

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 22:12:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231721.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_SRR6231721 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231721.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 22:12:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231721.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,355,059
Mapped reads	878,766 / 64.85%
Unmapped reads	476,293 / 35.15%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,377 / 0.25%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	43,376 / 3.2%
Duplication rate	4.12%
Clipped reads	625,147 / 46.13%

2.2. ACGT Content

Number/percentage of A's	13,582,214 / 25.56%
Number/percentage of C's	9,543,797 / 17.96%
Number/percentage of T's	16,847,923 / 31.71%
Number/percentage of G's	13,148,324 / 24.75%
Number/percentage of N's	8,303 / 0.02%
GC Percentage	42.71%

2.3. Coverage

Mean	0.0172

Standard Deviation	0.1849
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2.4. Mapping Quality

Mean Mapping Quality	42.54
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2.5. Mismatches and indels

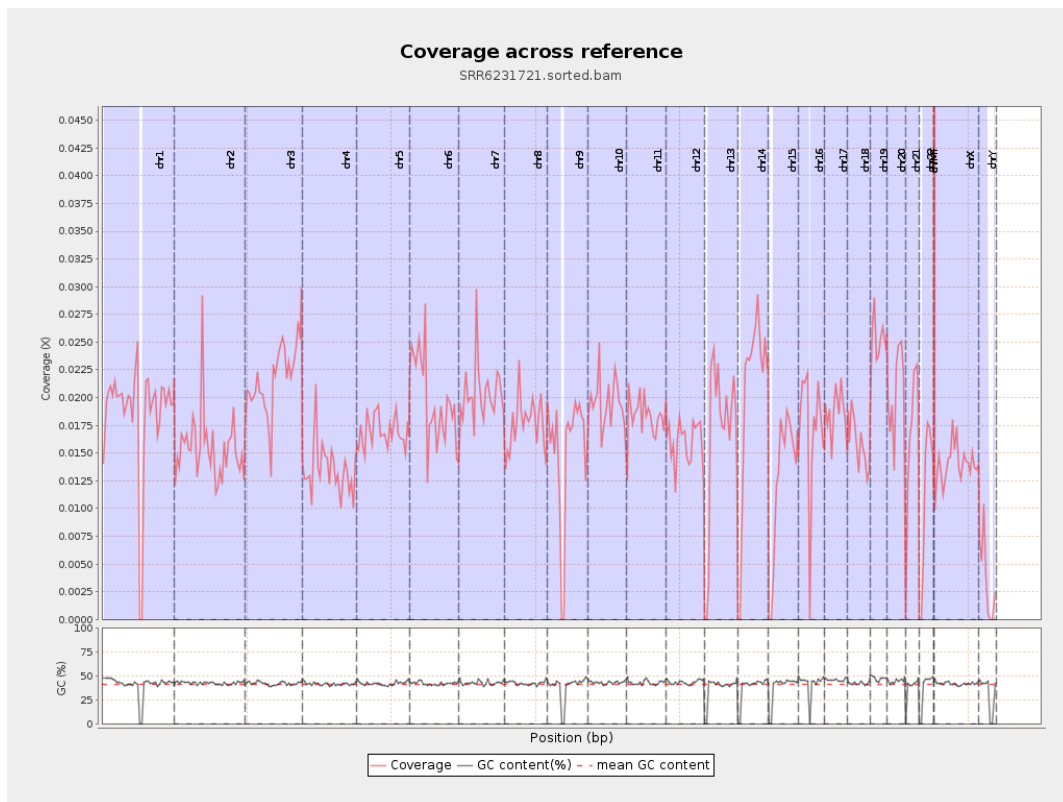
General error rate	0.95%
Mismatches	494,056
Insertions	4,402
Mapped reads with at least one insertion	0.5%
Deletions	21,262
Mapped reads with at least one deletion	2.38%
Homopolymer indels	46.24%

2.6. Chromosome stats

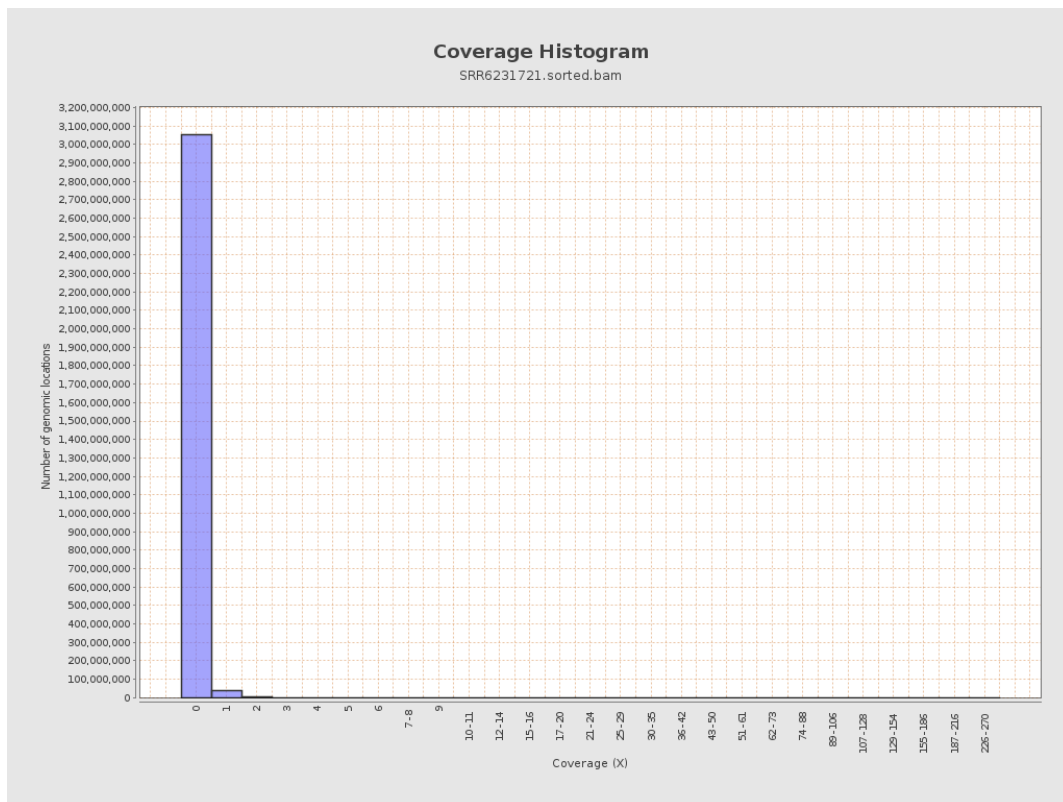
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4623141	0.0185	0.242
chr2	243199373	3761948	0.0155	0.2077
chr3	198022430	4294483	0.0217	0.1703
chr4	191154276	2585385	0.0135	0.1405
chr5	180915260	3074906	0.017	0.1531
chr6	171115067	3366049	0.0197	0.19
chr7	159138663	3234741	0.0203	0.2529

chr8	146364022	2573802	0.0176	0.1945
chr9	141213431	2140586	0.0152	0.1742
chr10	135534747	2636511	0.0195	0.1793
chr11	135006516	2489182	0.0184	0.1943
chr12	133851895	2135692	0.016	0.1472
chr13	115169878	1909885	0.0166	0.1646
chr14	107349540	2177092	0.0203	0.1714
chr15	102531392	1306979	0.0127	0.1381
chr16	90354753	1545562	0.0171	0.1569
chr17	81195210	1512035	0.0186	0.1691
chr18	78077248	1231447	0.0158	0.2527
chr19	59128983	1491769	0.0252	0.2248
chr20	63025520	1271781	0.0202	0.1745
chr21	48129895	806159	0.0167	0.1536
chr22	51304566	566516	0.011	0.1206
chrMT	16571	40887	2.4674	3.3001
chrX	155270560	2179980	0.014	0.145
chrY	59373566	211532	0.0036	0.0752

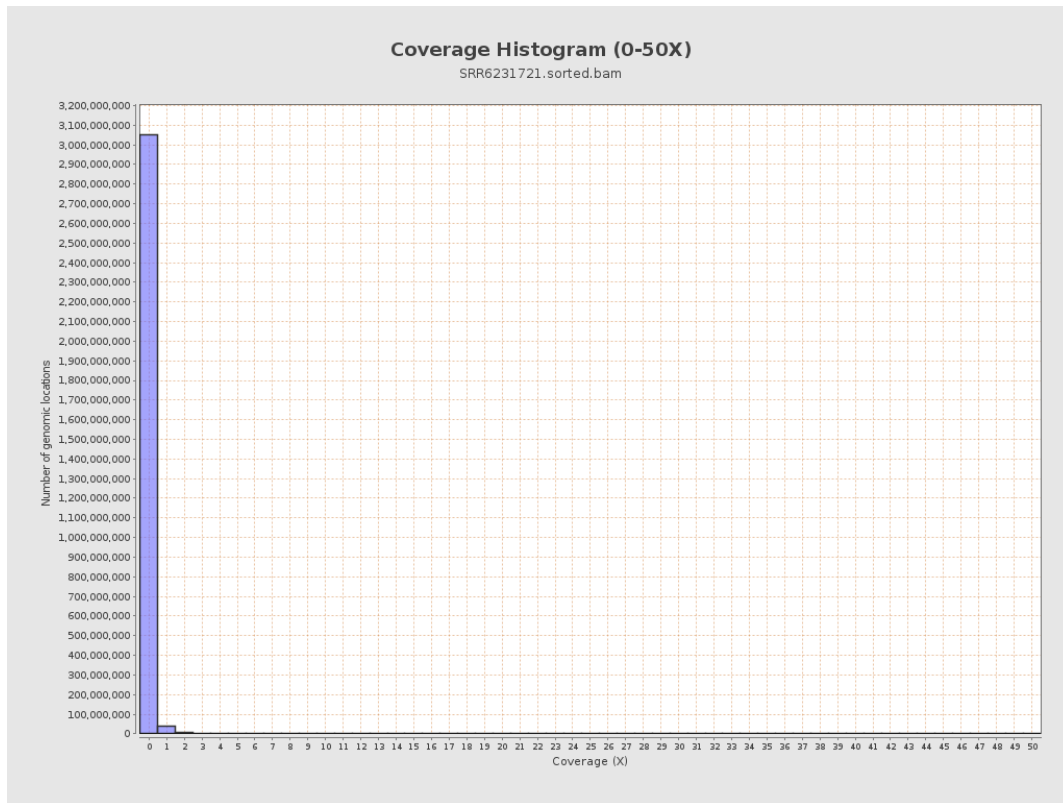
3. Results : Coverage across reference



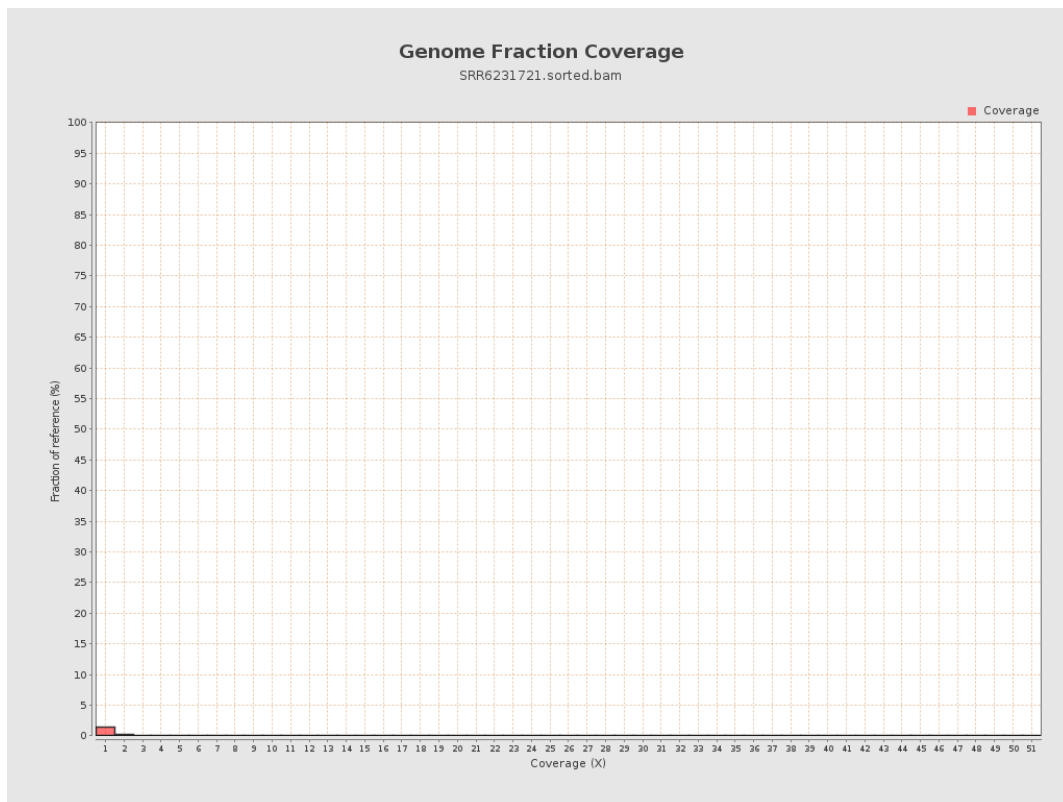
4. Results : Coverage Histogram



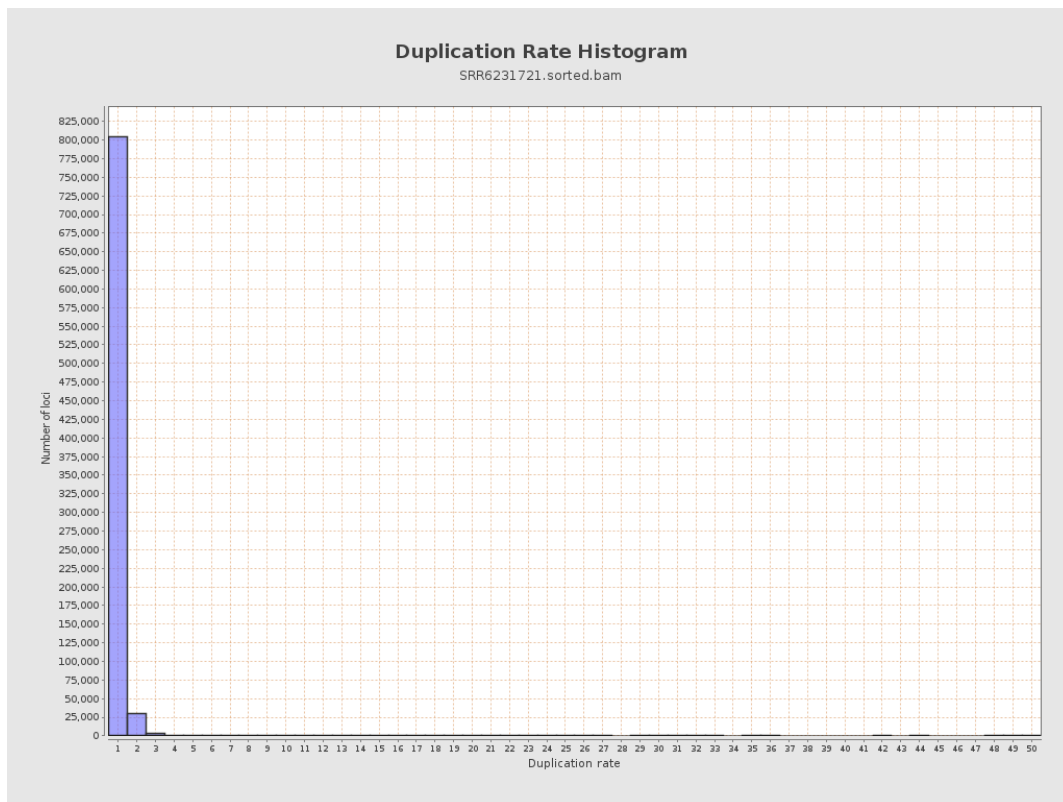
5. Results : Coverage Histogram (0-50X)



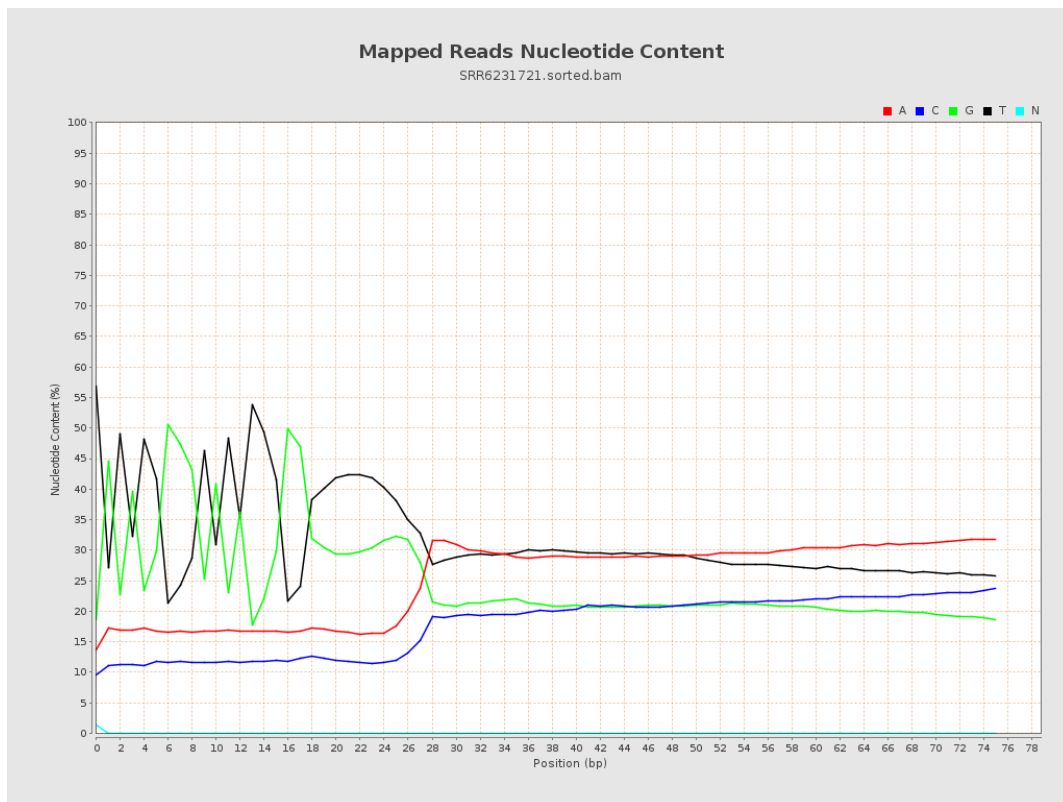
6. Results : Genome Fraction Coverage



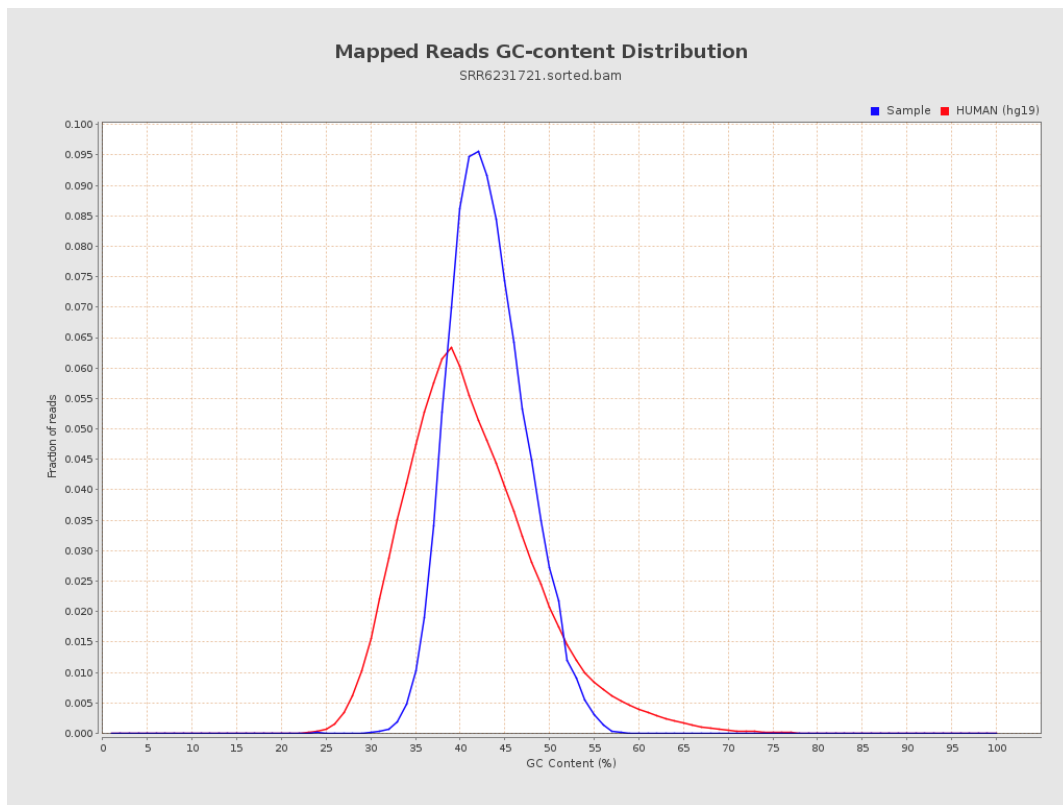
7. Results : Duplication Rate Histogram



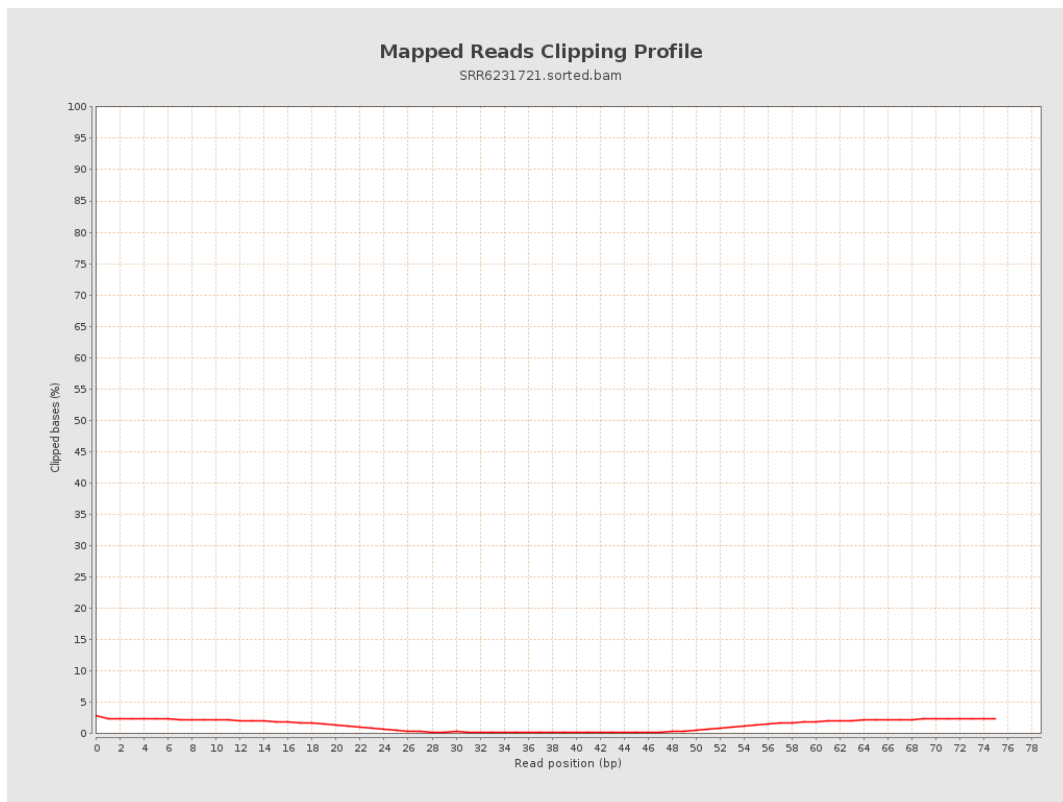
8. Results : Mapped Reads Nucleotide Content



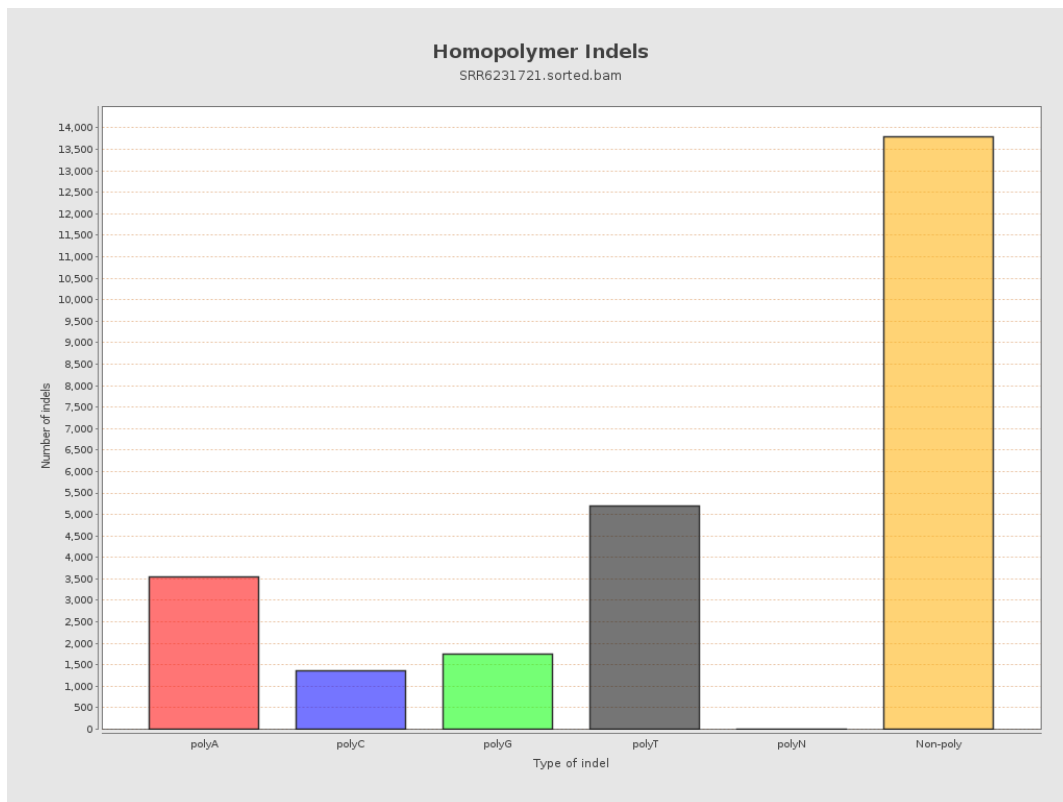
9. Results : Mapped Reads GC-content Distribution



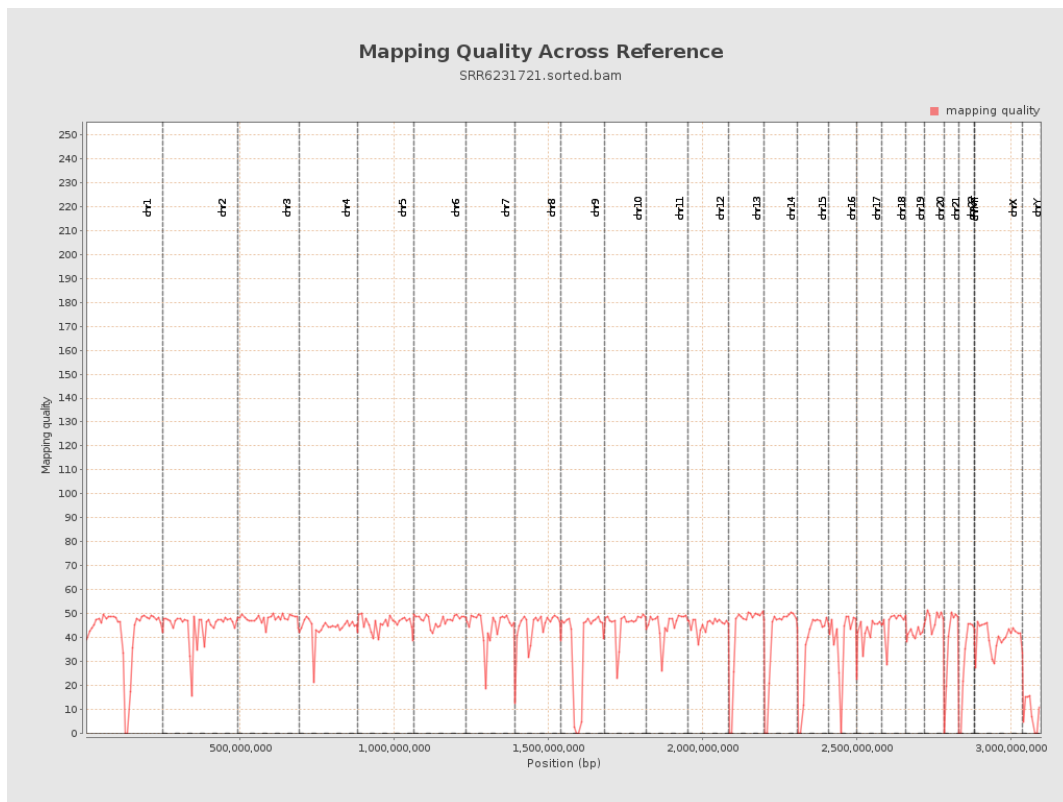
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

