Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:31:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231727.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_SRR6231727 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231727.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:31:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231727.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,870,712
Mapped reads	4,555,533 / 93.53%
Unmapped reads	315,179 / 6.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,837 / 0.78%
Read min/max/mean length	30 / 76 / 76.27
Duplicated reads (estimated)	493,490 / 10.13%
Duplication rate	4.99%
Clipped reads	1,704,381 / 34.99%

2.2. ACGT Content

Number/percentage of A's	82,830,225 / 26.6%
Number/percentage of C's	56,852,812 / 18.26%
Number/percentage of T's	90,175,604 / 28.96%
Number/percentage of G's	81,426,010 / 26.15%
Number/percentage of N's	66,490 / 0.02%
GC Percentage	44.41%

2.3. Coverage

Mean	0.1006

Standard Deviation	32.4908

2.4. Mapping Quality

Mean Mapping Quality	46.26

2.5. Mismatches and indels

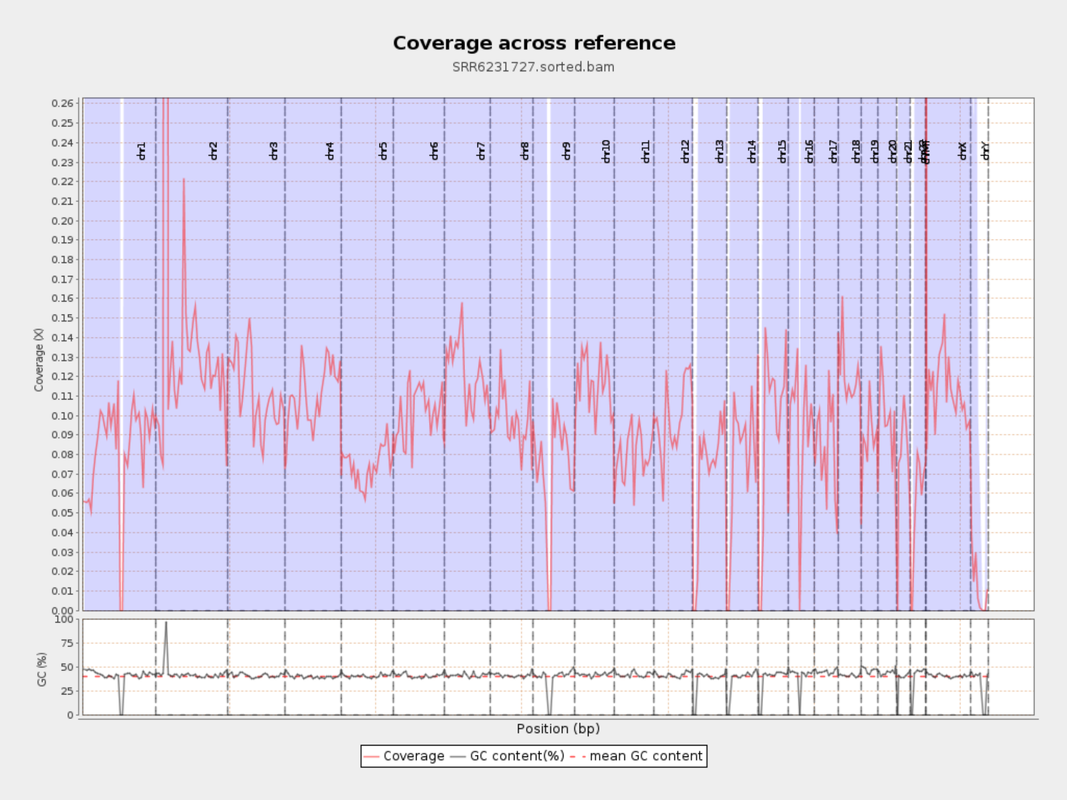
General error rate	0.65%
Mismatches	1,987,908
Insertions	20,413
Mapped reads with at least one insertion	0.44%
Deletions	68,264
Mapped reads with at least one deletion	1.48%
Homopolymer indels	47.3%

2.6. Chromosome stats

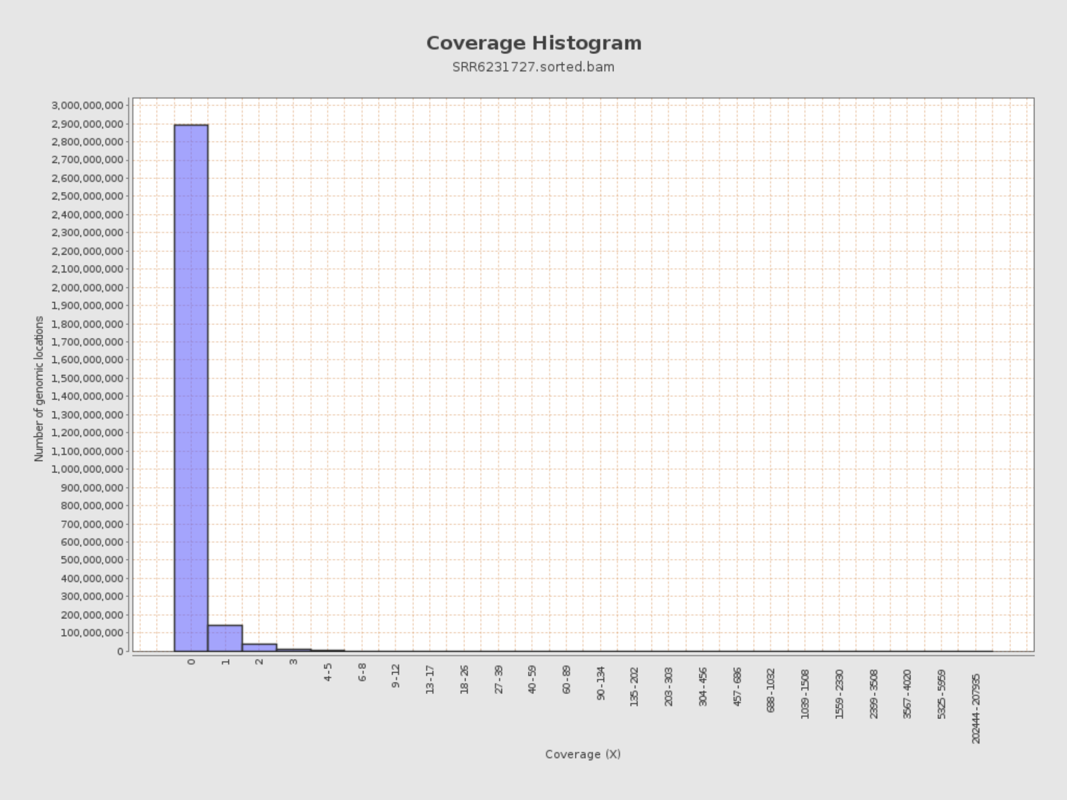
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20609878	0.0827	0.829
chr2	243199373	46008165	0.1892	115.8974
chr3	198022430	22130655	0.1118	0.4566
chr4	191154276	21328919	0.1116	0.4754
chr5	180915260	13487175	0.0745	0.3751
chr6	171115067	17435900	0.1019	0.5158
chr7	159138663	19298795	0.1213	1.027

chr8	146364022	14276005	0.0975	0.8441
chr9	141213431	10325342	0.0731	0.7521
chr10	135534747	15783317	0.1165	0.6433
chr11	135006516	10813910	0.0801	0.7643
chr12	133851895	13298267	0.0994	0.4468
chr13	115169878	8140031	0.0707	0.3627
chr14	107349540	8154509	0.076	0.524
chr15	102531392	9689611	0.0945	0.424
chr16	90354753	8292584	0.0918	0.5062
chr17	81195210	6841806	0.0843	0.4886
chr18	78077248	9470151	0.1213	1.6793
chr19	59128983	5222293	0.0883	0.7216
chr20	63025520	6292324	0.0998	0.4728
chr21	48129895	3655124	0.0759	0.4162
chr22	51304566	2675450	0.0521	0.3088
chrMT	16571	20574	1.2416	1.7616
chrX	155270560	17521874	0.1128	0.5674
chrY	59373566	688554	0.0116	0.1964

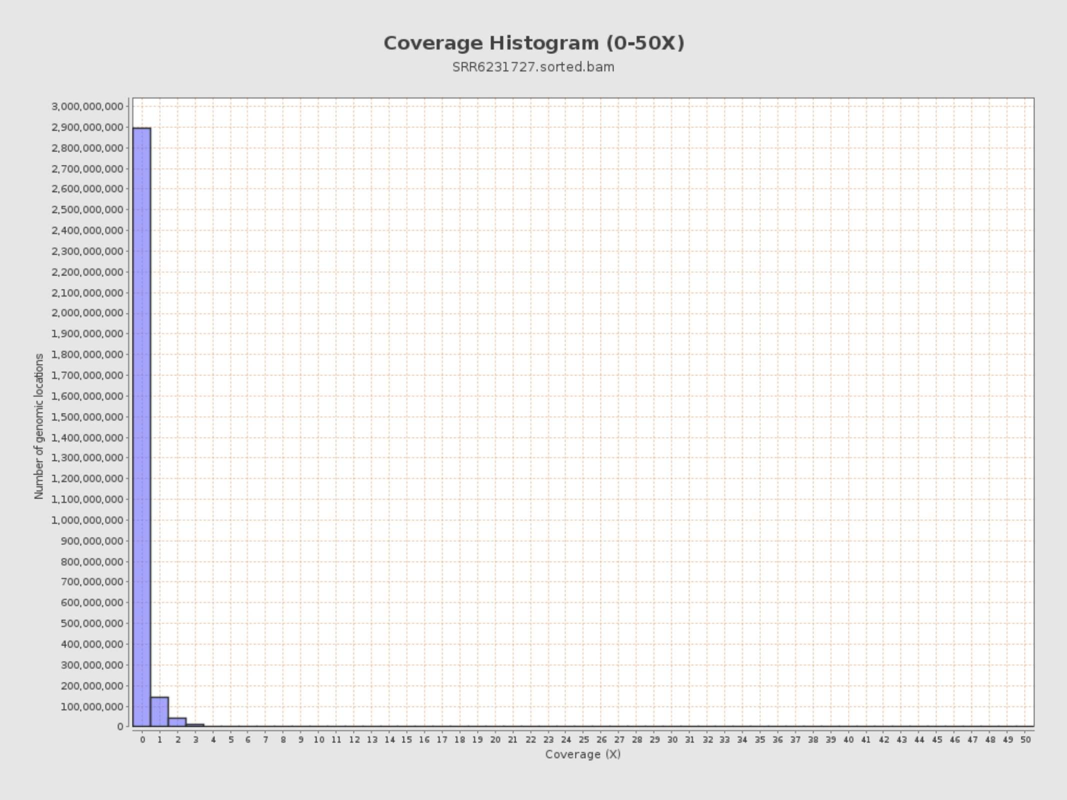
3. Results : Coverage across reference



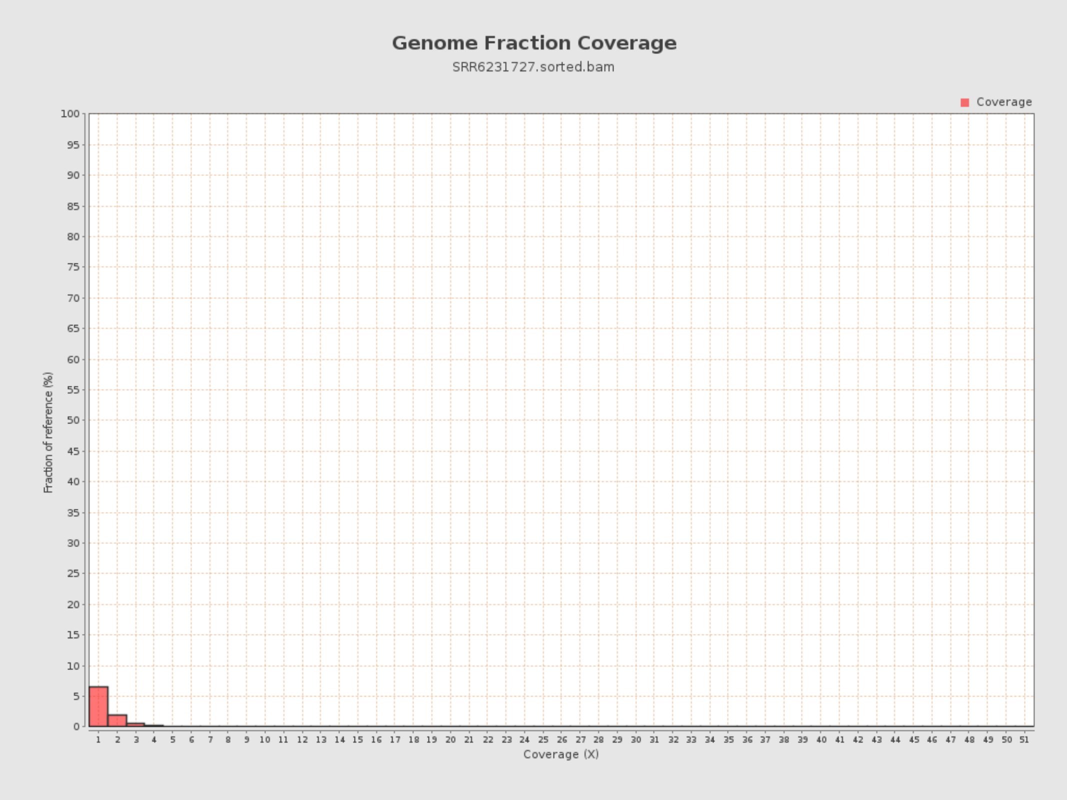
4. Results : Coverage Histogram



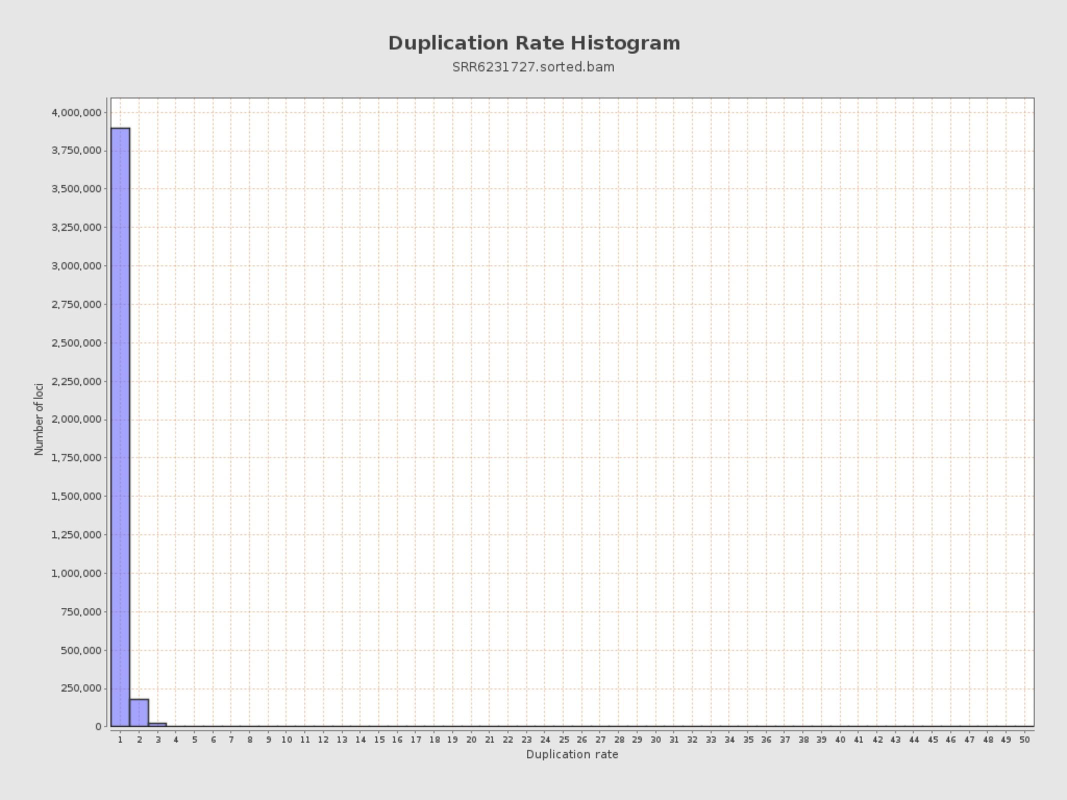
5. Results : Coverage Histogram (0-50X)



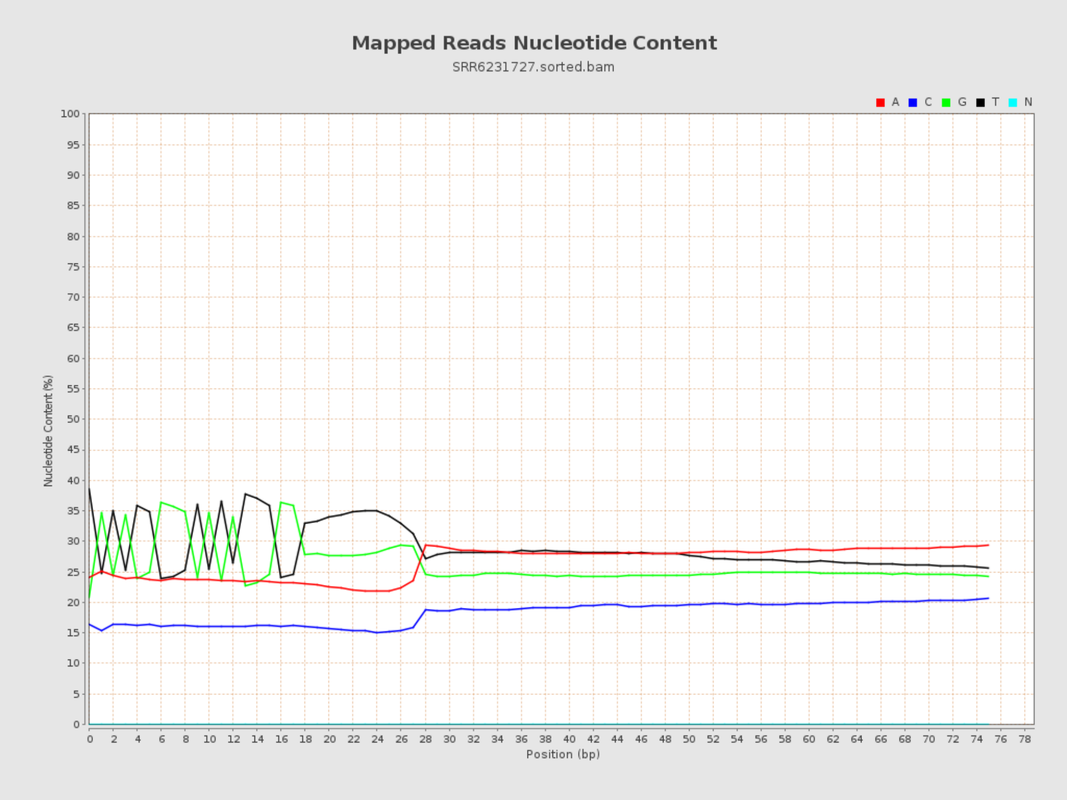
6. Results : Genome Fraction Coverage



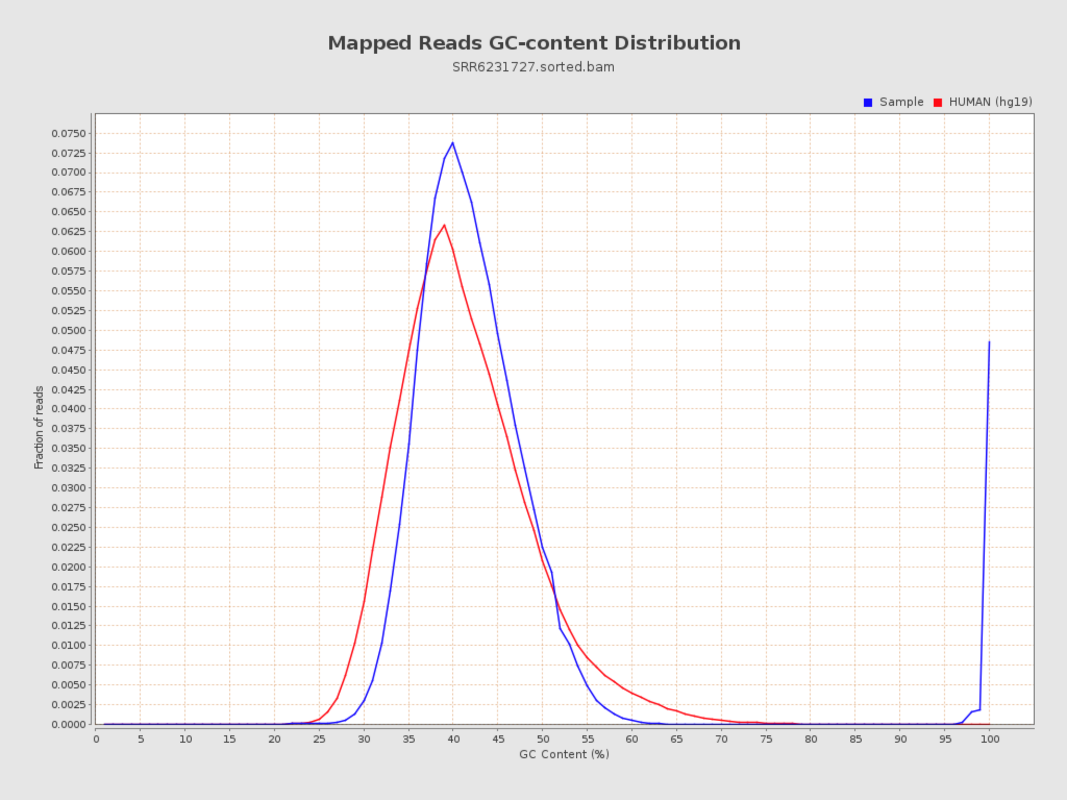
7. Results : Duplication Rate Histogram



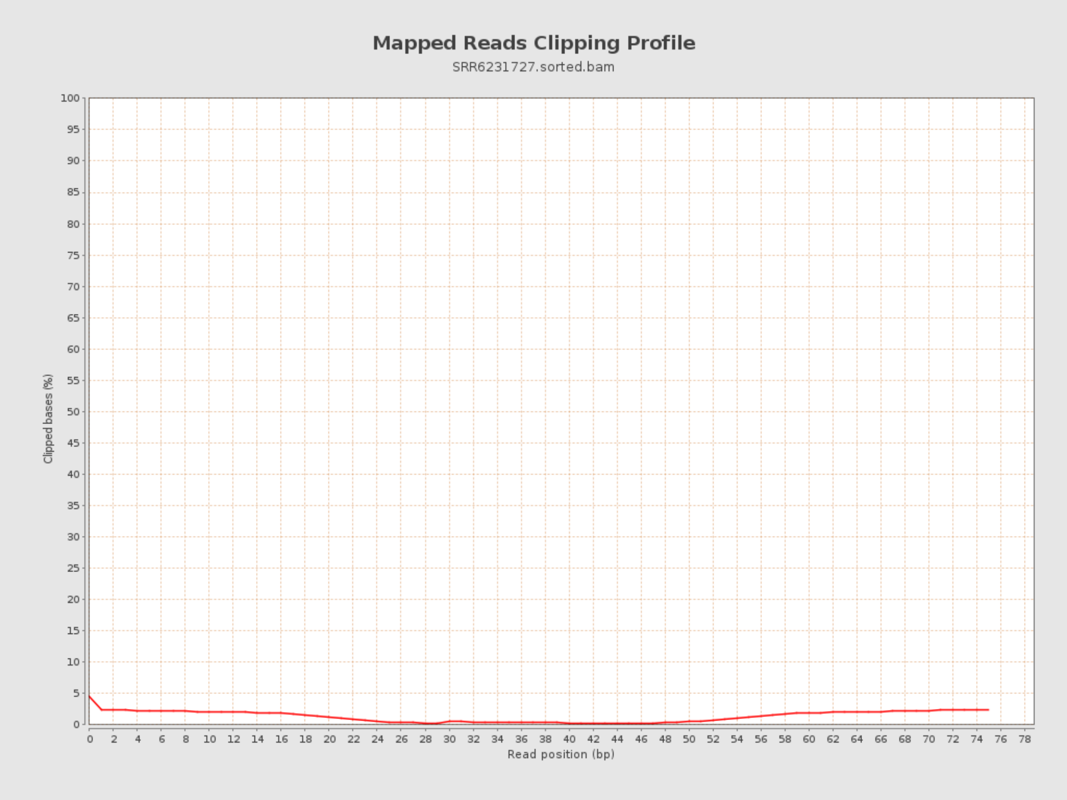
8. Results : Mapped Reads Nucleotide Content



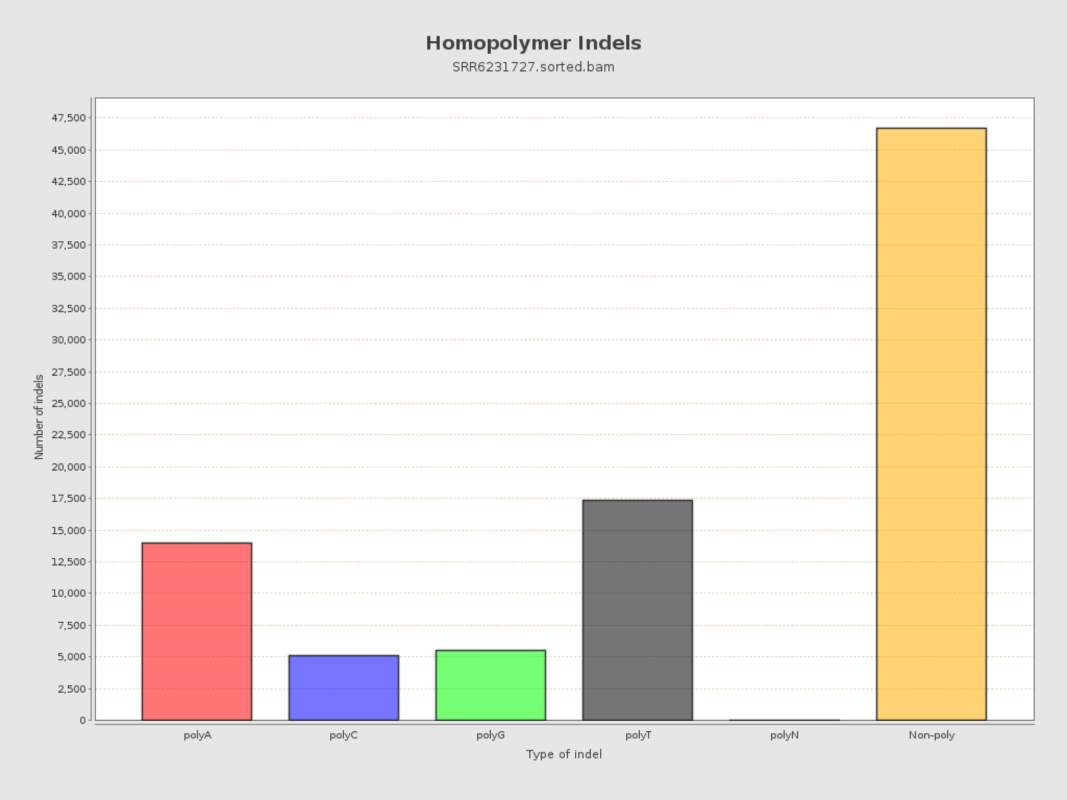
9. Results : Mapped Reads GC-content Distribution



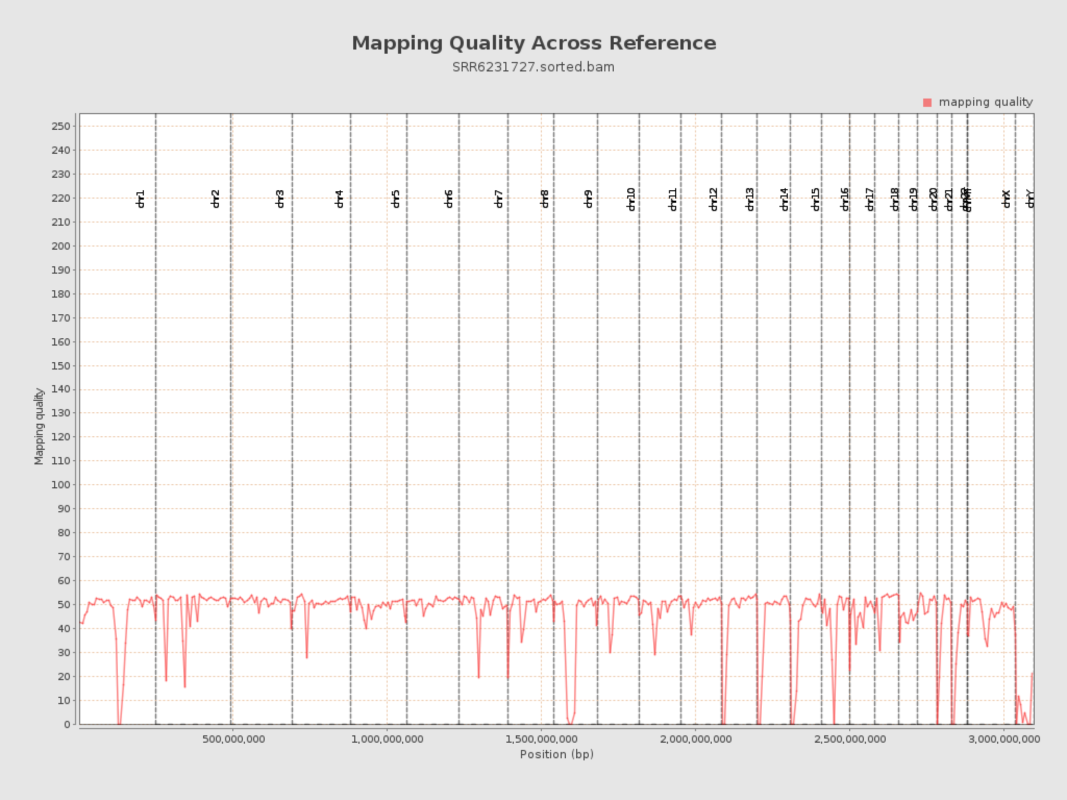
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram