

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 20:27:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819080.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_SRR1819080 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819080.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 20:27:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819080.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,408,316
Mapped reads	1,290,176 / 91.61%
Unmapped reads	118,140 / 8.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,079 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	44,397 / 3.15%
Duplication rate	2.52%
Clipped reads	1,293,665 / 91.86%

2.2. ACGT Content

Number/percentage of A's	18,454,932 / 24.64%
Number/percentage of C's	14,723,825 / 19.66%
Number/percentage of T's	23,299,093 / 31.11%
Number/percentage of G's	18,411,627 / 24.58%
Number/percentage of N's	1,152 / 0%
GC Percentage	44.25%

2.3. Coverage

Mean	0.0242

Standard Deviation	0.2388
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2.4. Mapping Quality

Mean Mapping Quality	44.57
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2.5. Mismatches and indels

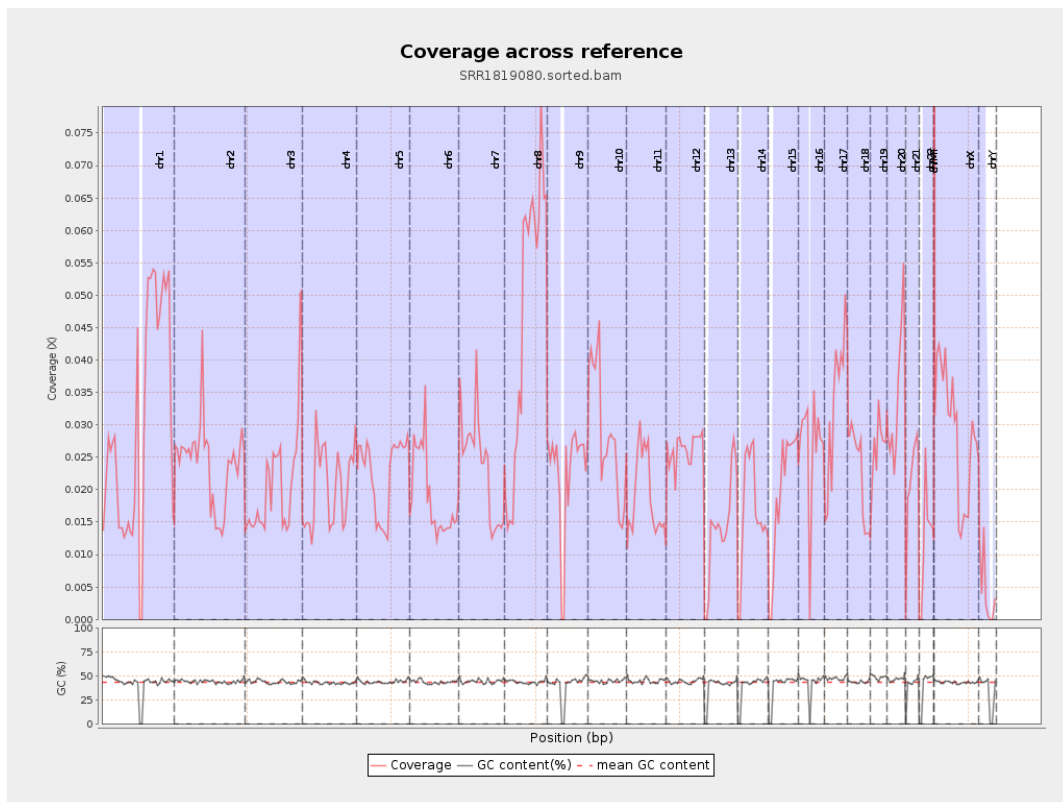
General error rate	0.52%
Mismatches	379,157
Insertions	4,178
Mapped reads with at least one insertion	0.32%
Deletions	14,198
Mapped reads with at least one deletion	1.09%
Homopolymer indels	44.75%

2.6. Chromosome stats

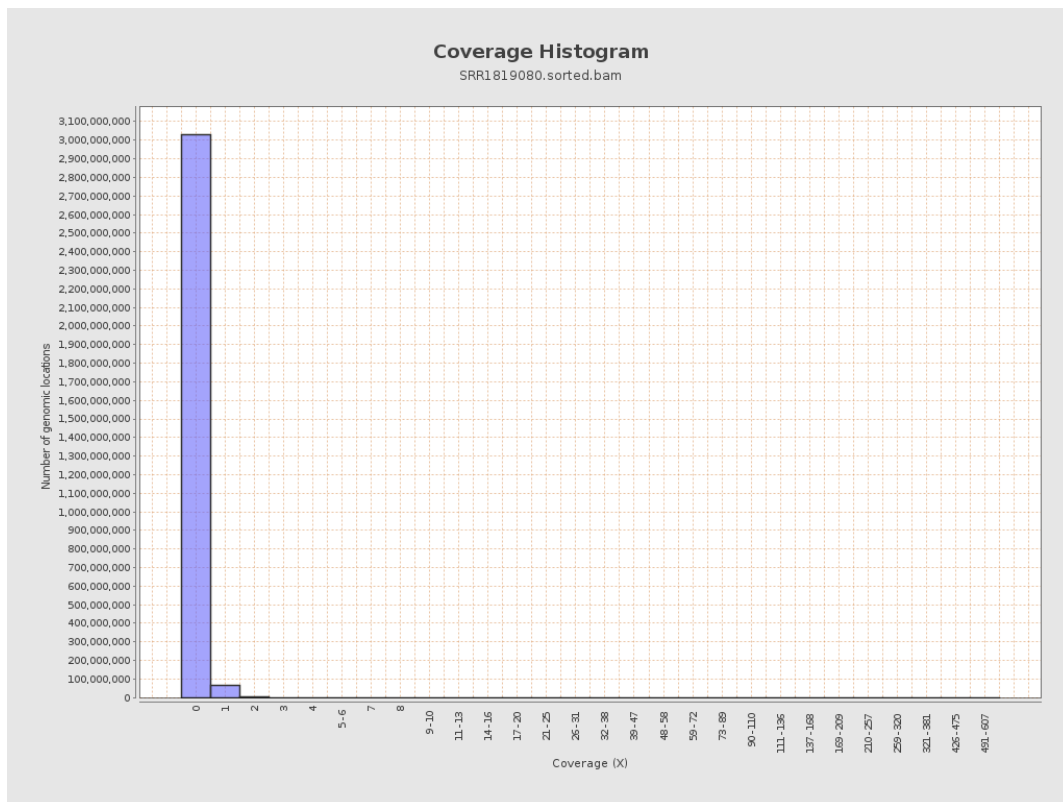
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7428398	0.0298	0.4467
chr2	243199373	5838185	0.024	0.2678
chr3	198022430	4077401	0.0206	0.1562
chr4	191154276	3890027	0.0204	0.1706
chr5	180915260	4084293	0.0226	0.1626
chr6	171115067	3252599	0.019	0.1908
chr7	159138663	3800508	0.0239	0.2805

chr8	146364022	6799955	0.0465	0.2715
chr9	141213431	3176229	0.0225	0.2073
chr10	135534747	3948029	0.0291	0.2477
chr11	135006516	2600802	0.0193	0.213
chr12	133851895	3512832	0.0262	0.1749
chr13	115169878	1659551	0.0144	0.1301
chr14	107349540	1789436	0.0167	0.1422
chr15	102531392	1993480	0.0194	0.1516
chr16	90354753	2377455	0.0263	0.186
chr17	81195210	2701511	0.0333	0.2043
chr18	78077248	1783031	0.0228	0.3501
chr19	59128983	1579652	0.0267	0.3021
chr20	63025520	2182335	0.0346	0.2024
chr21	48129895	1037322	0.0216	0.1684
chr22	51304566	641574	0.0125	0.1208
chrMT	16571	6017	0.3631	0.6518
chrX	155270560	4503238	0.029	0.2012
chrY	59373566	250556	0.0042	0.1246

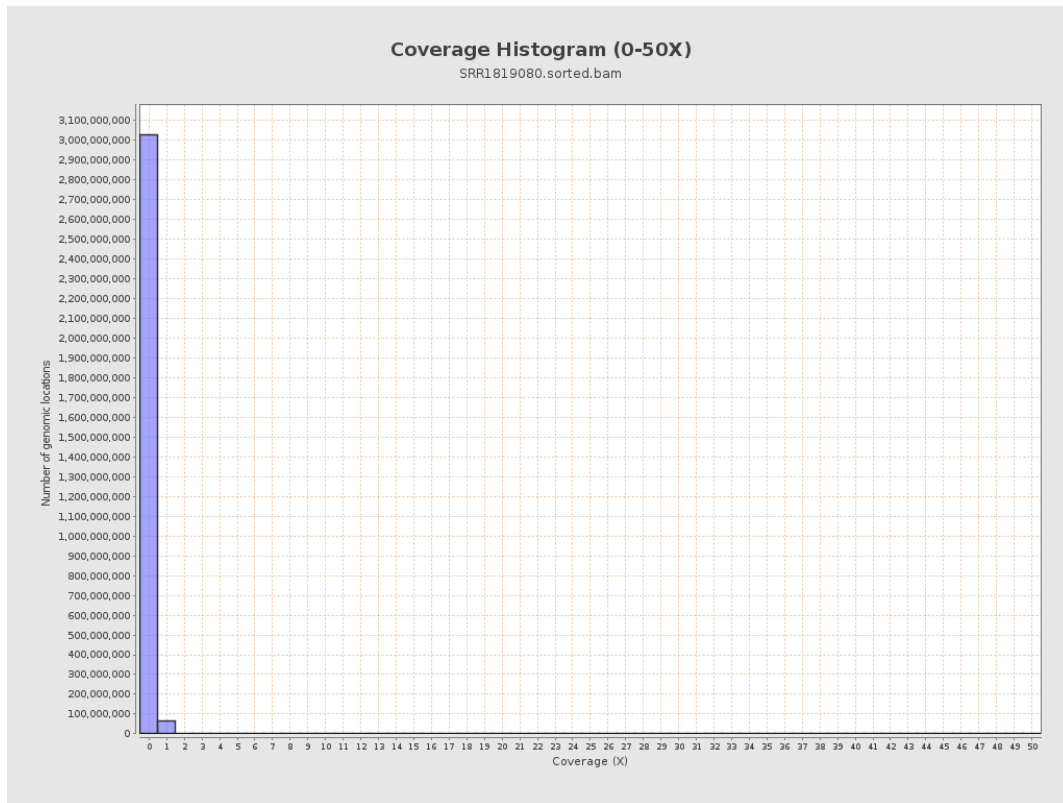
3. Results : Coverage across reference



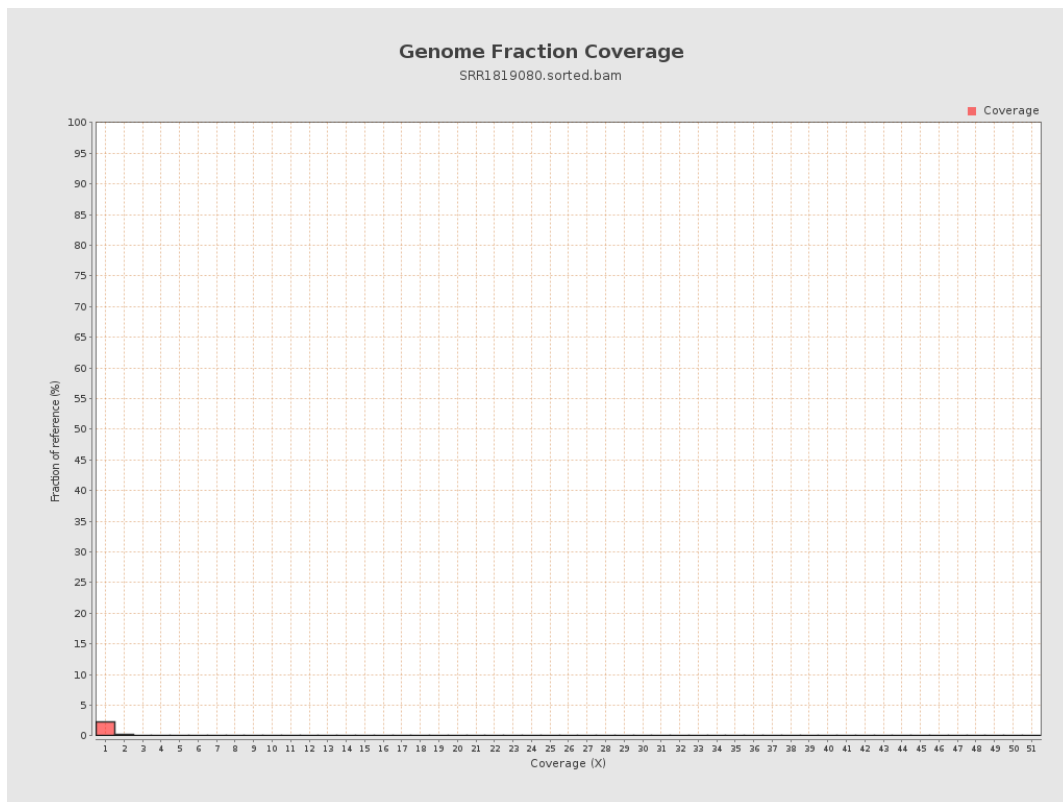
4. Results : Coverage Histogram



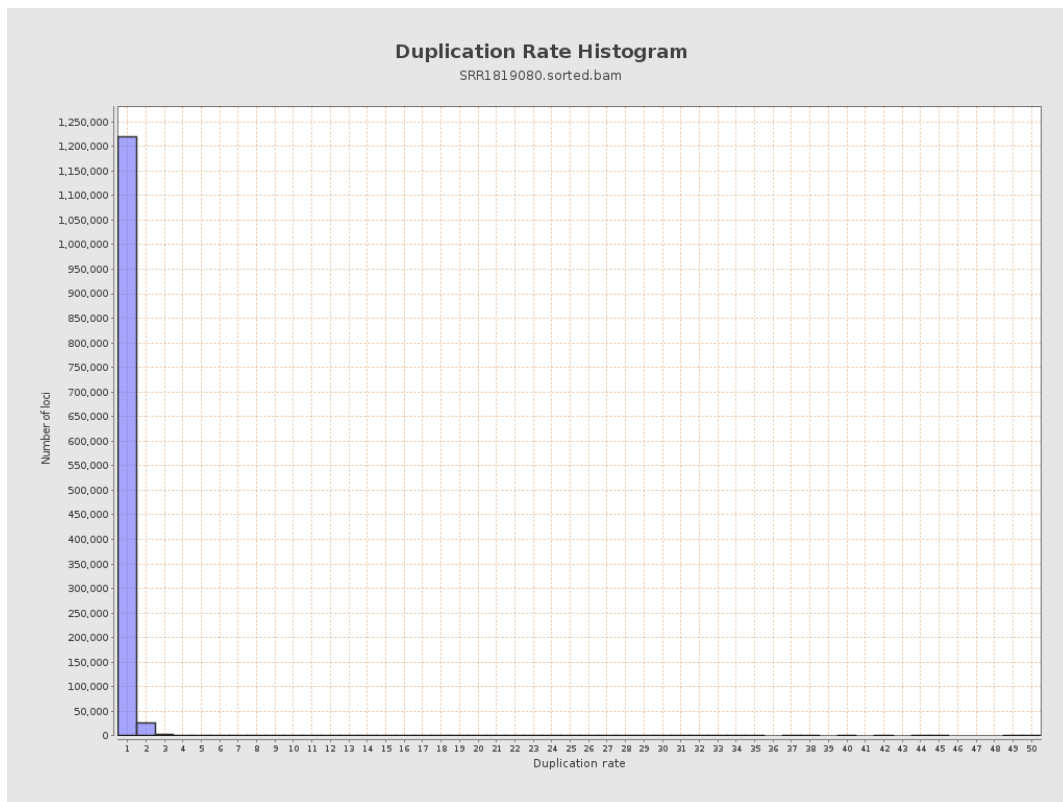
5. Results : Coverage Histogram (0-50X)



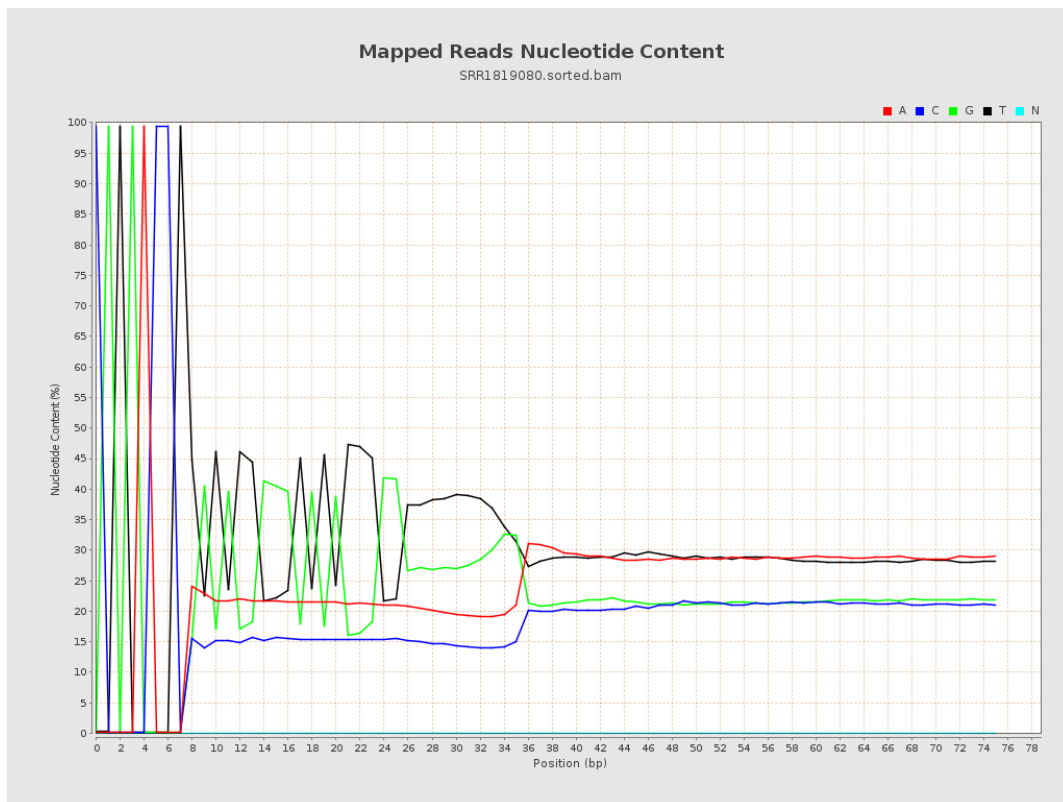
6. Results : Genome Fraction Coverage



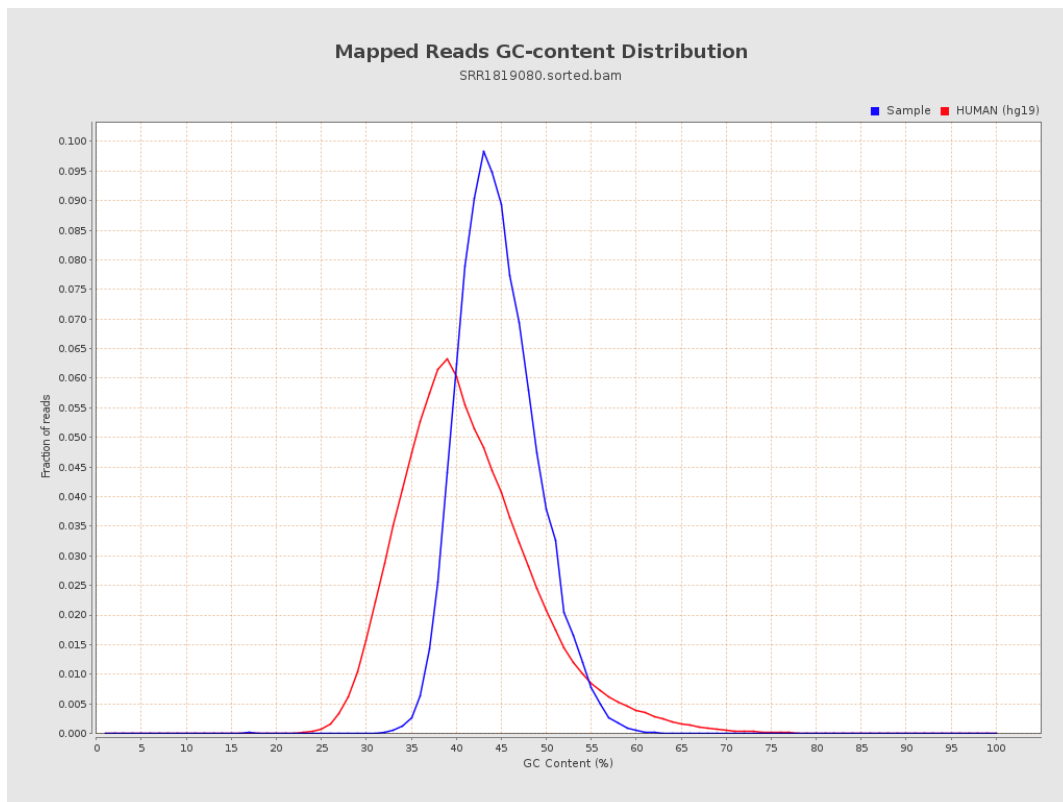
7. Results : Duplication Rate Histogram



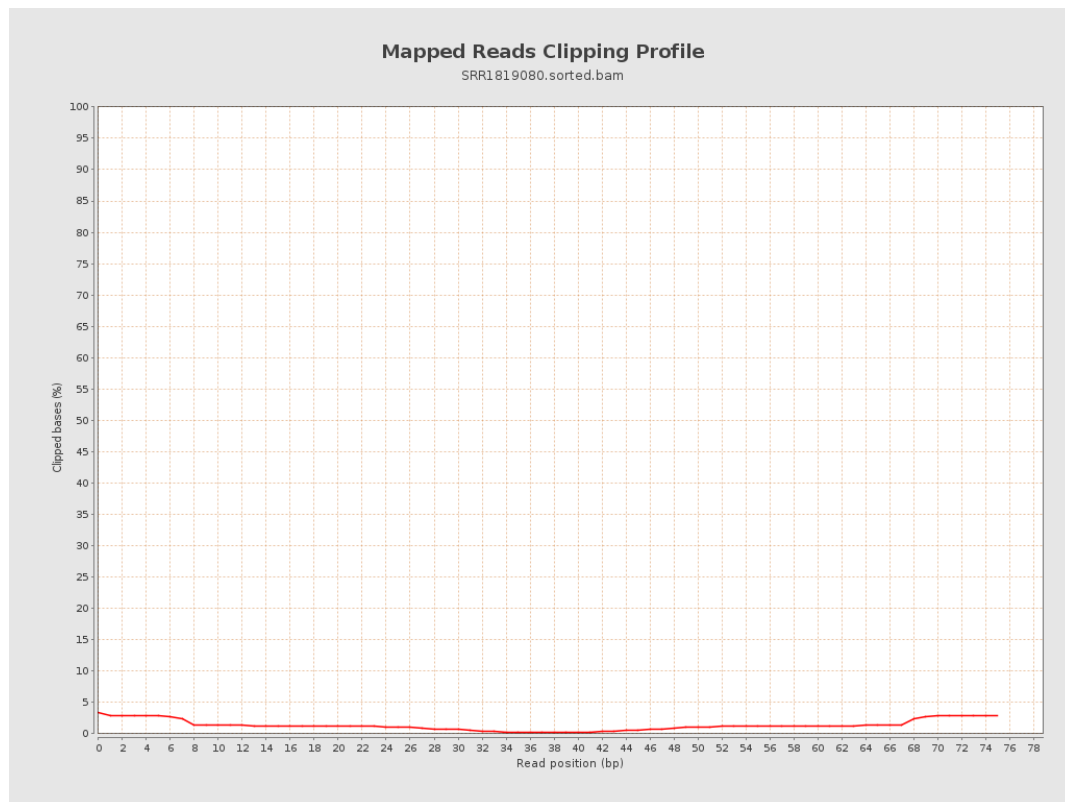
8. Results : Mapped Reads Nucleotide Content



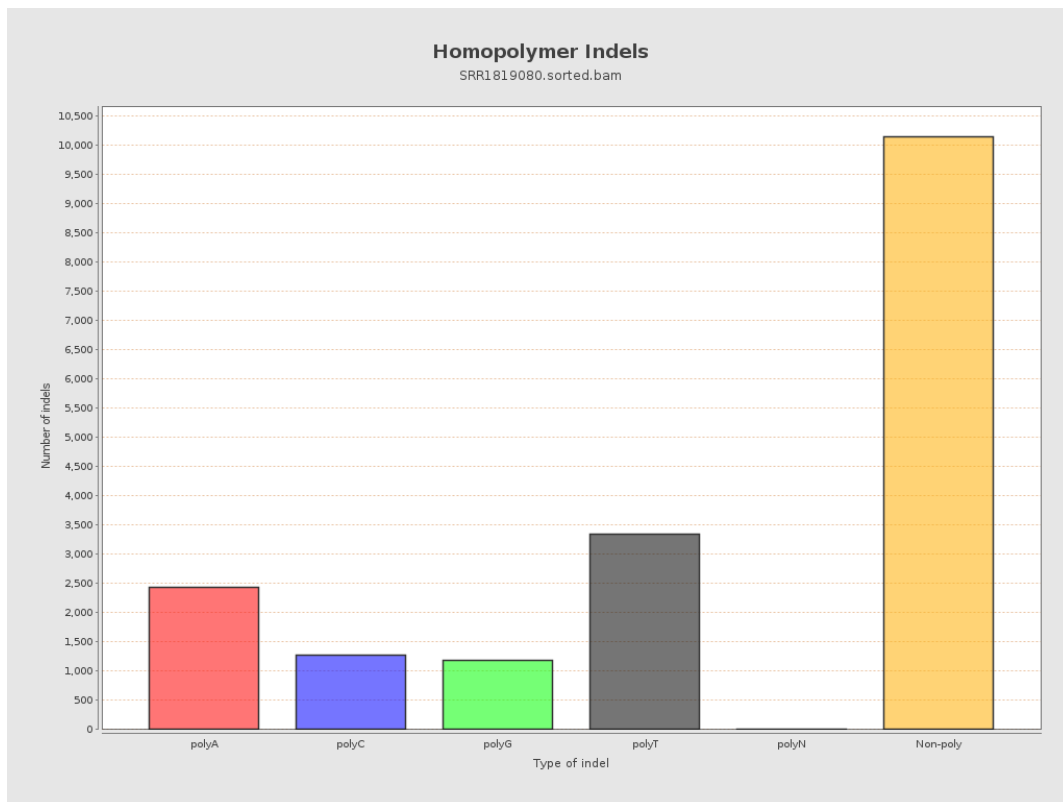
9. Results : Mapped Reads GC-content Distribution



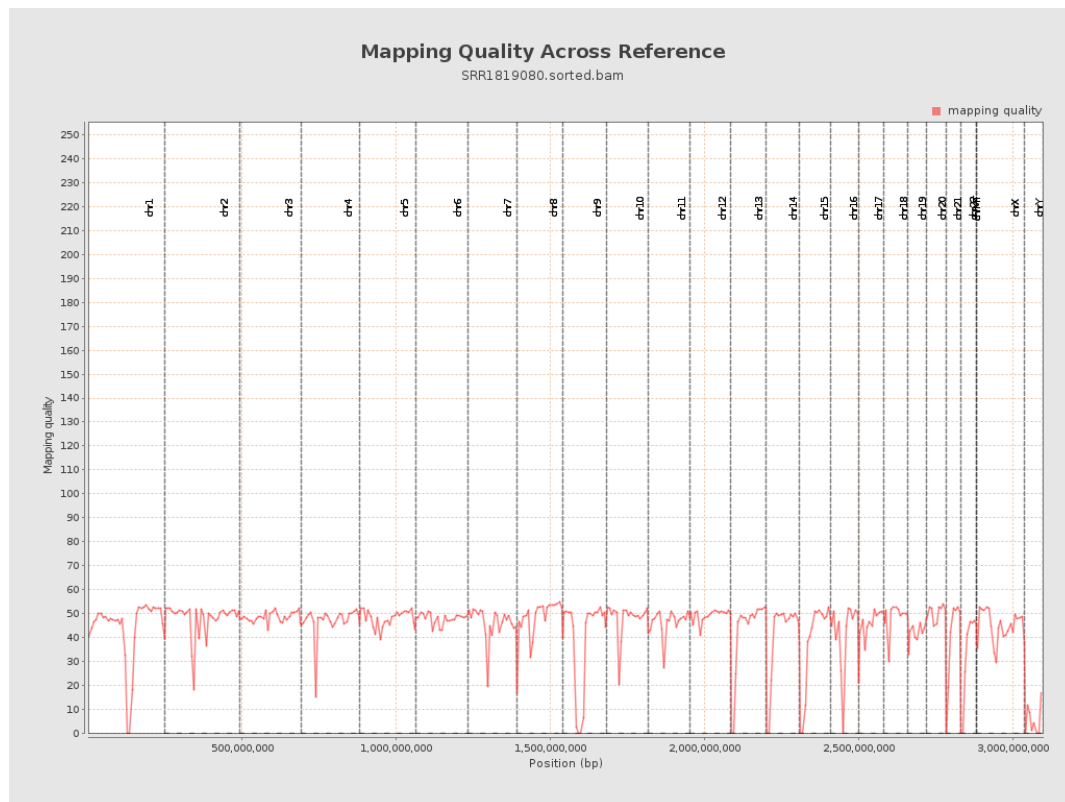
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

