Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:13:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231722.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_SRR6231722 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231722.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:13:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231722.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	836,426
Mapped reads	356,094 / 42.57%
Unmapped reads	480,332 / 57.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,597 / 0.19%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	9,403 / 1.12%
Duplication rate	2.17%
Clipped reads	224,220 / 26.81%

2.2. ACGT Content

Number/percentage of A's	6,075,022 / 27.58%
Number/percentage of C's	3,766,579 / 17.1%
Number/percentage of T's	7,135,751 / 32.4%
Number/percentage of G's	5,047,569 / 22.92%
Number/percentage of N's	448 / 0%
GC Percentage	40.02%

2.3. Coverage

Mean	0.0071

Standard Deviation	0.1041

2.4. Mapping Quality

Mean Mapping Quality	44.63

2.5. Mismatches and indels

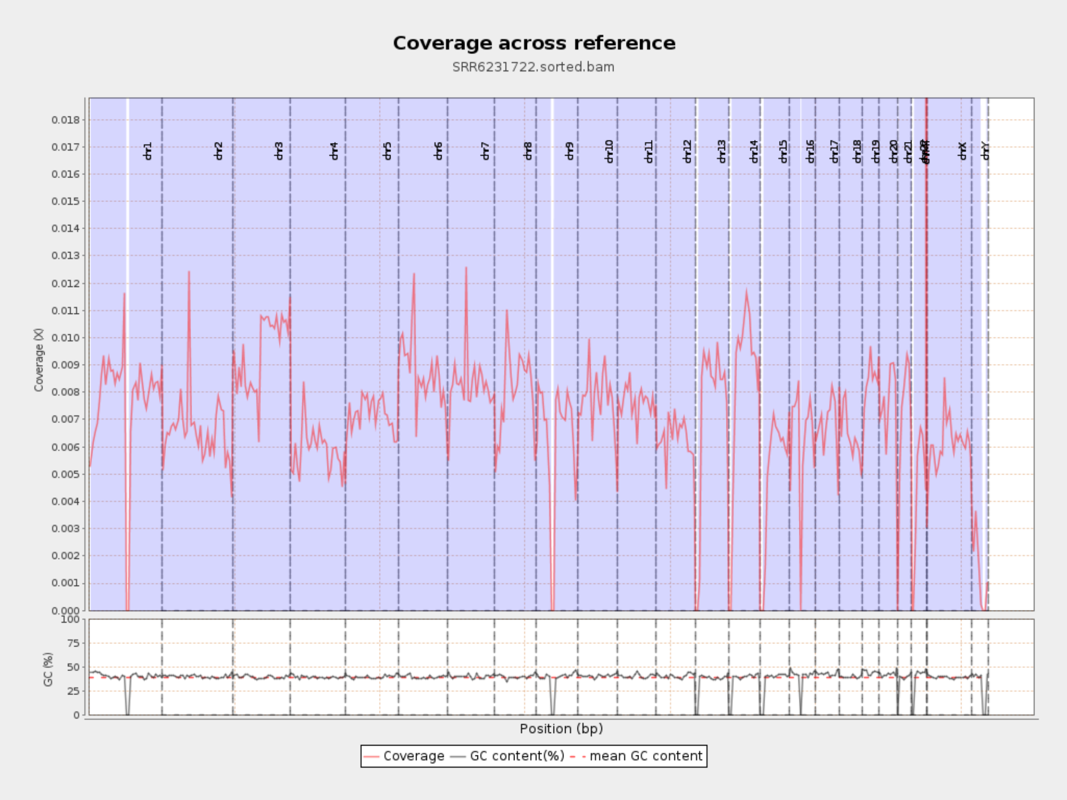
General error rate	1.18%
Mismatches	257,249
Insertions	1,847
Mapped reads with at least one insertion	0.51%
Deletions	8,804
Mapped reads with at least one deletion	2.44%
Homopolymer indels	47.14%

2.6. Chromosome stats

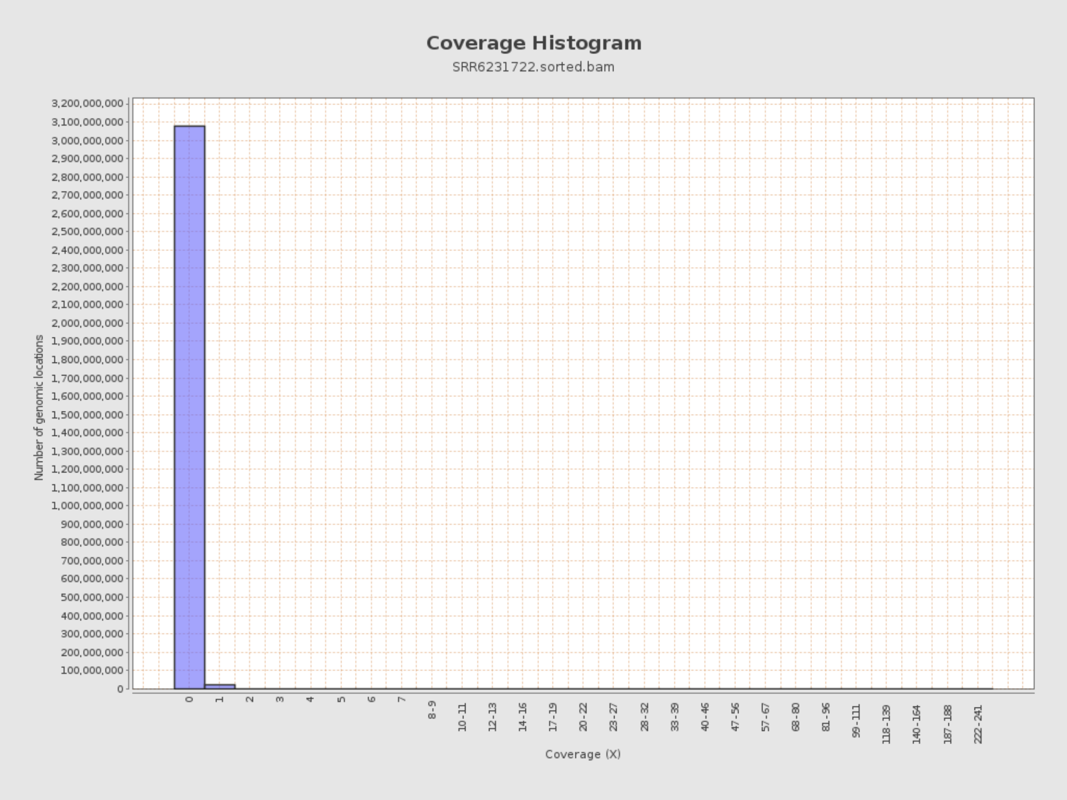
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1905618	0.0076	0.125
chr2	243199373	1610694	0.0066	0.1059
chr3	198022430	1874255	0.0095	0.1034
chr4	191154276	1123599	0.0059	0.0828
chr5	180915260	1298225	0.0072	0.0922
chr6	171115067	1499066	0.0088	0.1049
chr7	159138663	1331163	0.0084	0.1238

chr8	146364022	1171611	0.008	0.1696
chr9	141213431	887811	0.0063	0.0926
chr10	135534747	1060064	0.0078	0.099
chr11	135006516	1024229	0.0076	0.1101
chr12	133851895	844235	0.0063	0.0844
chr13	115169878	830368	0.0072	0.0909
chr14	107349540	882893	0.0082	0.0981
chr15	102531392	513051	0.005	0.076
chr16	90354753	568890	0.0063	0.085
chr17	81195210	544439	0.0067	0.0902
chr18	78077248	507866	0.0065	0.1263
chr19	59128983	494241	0.0084	0.1088
chr20	63025520	479600	0.0076	0.0933
chr21	48129895	335154	0.007	0.0889
chr22	51304566	214615	0.0042	0.0688
chrMT	16571	13468	0.8127	1.1842
chrX	155270560	945005	0.0061	0.0847
chrY	59373566	80547	0.0014	0.0406

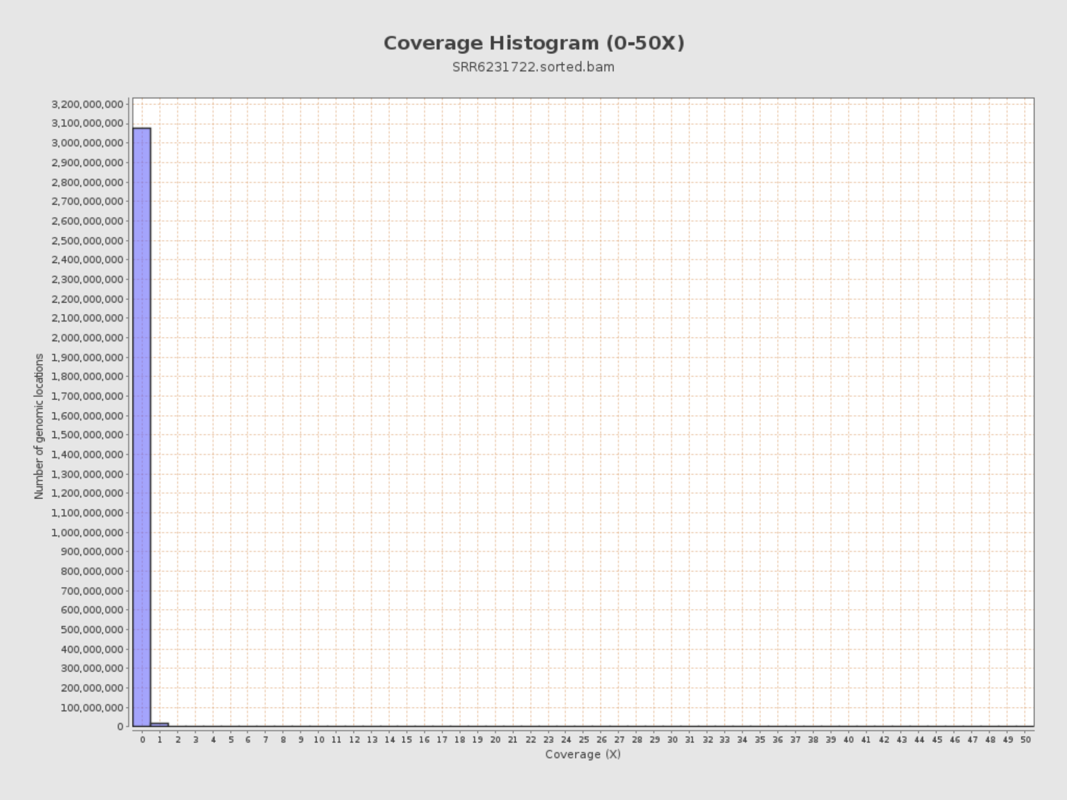
3. Results : Coverage across reference



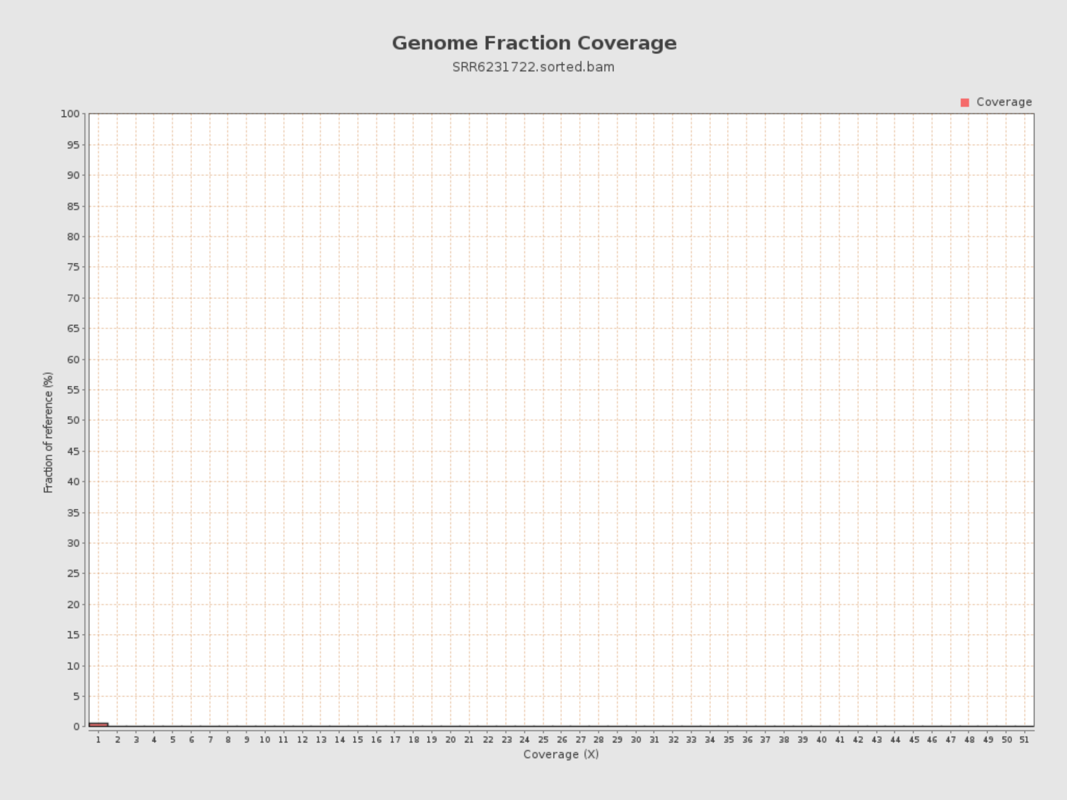
4. Results : Coverage Histogram



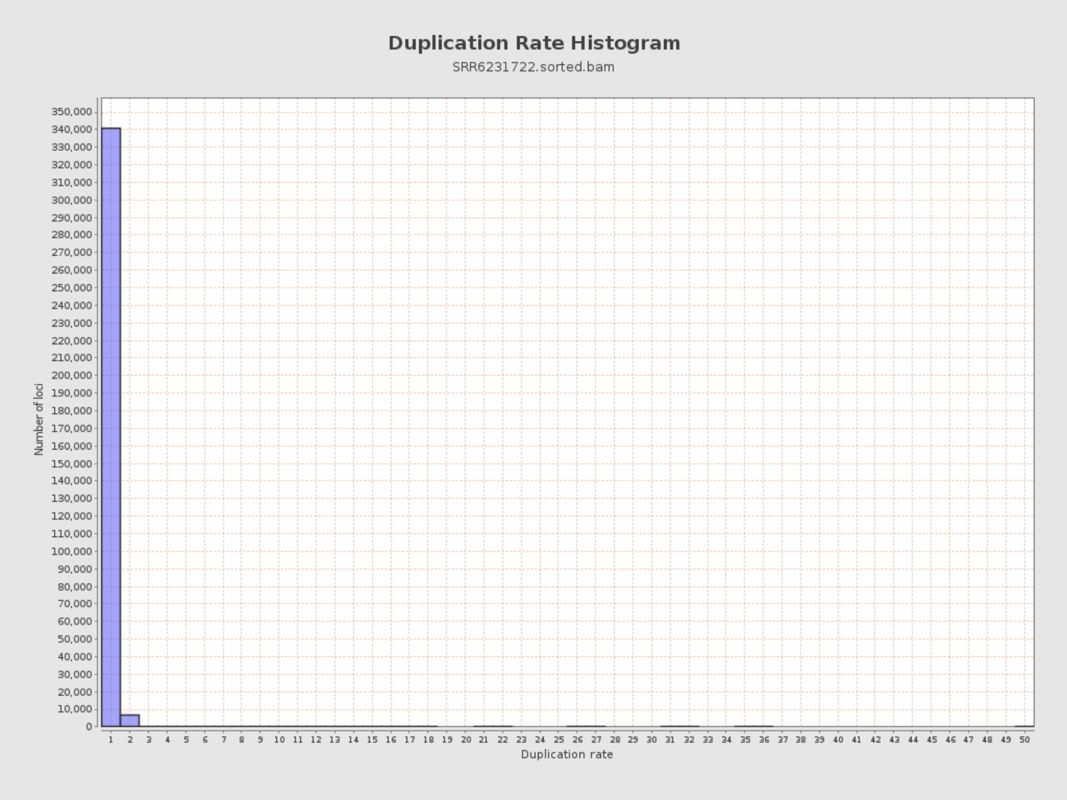
5. Results : Coverage Histogram (0-50X)



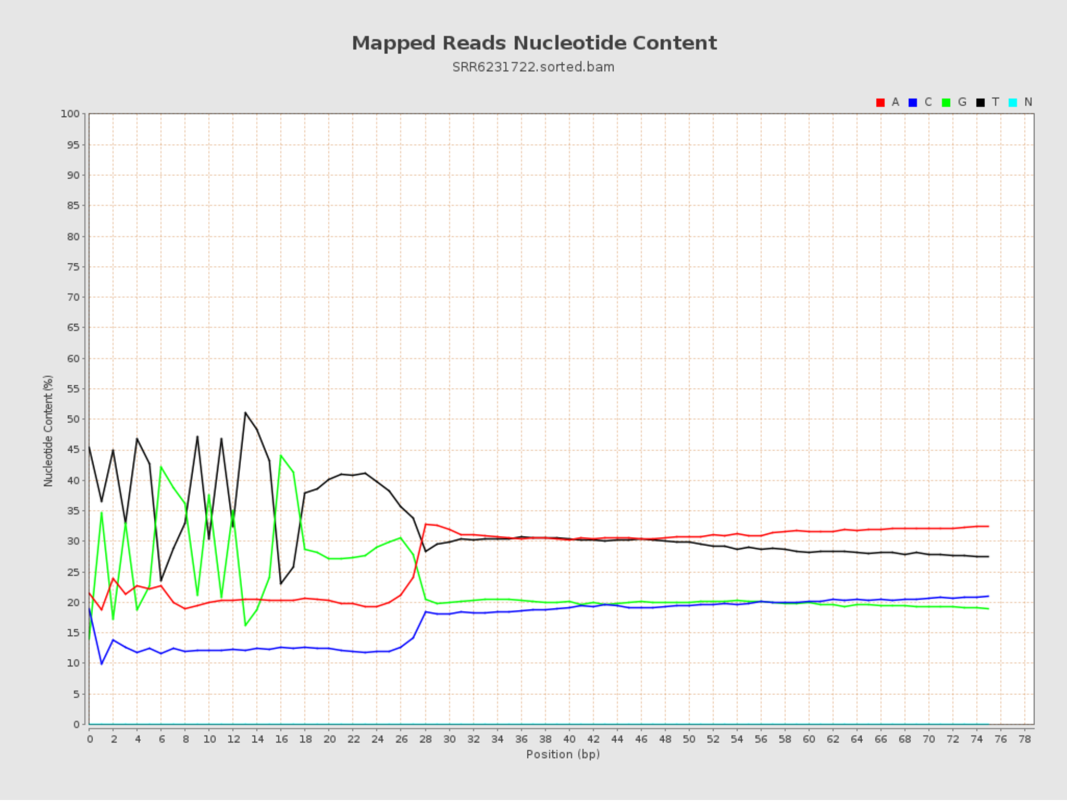
6. Results : Genome Fraction Coverage



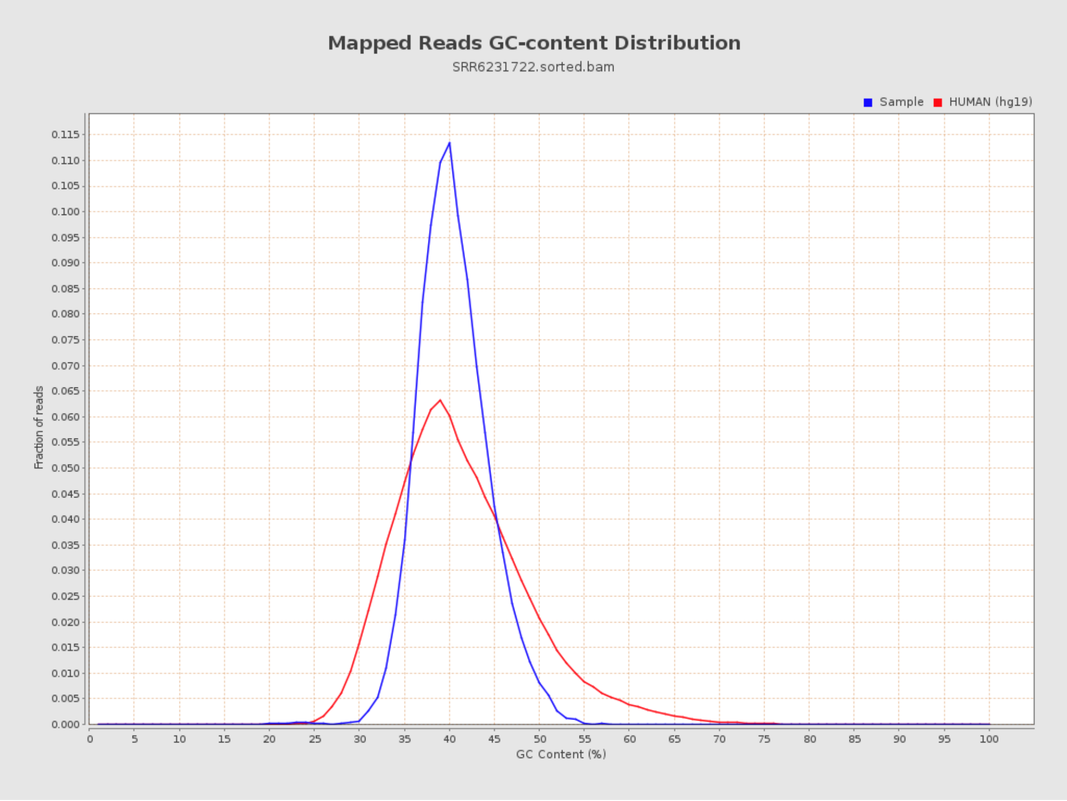
7. Results : Duplication Rate Histogram



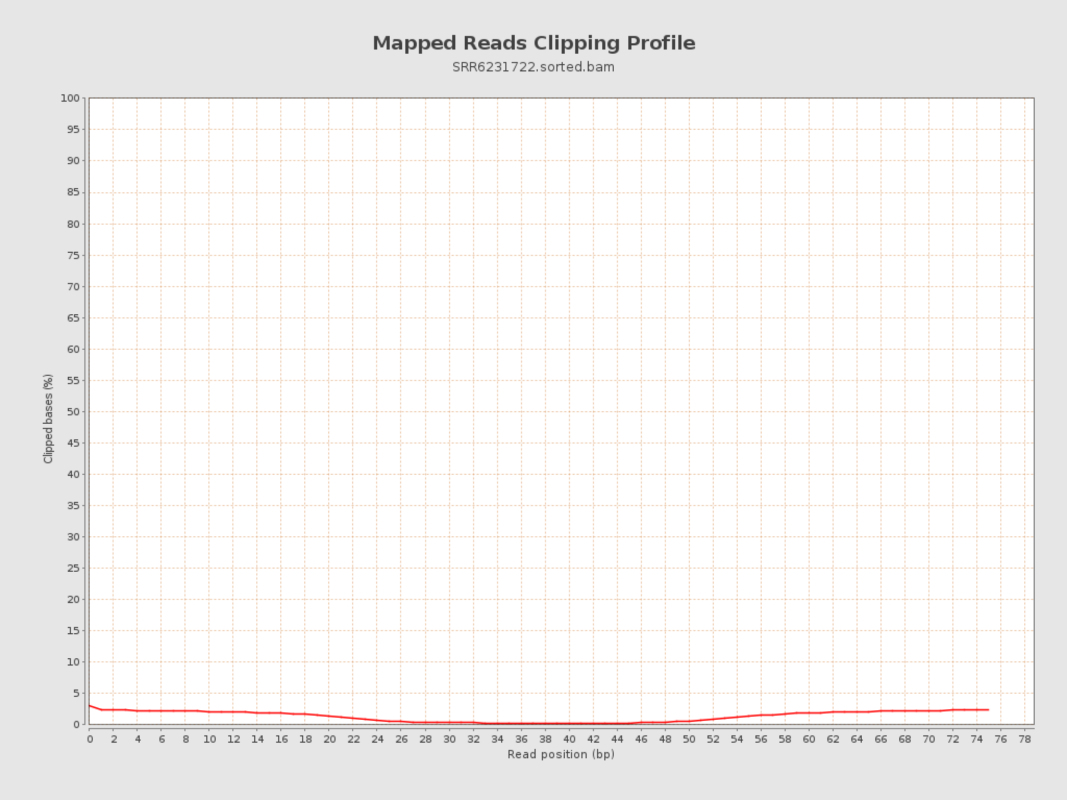
8. Results : Mapped Reads Nucleotide Content



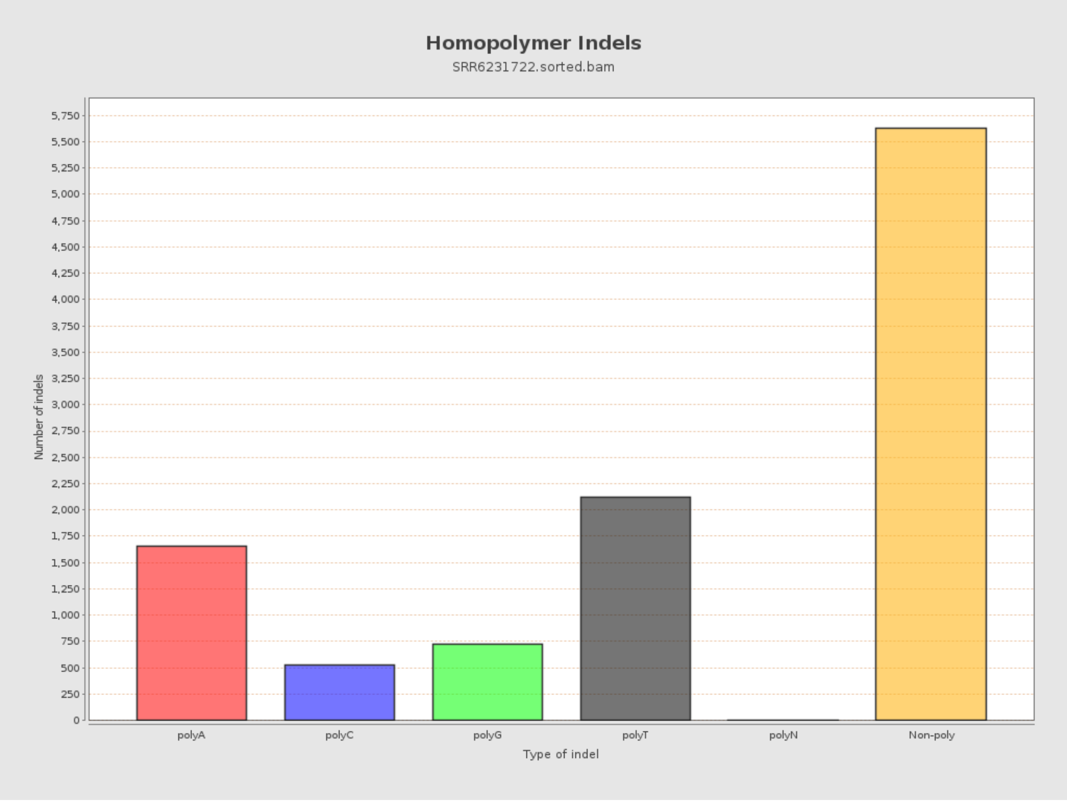
9. Results : Mapped Reads GC-content Distribution



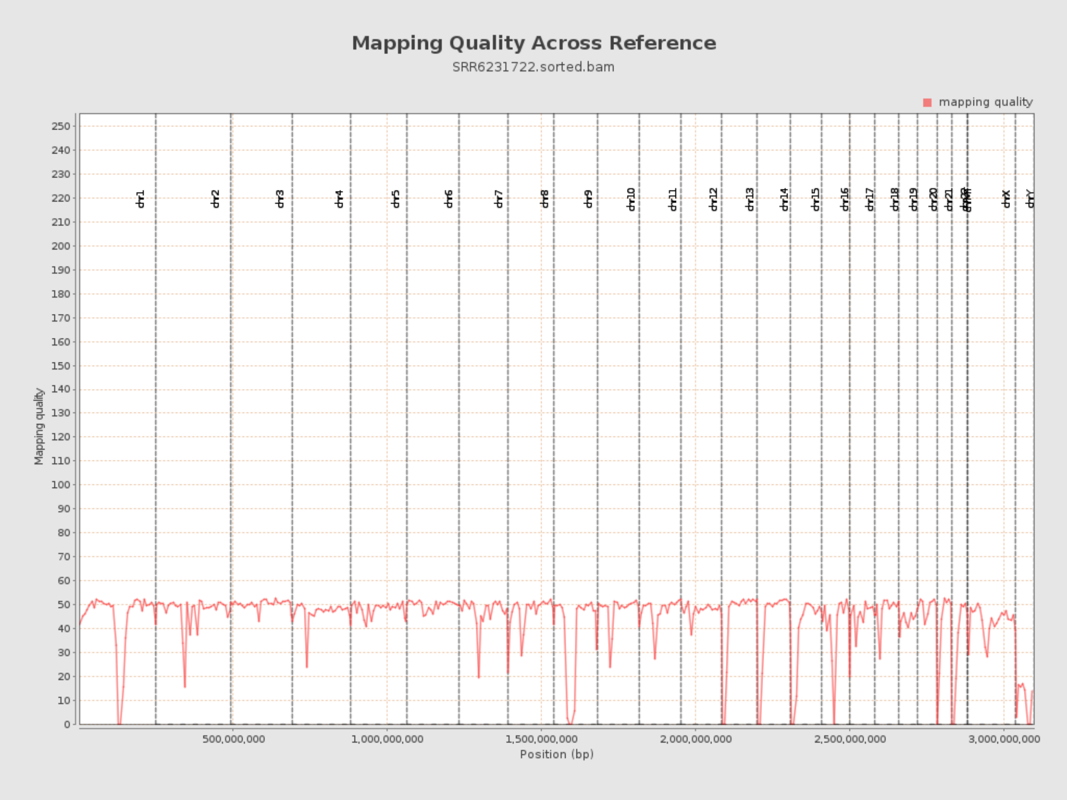
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram