

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/13 19:23:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6003990.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_SRR6003990 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6003990.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Sep 13 19:23:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6003990.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,329,390
Mapped reads	1,679,619 / 72.11%
Unmapped reads	649,771 / 27.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,416 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	267,978 / 11.5%
Duplication rate	12.2%
Clipped reads	928,510 / 39.86%

2.2. ACGT Content

Number/percentage of A's	29,092,376 / 27.05%
Number/percentage of C's	18,585,928 / 17.28%
Number/percentage of T's	36,301,917 / 33.76%
Number/percentage of G's	23,549,924 / 21.9%
Number/percentage of N's	10,527 / 0.01%
GC Percentage	39.18%

2.3. Coverage

Mean	0.0348

Standard Deviation	0.3966
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2.4. Mapping Quality

Mean Mapping Quality	46.15
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2.5. Mismatches and indels

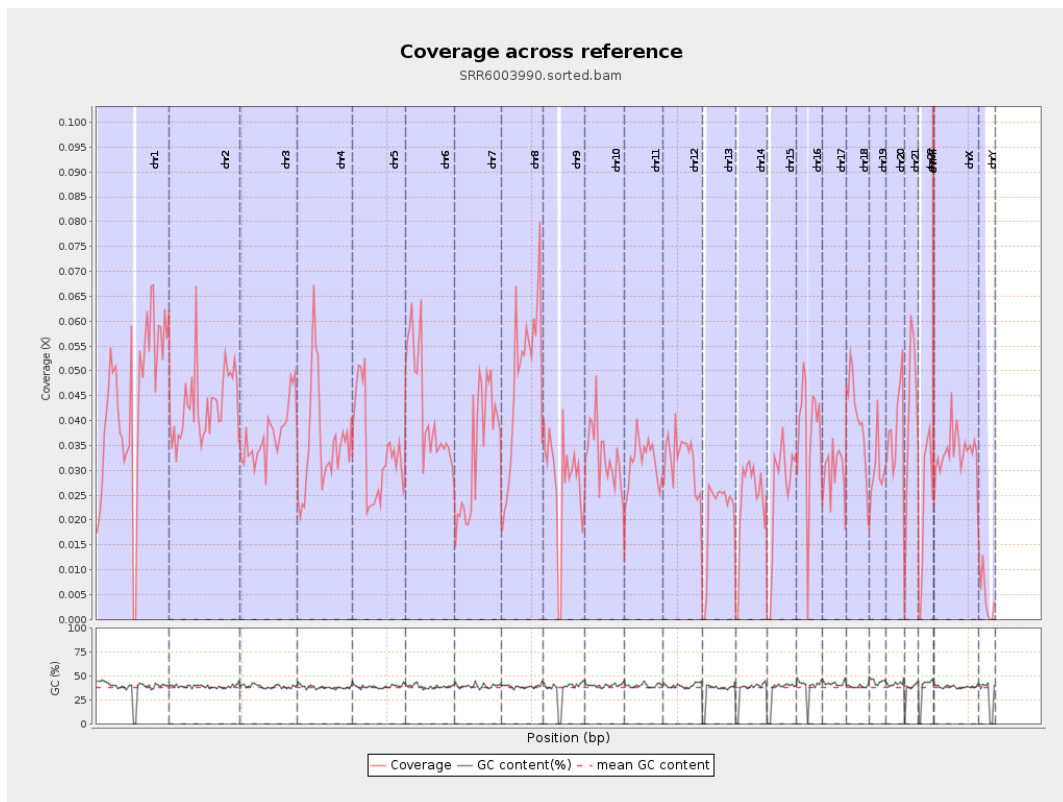
General error rate	1.05%
Mismatches	1,112,597
Insertions	9,438
Mapped reads with at least one insertion	0.56%
Deletions	34,286
Mapped reads with at least one deletion	2.02%
Homopolymer indels	49.52%

2.6. Chromosome stats

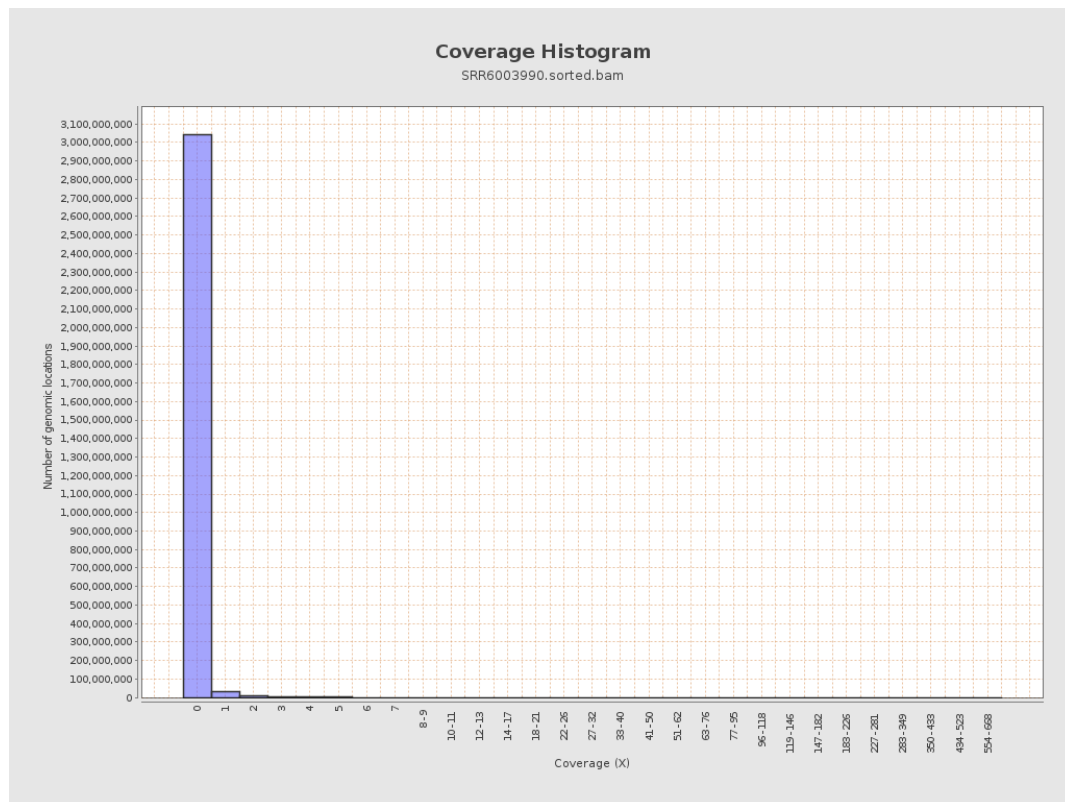
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10954078	0.0439	0.6047
chr2	243199373	10484604	0.0431	0.5112
chr3	198022430	7367912	0.0372	0.3304
chr4	191154276	6733184	0.0352	0.3249
chr5	180915260	6079789	0.0336	0.3126
chr6	171115067	7213628	0.0422	0.3845
chr7	159138663	5468407	0.0344	0.4081

chr8	146364022	6995319	0.0478	0.5247
chr9	141213431	3868760	0.0274	0.3633
chr10	135534747	4478707	0.033	0.3545
chr11	135006516	4247565	0.0315	0.3672
chr12	133851895	4273199	0.0319	0.3052
chr13	115169878	2391690	0.0208	0.2445
chr14	107349540	2517400	0.0235	0.2747
chr15	102531392	2603649	0.0254	0.2714
chr16	90354753	3392359	0.0375	0.3325
chr17	81195210	2400061	0.0296	0.2941
chr18	78077248	3186722	0.0408	0.6226
chr19	59128983	1788618	0.0302	0.4124
chr20	63025520	2432426	0.0386	0.3352
chr21	48129895	1961286	0.0407	0.3527
chr22	51304566	1193220	0.0233	0.2461
chrMT	16571	83546	5.0417	5.3357
chrX	155270560	5225158	0.0337	0.3259
chrY	59373566	256048	0.0043	0.1109

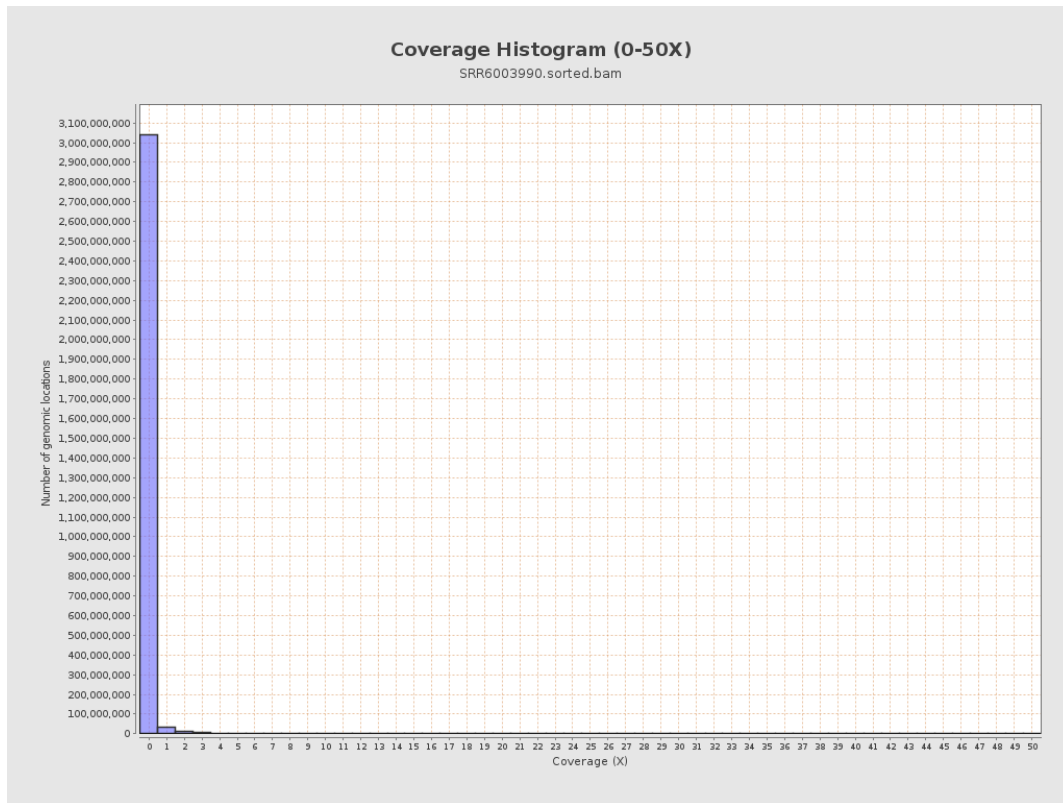
3. Results : Coverage across reference



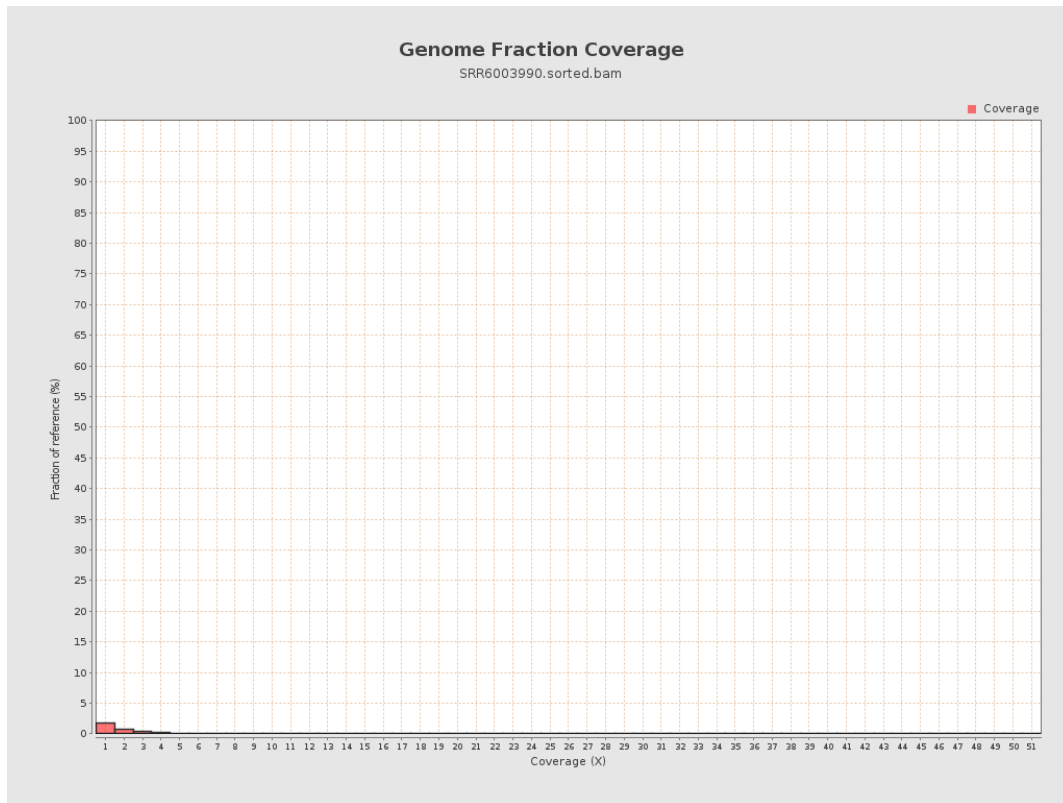
4. Results : Coverage Histogram



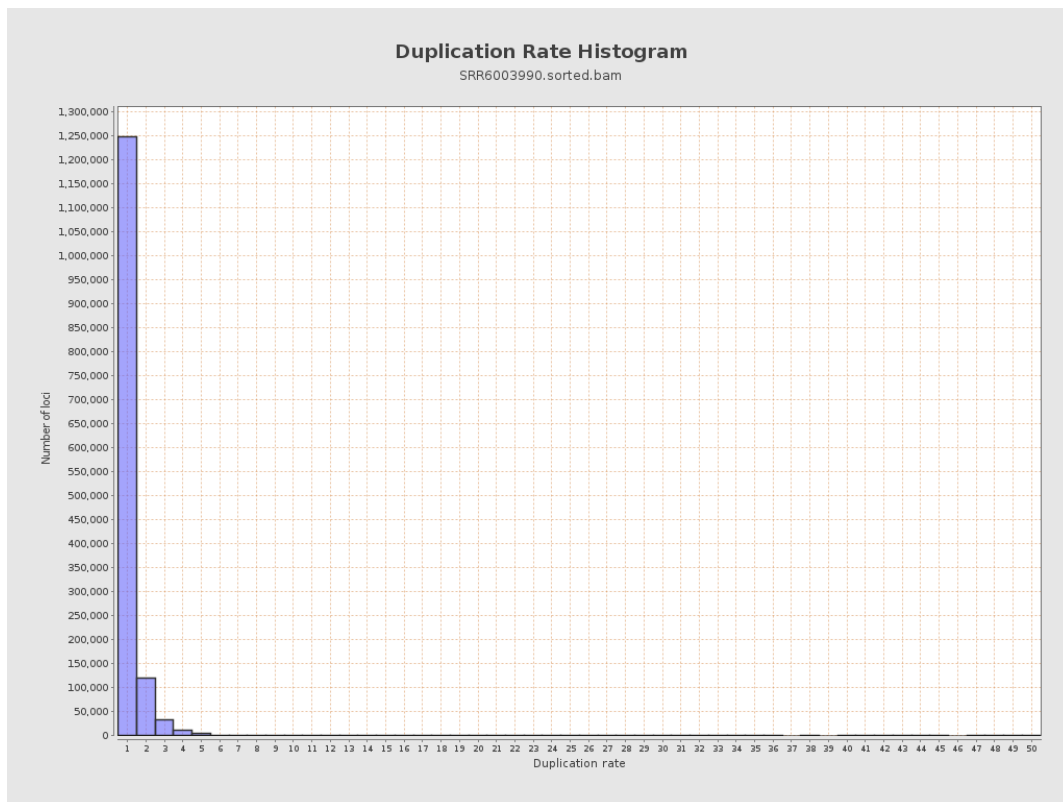
5. Results : Coverage Histogram (0-50X)



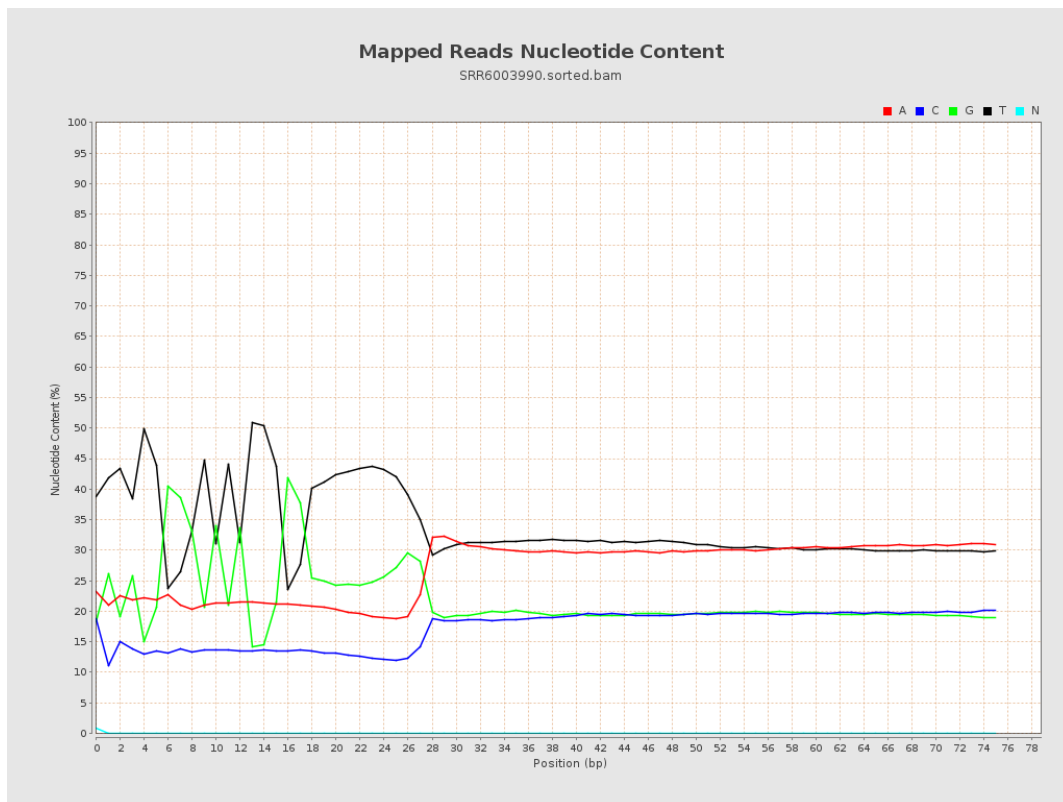
6. Results : Genome Fraction Coverage



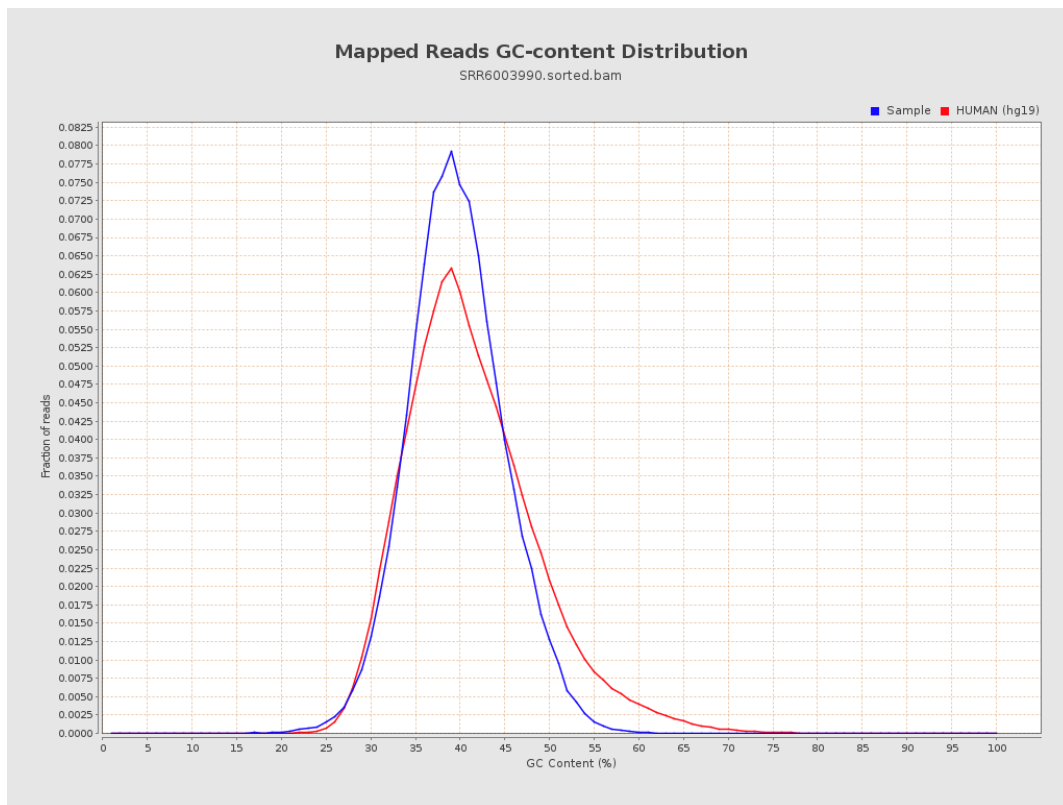
7. Results : Duplication Rate Histogram



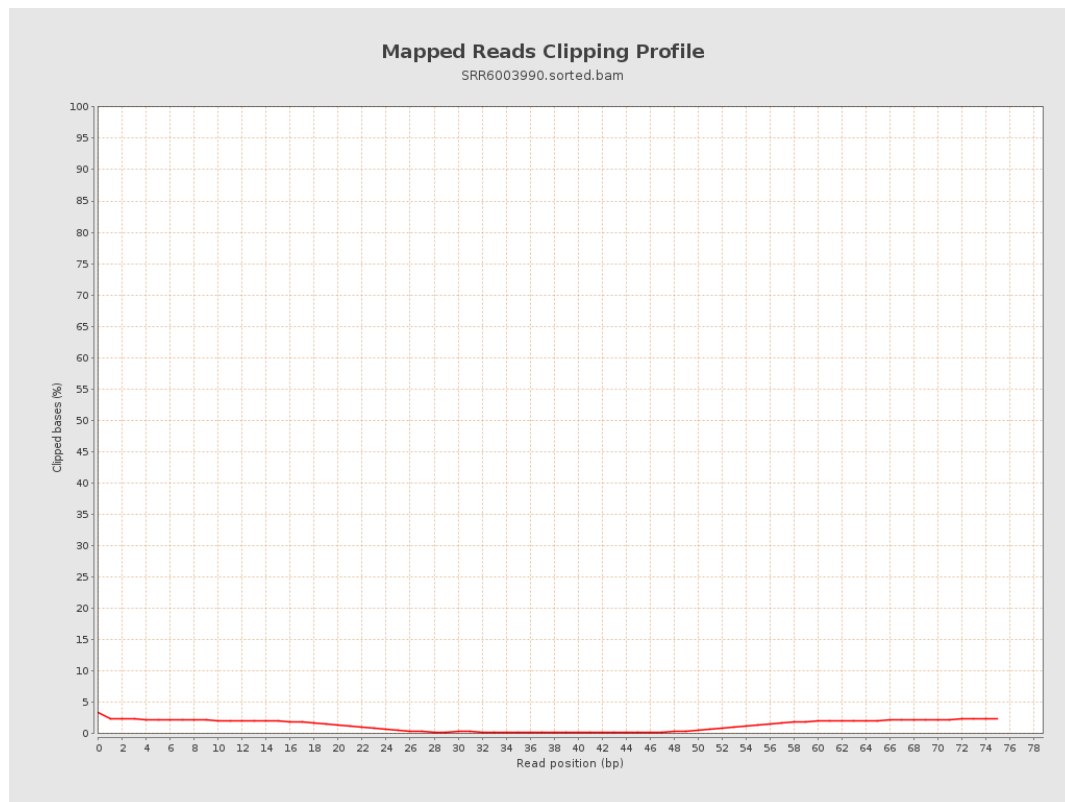
8. Results : Mapped Reads Nucleotide Content



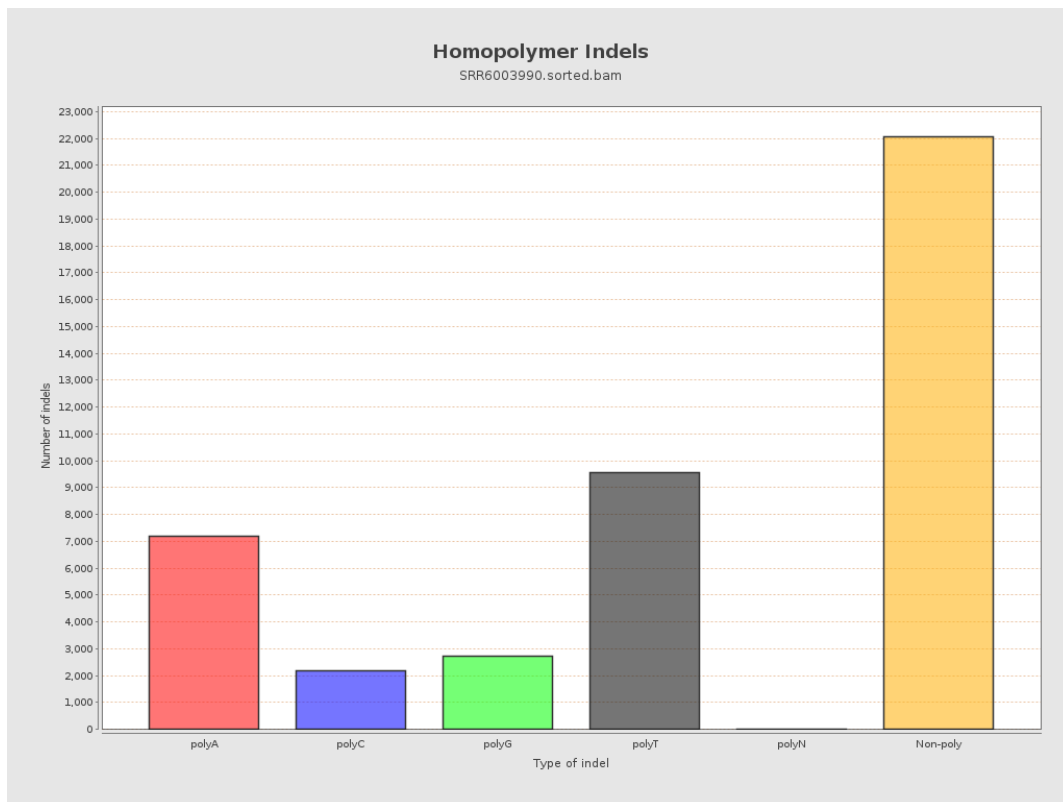
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

