Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 01:37:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231773.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_SRR6231773 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231773.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 01:37:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231773.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	542,498
Mapped reads	363,369 / 66.98%
Unmapped reads	179,129 / 33.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,117 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	9,283 / 1.71%
Duplication rate	2.18%
Clipped reads	153,215 / 28.24%

2.2. ACGT Content

Number/percentage of A's	7,041,860 / 28.92%
Number/percentage of C's	4,258,685 / 17.49%
Number/percentage of T's	7,930,992 / 32.57%
Number/percentage of G's	5,114,454 / 21.01%
Number/percentage of N's	1,281 / 0.01%
GC Percentage	38.5%

2.3. Coverage

Mean	0.0079

Standard Deviation	0.1122

2.4. Mapping Quality

Mean Mapping Quality	47.31

2.5. Mismatches and indels

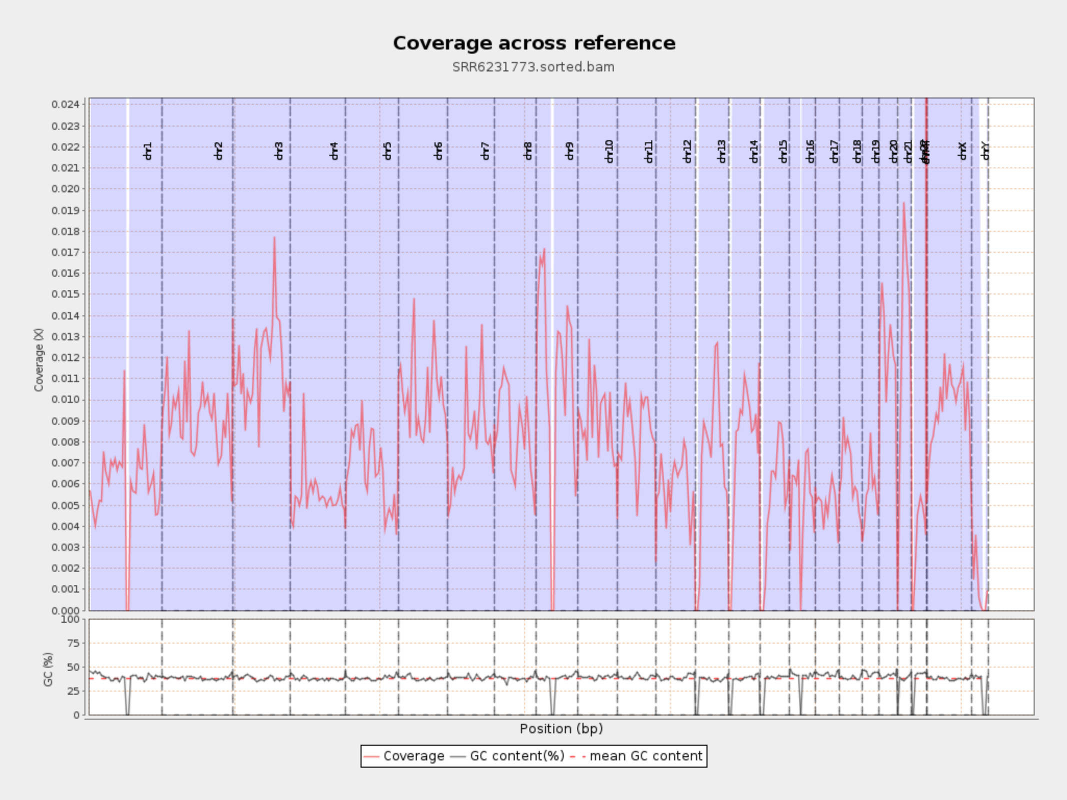
General error rate	0.89%
Mismatches	211,762
Insertions	2,244
Mapped reads with at least one insertion	0.61%
Deletions	7,876
Mapped reads with at least one deletion	2.13%
Homopolymer indels	45.66%

2.6. Chromosome stats

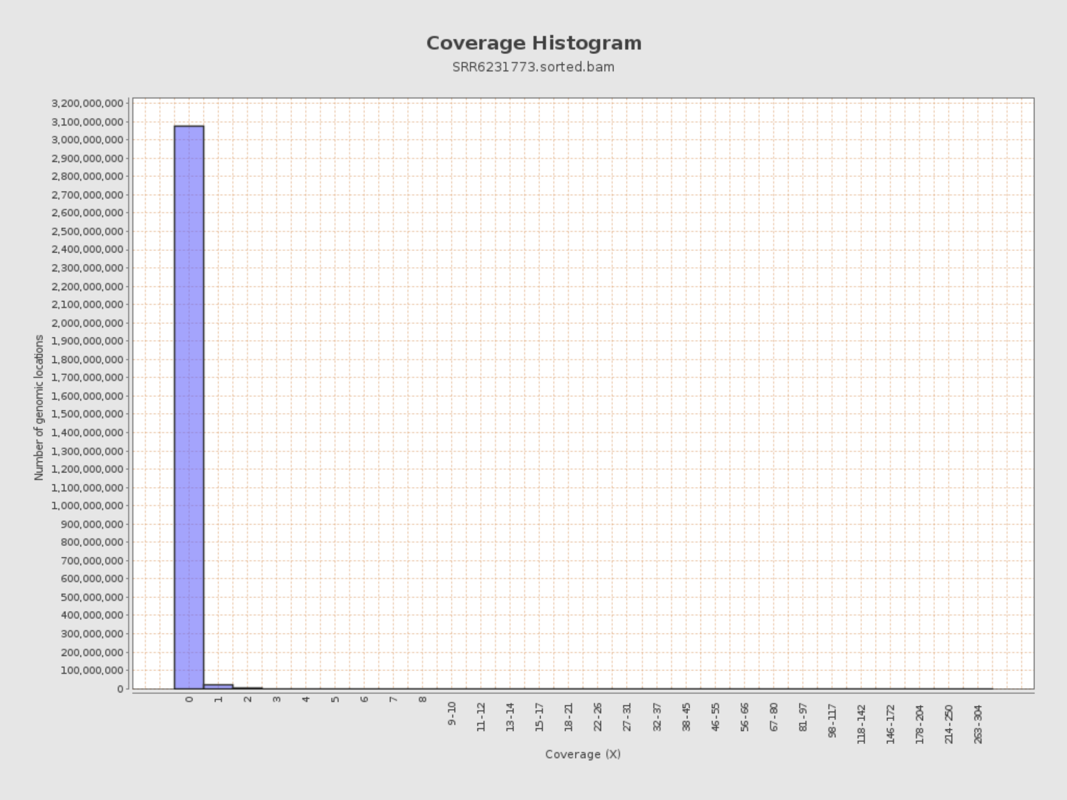
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1487046	0.006	0.1365
chr2	243199373	2254037	0.0093	0.1169
chr3	198022430	2330309	0.0118	0.1145
chr4	191154276	1047680	0.0055	0.0814
chr5	180915260	1219632	0.0067	0.0871
chr6	171115067	1757358	0.0103	0.1131
chr7	159138663	1271765	0.008	0.1113

chr8	146364022	1231184	0.0084	0.2056
chr9	141213431	1566416	0.0111	0.1204
chr10	135534747	1228200	0.0091	0.1091
chr11	135006516	1143956	0.0085	0.1039
chr12	133851895	796430	0.006	0.083
chr13	115169878	808300	0.007	0.0886
chr14	107349540	821592	0.0077	0.0938
chr15	102531392	531850	0.0052	0.0774
chr16	90354753	476270	0.0053	0.0782
chr17	81195210	404487	0.005	0.0768
chr18	78077248	507706	0.0065	0.1459
chr19	59128983	333616	0.0056	0.0965
chr20	63025520	780916	0.0124	0.119
chr21	48129895	598920	0.0124	0.12
chr22	51304566	172667	0.0034	0.061
chrMT	16571	19908	1.2014	1.2899
chrX	155270560	1501682	0.0097	0.1059
chrY	59373566	69005	0.0012	0.0426

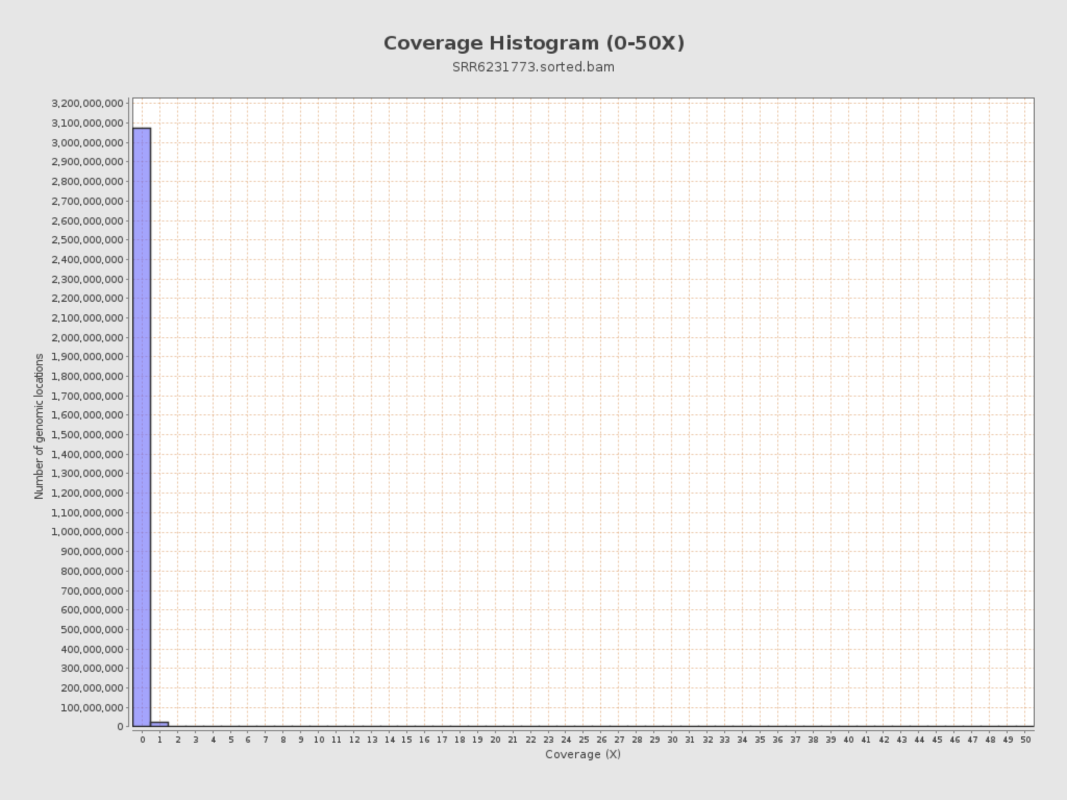
3. Results : Coverage across reference



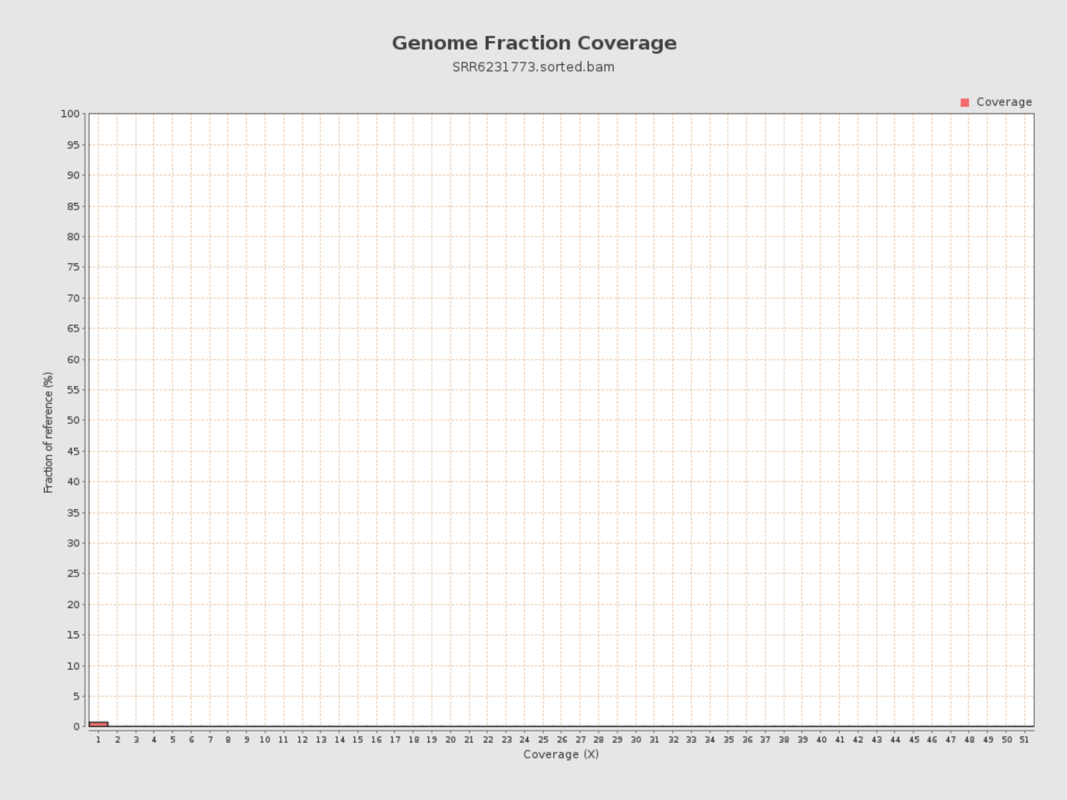
4. Results : Coverage Histogram



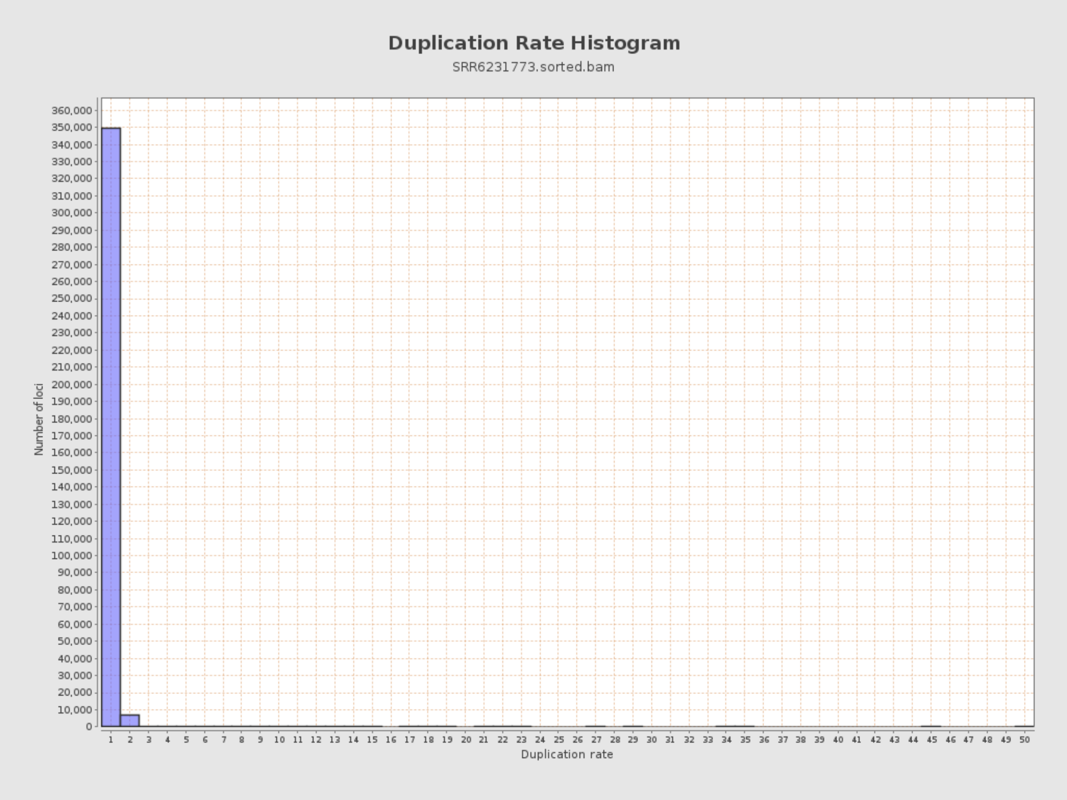
5. Results : Coverage Histogram (0-50X)



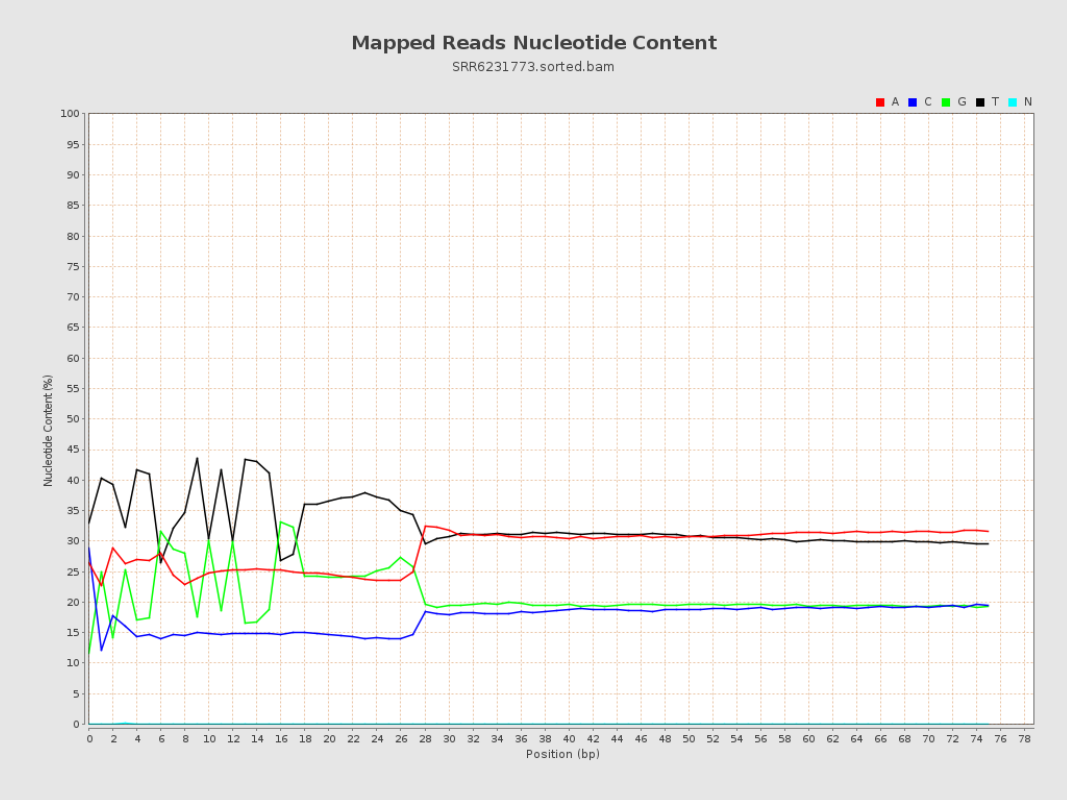
6. Results : Genome Fraction Coverage



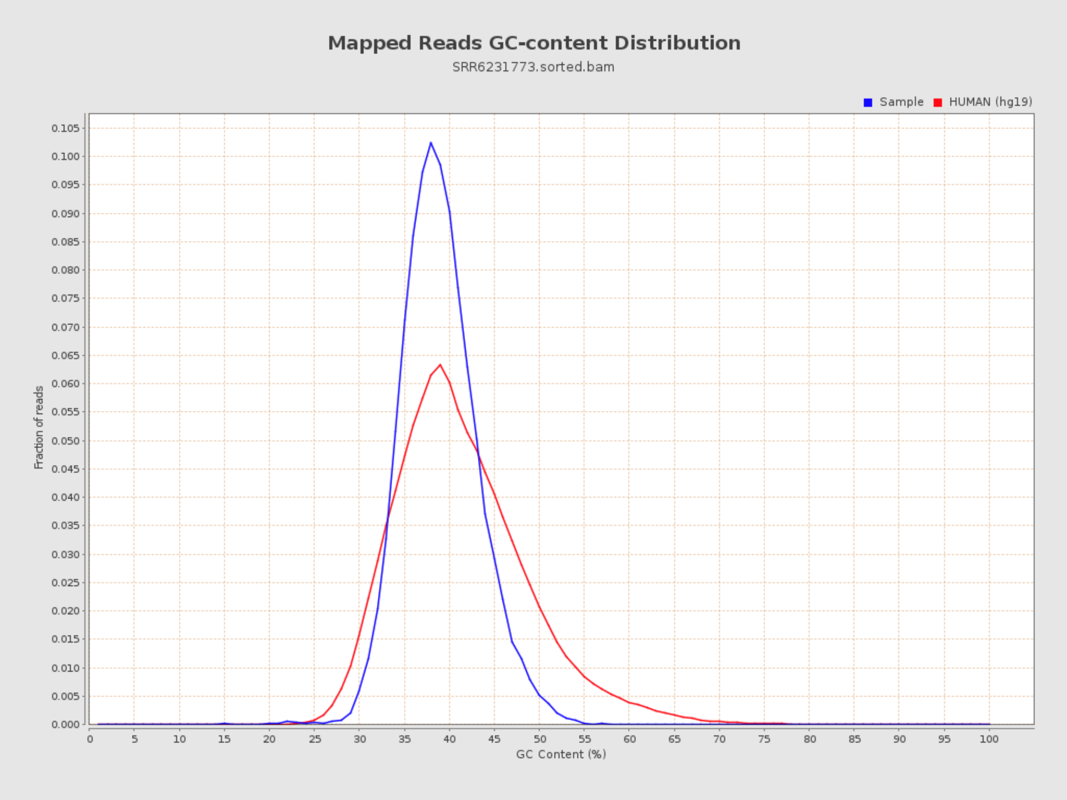
7. Results : Duplication Rate Histogram



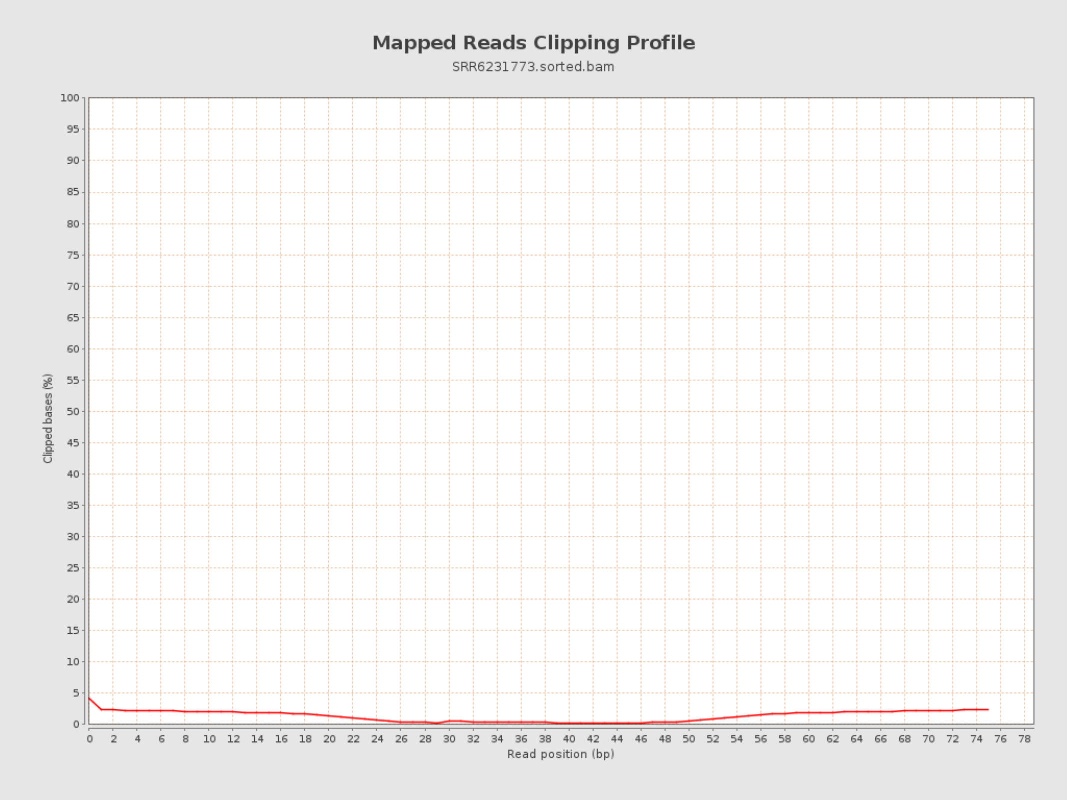
8. Results : Mapped Reads Nucleotide Content



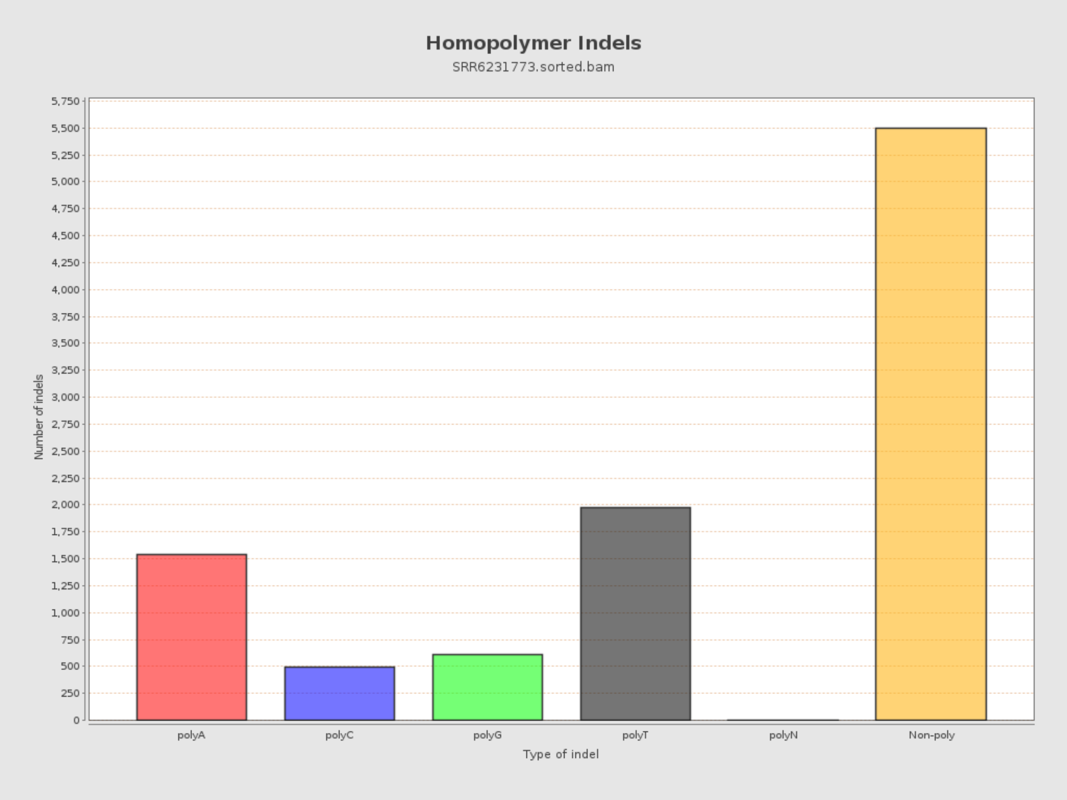
9. Results : Mapped Reads GC-content Distribution



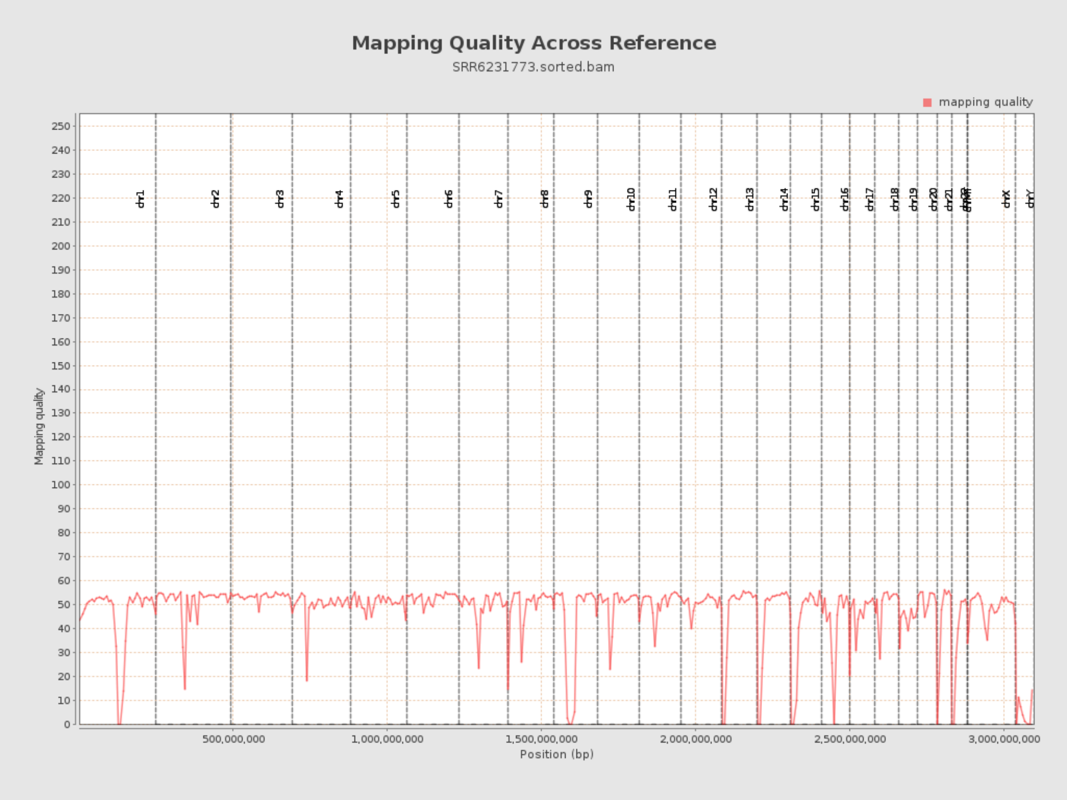
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram