Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 16:50:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819030.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_SRR1819030 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819030.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 16:50:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819030.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,586,535
Mapped reads	1,399,424 / 88.21%
Unmapped reads	187,111 / 11.79%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,623 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	34,588 / 2.18%
Duplication rate	1.91%
Clipped reads	1,401,875 / 88.36%

2.2. ACGT Content

Number/percentage of A's	20,879,207 / 26.12%
Number/percentage of C's	14,879,568 / 18.62%
Number/percentage of T's	24,369,136 / 30.49%
Number/percentage of G's	19,796,897 / 24.77%
Number/percentage of N's	1,778 / 0%
GC Percentage	43.39%

2.3. Coverage

Mean	0.0258

Standard Deviation	0.2084

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

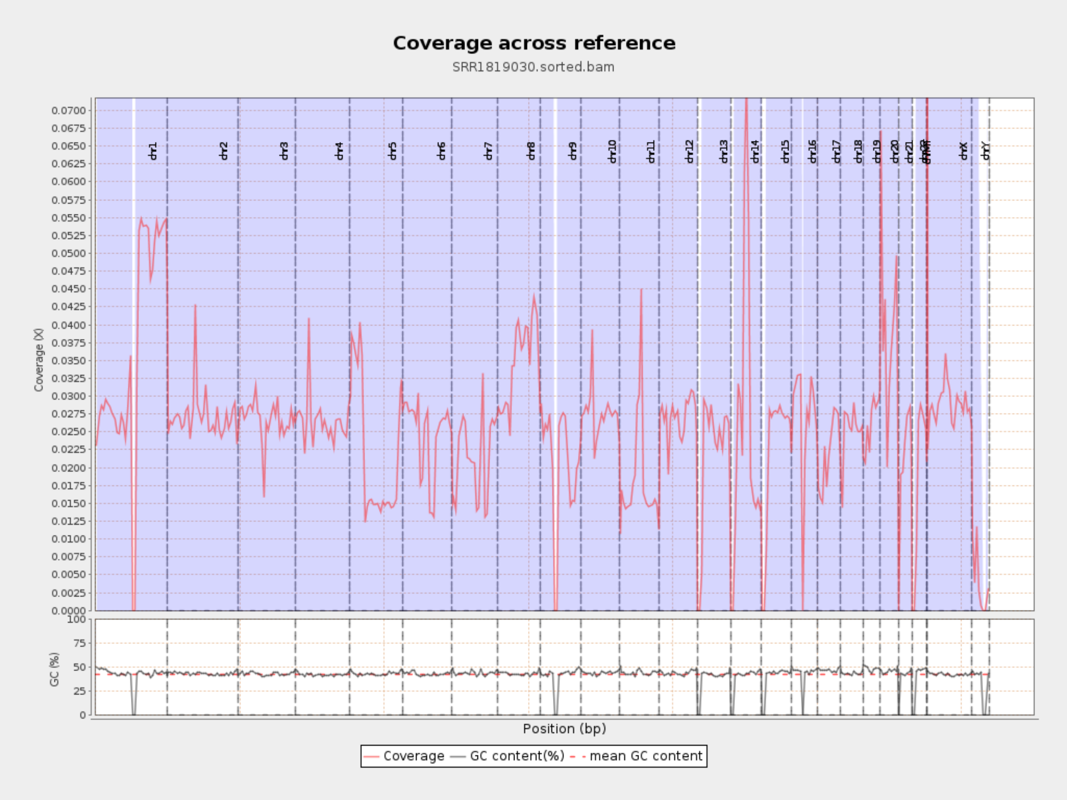
General error rate	0.51%
Mismatches	395,399
Insertions	4,906
Mapped reads with at least one insertion	0.35%
Deletions	12,185
Mapped reads with at least one deletion	0.87%
Homopolymer indels	39.79%

2.6. Chromosome stats

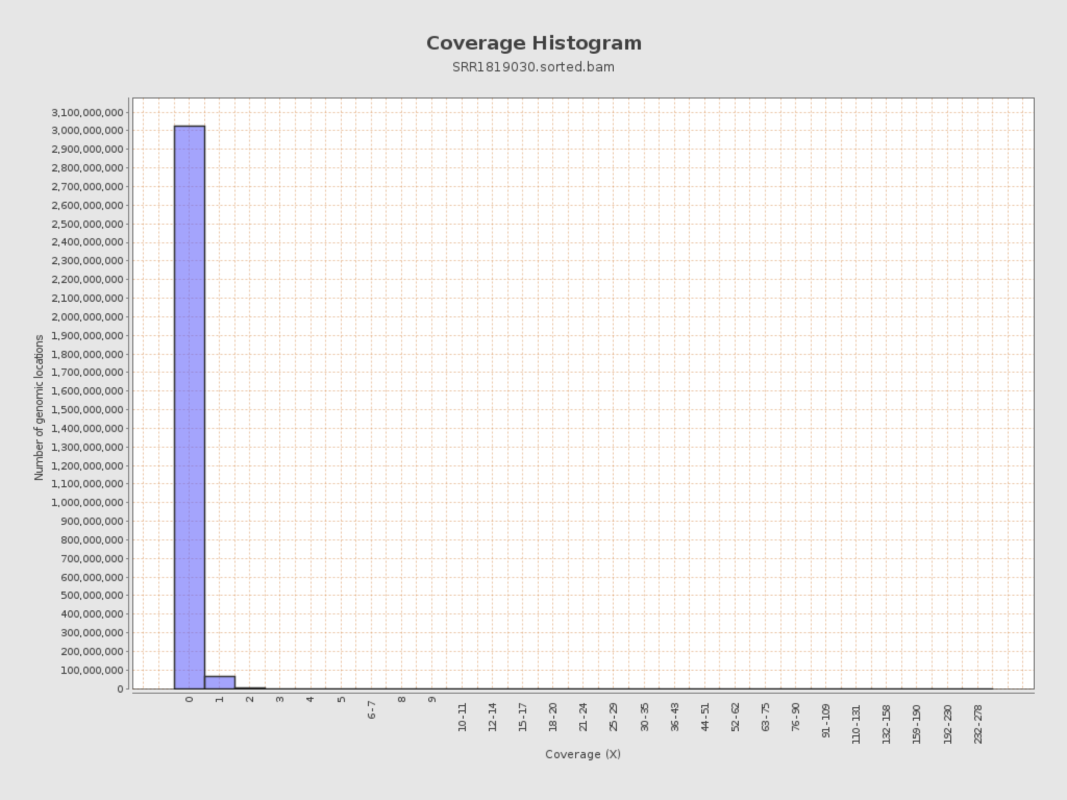
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9037208	0.0363	0.3038
chr2	243199373	6618260	0.0272	0.2367
chr3	198022430	5290454	0.0267	0.1758
chr4	191154276	5076069	0.0266	0.1867
chr5	180915260	3956641	0.0219	0.1604
chr6	171115067	4207782	0.0246	0.1786
chr7	159138663	3427628	0.0215	0.1845

chr8	146364022	5095174	0.0348	0.2246
chr9	141213431	2882252	0.0204	0.2007
chr10	135534747	3751887	0.0277	0.2206
chr11	135006516	2531206	0.0187	0.1832
chr12	133851895	3630576	0.0271	0.1794
chr13	115169878	2499682	0.0217	0.158
chr14	107349540	2820173	0.0263	0.1837
chr15	102531392	2277249	0.0222	0.1603
chr16	90354753	2384408	0.0264	0.1854
chr17	81195210	1783224	0.022	0.1628
chr18	78077248	1933112	0.0248	0.3704
chr19	59128983	1555727	0.0263	0.2435
chr20	63025520	2493323	0.0396	0.2195
chr21	48129895	1029498	0.0214	0.1699
chr22	51304566	947426	0.0185	0.1451
chrMT	16571	6060	0.3657	0.6415
chrX	155270560	4486872	0.0289	0.2011
chrY	59373566	225303	0.0038	0.0876

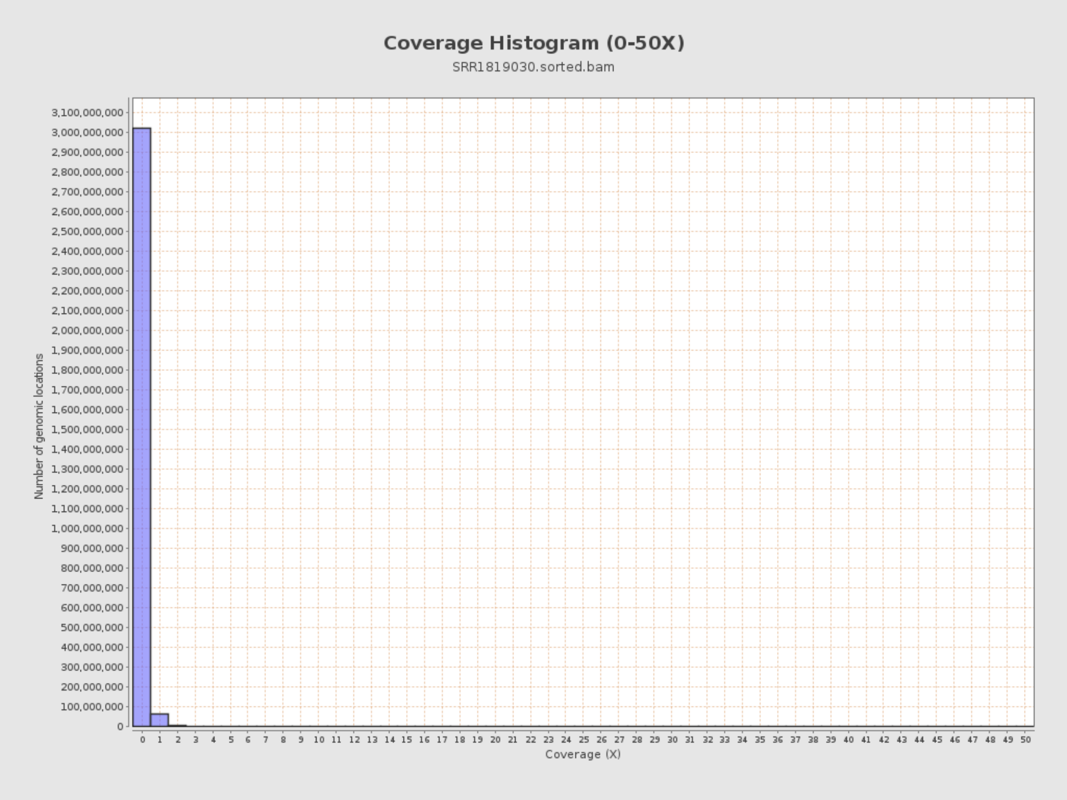
3. Results : Coverage across reference



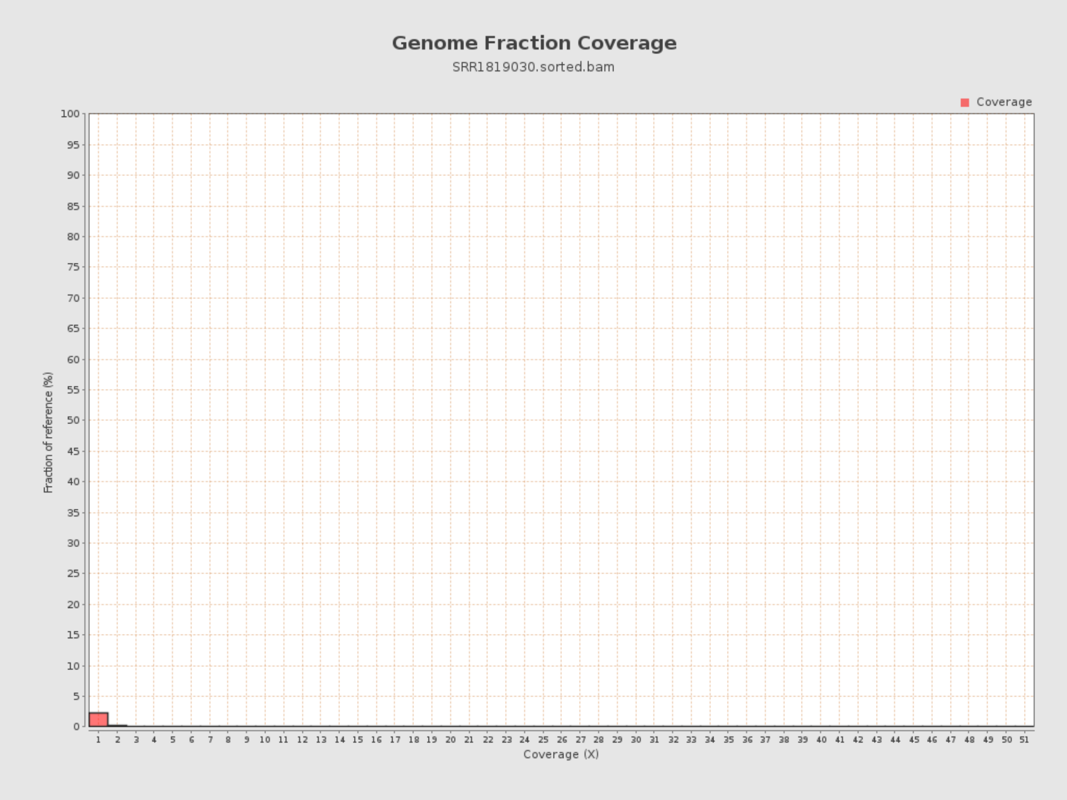
4. Results : Coverage Histogram



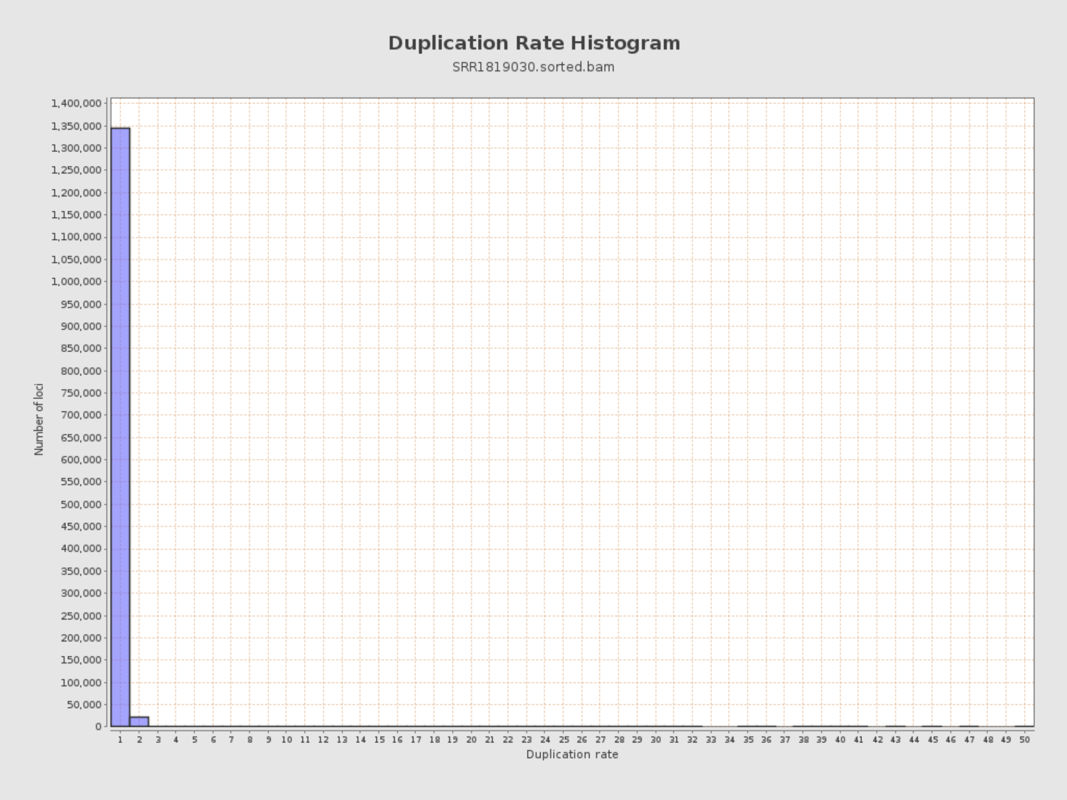
5. Results : Coverage Histogram (0-50X)



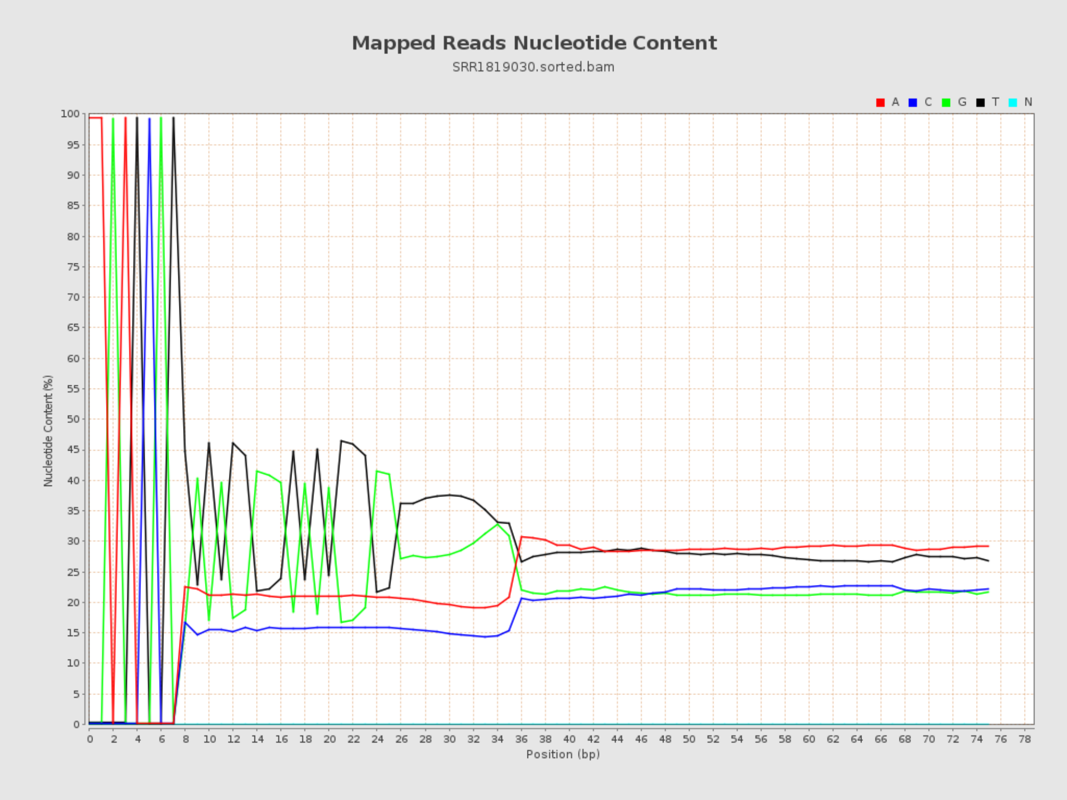
6. Results : Genome Fraction Coverage



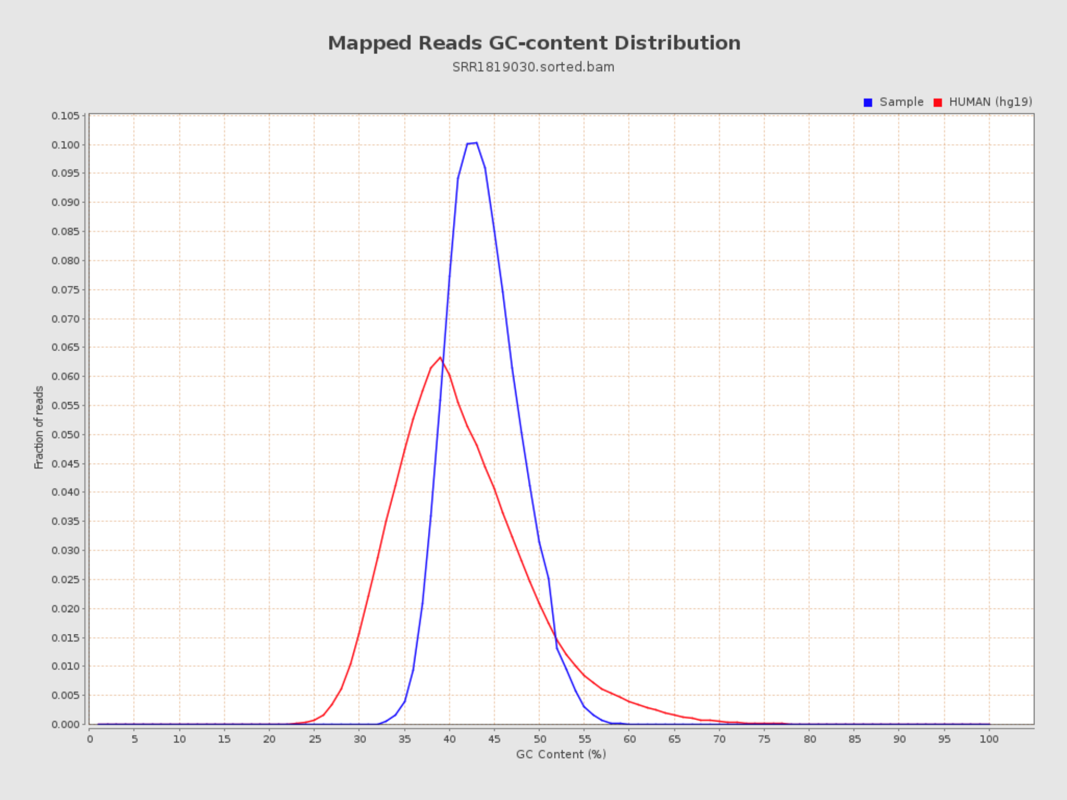
7. Results : Duplication Rate Histogram



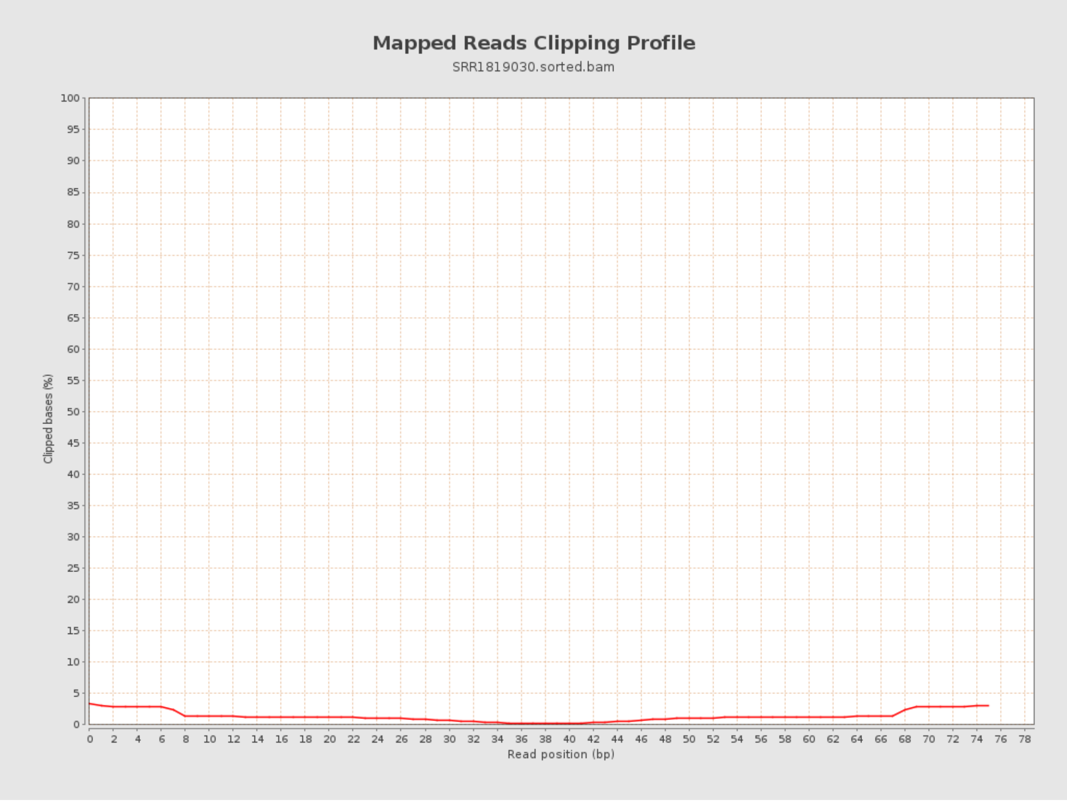
8. Results : Mapped Reads Nucleotide Content



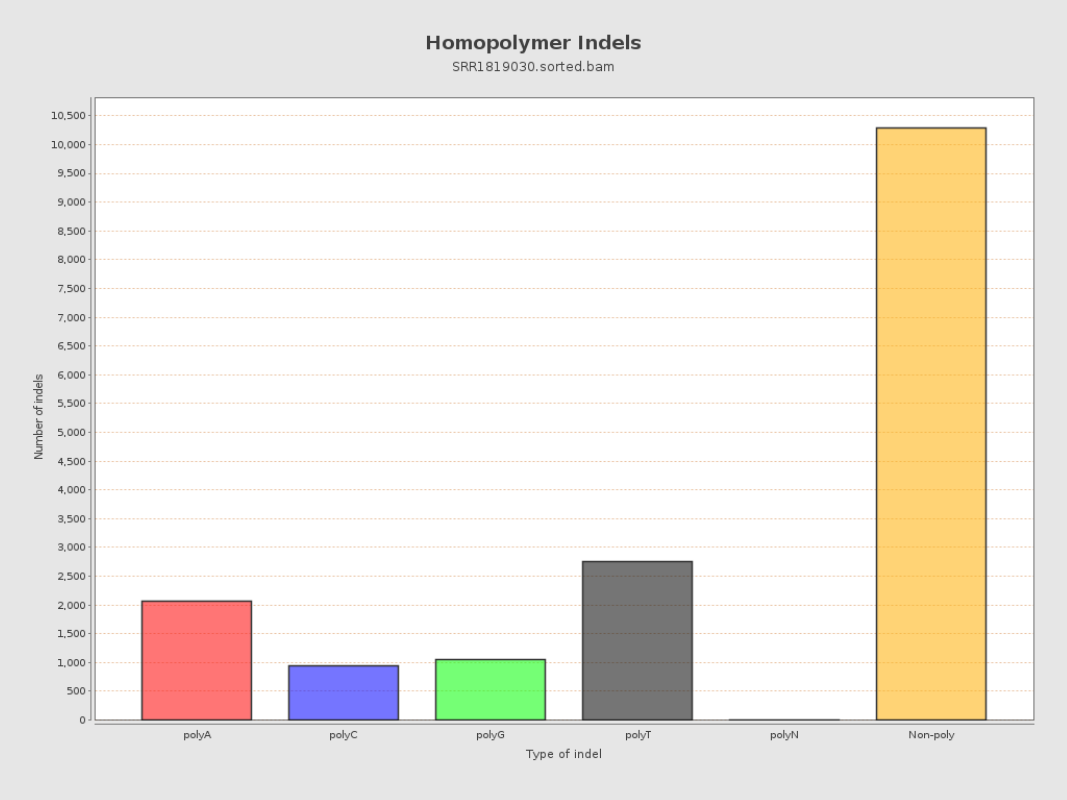
9. Results : Mapped Reads GC-content Distribution



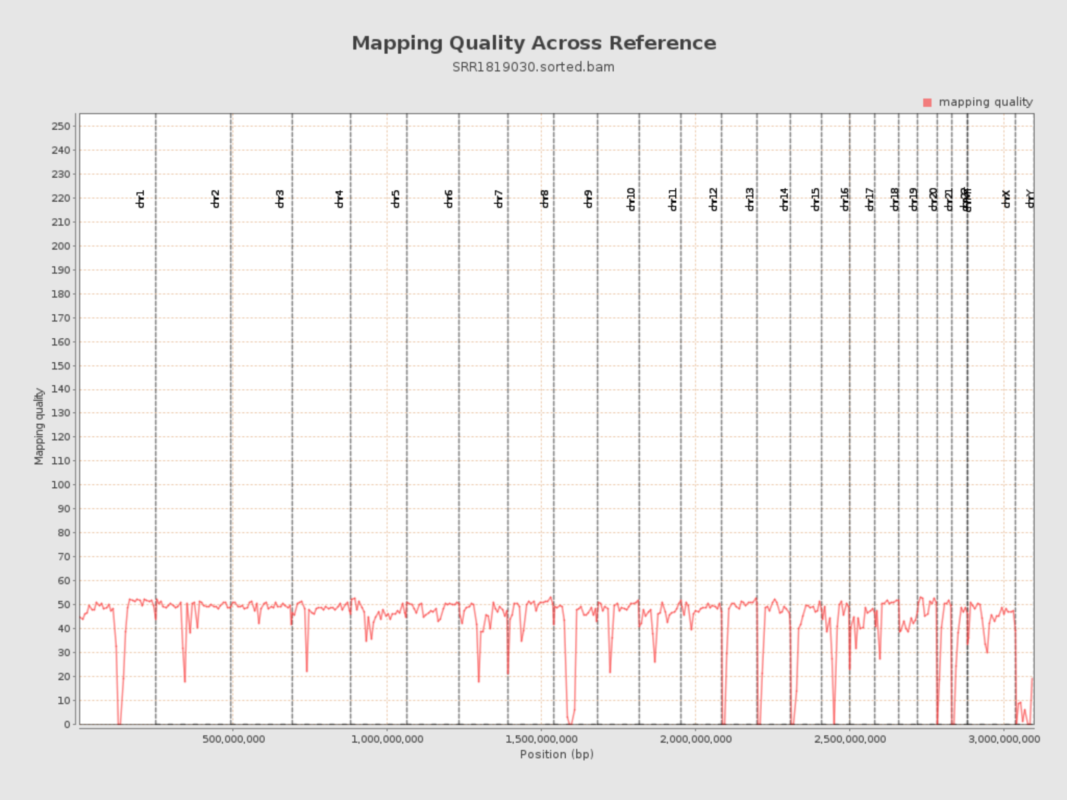
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram