Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:42:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231729.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_SRR6231729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231729.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:42:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,125,664
Mapped reads	4,700,602 / 91.71%
Unmapped reads	425,062 / 8.29%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	54,450 / 1.06%
Read min/max/mean length	30 / 76 / 76.37
Duplicated reads (estimated)	817,429 / 15.95%
Duplication rate	8.57%
Clipped reads	1,690,257 / 32.98%

2.2. ACGT Content

Number/percentage of A's	84,481,735 / 26.13%
Number/percentage of C's	59,216,254 / 18.31%
Number/percentage of T's	90,776,318 / 28.07%
Number/percentage of G's	88,821,055 / 27.47%
Number/percentage of N's	71,537 / 0.02%
GC Percentage	45.78%

2.3. Coverage

Mean	0.1045

Standard Deviation	45.6657

2.4. Mapping Quality

Mean Mapping Quality	46.24

2.5. Mismatches and indels

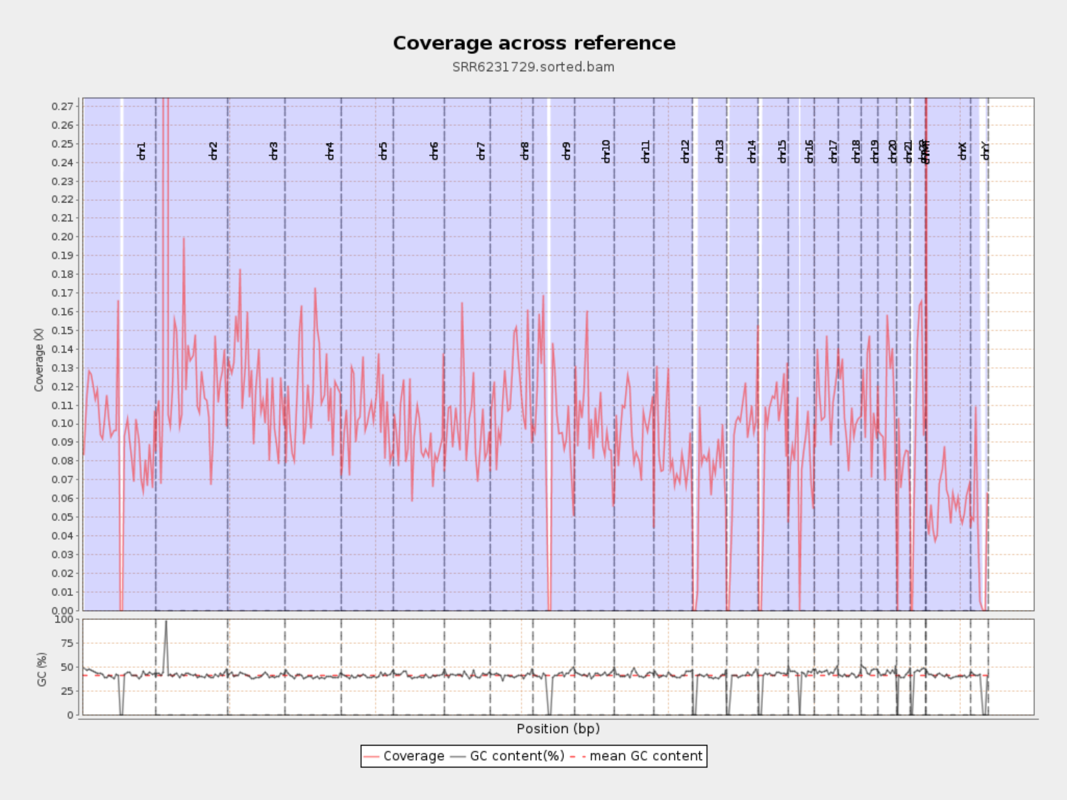
General error rate	0.64%
Mismatches	2,038,998
Insertions	22,237
Mapped reads with at least one insertion	0.47%
Deletions	67,795
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.48%

2.6. Chromosome stats

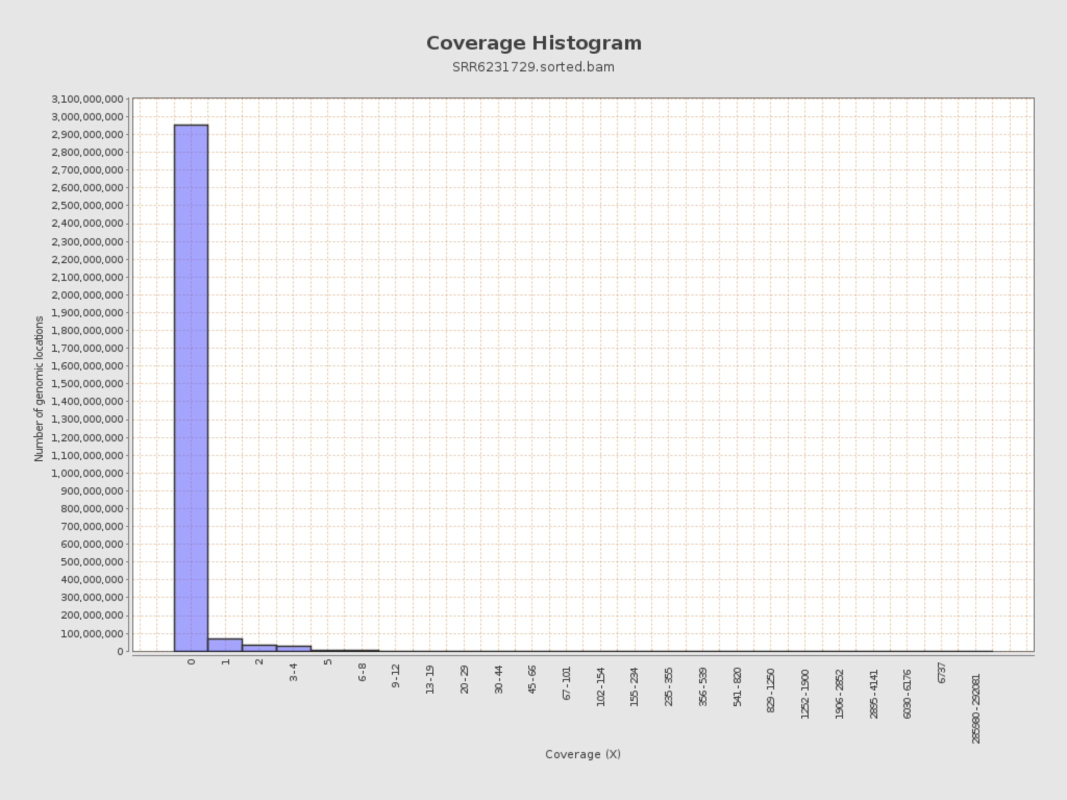
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	22867805	0.0917	1.9684
chr2	243199373	51499886	0.2118	162.8898
chr3	198022430	23796423	0.1202	0.6322
chr4	191154276	22310616	0.1167	0.6664
chr5	180915260	18744470	0.1036	0.5936
chr6	171115067	15706398	0.0918	0.6768
chr7	159138663	15832667	0.0995	1.0885

chr8	146364022	16936899	0.1157	1.4162
chr9	141213431	13767519	0.0975	0.8874
chr10	135534747	13619294	0.1005	0.8284
chr11	135006516	13111630	0.0971	1.0368
chr12	133851895	11474609	0.0857	0.5705
chr13	115169878	7826192	0.068	0.4668
chr14	107349540	9268321	0.0863	0.7128
chr15	102531392	9143627	0.0892	0.5482
chr16	90354753	6808589	0.0754	0.5798
chr17	81195210	9277266	0.1143	0.7074
chr18	78077248	8219887	0.1053	1.7266
chr19	59128983	6555748	0.1109	1.3641
chr20	63025520	6903600	0.1095	0.6452
chr21	48129895	3563997	0.074	0.6438
chr22	51304566	5094569	0.0993	0.637
chrMT	16571	38256	2.3086	3.2407
chrX	155270560	8745224	0.0563	0.5337
chrY	59373566	2364565	0.0398	0.4636

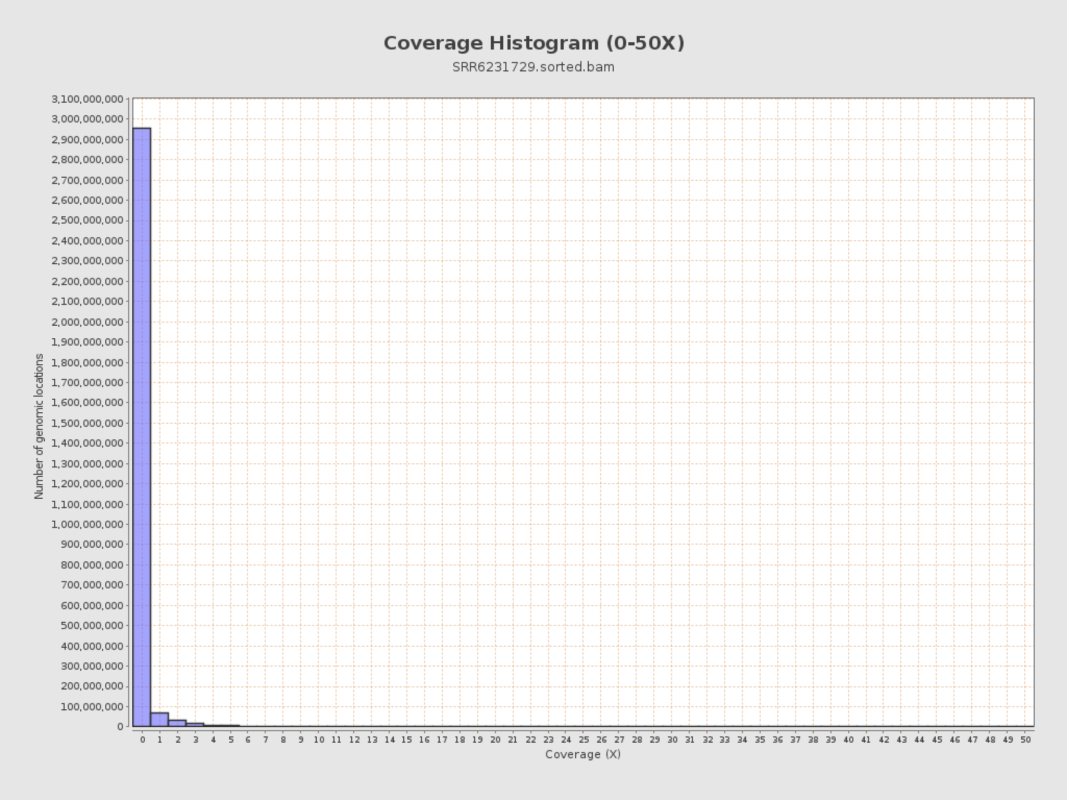
3. Results : Coverage across reference



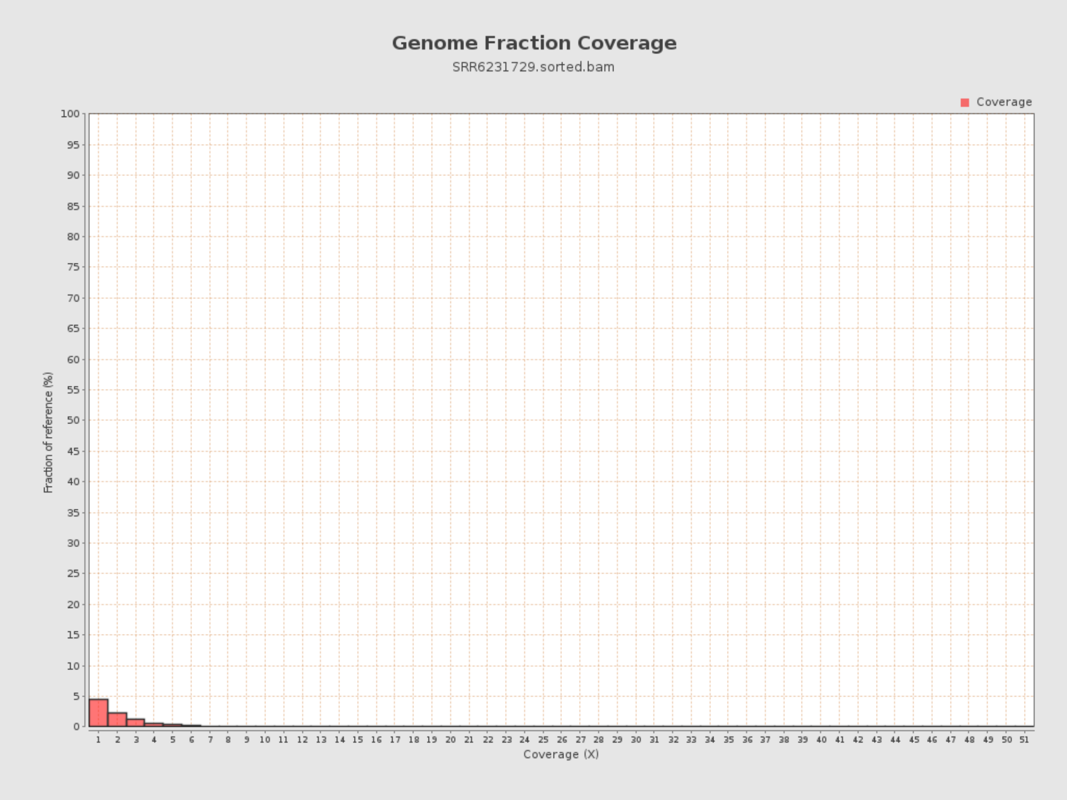
4. Results : Coverage Histogram



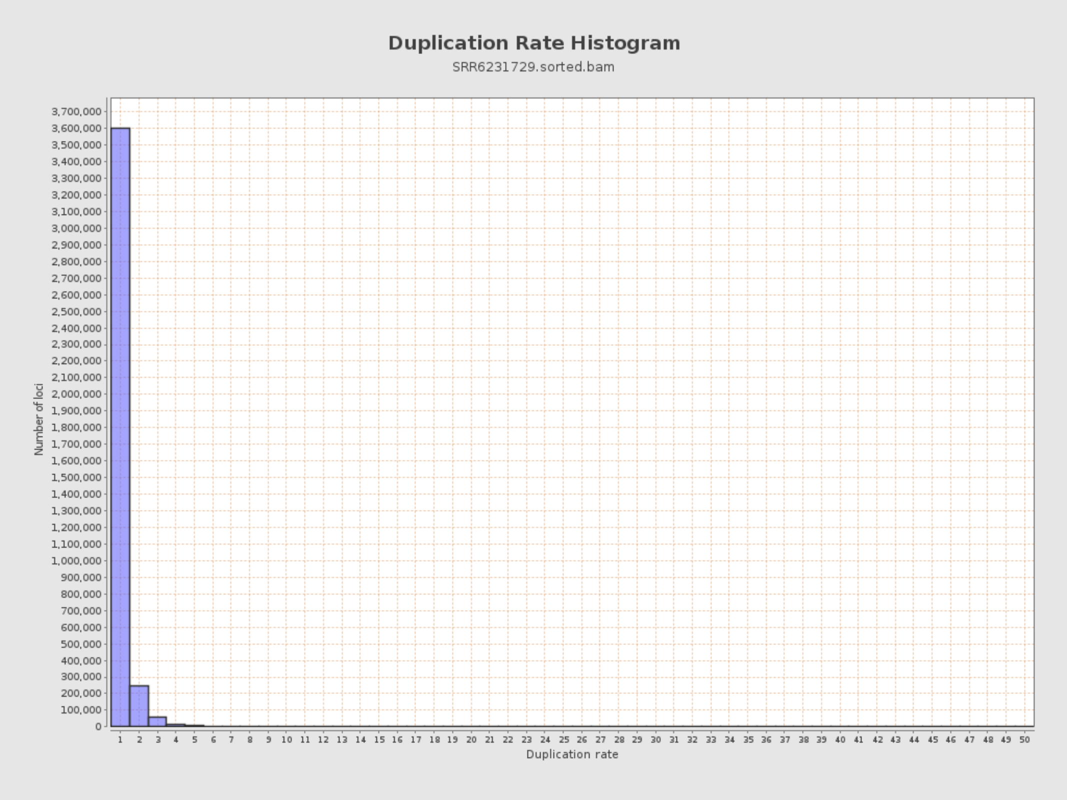
5. Results : Coverage Histogram (0-50X)



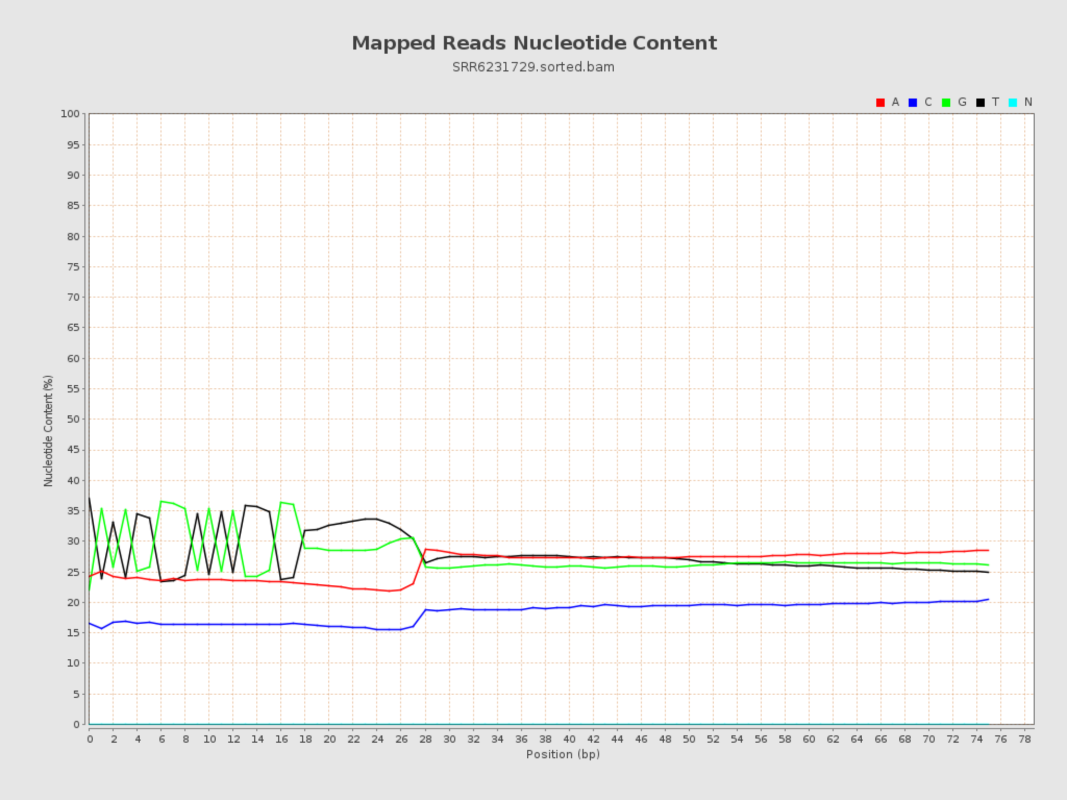
6. Results : Genome Fraction Coverage



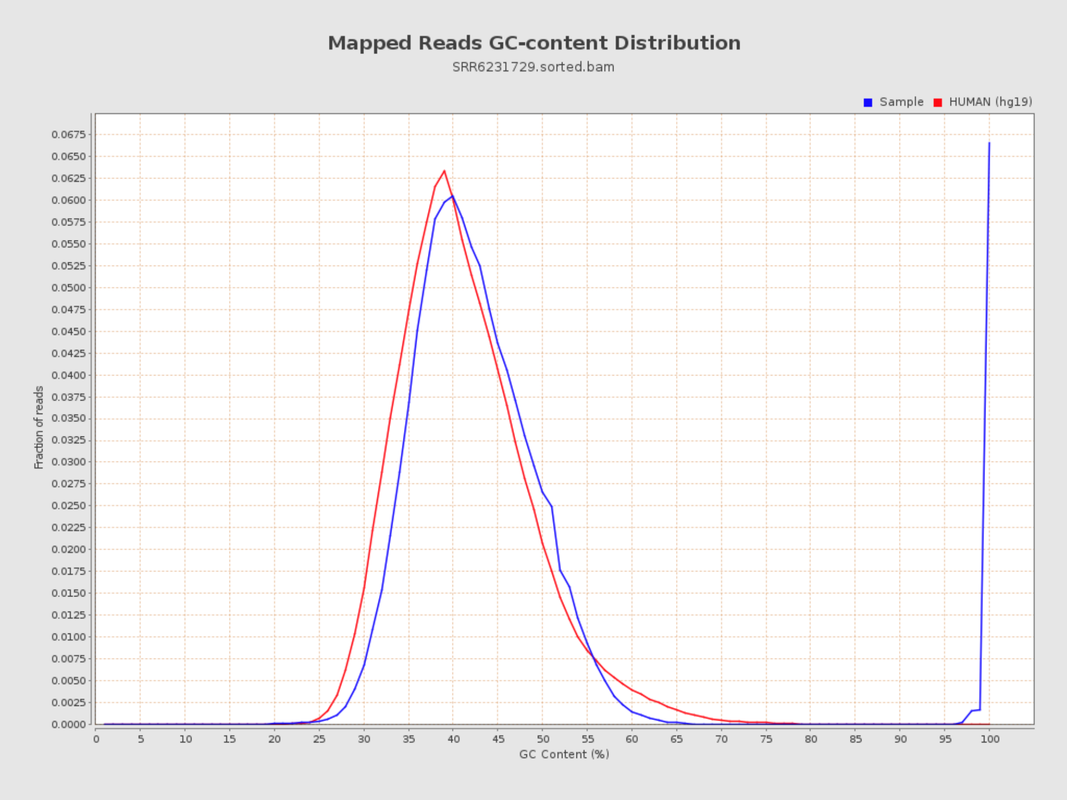
7. Results : Duplication Rate Histogram



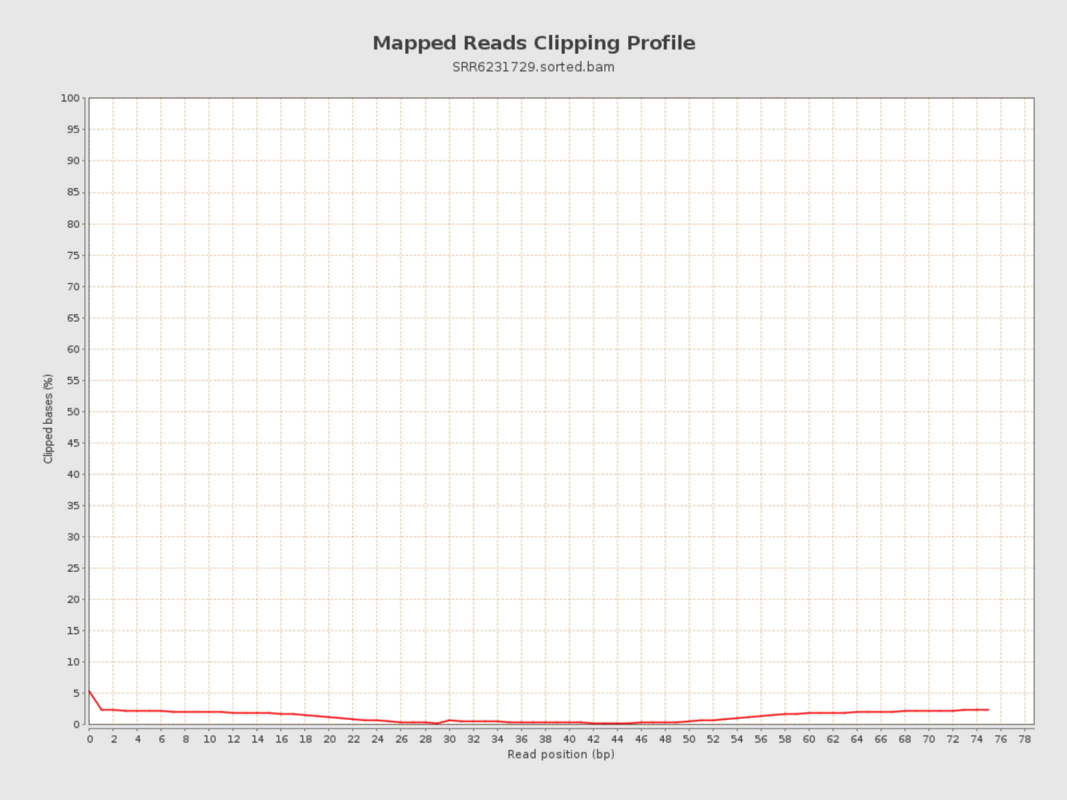
8. Results : Mapped Reads Nucleotide Content



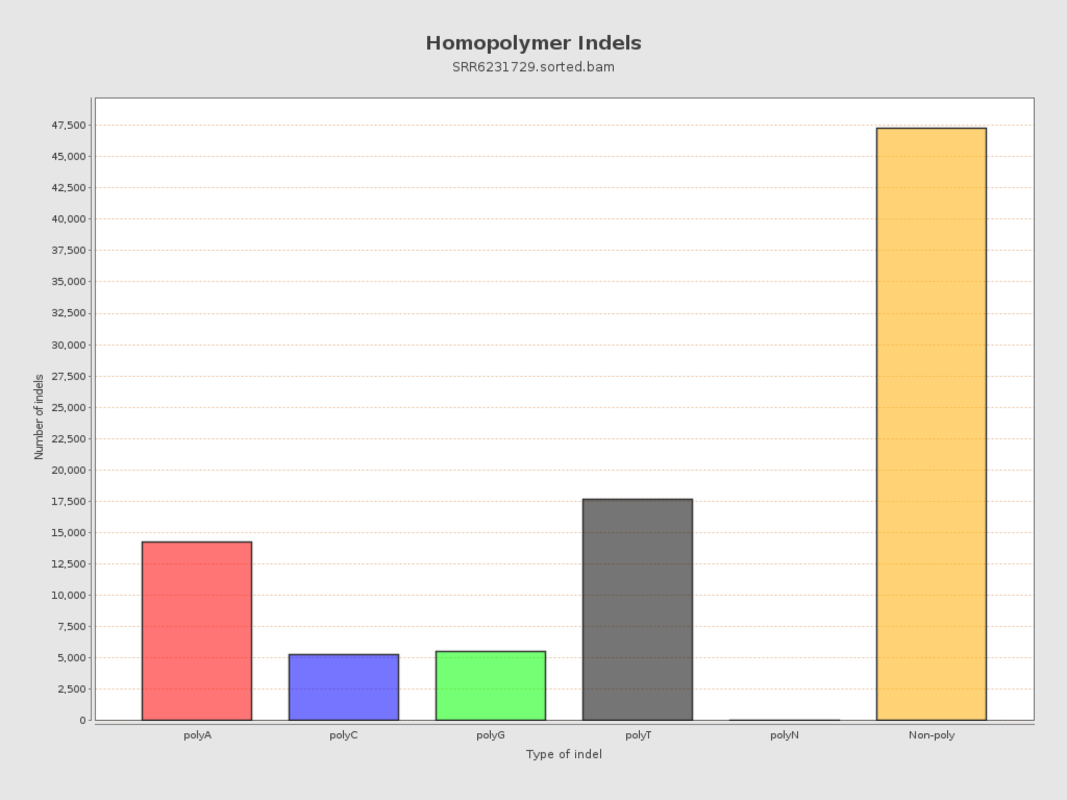
9. Results : Mapped Reads GC-content Distribution



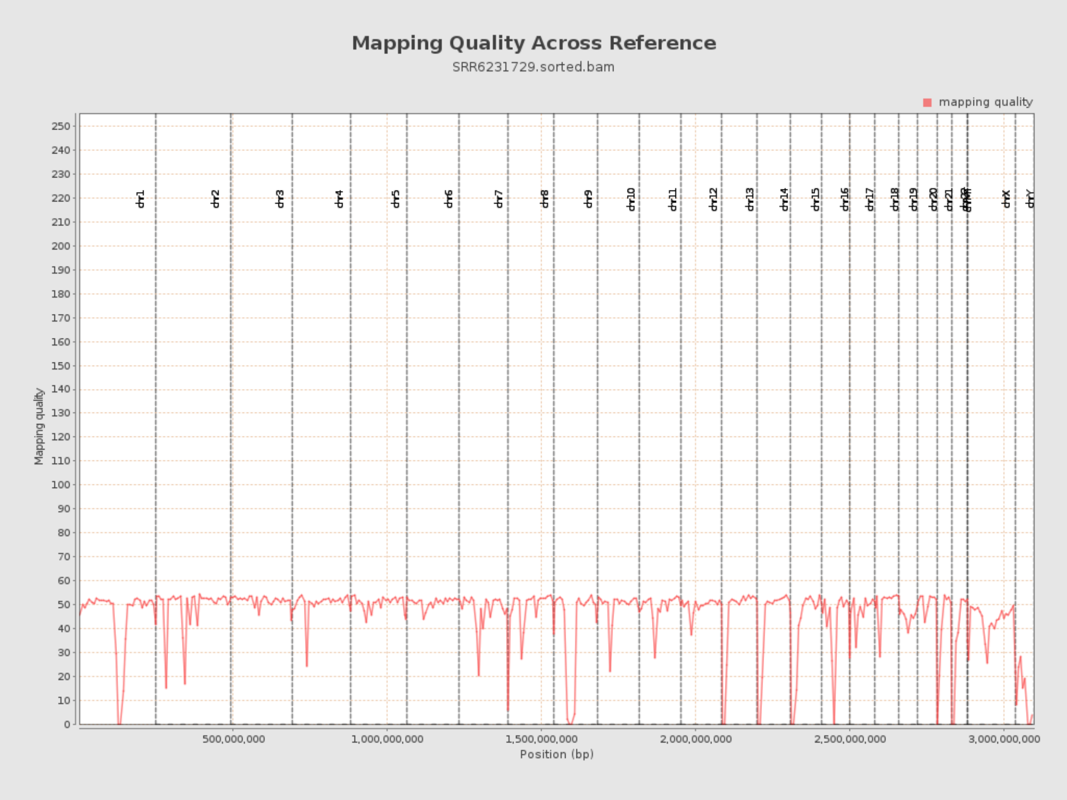
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram