

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:32:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008745.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_SRR6008745 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008745.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:32:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008745.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,971,117
Mapped reads	2,687,501 / 90.45%
Unmapped reads	283,616 / 9.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,719 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	127,103 / 4.28%
Duplication rate	3.14%
Clipped reads	1,310,686 / 44.11%

2.2. ACGT Content

Number/percentage of A's	47,542,585 / 27.07%
Number/percentage of C's	31,700,791 / 18.05%
Number/percentage of T's	55,794,320 / 31.76%
Number/percentage of G's	40,576,247 / 23.1%
Number/percentage of N's	33,996 / 0.02%
GC Percentage	41.15%

2.3. Coverage

Mean	0.0568

Standard Deviation	0.6717
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2.4. Mapping Quality

Mean Mapping Quality	44
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2.5. Mismatches and indels

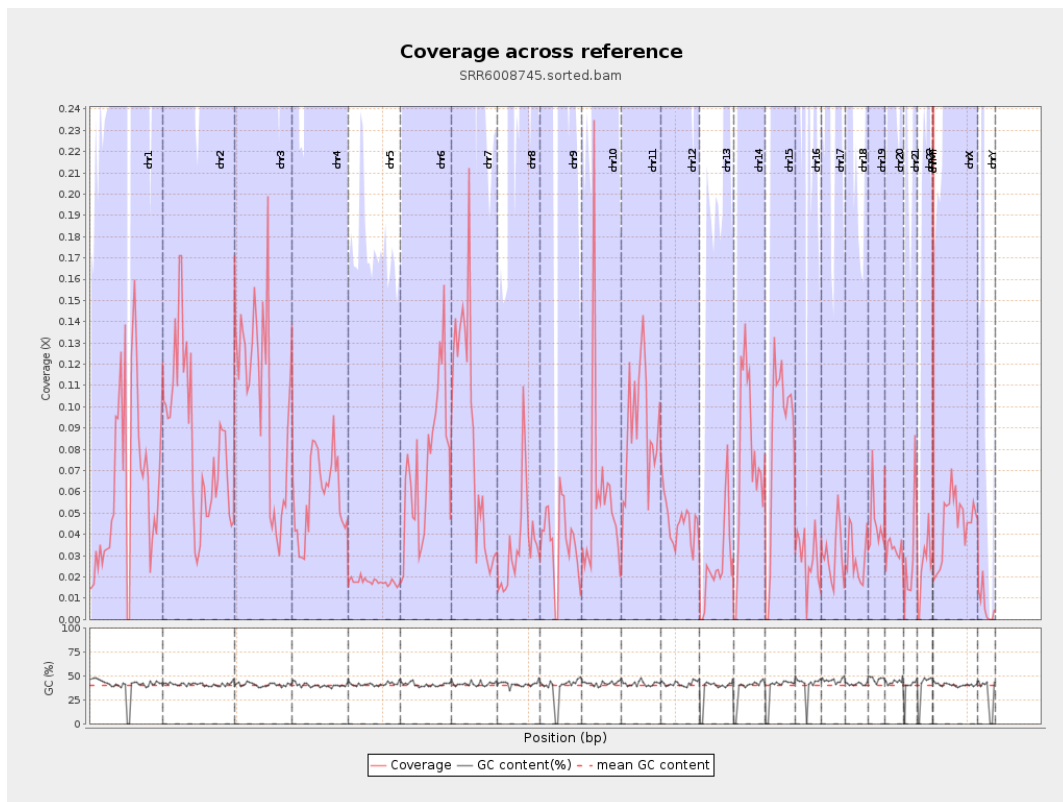
General error rate	0.73%
Mismatches	1,259,245
Insertions	13,906
Mapped reads with at least one insertion	0.51%
Deletions	49,311
Mapped reads with at least one deletion	1.82%
Homopolymer indels	47.26%

