

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 22:42:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3080719.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_SRR3080719 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3080719.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 22:42:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3080719.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,313,273
Mapped reads	2,086,923 / 90.22%
Unmapped reads	226,350 / 9.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,378 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	113,360 / 4.9%
Duplication rate	4.48%
Clipped reads	815,170 / 35.24%

2.2. ACGT Content

Number/percentage of A's	39,833,656 / 28.13%
Number/percentage of C's	26,180,486 / 18.49%
Number/percentage of T's	45,030,459 / 31.8%
Number/percentage of G's	30,572,555 / 21.59%
Number/percentage of N's	2,097 / 0%
GC Percentage	40.07%

2.3. Coverage

Mean	0.0458

Standard Deviation	0.4183
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2.4. Mapping Quality

Mean Mapping Quality	46.5
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2.5. Mismatches and indels

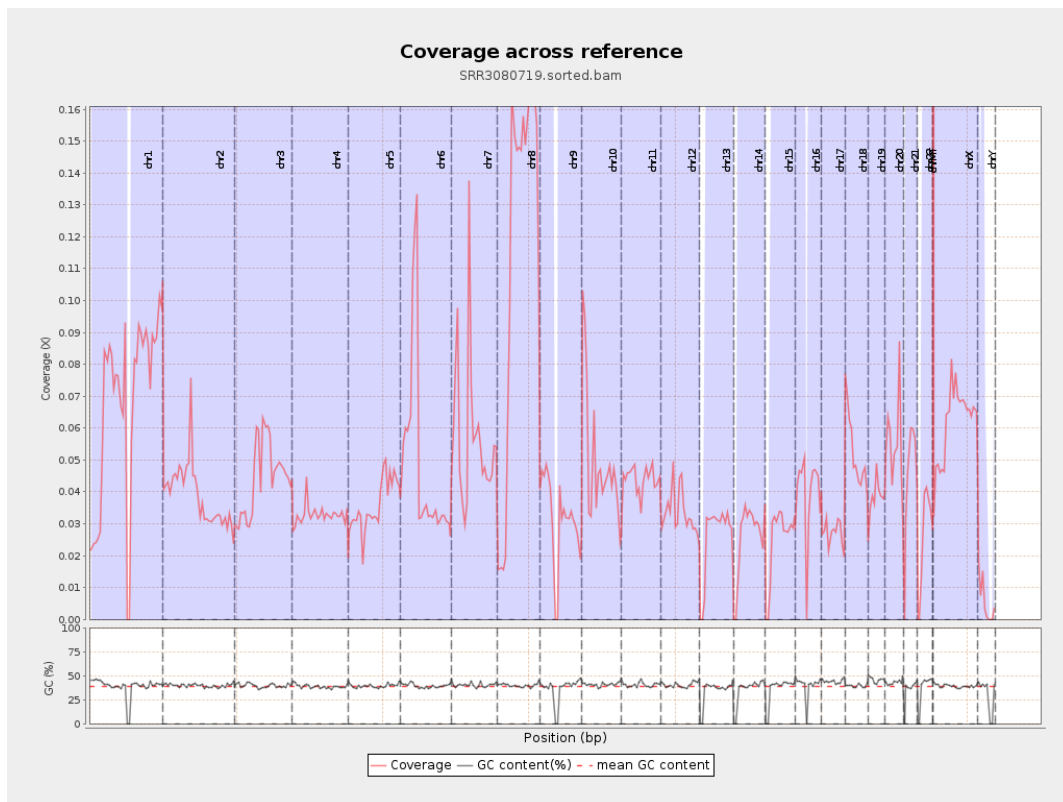
General error rate	0.83%
Mismatches	1,149,473
Insertions	10,282
Mapped reads with at least one insertion	0.49%
Deletions	29,266
Mapped reads with at least one deletion	1.39%
Homopolymer indels	47.85%

2.6. Chromosome stats

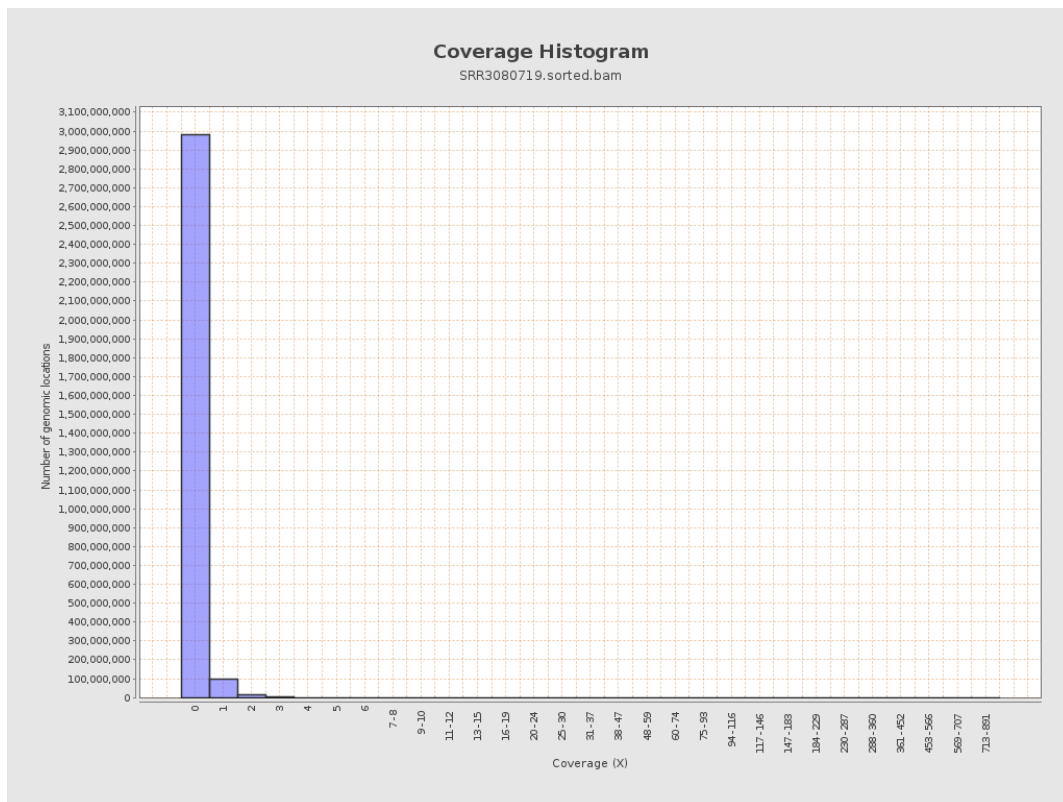
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16881421	0.0677	0.5969
chr2	243199373	9482664	0.039	0.3978
chr3	198022430	8789079	0.0444	0.2444
chr4	191154276	6272692	0.0328	0.2207
chr5	180915260	6470356	0.0358	0.2193
chr6	171115067	8489619	0.0496	0.3613
chr7	159138663	9173834	0.0576	1.1099

chr8	146364022	17071038	0.1166	0.5554
chr9	141213431	4464080	0.0316	0.2852
chr10	135534747	6812650	0.0503	0.3636
chr11	135006516	5893152	0.0437	0.2823
chr12	133851895	4498073	0.0336	0.2159
chr13	115169878	2994360	0.026	0.1855
chr14	107349540	2766774	0.0258	0.1957
chr15	102531392	2506355	0.0244	0.1805
chr16	90354753	3500431	0.0387	0.248
chr17	81195210	2223201	0.0274	0.2003
chr18	78077248	4086379	0.0523	0.4744
chr19	59128983	2296859	0.0388	0.3934
chr20	63025520	3520806	0.0559	0.2793
chr21	48129895	2169464	0.0451	0.2569
chr22	51304566	1350086	0.0263	0.186
chrMT	16571	61560	3.7149	2.8423
chrX	155270560	9566906	0.0616	0.3126
chrY	59373566	329455	0.0055	0.1219

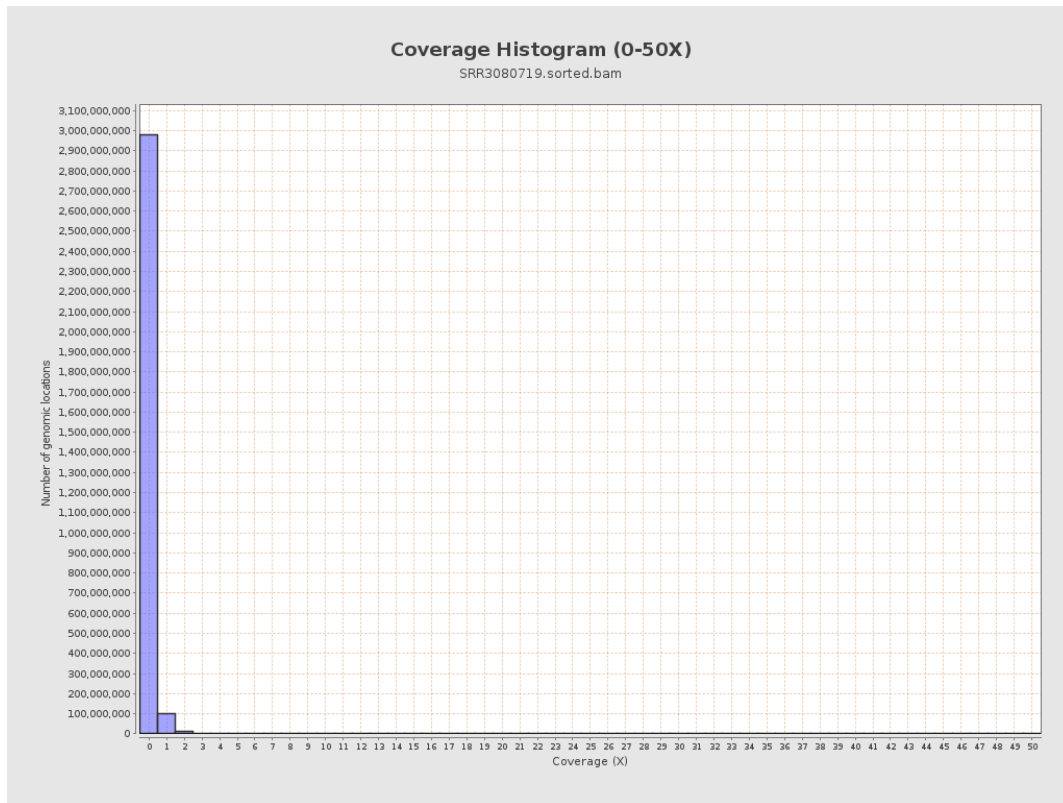
3. Results : Coverage across reference



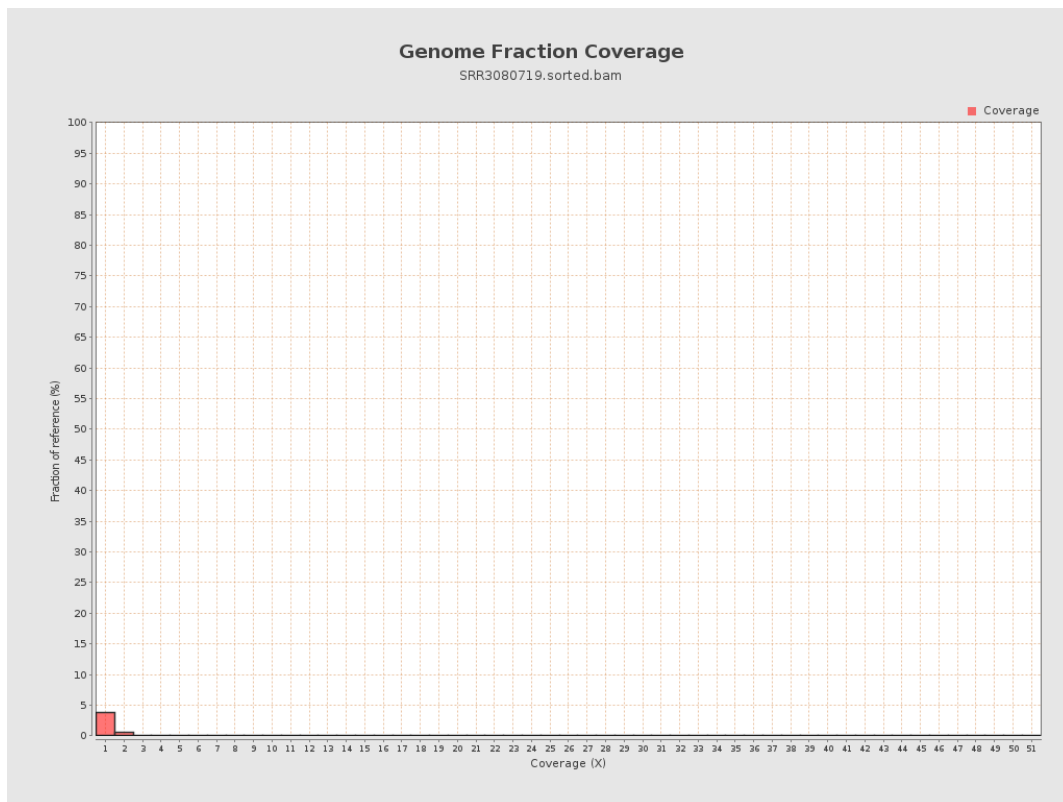
4. Results : Coverage Histogram



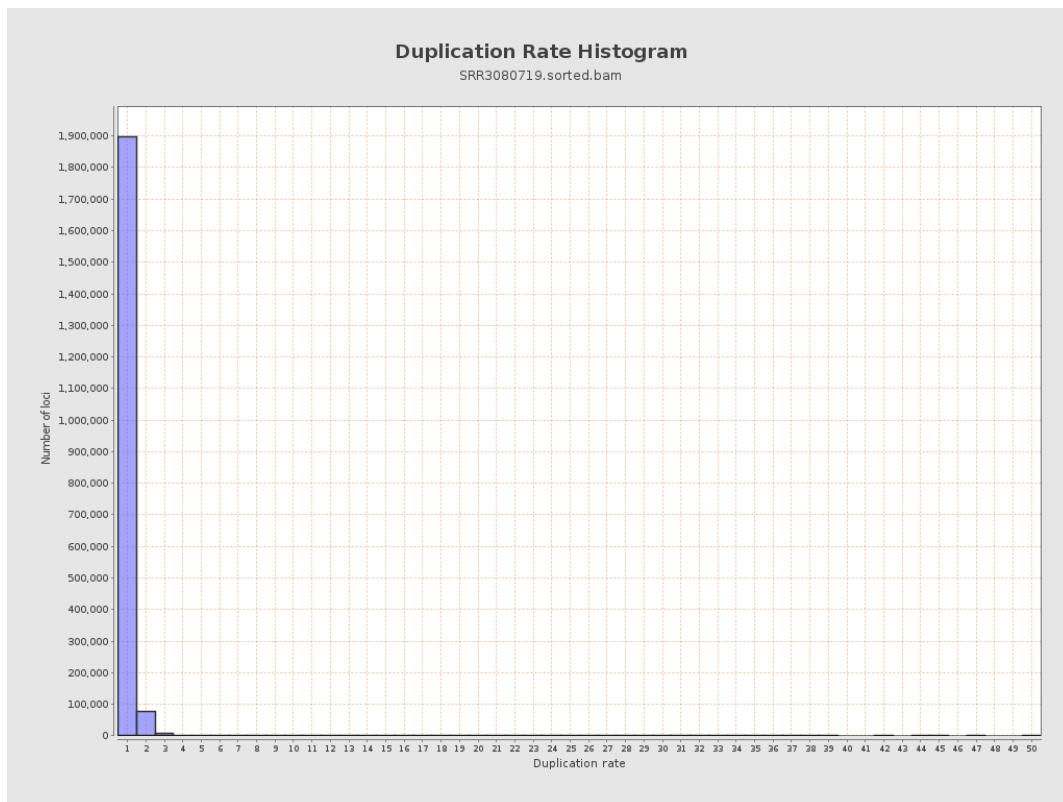
5. Results : Coverage Histogram (0-50X)



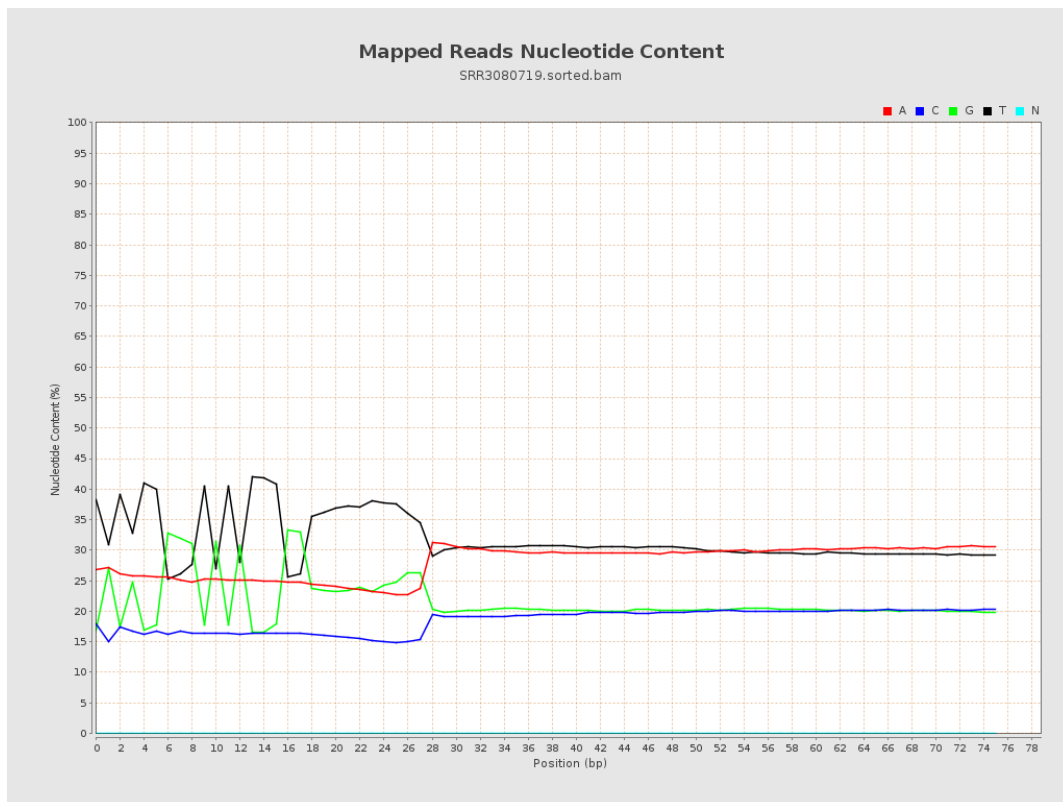
6. Results : Genome Fraction Coverage



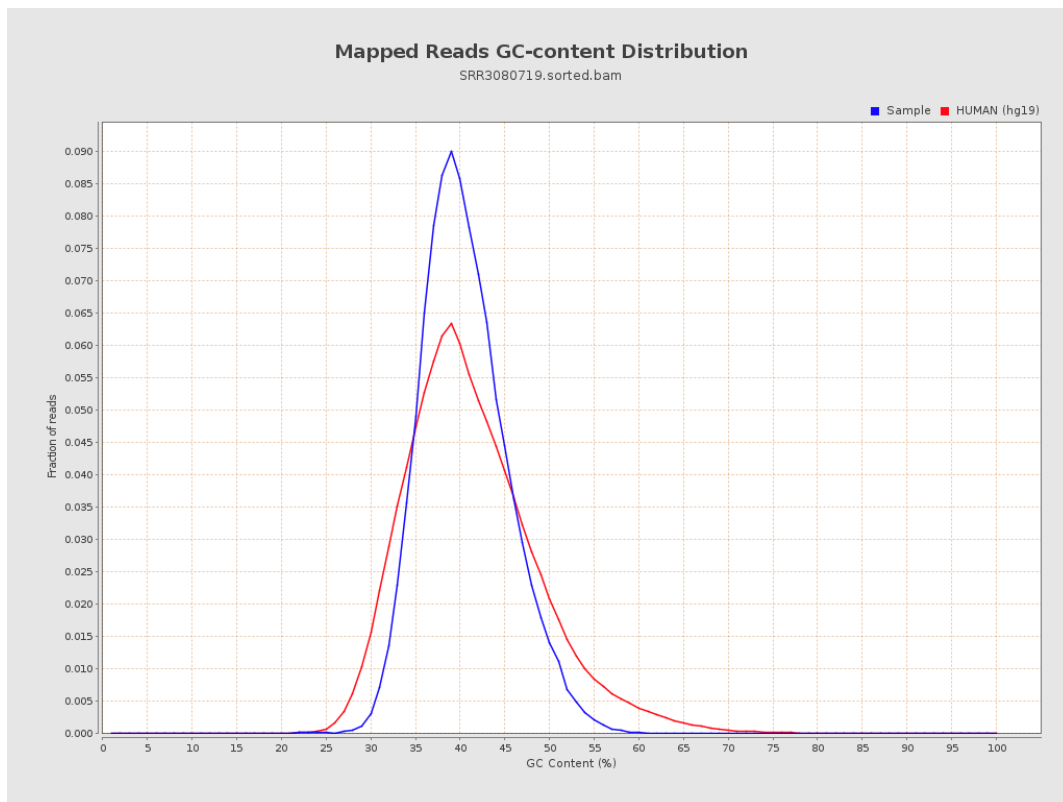
7. Results : Duplication Rate Histogram



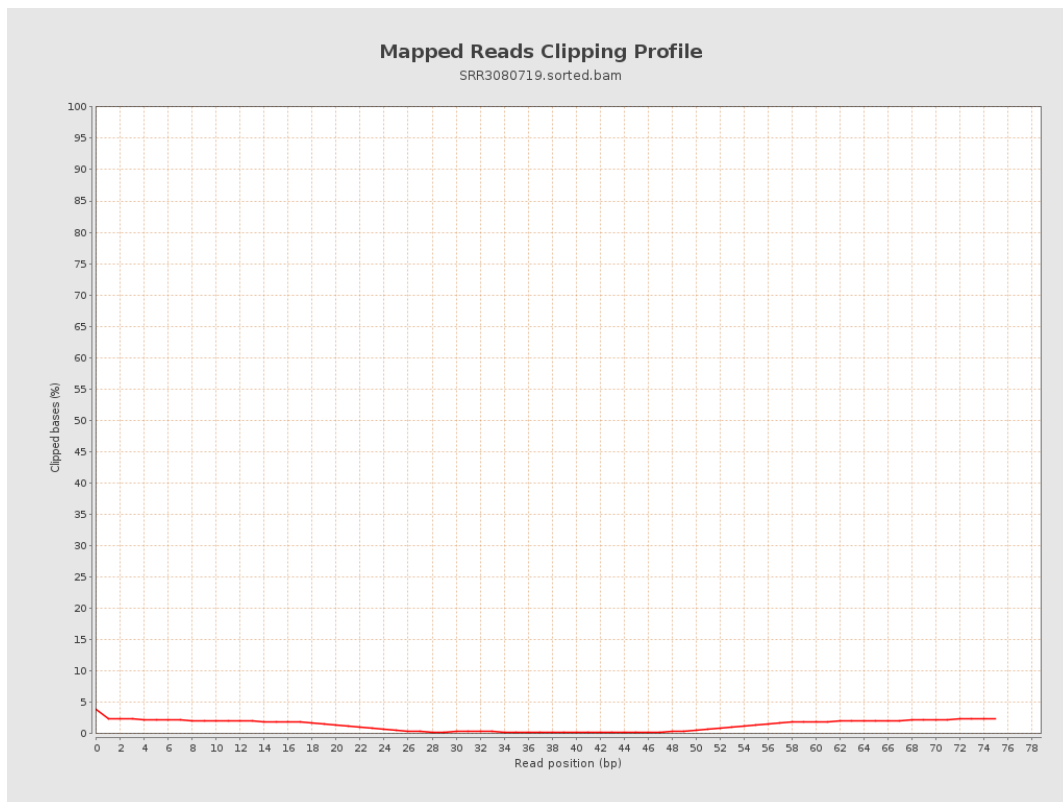
8. Results : Mapped Reads Nucleotide Content



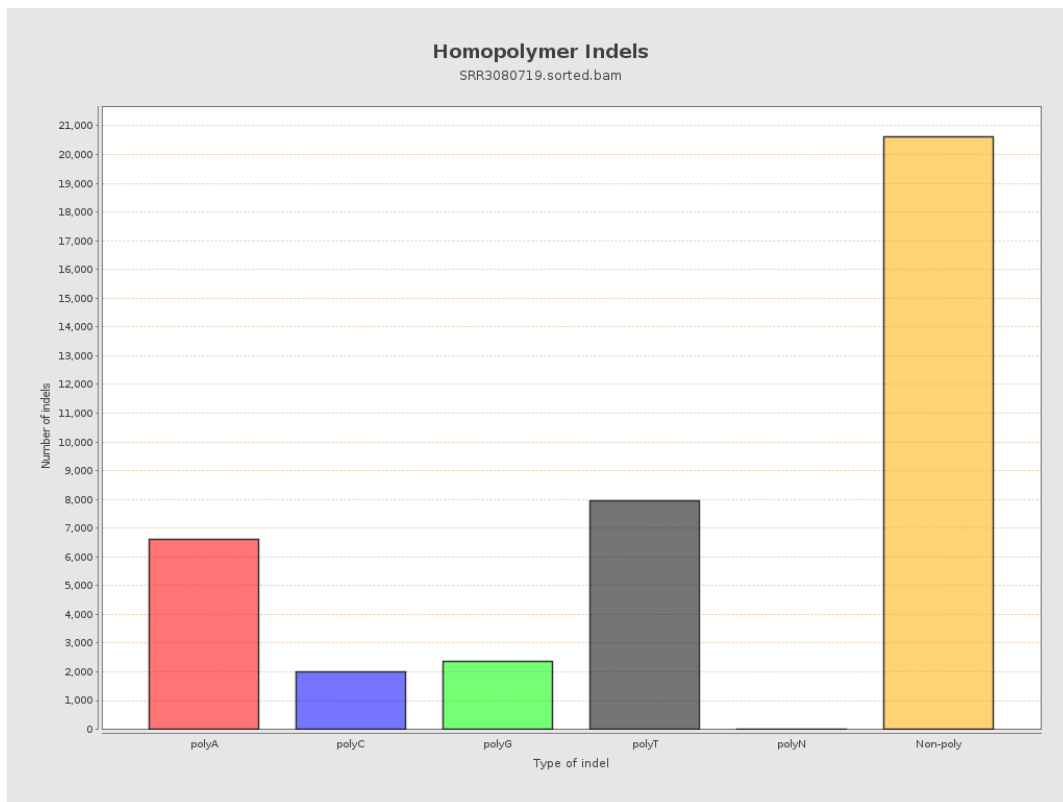
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

