Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:02:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819103.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_SRR1819103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:02:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,396,882
Mapped reads	1,260,911 / 90.27%
Unmapped reads	135,971 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,029 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	36,596 / 2.62%
Duplication rate	2.08%
Clipped reads	1,264,239 / 90.5%

2.2. ACGT Content

Number/percentage of A's	18,440,159 / 24.99%
Number/percentage of C's	13,978,049 / 18.95%
Number/percentage of T's	22,192,232 / 30.08%
Number/percentage of G's	19,167,061 / 25.98%
Number/percentage of N's	984 / 0%
GC Percentage	44.93%

2.3. Coverage

Mean	0.0238

Standard Deviation	0.2319

2.4. Mapping Quality

Mean Mapping Quality	44.72

2.5. Mismatches and indels

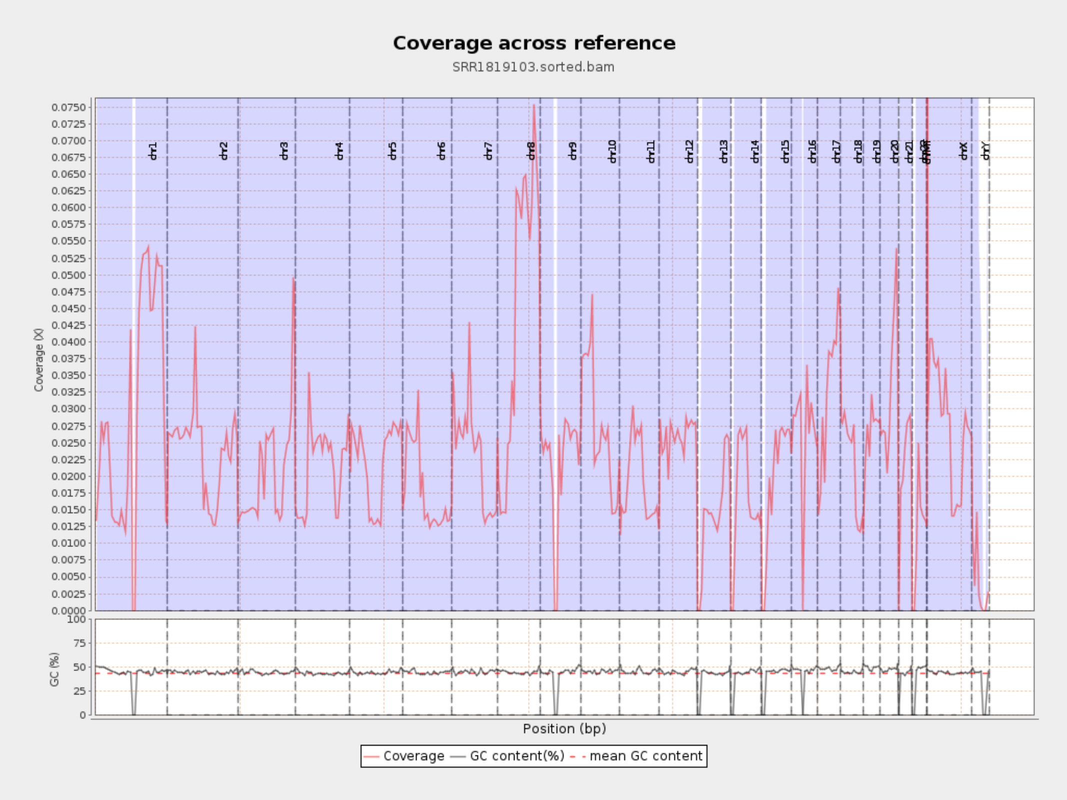
General error rate	0.54%
Mismatches	389,100
Insertions	4,181
Mapped reads with at least one insertion	0.33%
Deletions	13,363
Mapped reads with at least one deletion	1.05%
Homopolymer indels	44.79%

2.6. Chromosome stats

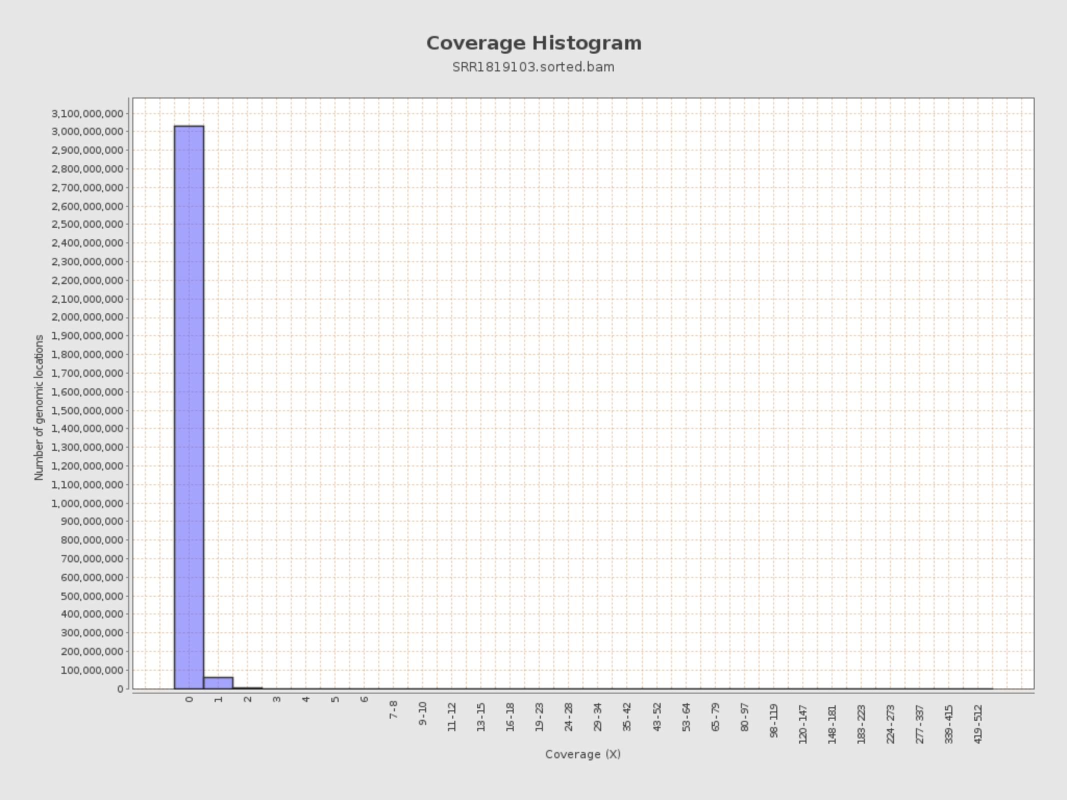
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7296654	0.0293	0.4145
chr2	243199373	5829012	0.024	0.2587
chr3	198022430	4075945	0.0206	0.155
chr4	191154276	4135251	0.0216	0.1752
chr5	180915260	4032706	0.0223	0.1604
chr6	171115067	3074778	0.018	0.1763
chr7	159138663	3738277	0.0235	0.2975

chr8	146364022	6622952	0.0452	0.2536
chr9	141213431	3097251	0.0219	0.1993
chr10	135534747	3777465	0.0279	0.248
chr11	135006516	2610326	0.0193	0.2143
chr12	133851895	3481793	0.026	0.1734
chr13	115169878	1663453	0.0144	0.1282
chr14	107349540	1780950	0.0166	0.1393
chr15	102531392	1969029	0.0192	0.1493
chr16	90354753	2362040	0.0261	0.1873
chr17	81195210	2627498	0.0324	0.2018
chr18	78077248	1713929	0.022	0.3574
chr19	59128983	1562068	0.0264	0.2885
chr20	63025520	2114960	0.0336	0.1986
chr21	48129895	1043698	0.0217	0.167
chr22	51304566	612096	0.0119	0.1164
chrMT	16571	14212	0.8576	1.054
chrX	155270560	4320832	0.0278	0.1943
chrY	59373566	243765	0.0041	0.1202

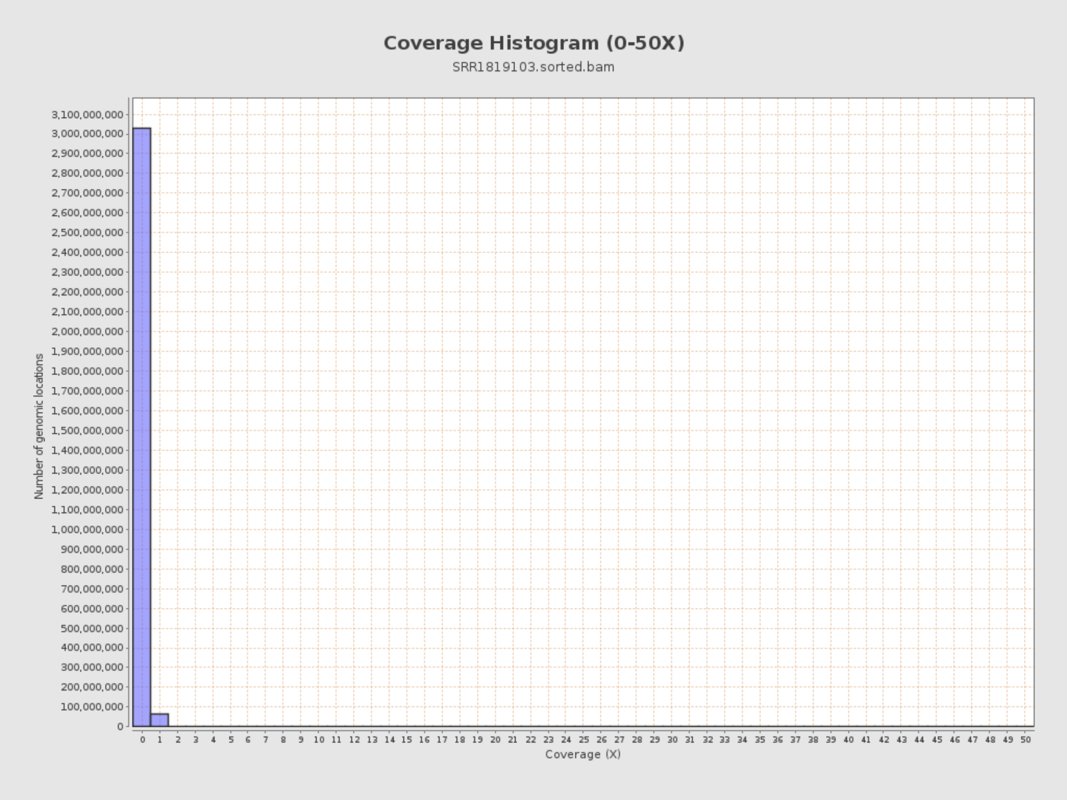
3. Results : Coverage across reference



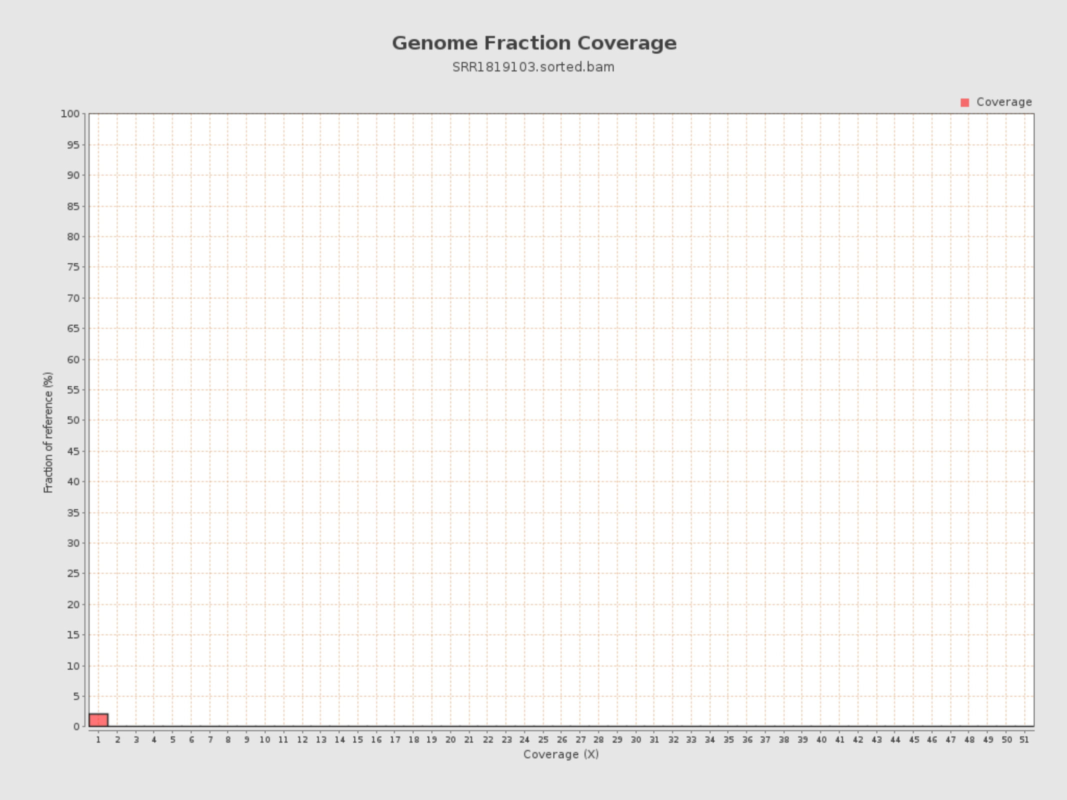
4. Results : Coverage Histogram



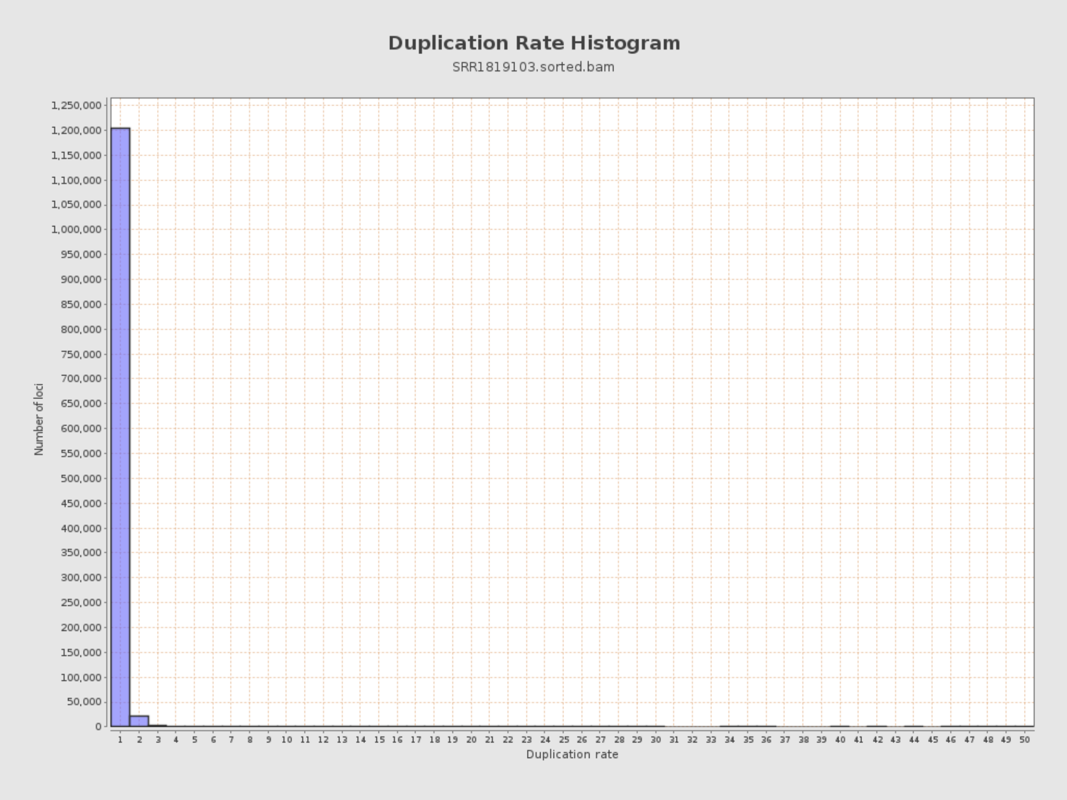
5. Results : Coverage Histogram (0-50X)



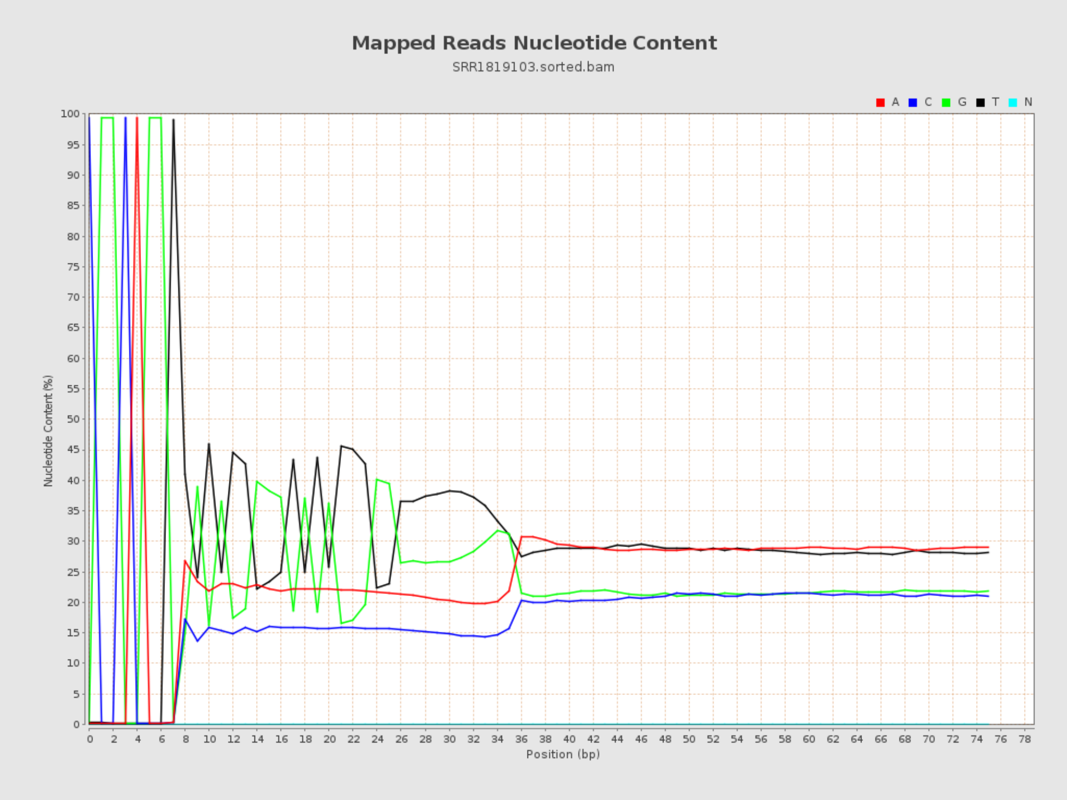
6. Results : Genome Fraction Coverage



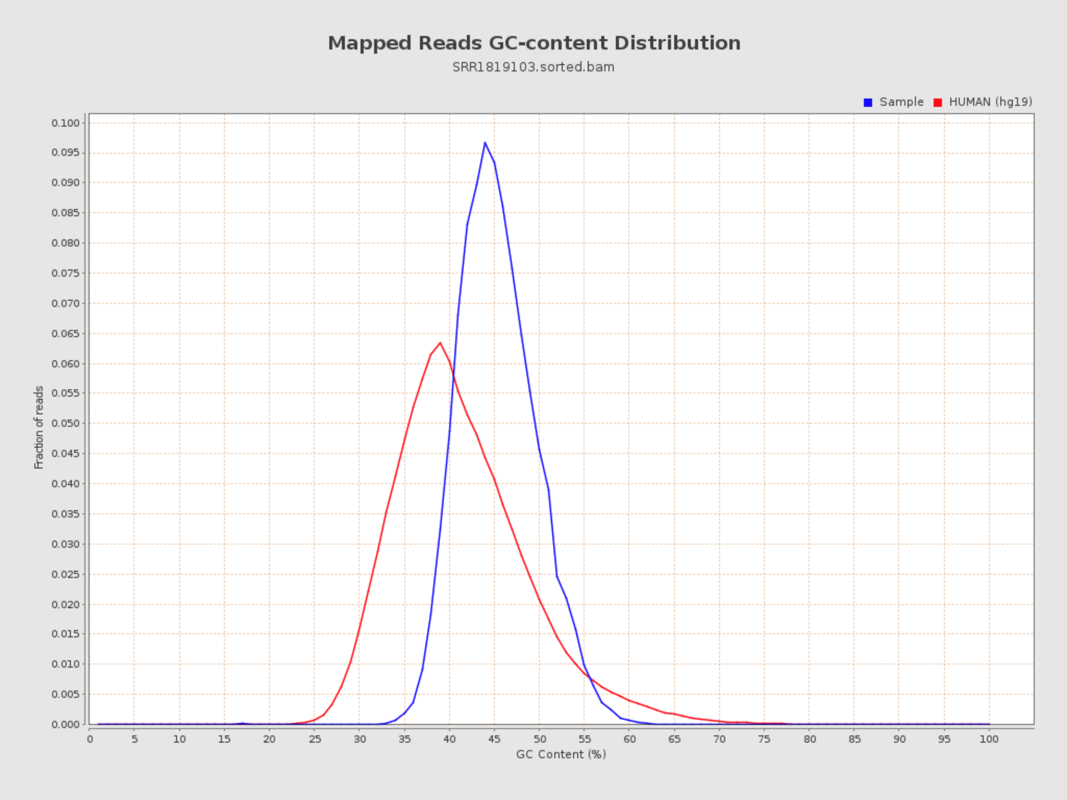
