Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:15:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231723.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_SRR6231723 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231723.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:15:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231723.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,502,786
Mapped reads	273,419 / 18.19%
Unmapped reads	1,229,367 / 81.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,605 / 0.17%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	24,395 / 1.62%
Duplication rate	6.97%
Clipped reads	181,978 / 12.11%

2.2. ACGT Content

Number/percentage of A's	4,267,776 / 26.1%
Number/percentage of C's	3,171,479 / 19.4%
Number/percentage of T's	5,021,611 / 30.72%
Number/percentage of G's	3,884,479 / 23.76%
Number/percentage of N's	3,529 / 0.02%
GC Percentage	43.16%

2.3. Coverage

Mean	0.0053

Standard Deviation	0.1124

2.4. Mapping Quality

Mean Mapping Quality	39.28

2.5. Mismatches and indels

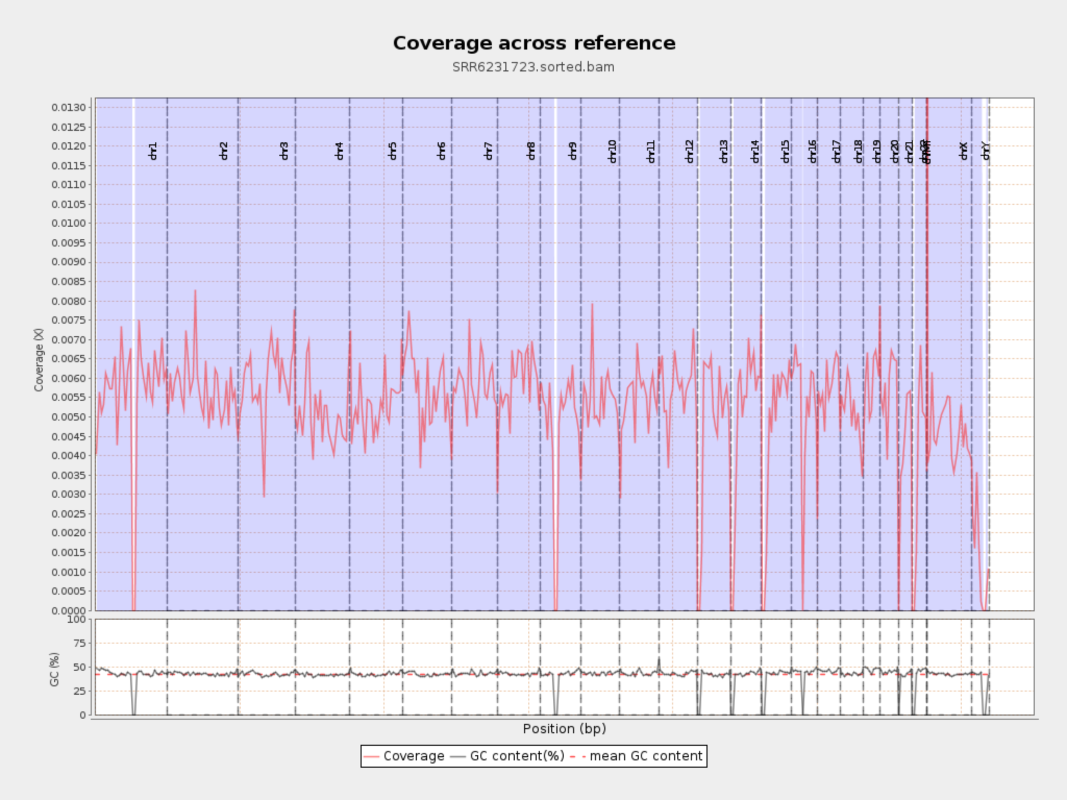
General error rate	1.05%
Mismatches	165,605
Insertions	2,444
Mapped reads with at least one insertion	0.87%
Deletions	5,421
Mapped reads with at least one deletion	1.95%
Homopolymer indels	39.5%

2.6. Chromosome stats

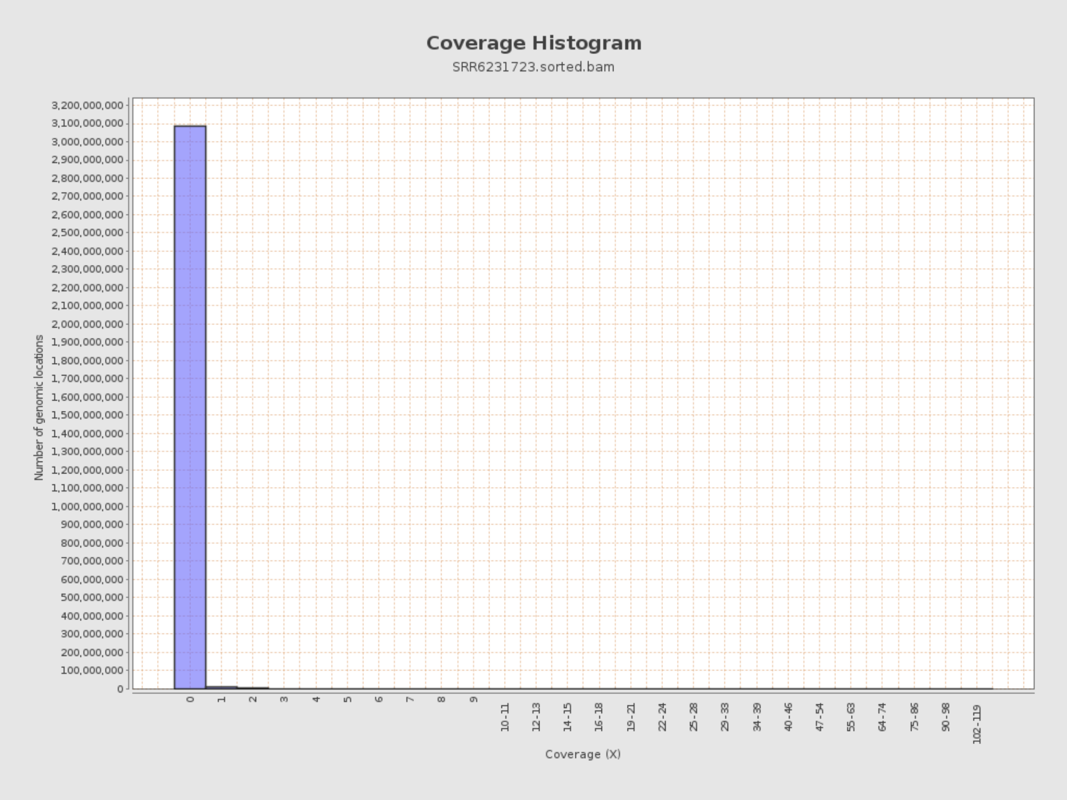
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1389094	0.0056	0.1206
chr2	243199373	1396110	0.0057	0.1252
chr3	198022430	1167617	0.0059	0.11
chr4	191154276	959197	0.005	0.1033
chr5	180915260	952815	0.0053	0.1082
chr6	171115067	976837	0.0057	0.1098
chr7	159138663	931346	0.0059	0.1183

chr8	146364022	866717	0.0059	0.1179
chr9	141213431	664602	0.0047	0.0999
chr10	135534747	742227	0.0055	0.1079
chr11	135006516	741180	0.0055	0.1077
chr12	133851895	769302	0.0057	0.1069
chr13	115169878	543064	0.0047	0.1471
chr14	107349540	533357	0.005	0.1191
chr15	102531392	466752	0.0046	0.0976
chr16	90354753	475301	0.0053	0.1241
chr17	81195210	470739	0.0058	0.1209
chr18	78077248	400233	0.0051	0.1147
chr19	59128983	353229	0.006	0.1098
chr20	63025520	358032	0.0057	0.1161
chr21	48129895	203574	0.0042	0.0867
chr22	51304566	191588	0.0037	0.0852
chrMT	16571	7518	0.4537	0.8636
chrX	155270560	721420	0.0046	0.1035
chrY	59373566	76343	0.0013	0.049

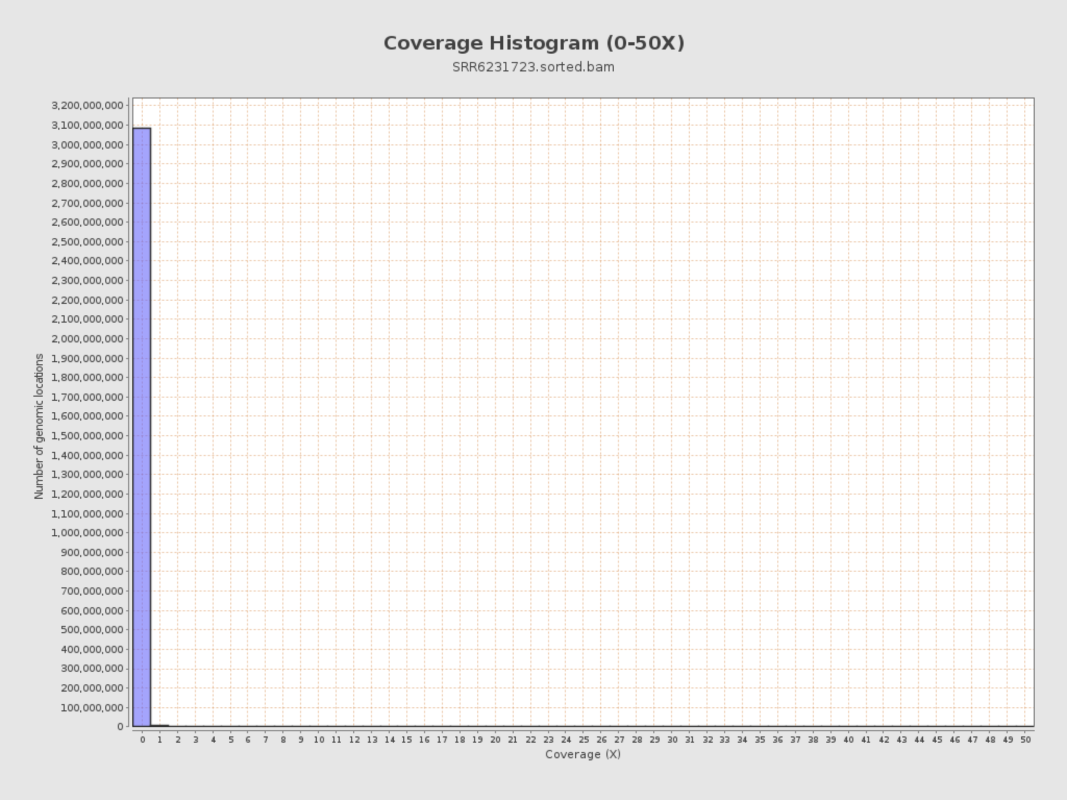
3. Results : Coverage across reference



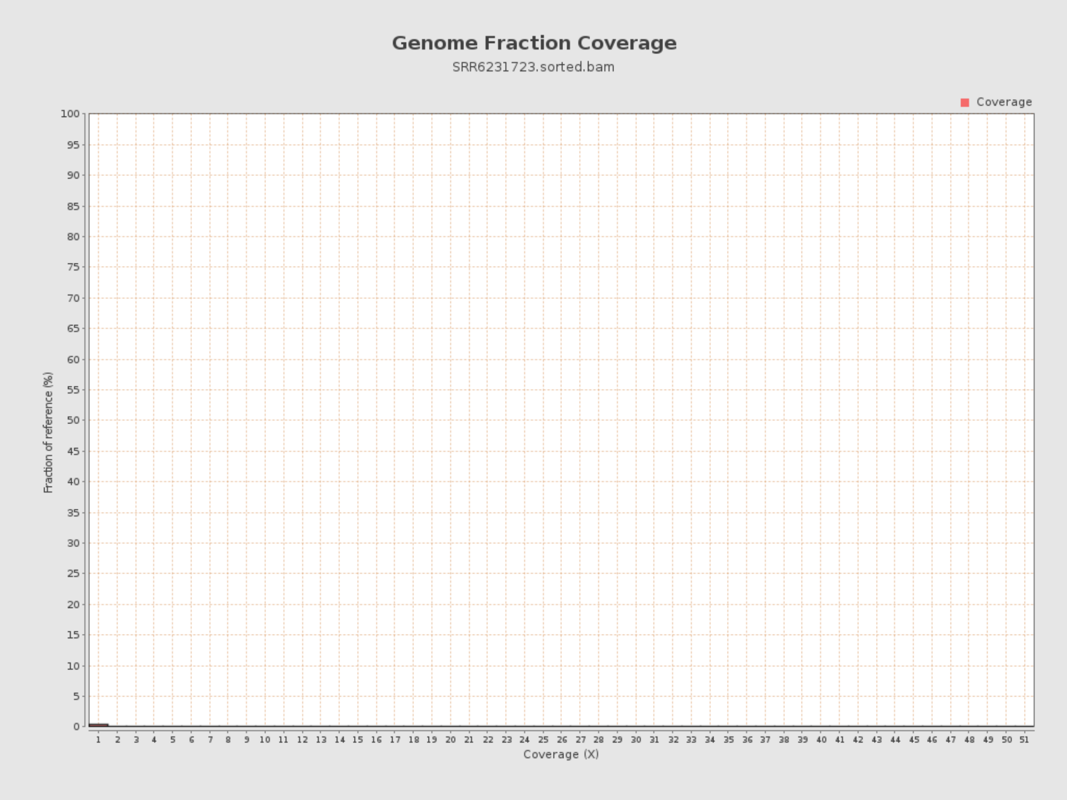
4. Results : Coverage Histogram



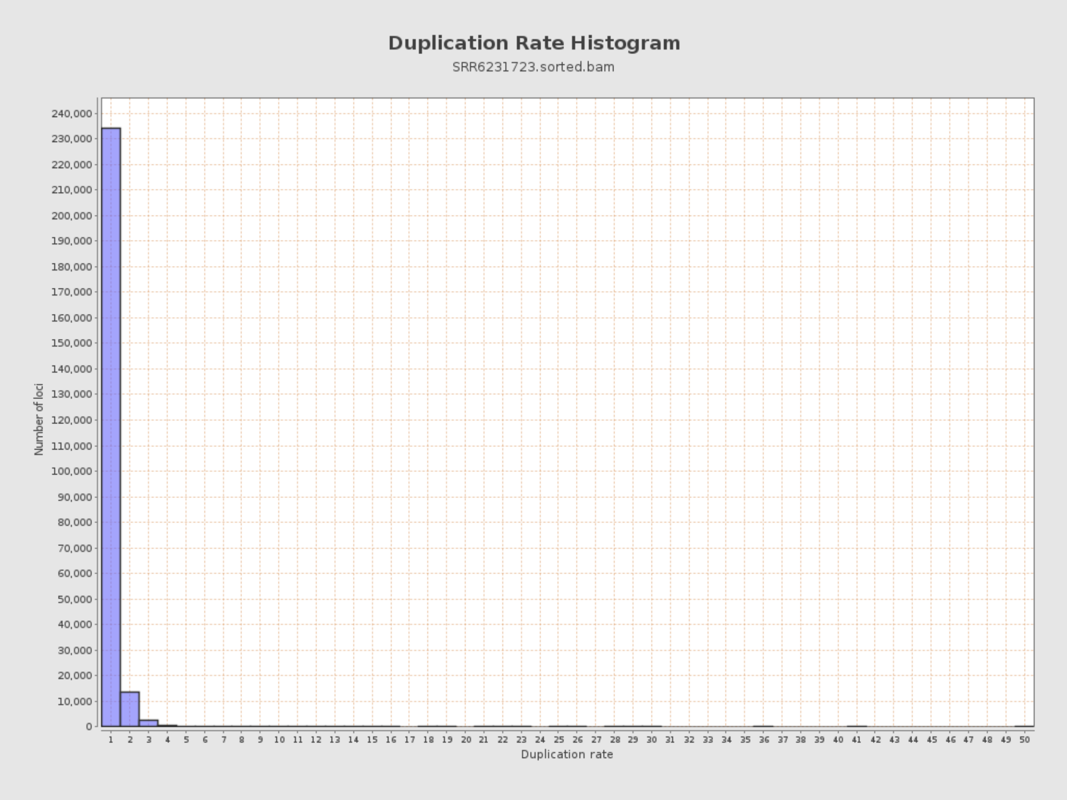
5. Results : Coverage Histogram (0-50X)



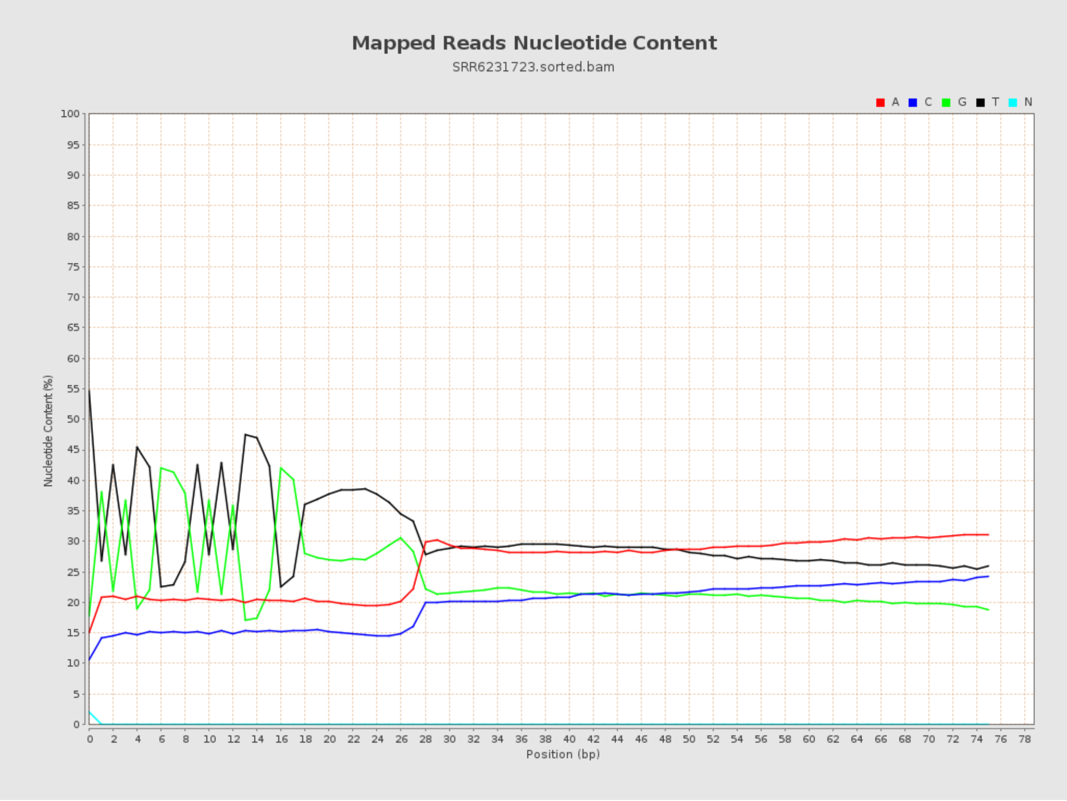
6. Results : Genome Fraction Coverage



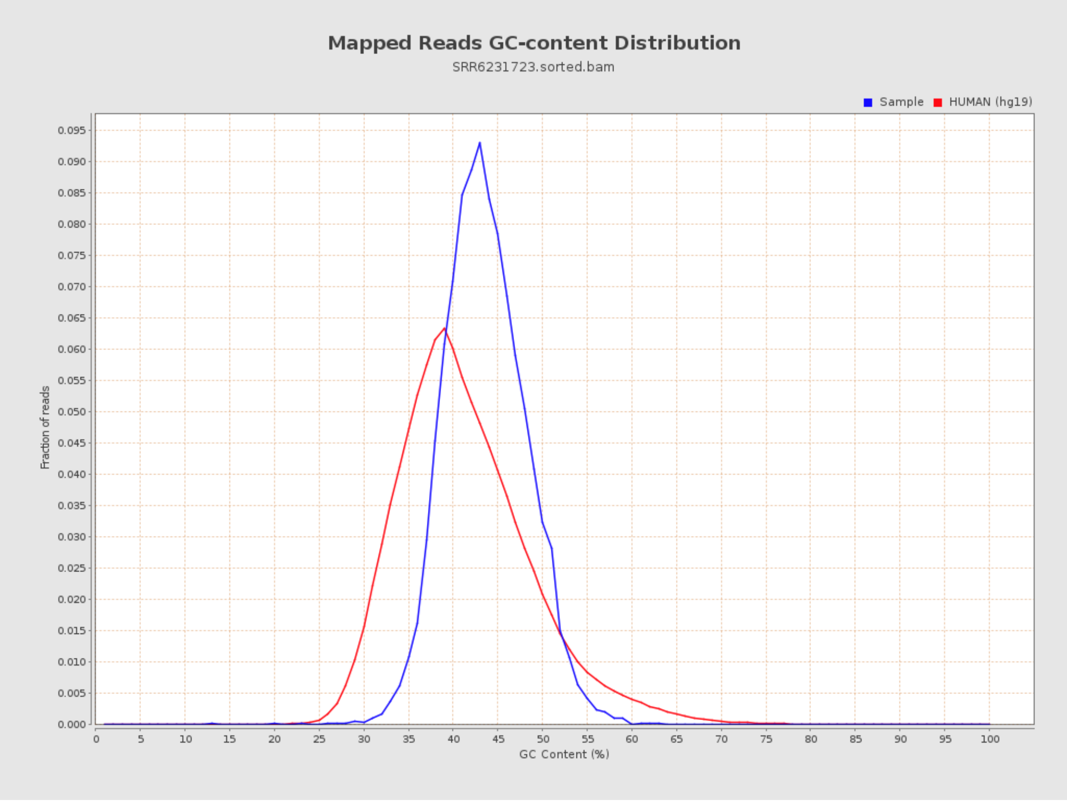
7. Results : Duplication Rate Histogram



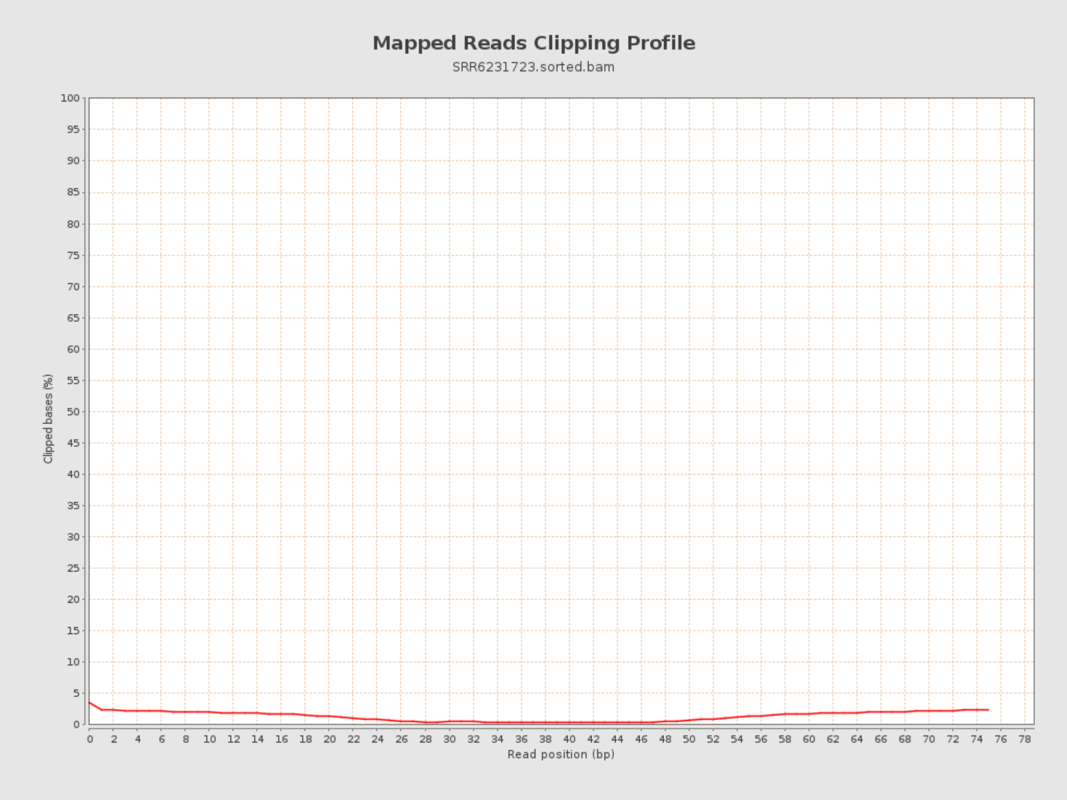
8. Results : Mapped Reads Nucleotide Content



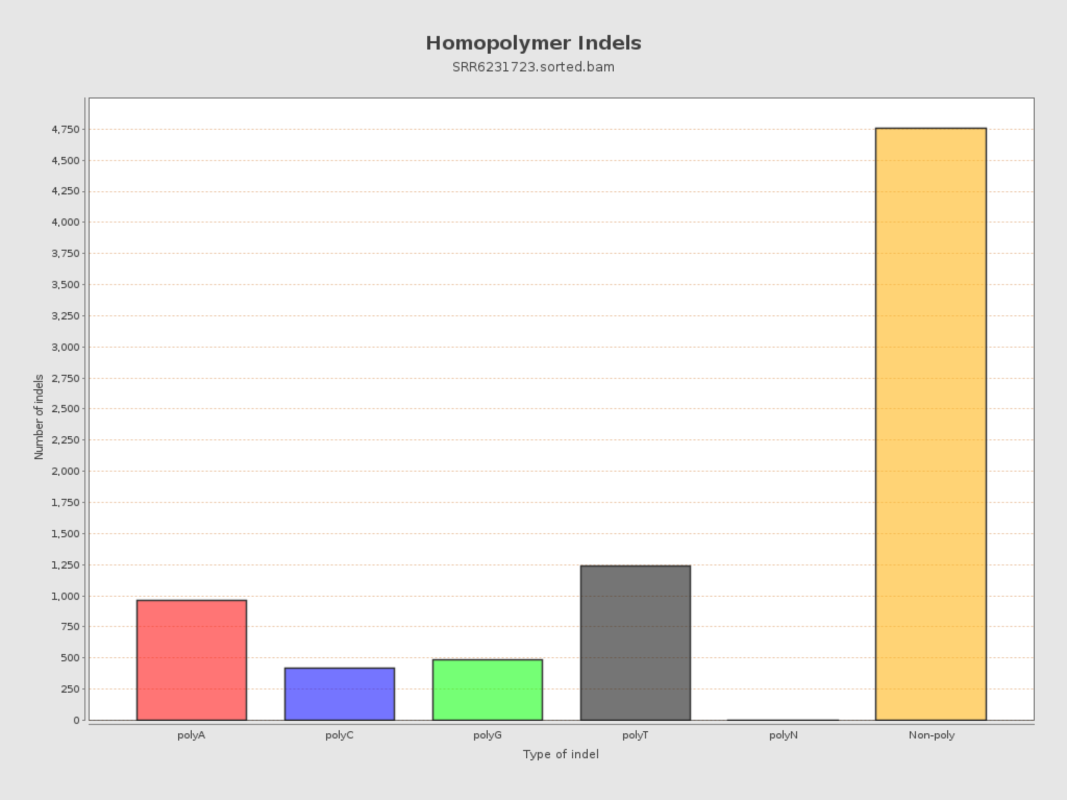
9. Results : Mapped Reads GC-content Distribution



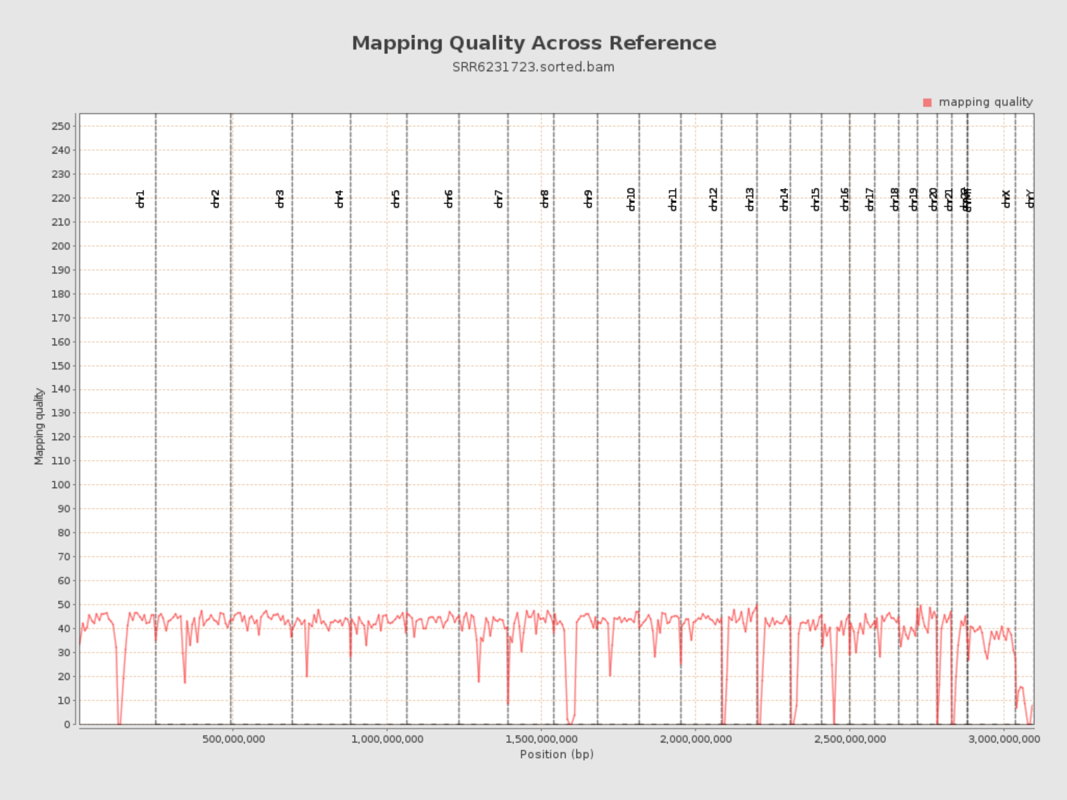
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram