

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:20:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716731.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_SRR9716731 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716731.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:20:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716731.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,668,712
Mapped reads	1,500,209 / 89.9%
Unmapped reads	168,503 / 10.1%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,760 / 0.52%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	58,248 / 3.49%
Duplication rate	2.81%
Clipped reads	1,504,308 / 90.15%

2.2. ACGT Content

Number/percentage of A's	21,425,773 / 24.59%
Number/percentage of C's	18,102,472 / 20.77%
Number/percentage of T's	27,526,911 / 31.59%
Number/percentage of G's	20,081,144 / 23.05%
Number/percentage of N's	1,160 / 0%
GC Percentage	43.82%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2826
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2.4. Mapping Quality

Mean Mapping Quality	44.3
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2.5. Mismatches and indels

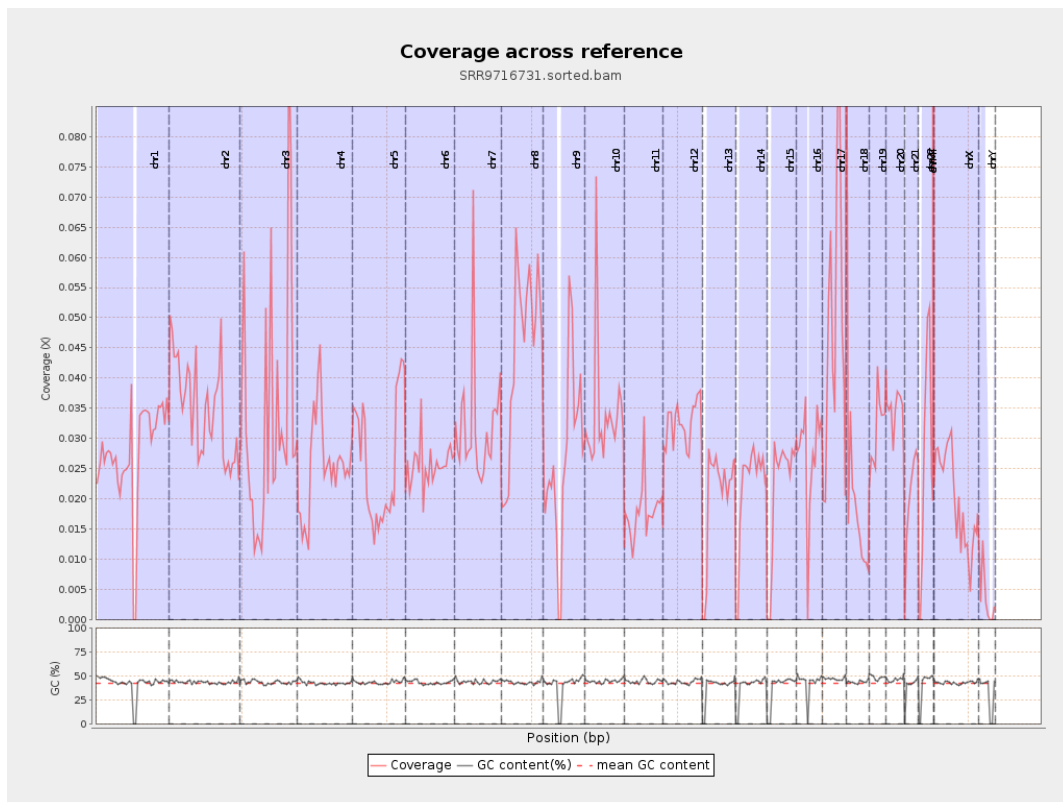
General error rate	0.52%
Mismatches	439,473
Insertions	5,762
Mapped reads with at least one insertion	0.38%
Deletions	16,433
Mapped reads with at least one deletion	1.09%
Homopolymer indels	41.51%

2.6. Chromosome stats

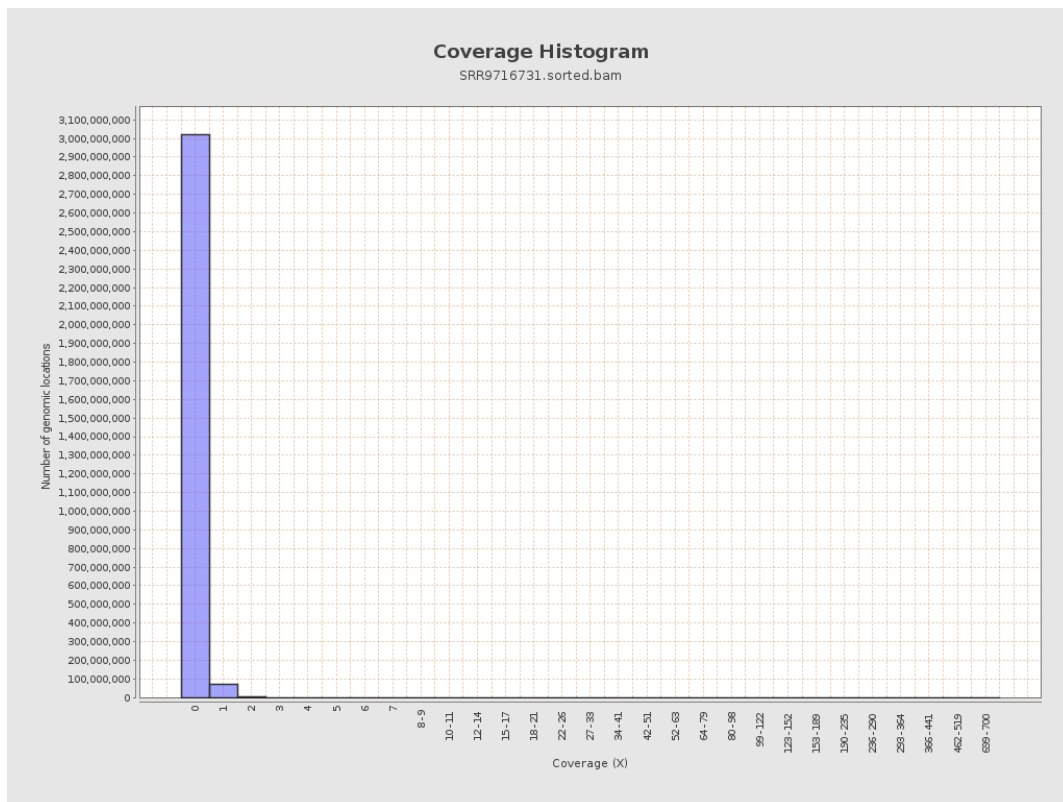
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6878480	0.0276	0.4036
chr2	243199373	8536135	0.0351	0.362
chr3	198022430	6490431	0.0328	0.2112
chr4	191154276	4840980	0.0253	0.1978
chr5	180915260	4682202	0.0259	0.1755
chr6	171115067	4358675	0.0255	0.1899
chr7	159138663	5077072	0.0319	0.5913

chr8	146364022	6522212	0.0446	0.2957
chr9	141213431	3753726	0.0266	0.2029
chr10	135534747	4577796	0.0338	0.3842
chr11	135006516	2399070	0.0178	0.1746
chr12	133851895	4337806	0.0324	0.2133
chr13	115169878	2351947	0.0204	0.1544
chr14	107349540	2338496	0.0218	0.163
chr15	102531392	2238682	0.0218	0.1634
chr16	90354753	2464036	0.0273	0.1918
chr17	81195210	3915798	0.0482	0.2478
chr18	78077248	1667297	0.0214	0.2961
chr19	59128983	1878267	0.0318	0.3495
chr20	63025520	2173435	0.0345	0.2145
chr21	48129895	973326	0.0202	0.166
chr22	51304566	1346644	0.0262	0.1772
chrMT	16571	23336	1.4082	1.4692
chrX	155270560	3120111	0.0201	0.1756
chrY	59373566	217720	0.0037	0.1112

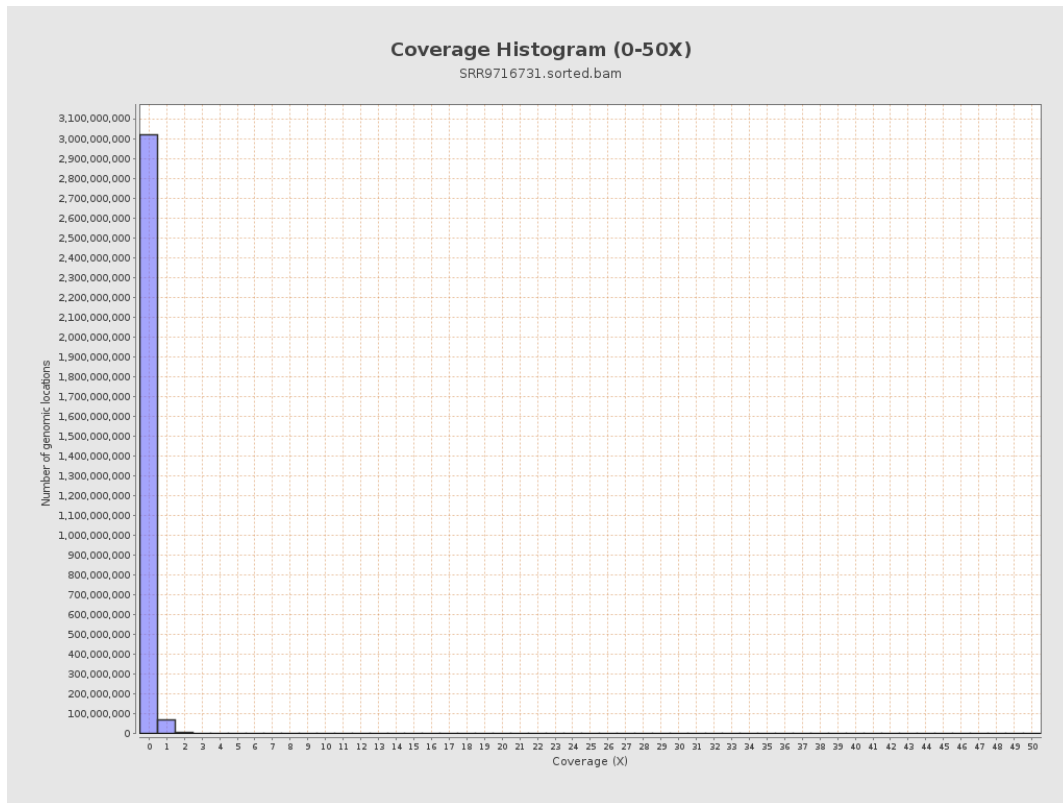
3. Results : Coverage across reference



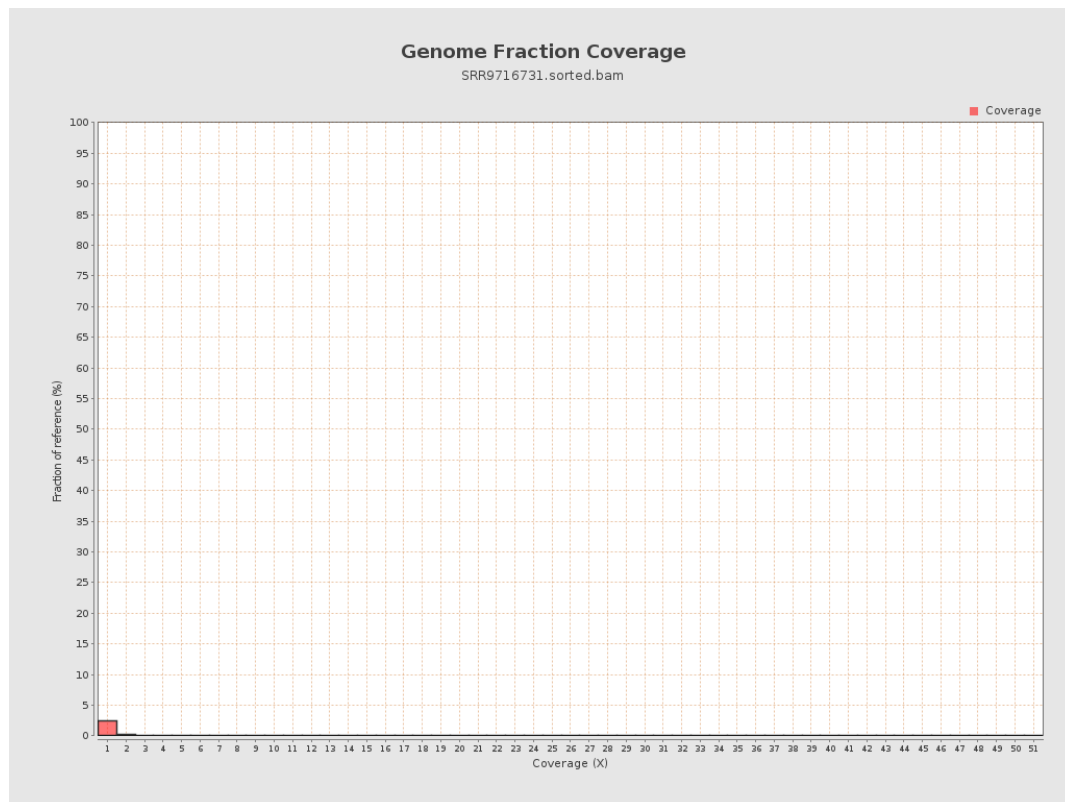
4. Results : Coverage Histogram



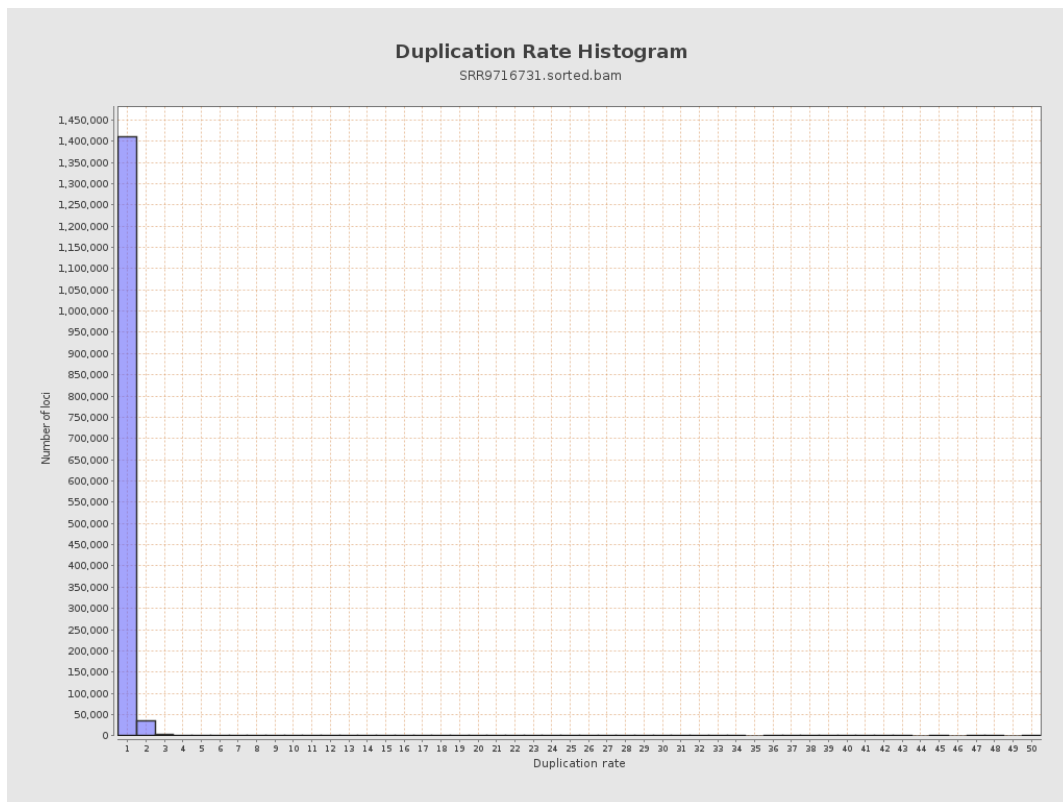
5. Results : Coverage Histogram (0-50X)



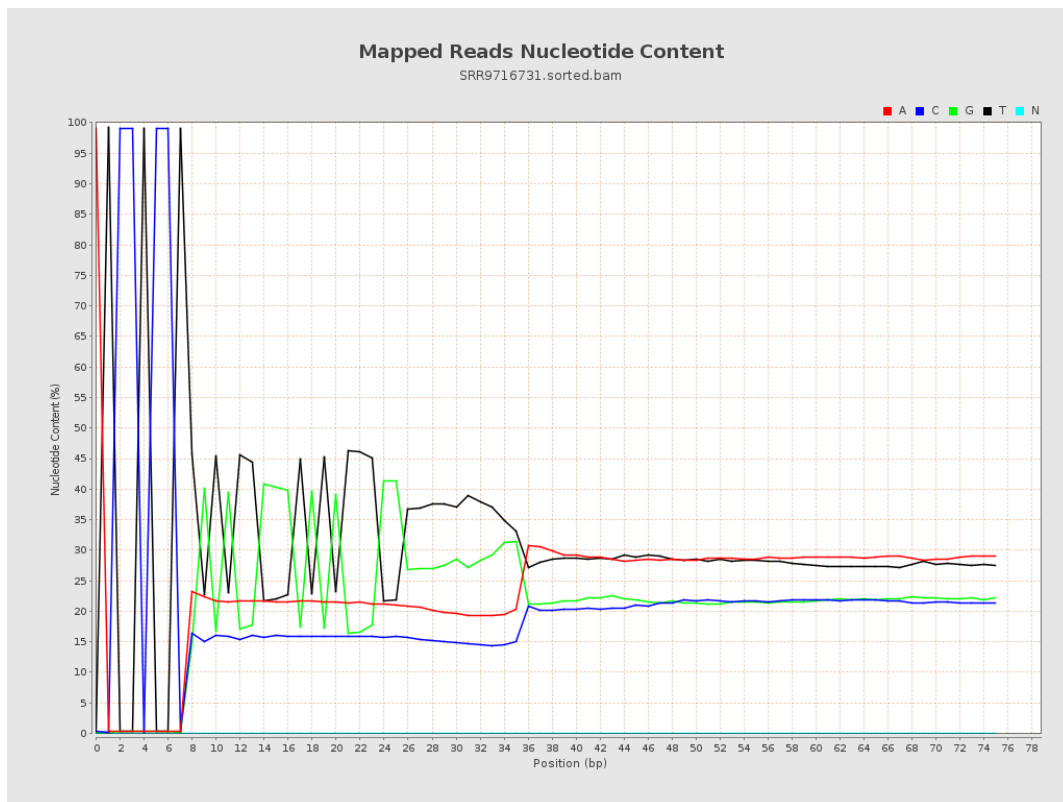
6. Results : Genome Fraction Coverage



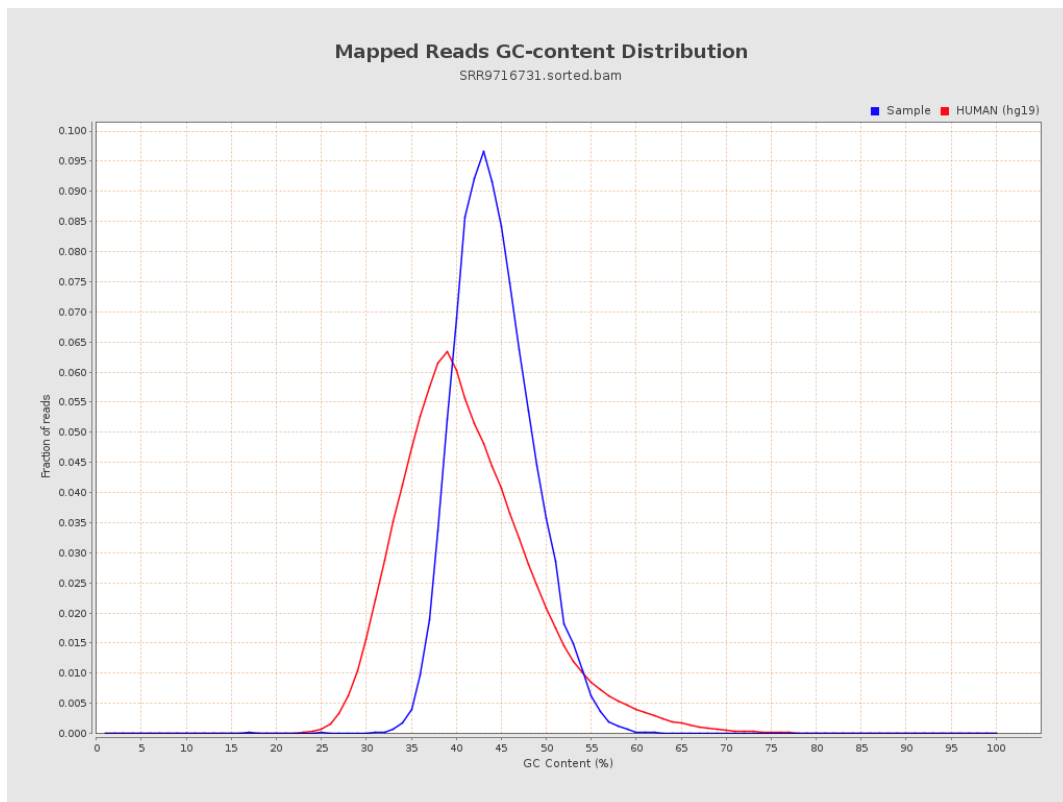
7. Results : Duplication Rate Histogram



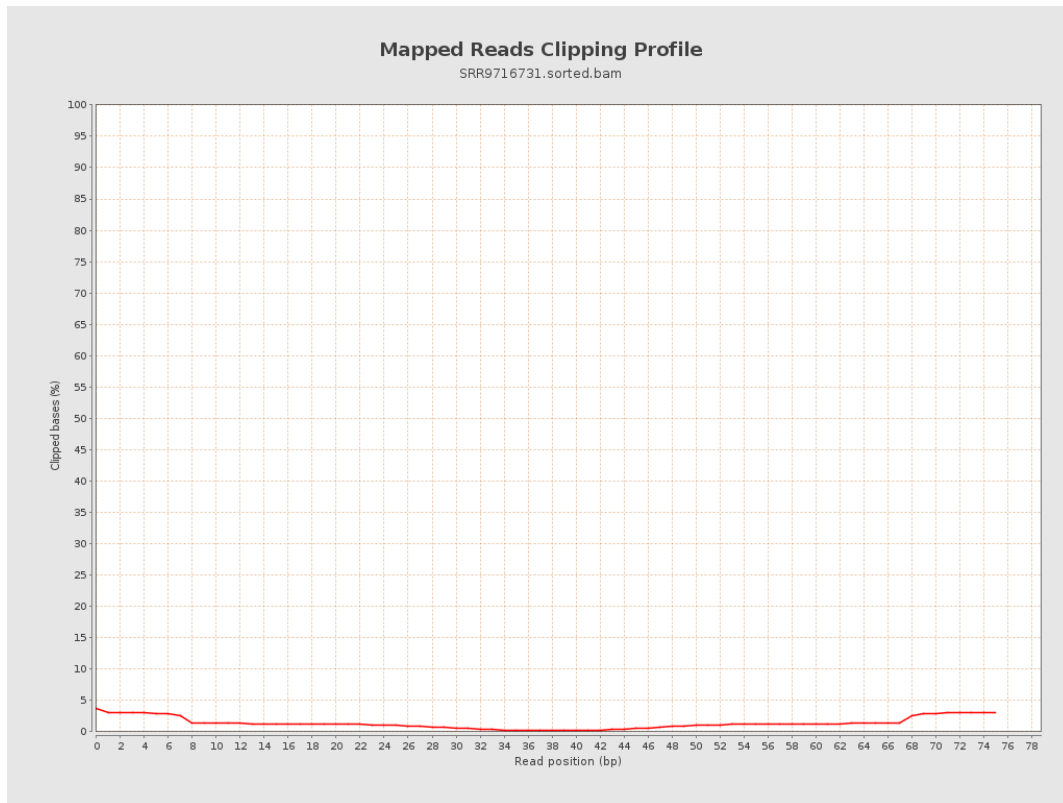
8. Results : Mapped Reads Nucleotide Content



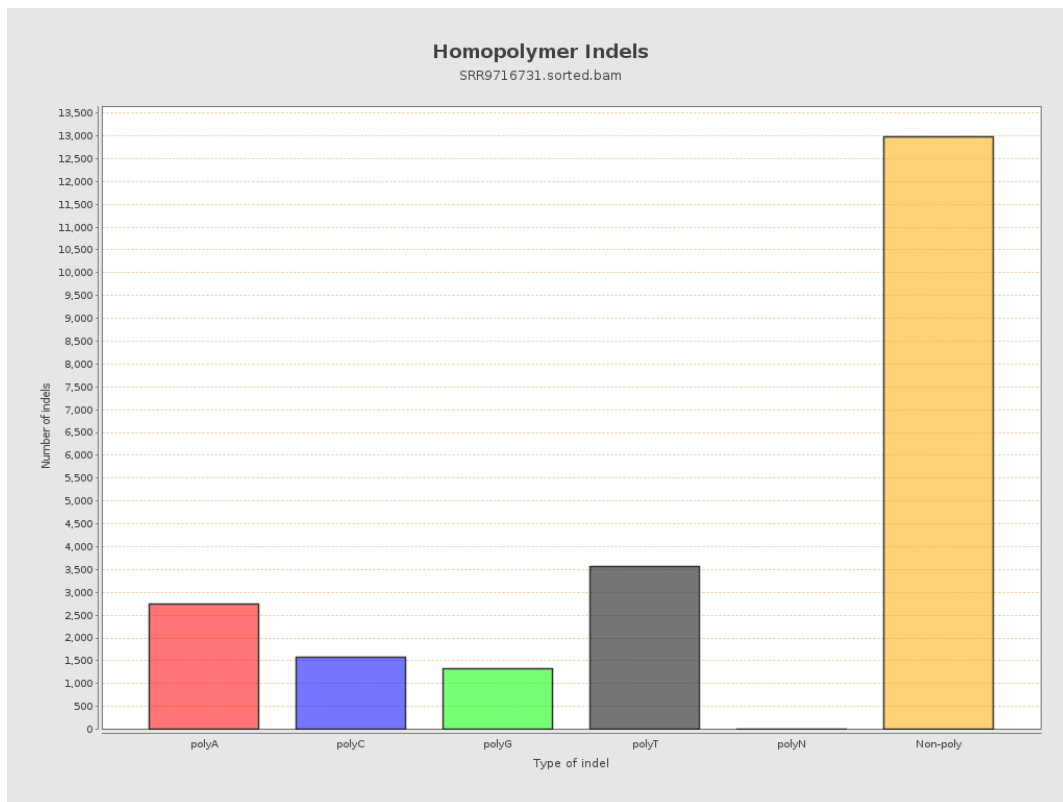
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