7. Results : Duplication Rate Histogram



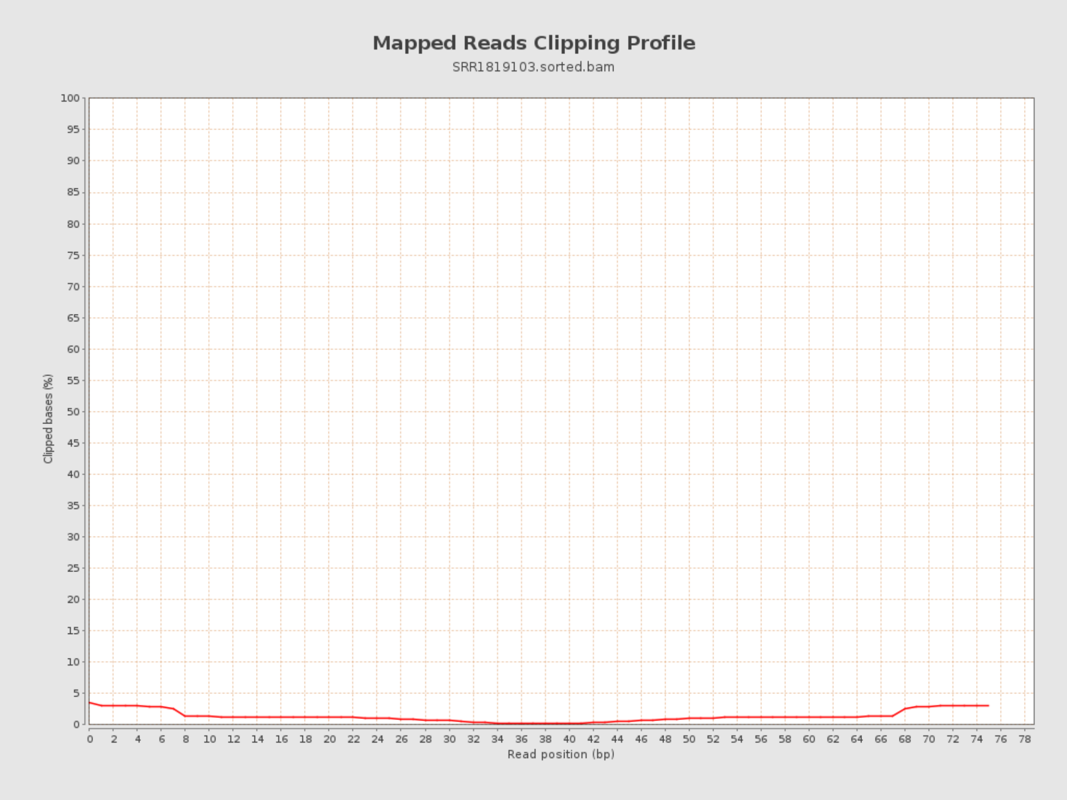
8. Results : Mapped Reads Nucleotide Content



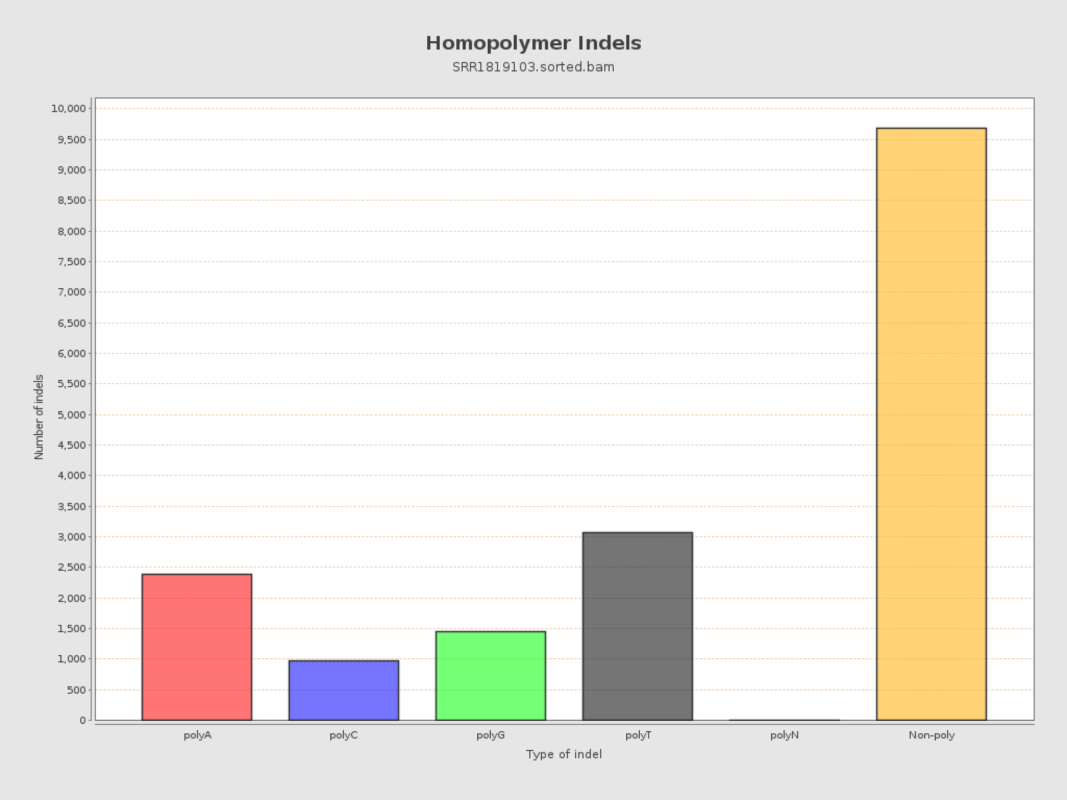
9. Results : Mapped Reads GC-content Distribution



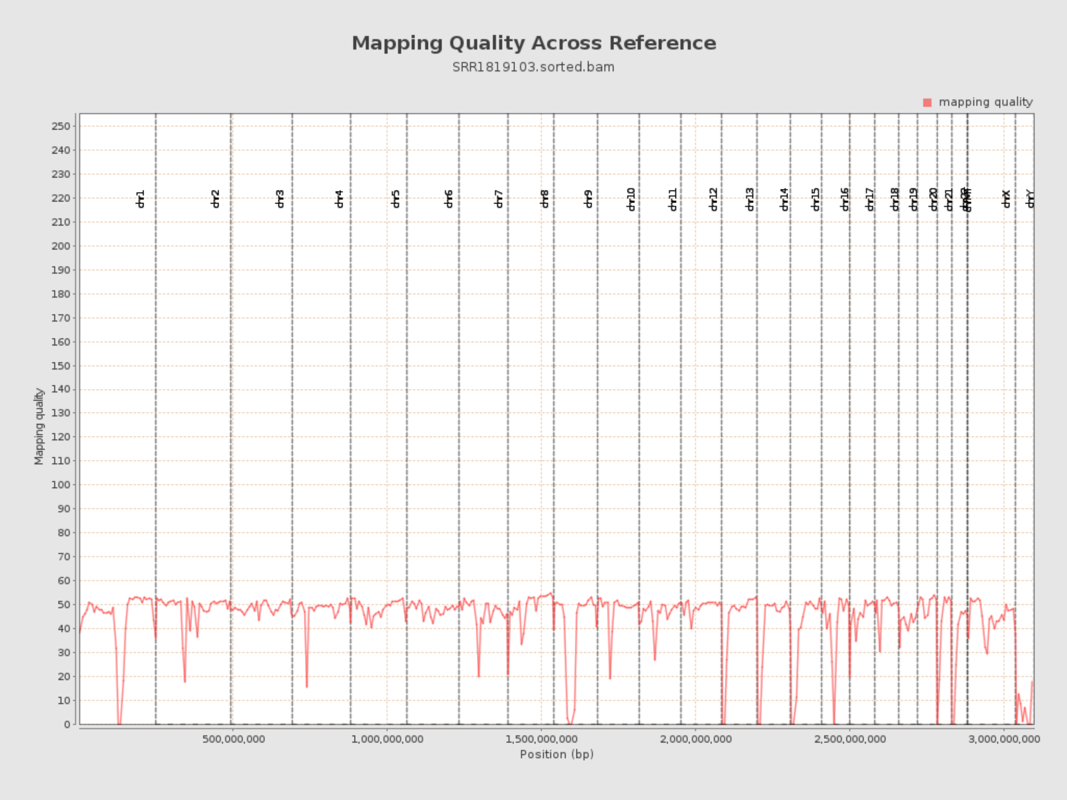
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram