

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 00:27:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6004081.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_SRR6004081 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6004081.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 00:27:35 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6004081.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,160,428
Mapped reads	1,857,458 / 85.98%
Unmapped reads	302,970 / 14.02%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,527 / 1.04%
Read min/max/mean length	30 / 76 / 76.36
Duplicated reads (estimated)	181,099 / 8.38%
Duplication rate	7.83%
Clipped reads	999,380 / 46.26%

2.2. ACGT Content

Number/percentage of A's	33,114,231 / 27.55%
Number/percentage of C's	22,275,631 / 18.53%
Number/percentage of T's	37,873,559 / 31.51%
Number/percentage of G's	26,908,061 / 22.39%
Number/percentage of N's	14,203 / 0.01%
GC Percentage	40.92%

2.3. Coverage

Mean	0.0388

Standard Deviation	0.378
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2.4. Mapping Quality

Mean Mapping Quality	41.17
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2.5. Mismatches and indels

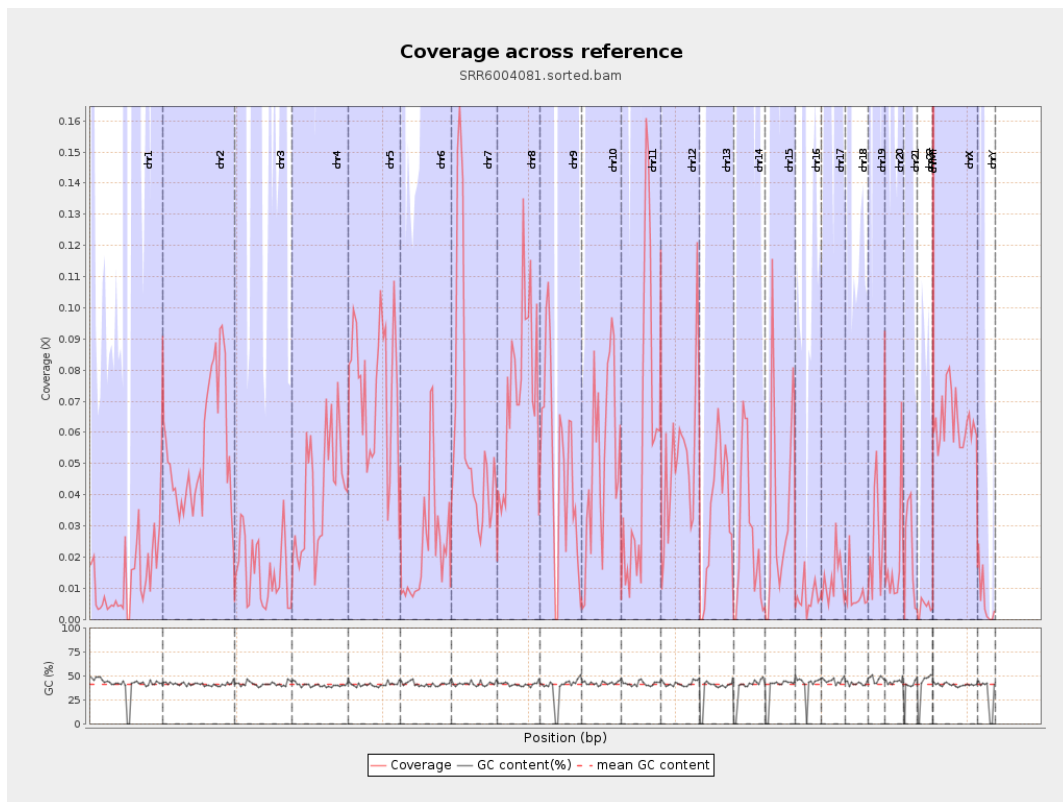
General error rate	0.78%
Mismatches	922,371
Insertions	8,201
Mapped reads with at least one insertion	0.44%
Deletions	30,679
Mapped reads with at least one deletion	1.63%
Homopolymer indels	44.32%

2.6. Chromosome stats

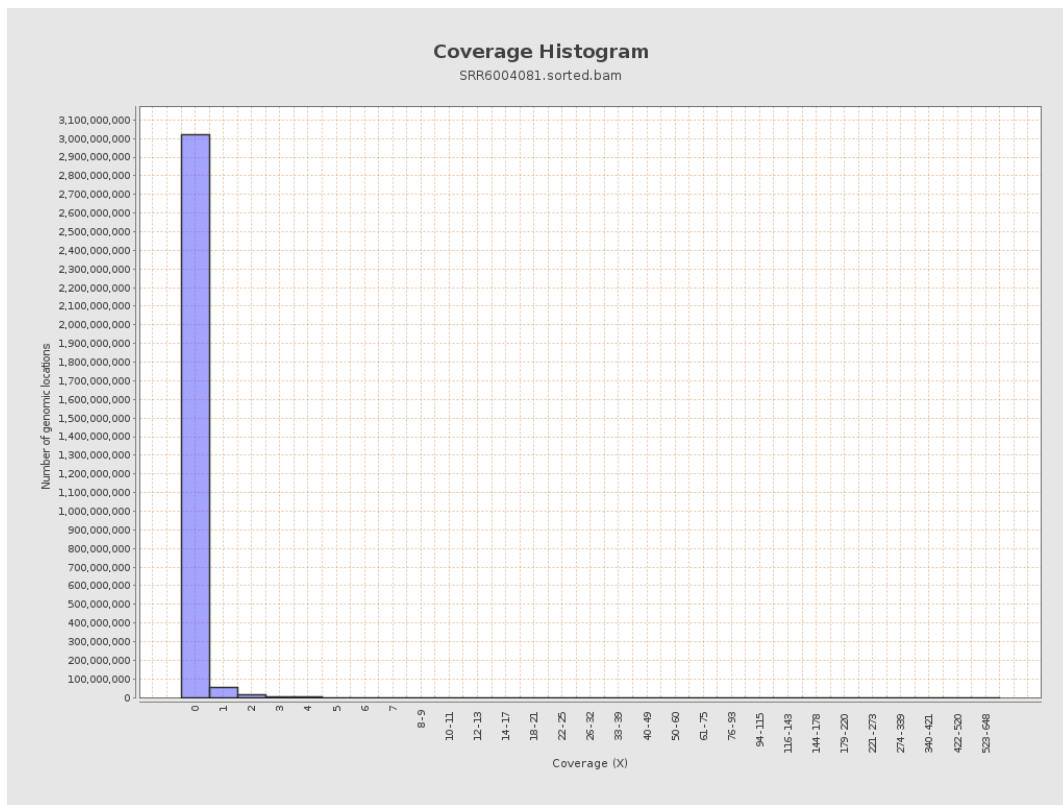
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3469633	0.0139	0.4589
chr2	243199373	13192178	0.0542	0.4627
chr3	198022430	3123018	0.0158	0.1757
chr4	191154276	7937422	0.0415	0.3201
chr5	180915260	13158784	0.0727	0.3984
chr6	171115067	3911389	0.0229	0.2322
chr7	159138663	9421380	0.0592	0.4448

chr8	146364022	10749276	0.0734	0.512
chr9	141213431	7080890	0.0501	0.5024
chr10	135534747	6989338	0.0516	0.4198
chr11	135006516	7206373	0.0534	0.3663
chr12	133851895	6708526	0.0501	0.3426
chr13	115169878	3919202	0.034	0.2648
chr14	107349540	2940818	0.0274	0.3325
chr15	102531392	3751761	0.0366	0.2879
chr16	90354753	628998	0.007	0.2264
chr17	81195210	1088811	0.0134	0.1695
chr18	78077248	637529	0.0082	0.6569
chr19	59128983	1736751	0.0294	0.3857
chr20	63025520	1254000	0.0199	0.2144
chr21	48129895	978432	0.0203	0.2595
chr22	51304566	200355	0.0039	0.0756
chrMT	16571	30627	1.8482	2.2329
chrX	155270560	9765158	0.0629	0.3918
chrY	59373566	358489	0.006	0.1503

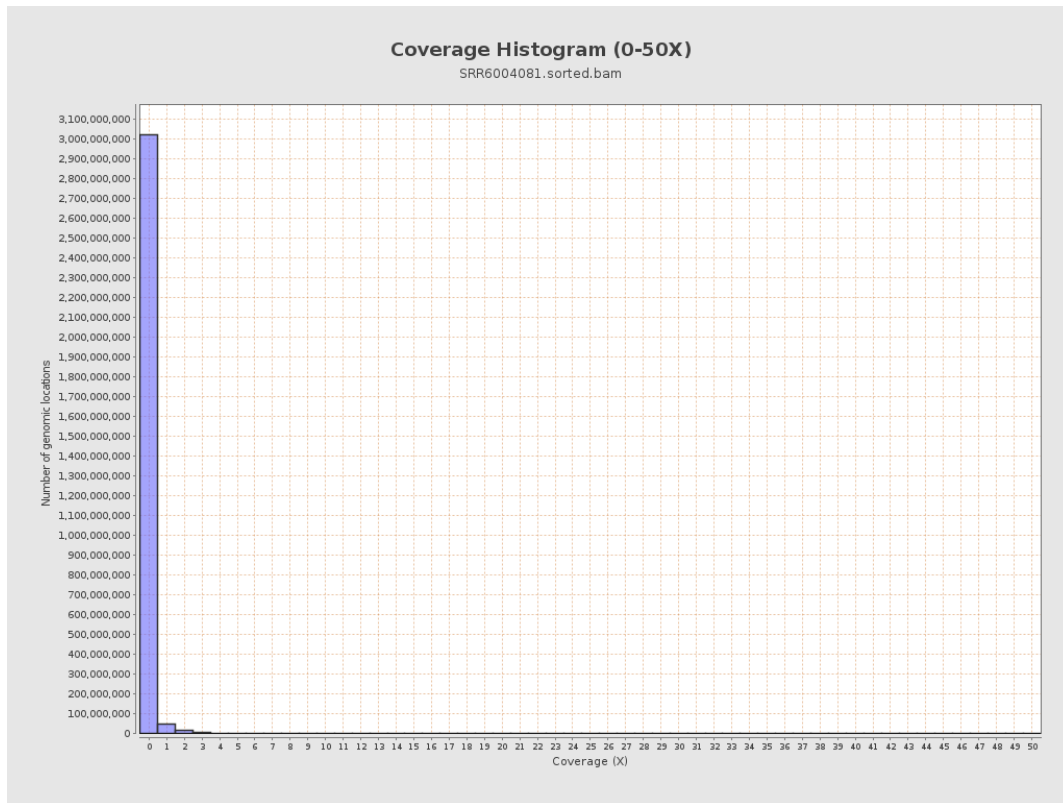
3. Results : Coverage across reference



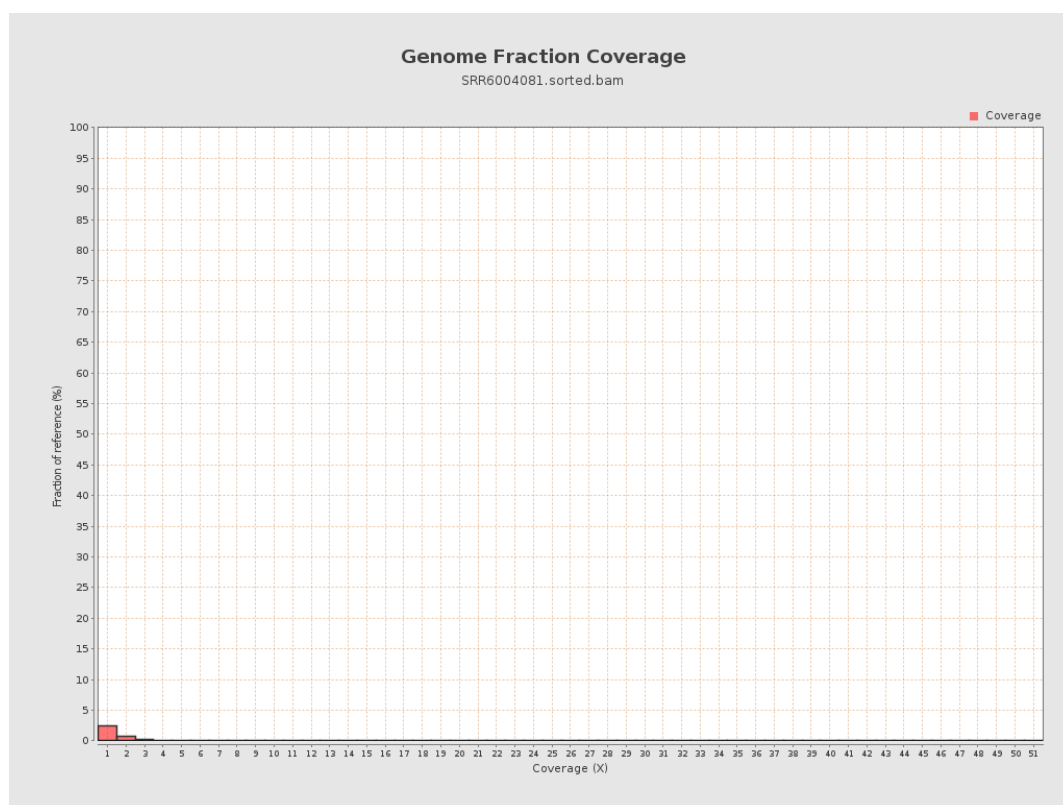
4. Results : Coverage Histogram



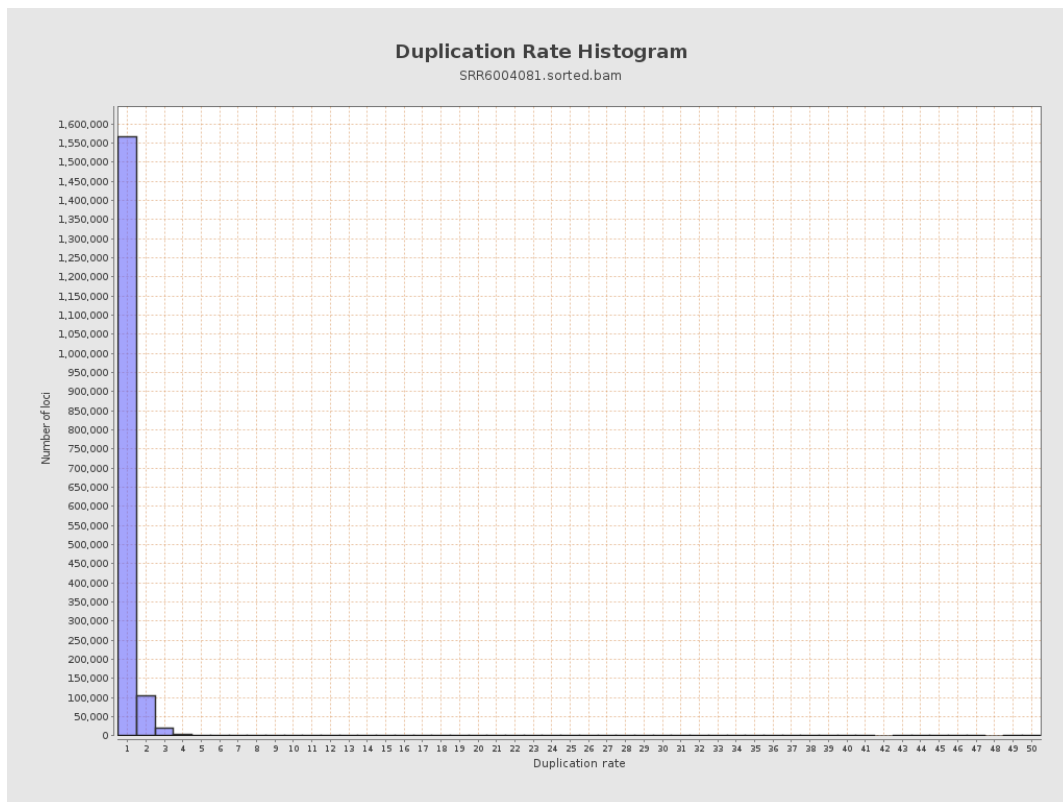
5. Results : Coverage Histogram (0-50X)



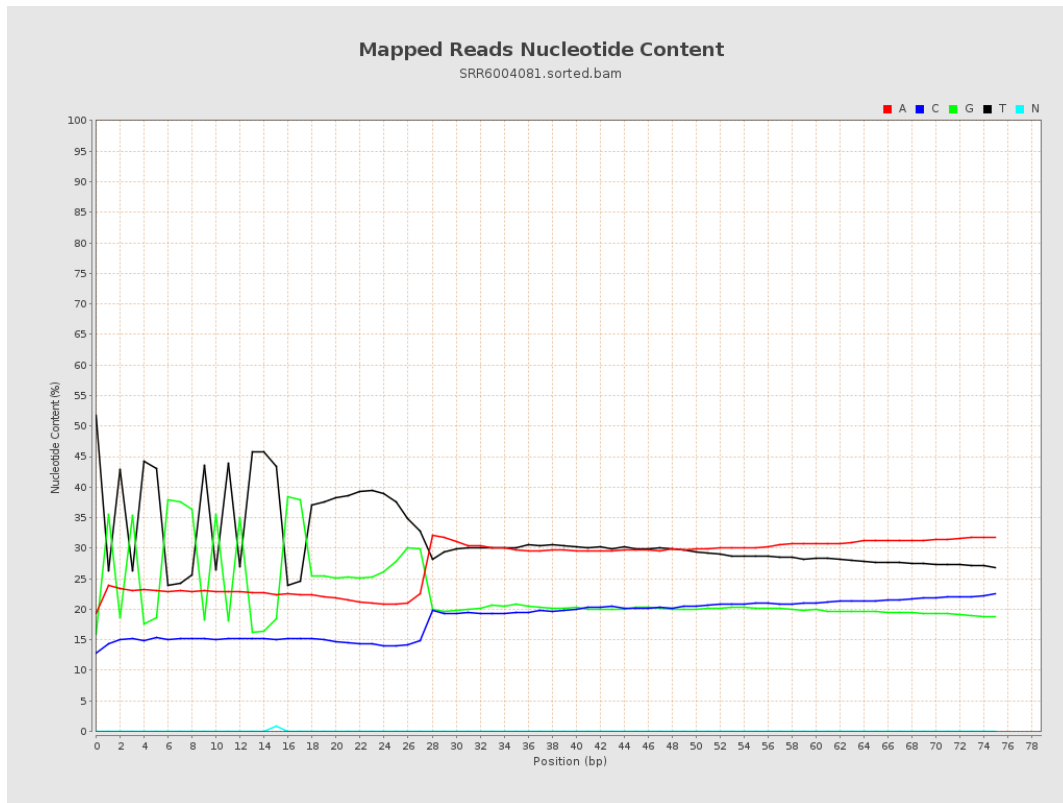
6. Results : Genome Fraction Coverage



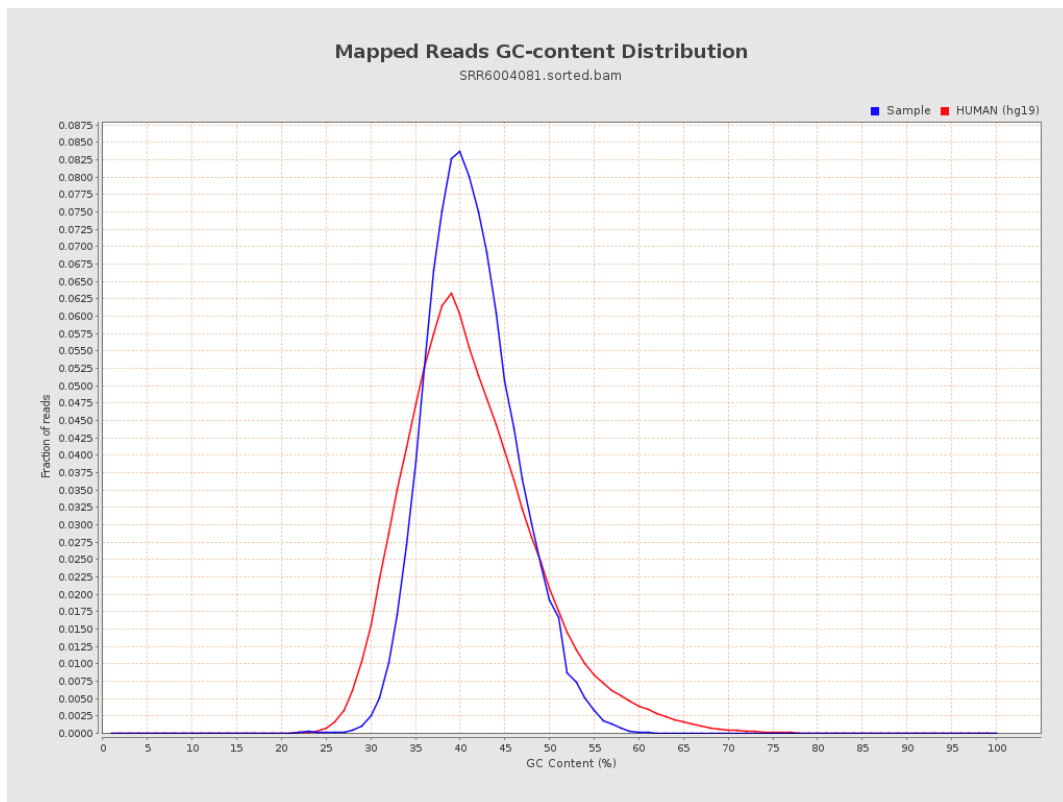
7. Results : Duplication Rate Histogram



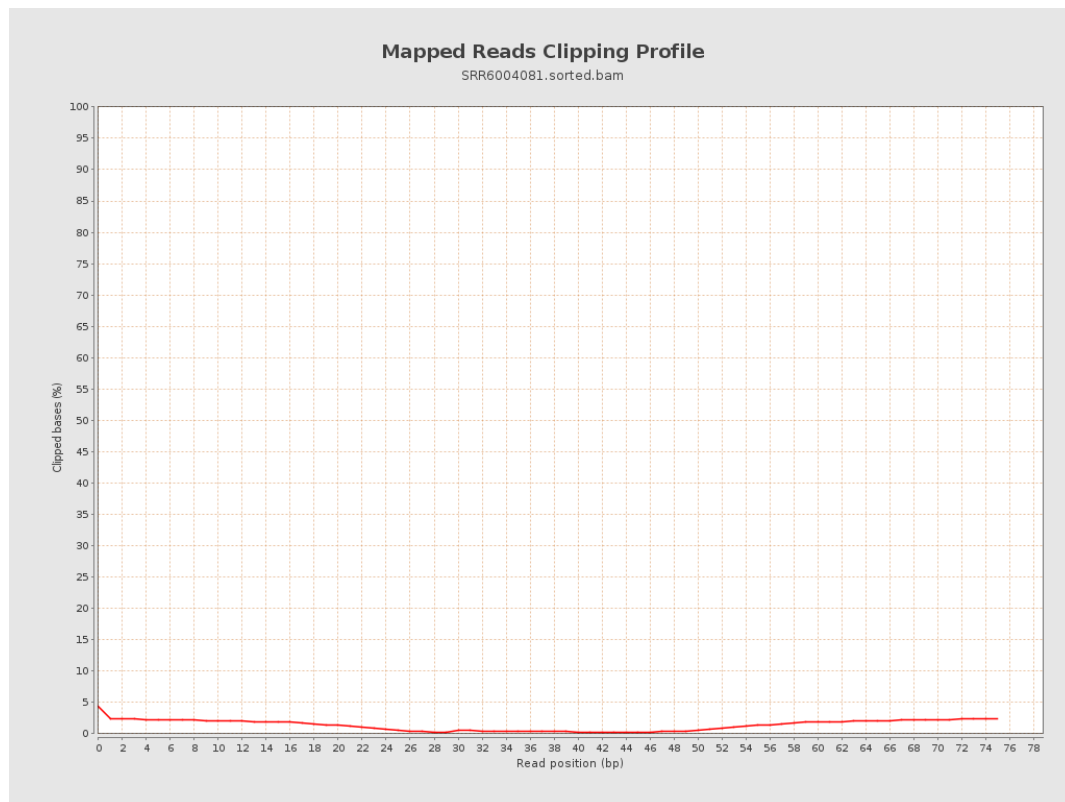
8. Results : Mapped Reads Nucleotide Content



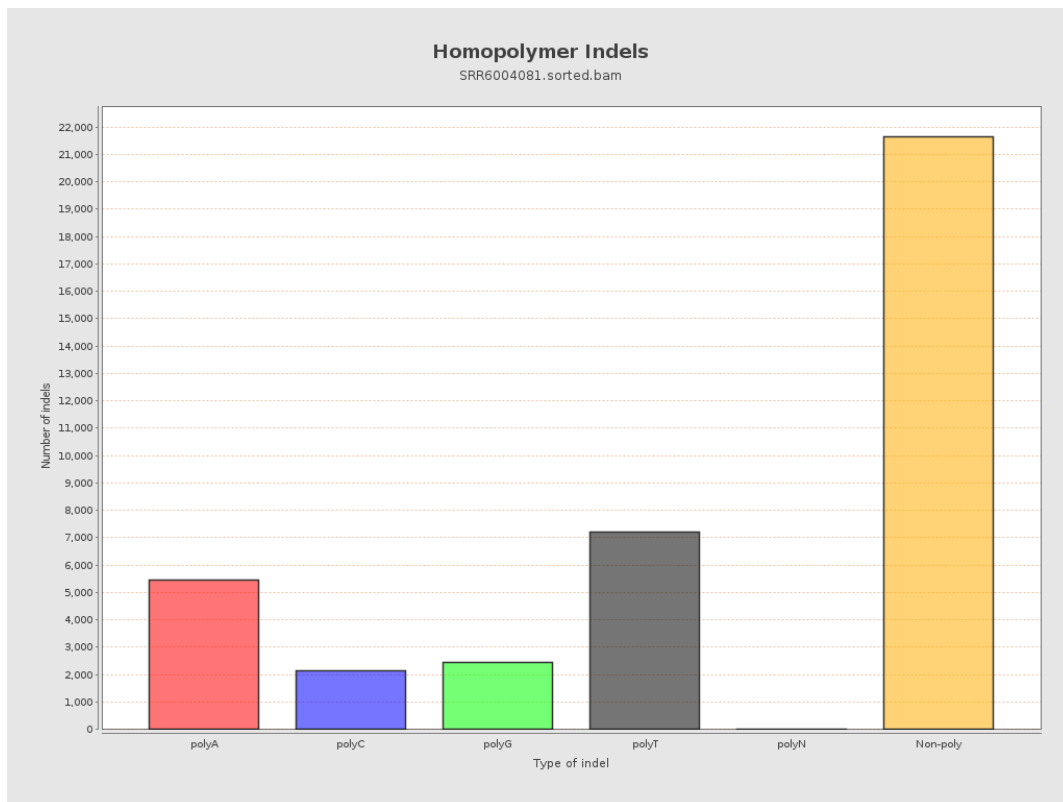
9. Results : Mapped Reads GC-content Distribution



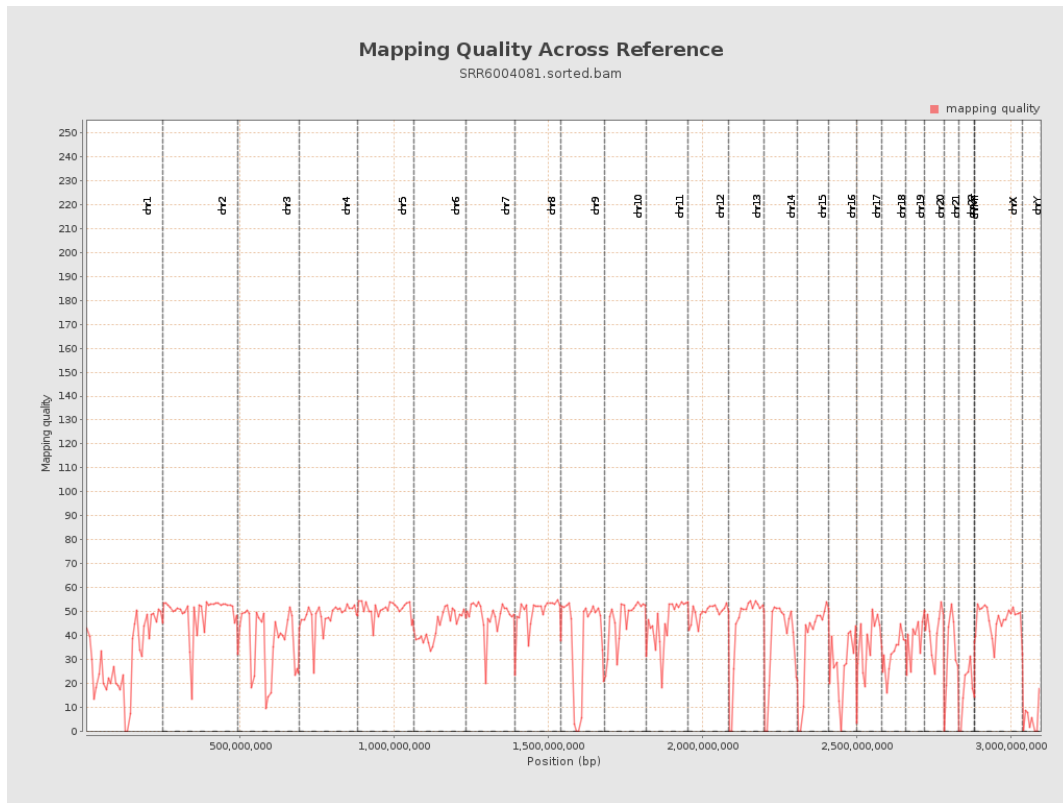
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

