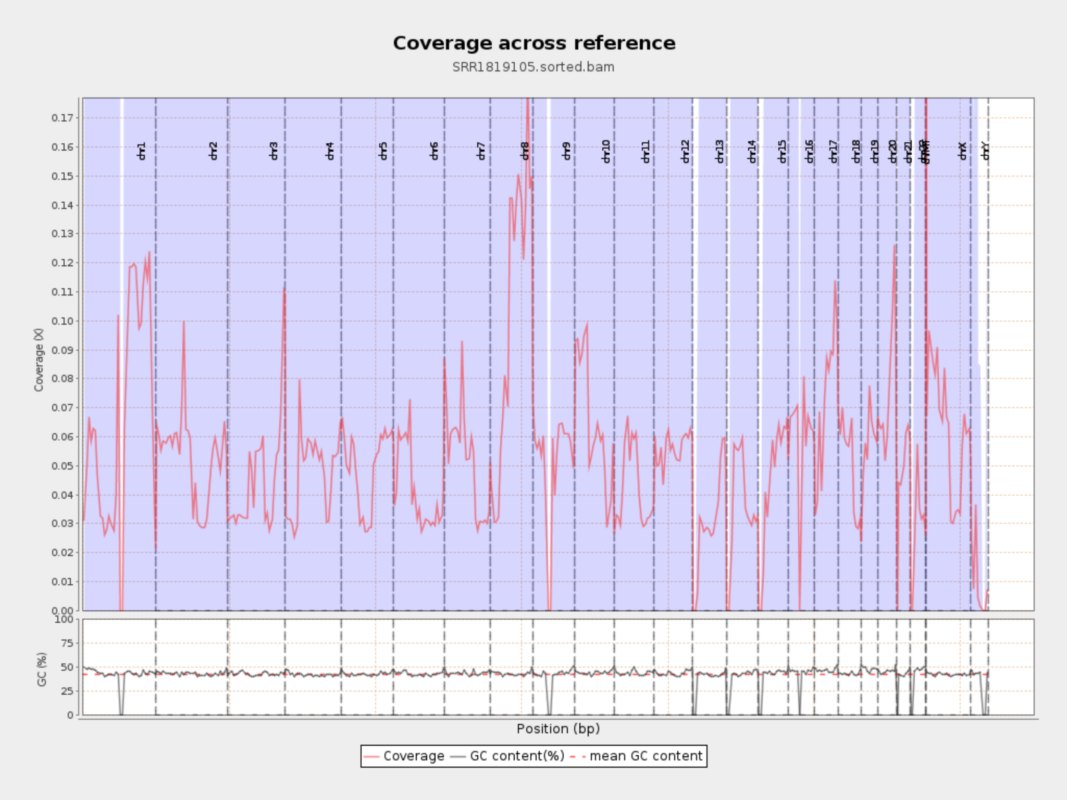
General error rate	0.51%
Mismatches	825,818
Insertions	10,734
Mapped reads with at least one insertion	0.38%
Deletions	30,055
Mapped reads with at least one deletion	1.06%
Homopolymer indels	43.48%

2.6. Chromosome stats

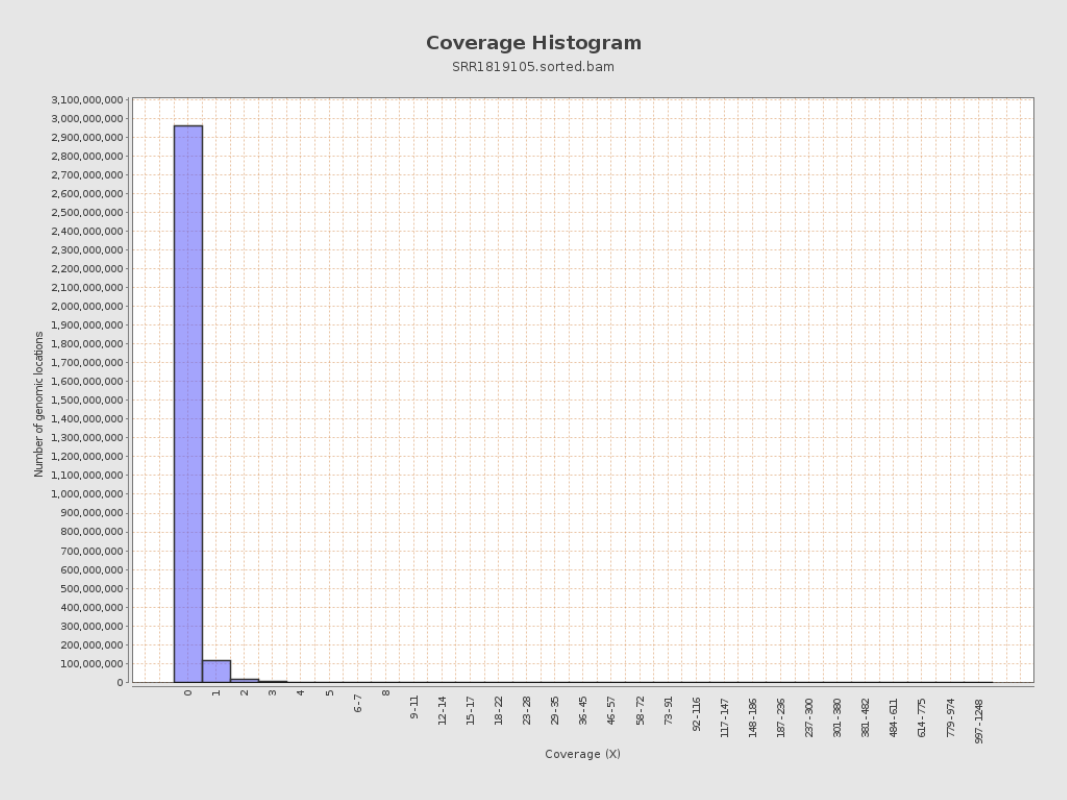
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16551980	0.0664	0.9575
chr2	243199373	12980368	0.0534	0.5465
chr3	198022430	8895171	0.0449	0.2521
chr4	191154276	9105611	0.0476	0.3415
chr5	180915260	8920260	0.0493	0.2679
chr6	171115067	7057761	0.0412	0.326
chr7	159138663	8318135	0.0523	0.6002

chr8	146364022	15338045	0.1048	0.5407
chr9	141213431	7113564	0.0504	0.3922
chr10	135534747	8757970	0.0646	0.4724
chr11	135006516	5701236	0.0422	0.4354
chr12	133851895	7536294	0.0563	0.2866
chr13	115169878	3546483	0.0308	0.2119
chr14	107349540	3907554	0.0364	0.2379
chr15	102531392	4402800	0.0429	0.2509
chr16	90354753	5265933	0.0583	0.3223
chr17	81195210	5948018	0.0733	0.3572
chr18	78077248	3971007	0.0509	0.7869
chr19	59128983	3462405	0.0586	0.6232
chr20	63025520	4964566	0.0788	0.3443
chr21	48129895	2323648	0.0483	0.3197
chr22	51304566	1418363	0.0276	0.1972
chrMT	16571	11564	0.6978	0.8913
chrX	155270560	9868299	0.0636	0.3492
chrY	59373566	572783	0.0096	0.3125

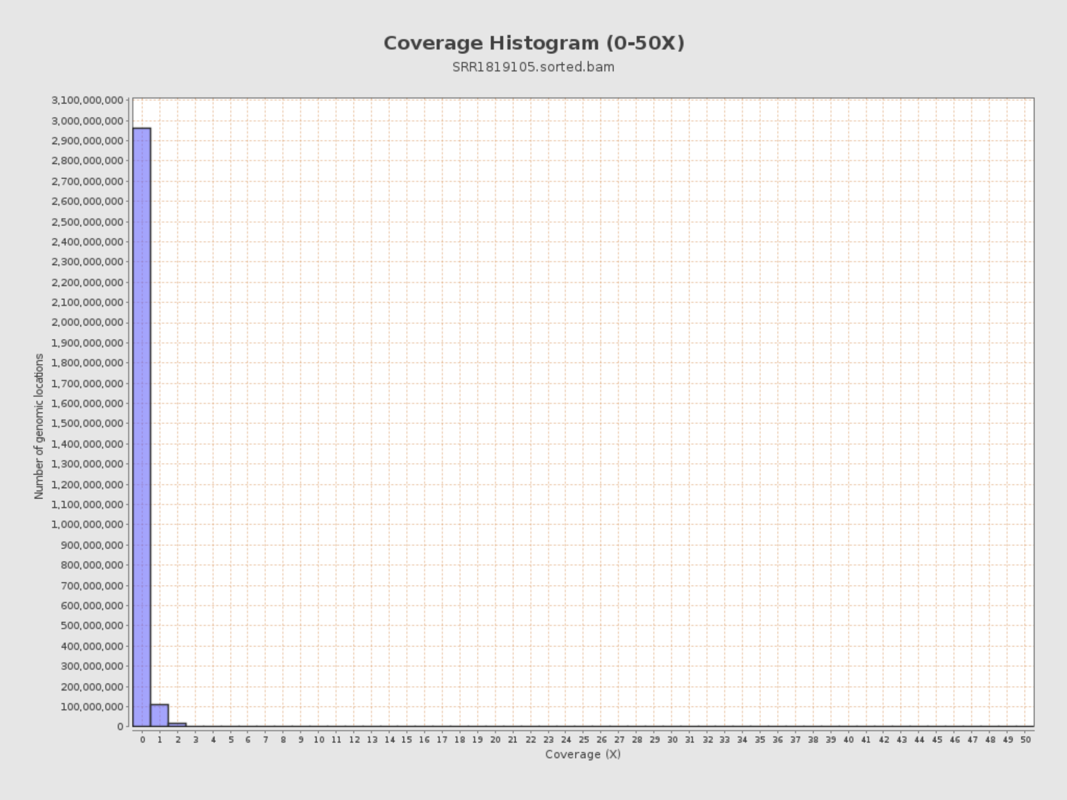
3. Results : Coverage across reference



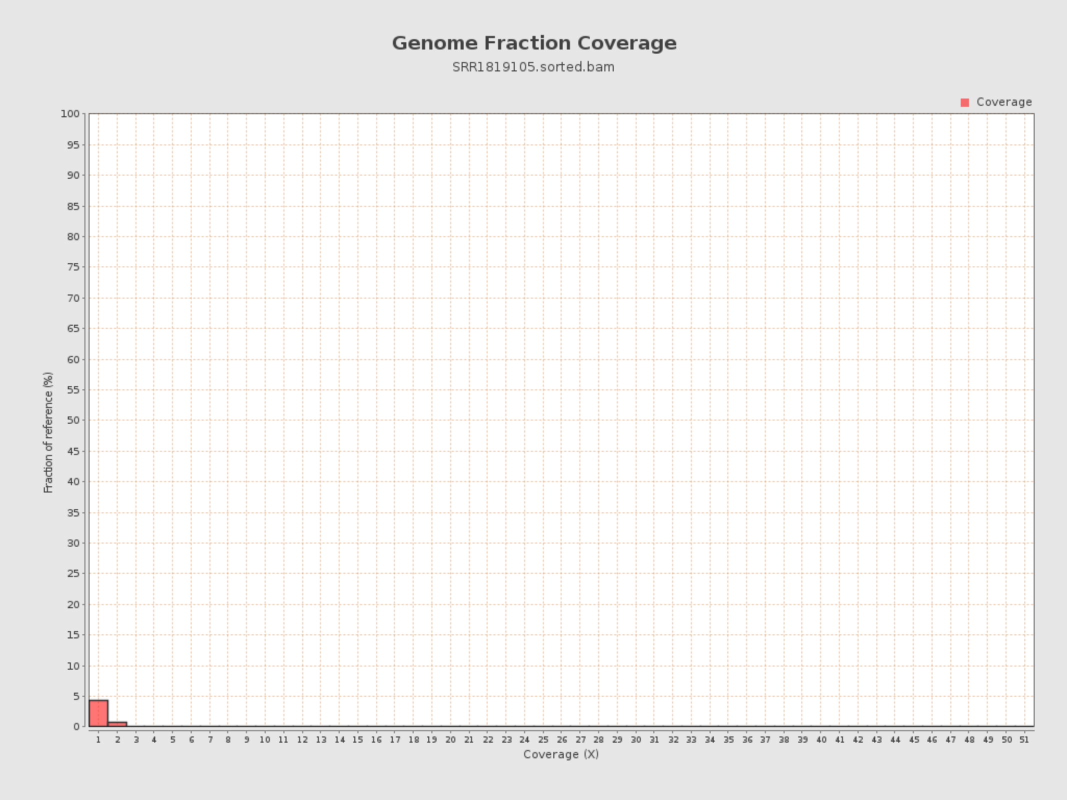
4. Results : Coverage Histogram



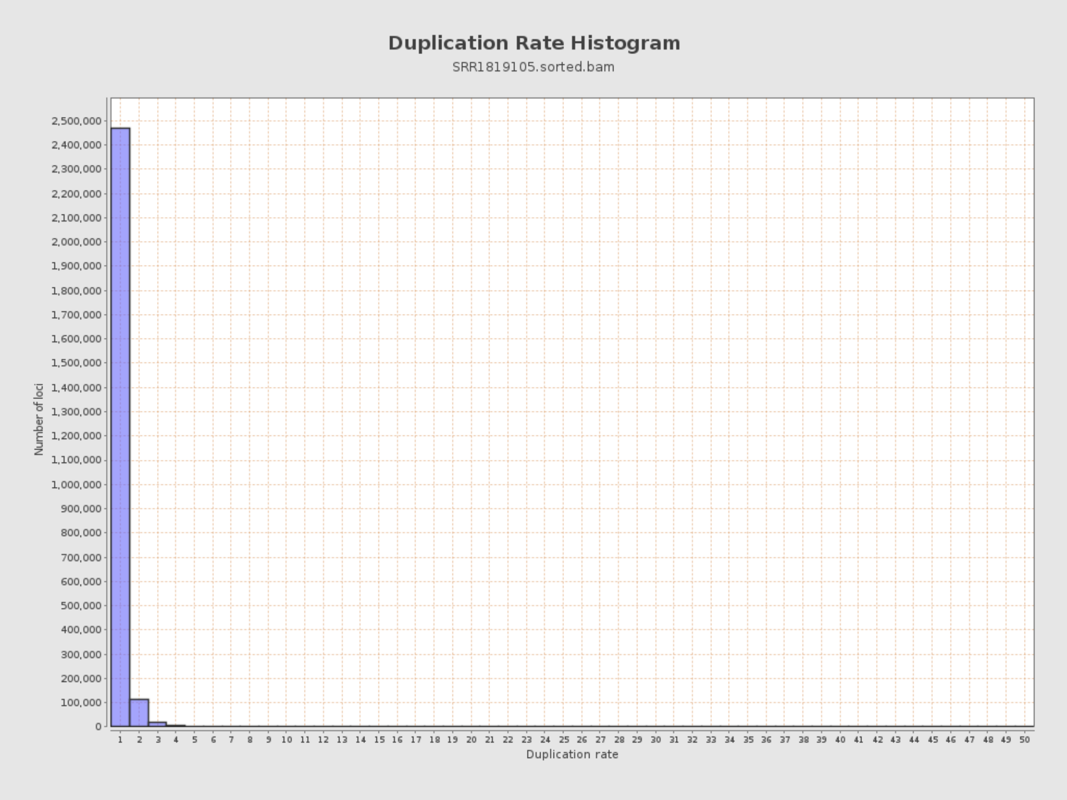
5. Results : Coverage Histogram (0-50X)



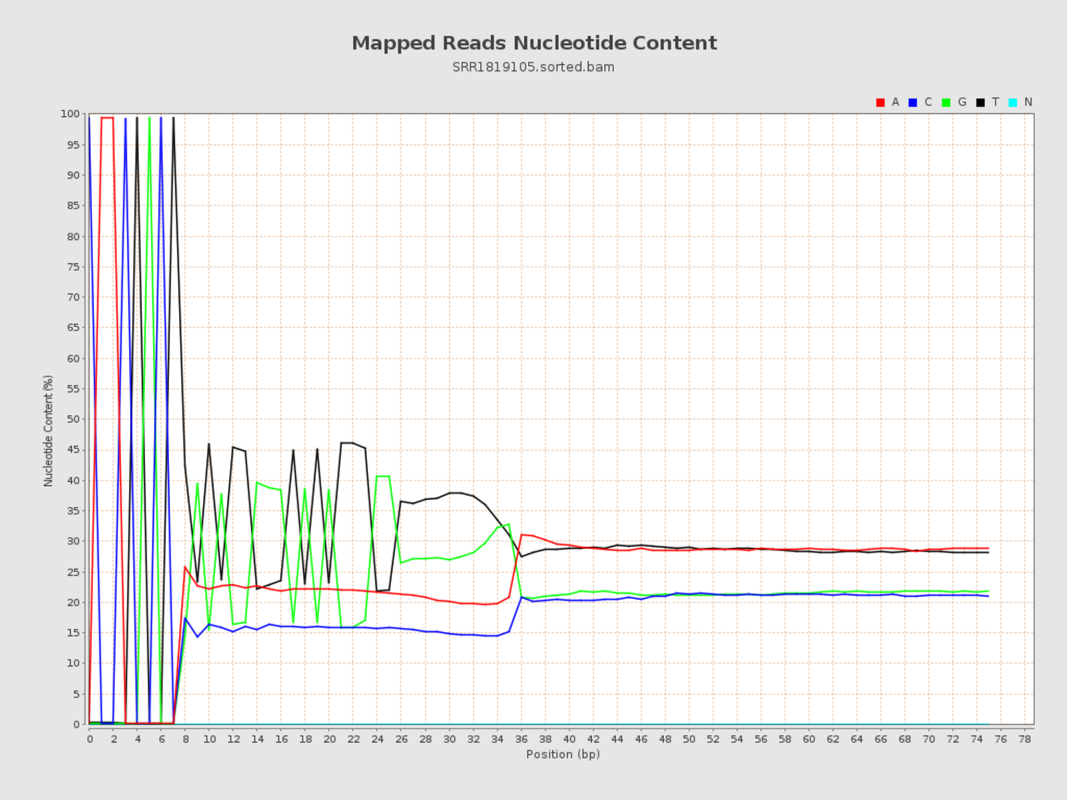
6. Results : Genome Fraction Coverage



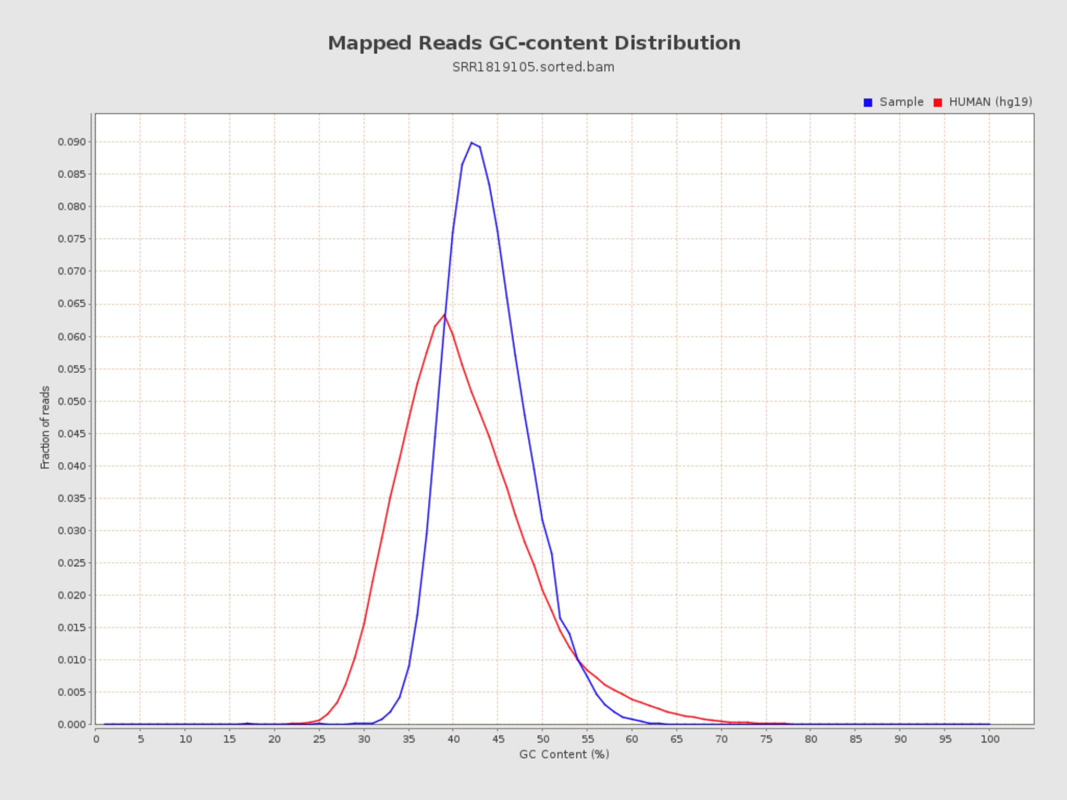
7. Results : Duplication Rate Histogram



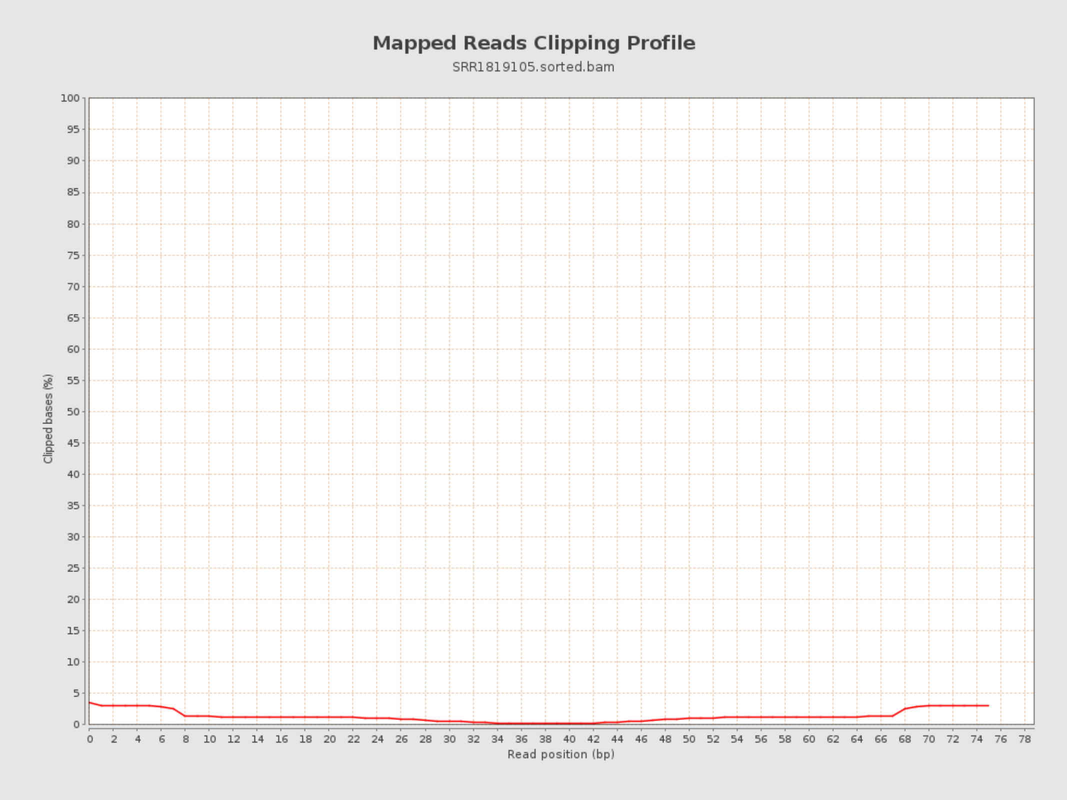
8. Results : Mapped Reads Nucleotide Content



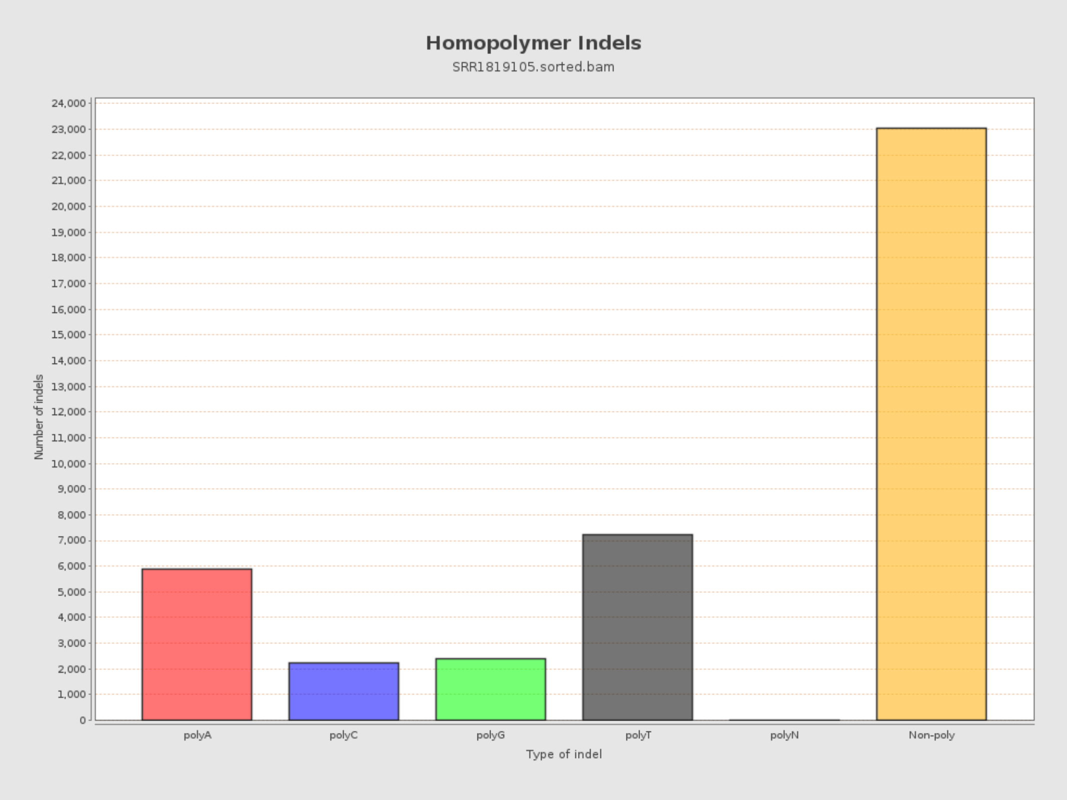
9. Results : Mapped Reads GC-content Distribution



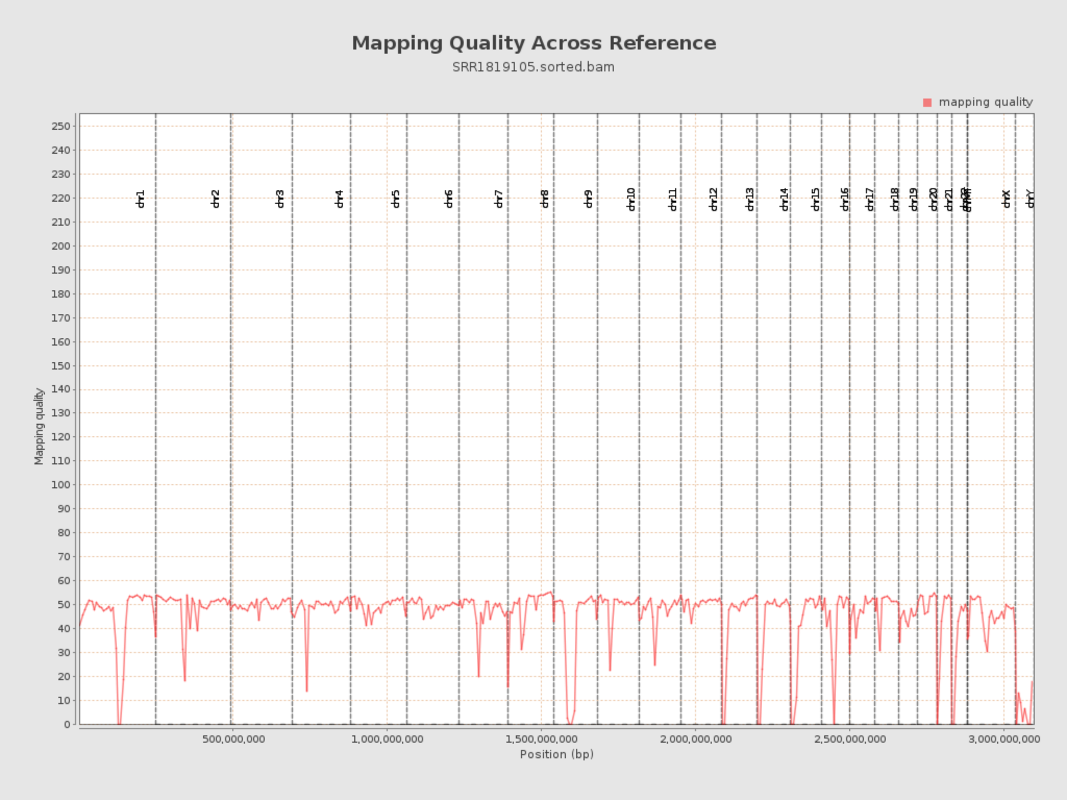
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram