

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 20:28:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004008.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_SRR6004008 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004008.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 20:28:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004008.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,761,479
Mapped reads	1,587,101 / 90.1%
Unmapped reads	174,378 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,932 / 0.56%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	67,067 / 3.81%
Duplication rate	3.43%
Clipped reads	660,160 / 37.48%

2.2. ACGT Content

Number/percentage of A's	29,950,542 / 28.06%
Number/percentage of C's	19,359,448 / 18.14%
Number/percentage of T's	34,283,902 / 32.12%
Number/percentage of G's	23,121,804 / 21.66%
Number/percentage of N's	18,542 / 0.02%
GC Percentage	39.8%

2.3. Coverage

Mean	0.0345

Standard Deviation	0.3082
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2.4. Mapping Quality

Mean Mapping Quality	46.39
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2.5. Mismatches and indels

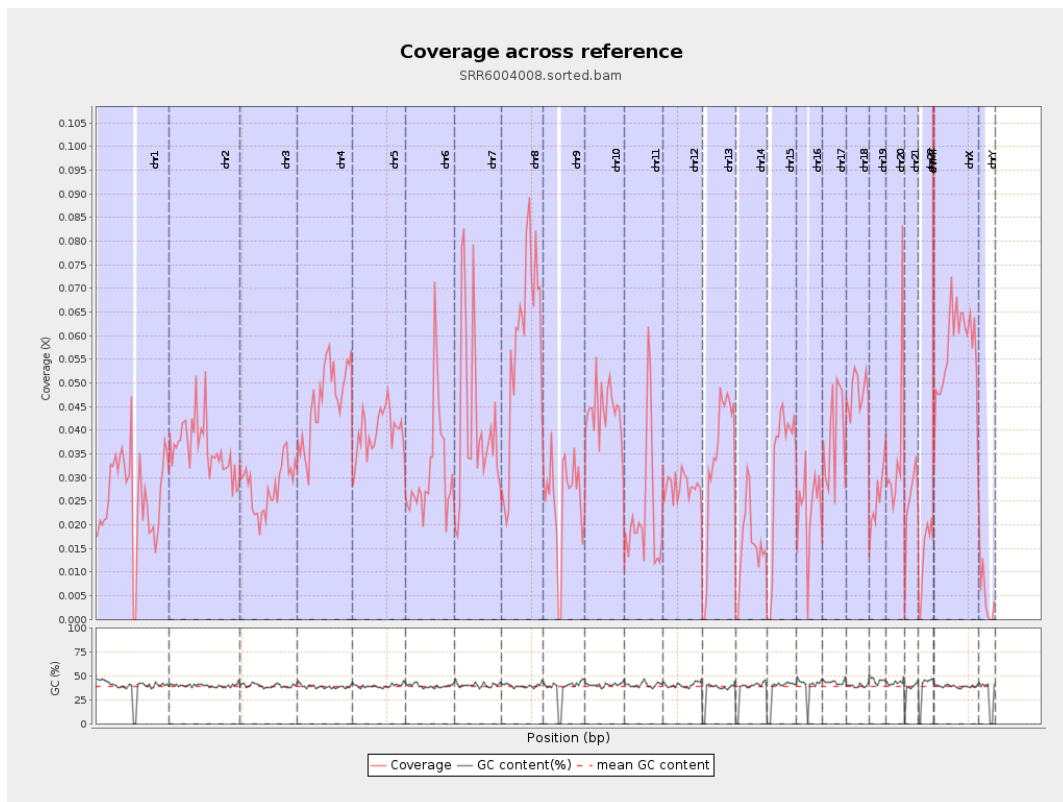
General error rate	0.86%
Mismatches	908,250
Insertions	7,616
Mapped reads with at least one insertion	0.48%
Deletions	25,917
Mapped reads with at least one deletion	1.62%
Homopolymer indels	46.72%

2.6. Chromosome stats

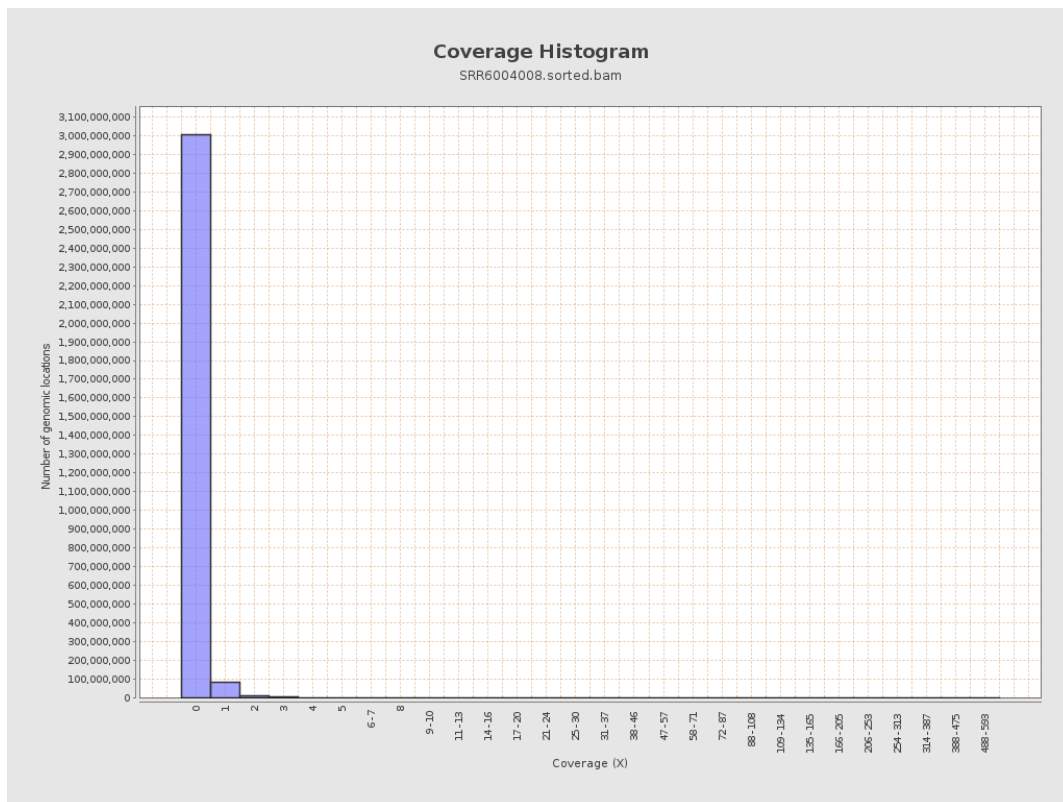
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6429694	0.0258	0.4434
chr2	243199373	8818227	0.0363	0.3528
chr3	198022430	5554925	0.0281	0.1876
chr4	191154276	8831735	0.0462	0.2567
chr5	180915260	7208912	0.0398	0.2261
chr6	171115067	5430017	0.0317	0.2131
chr7	159138663	6771917	0.0426	0.5935

chr8	146364022	8358845	0.0571	0.4447
chr9	141213431	3575035	0.0253	0.2645
chr10	135534747	5996403	0.0442	0.289
chr11	135006516	3129843	0.0232	0.1979
chr12	133851895	3743321	0.028	0.1924
chr13	115169878	3885759	0.0337	0.2104
chr14	107349540	1690001	0.0157	0.1526
chr15	102531392	3308936	0.0323	0.202
chr16	90354753	2147536	0.0238	0.1853
chr17	81195210	3169579	0.039	0.2366
chr18	78077248	3754708	0.0481	0.4451
chr19	59128983	1539549	0.026	0.3254
chr20	63025520	2293465	0.0364	0.2188
chr21	48129895	1193671	0.0248	0.1947
chr22	51304566	696501	0.0136	0.1281
chrMT	16571	53864	3.2505	2.8817
chrX	155270560	8908650	0.0574	0.2933
chrY	59373566	288428	0.0049	0.1138

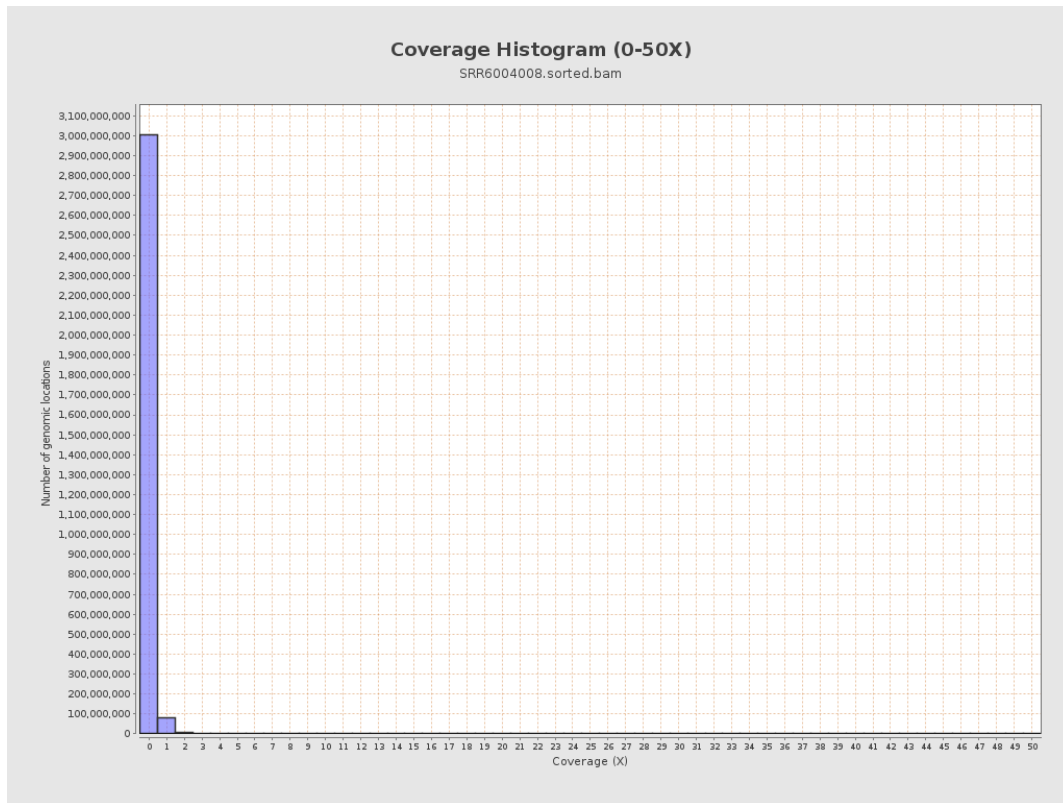
3. Results : Coverage across reference



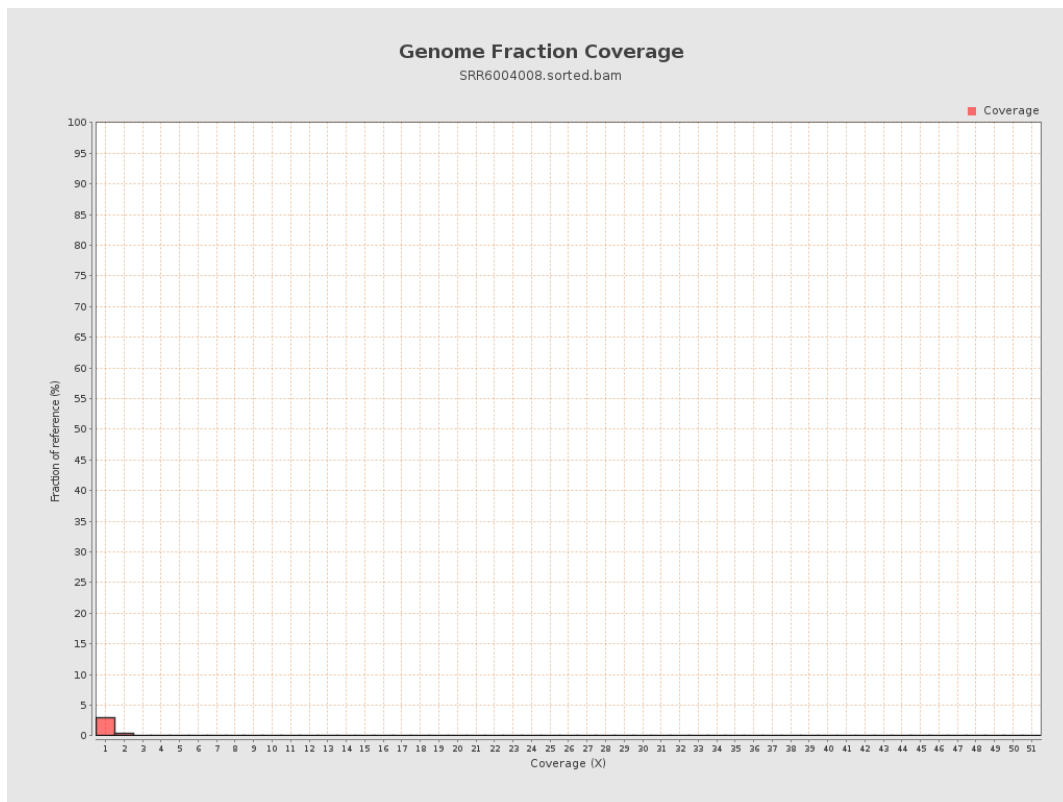
4. Results : Coverage Histogram



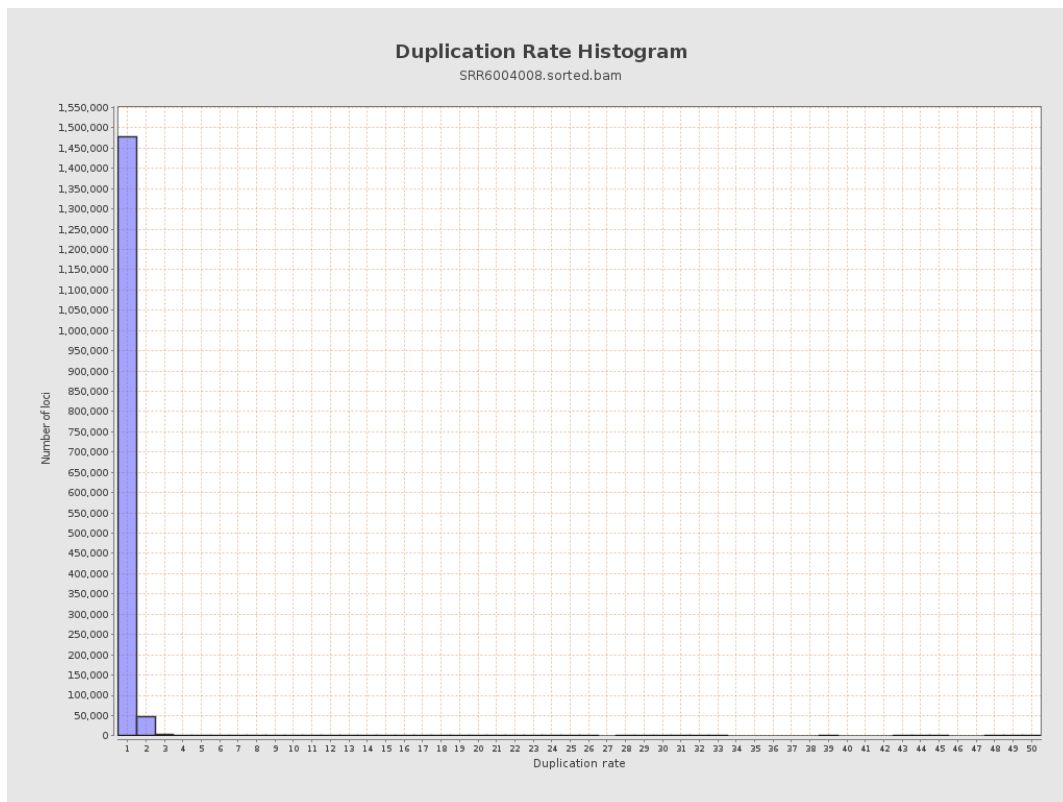
5. Results : Coverage Histogram (0-50X)



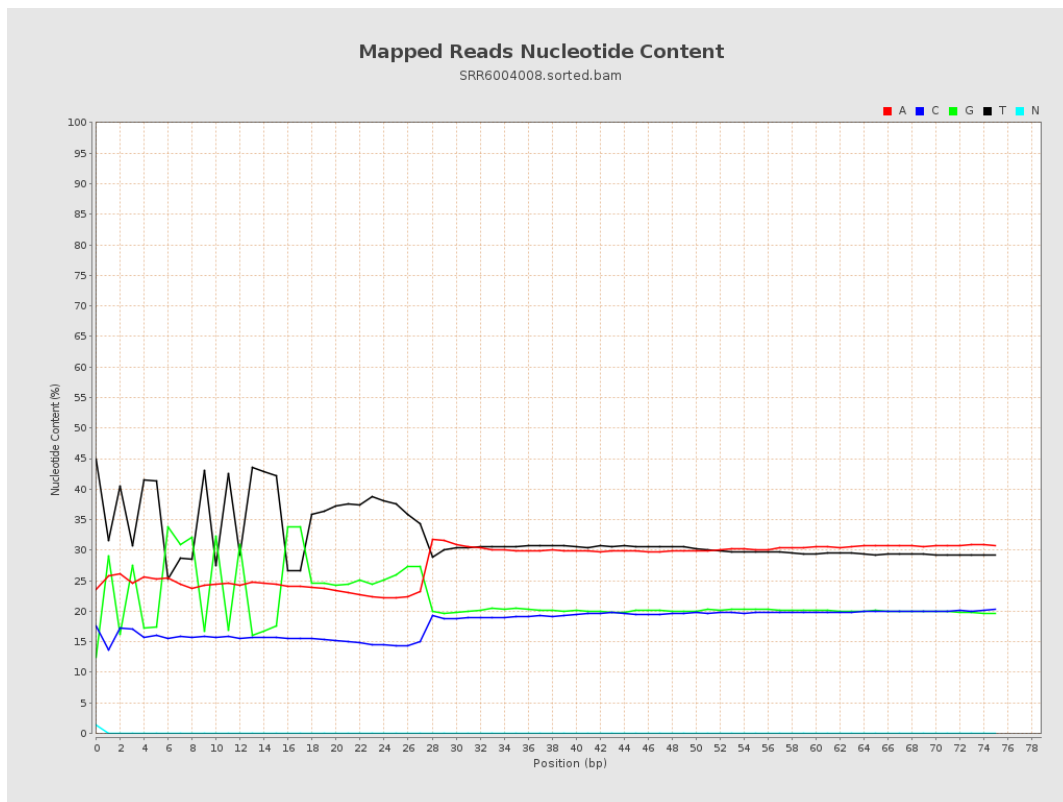
6. Results : Genome Fraction Coverage



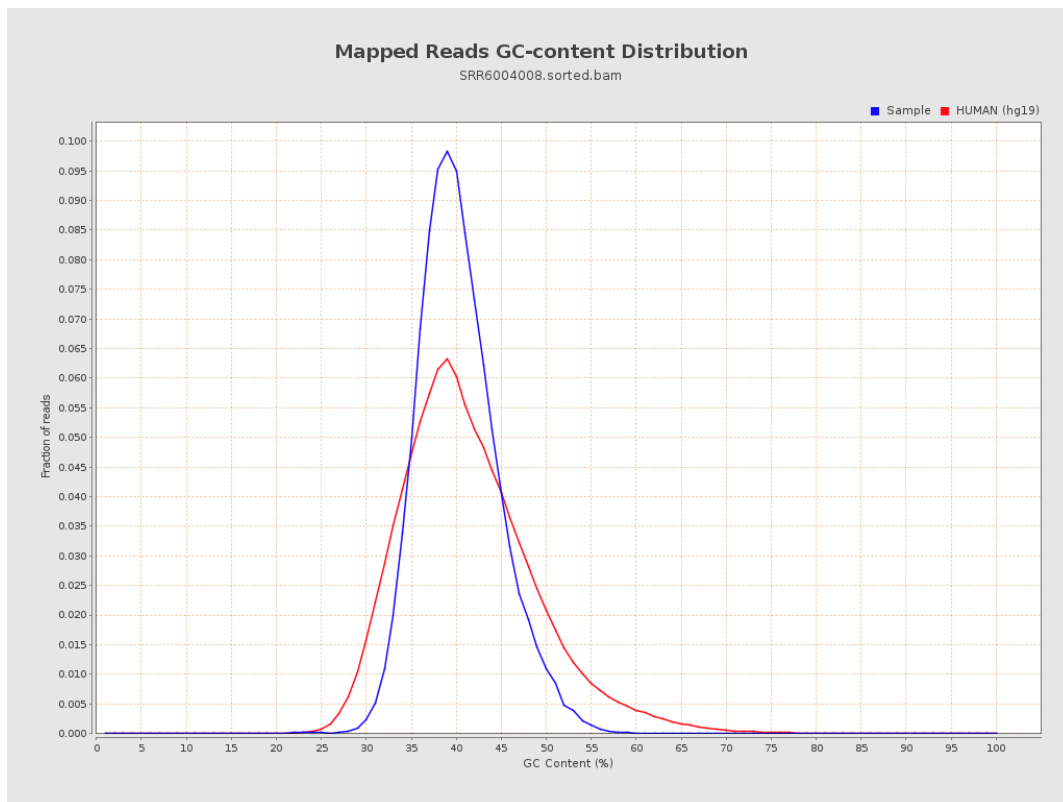
7. Results : Duplication Rate Histogram



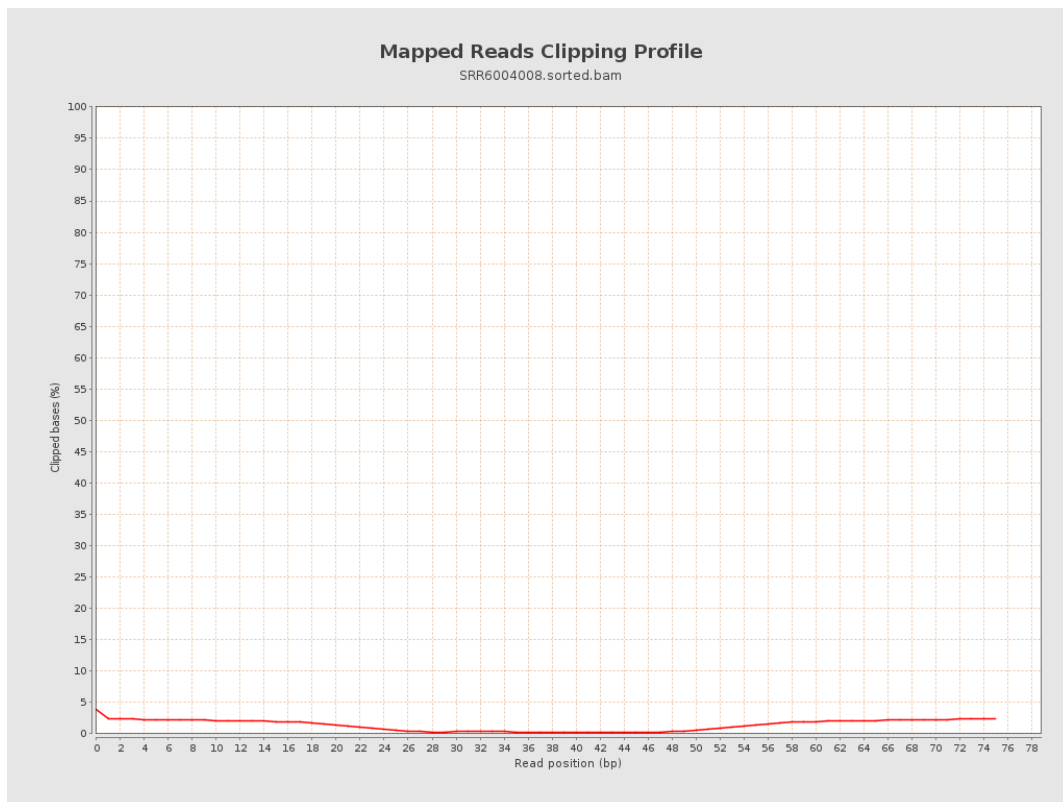
8. Results : Mapped Reads Nucleotide Content



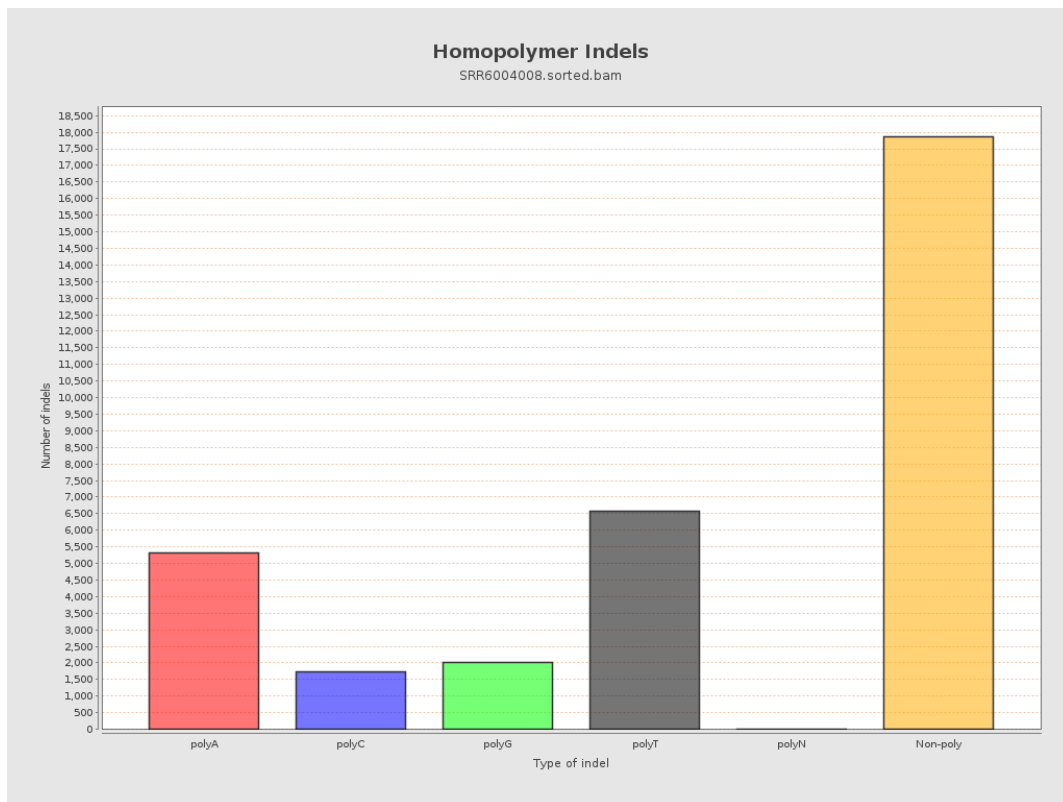
9. Results : Mapped Reads GC-content Distribution



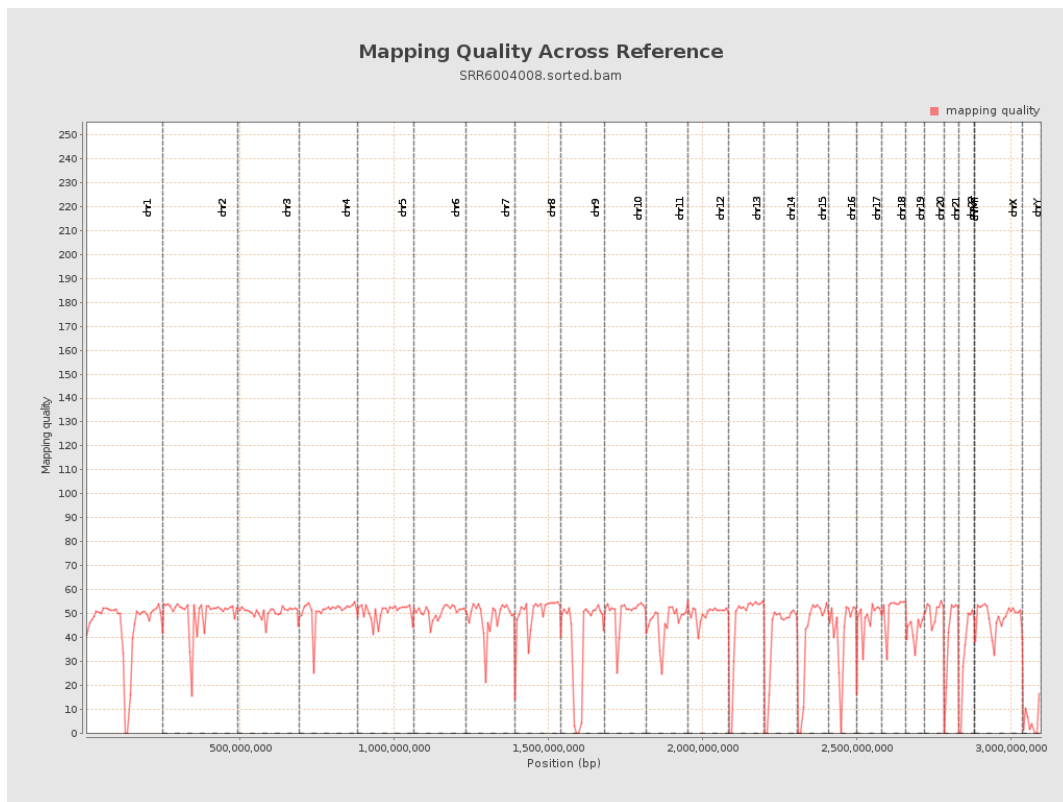
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