2.6. Chromosome stats

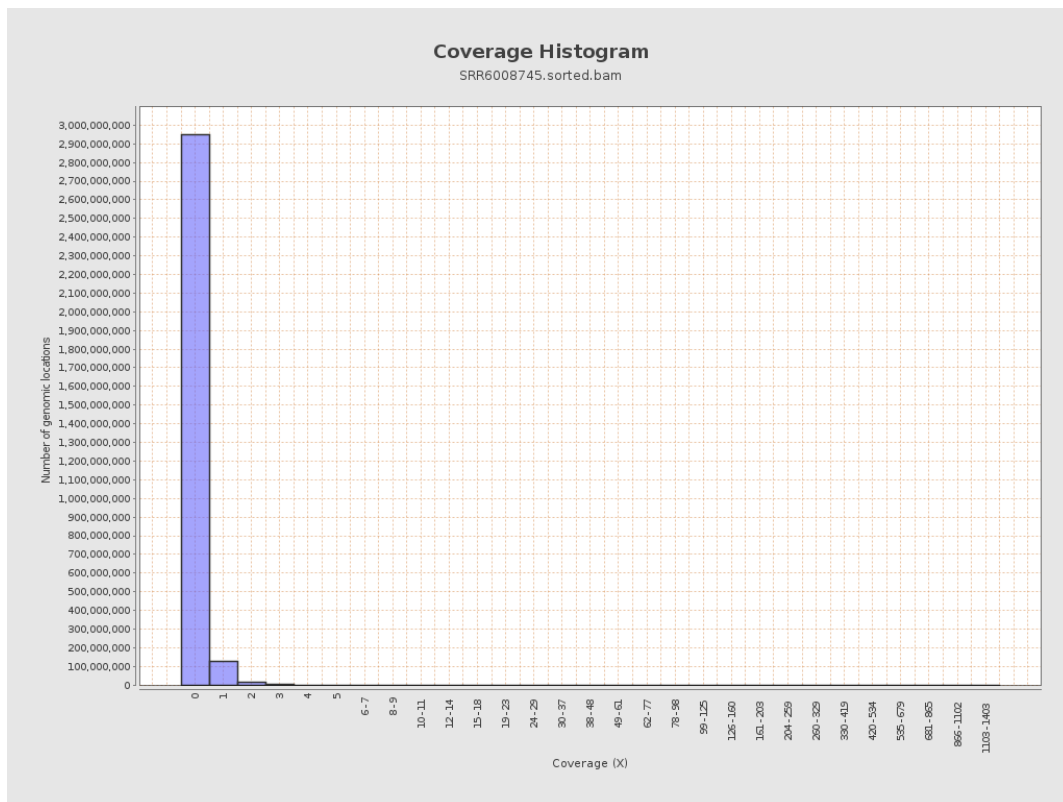
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	15401522	0.0618	0.9994
chr2	243199373	20392684	0.0839	0.4938
chr3	198022430	20493778	0.1035	0.4382
chr4	191154276	11256414	0.0589	0.2928
chr5	180915260	3211150	0.0177	0.1568
chr6	171115067	12662635	0.074	0.4166
chr7	159138663	13550988	0.0852	1.7225

chr8	146364022	5254896	0.0359	0.5454
chr9	141213431	5256376	0.0372	0.3872
chr10	135534747	7614177	0.0562	1.4443
chr11	135006516	12194517	0.0903	0.4736
chr12	133851895	6149555	0.0459	0.2544
chr13	115169878	3016797	0.0262	0.1845
chr14	107349540	8192192	0.0763	0.3278
chr15	102531392	8677042	0.0846	0.3338
chr16	90354753	2518586	0.0279	0.2827
chr17	81195210	2546395	0.0314	0.2221
chr18	78077248	2247917	0.0288	0.844
chr19	59128983	2735799	0.0463	0.607
chr20	63025520	2064265	0.0328	0.2239
chr21	48129895	1529433	0.0318	0.2243
chr22	51304566	1302671	0.0254	0.1814
chrMT	16571	109988	6.6374	4.4799
chrX	155270560	6956538	0.0448	0.3004
chrY	59373566	392805	0.0066	0.1669

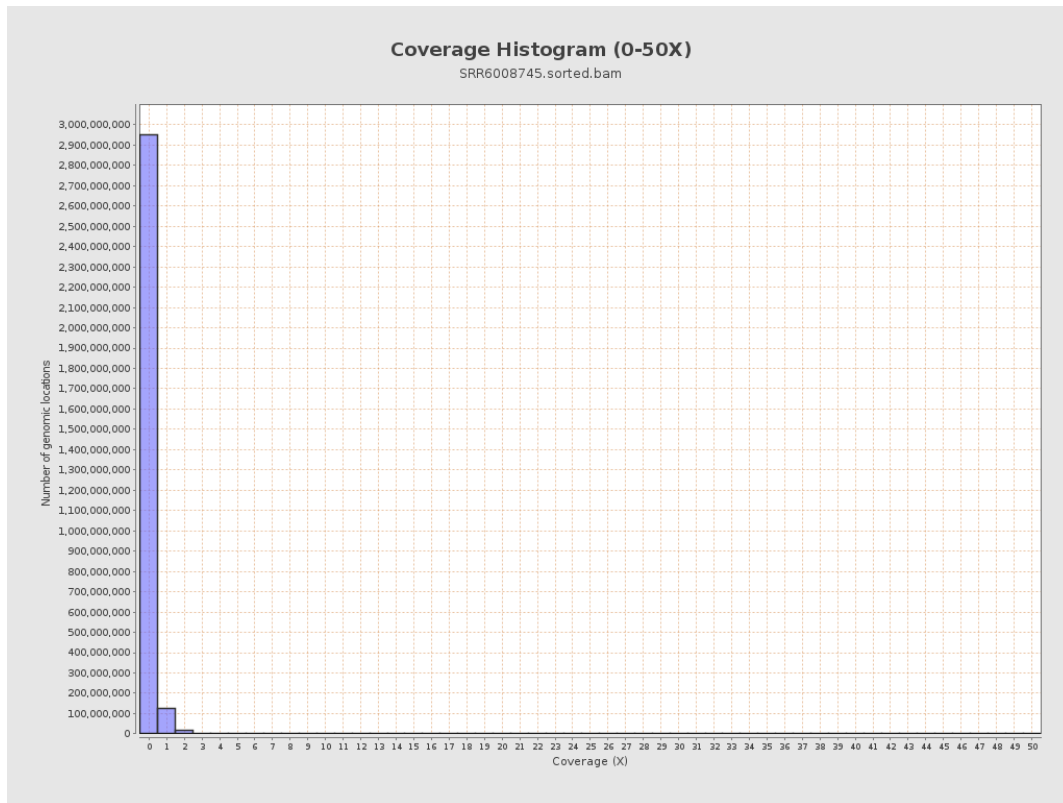
3. Results : Coverage across reference



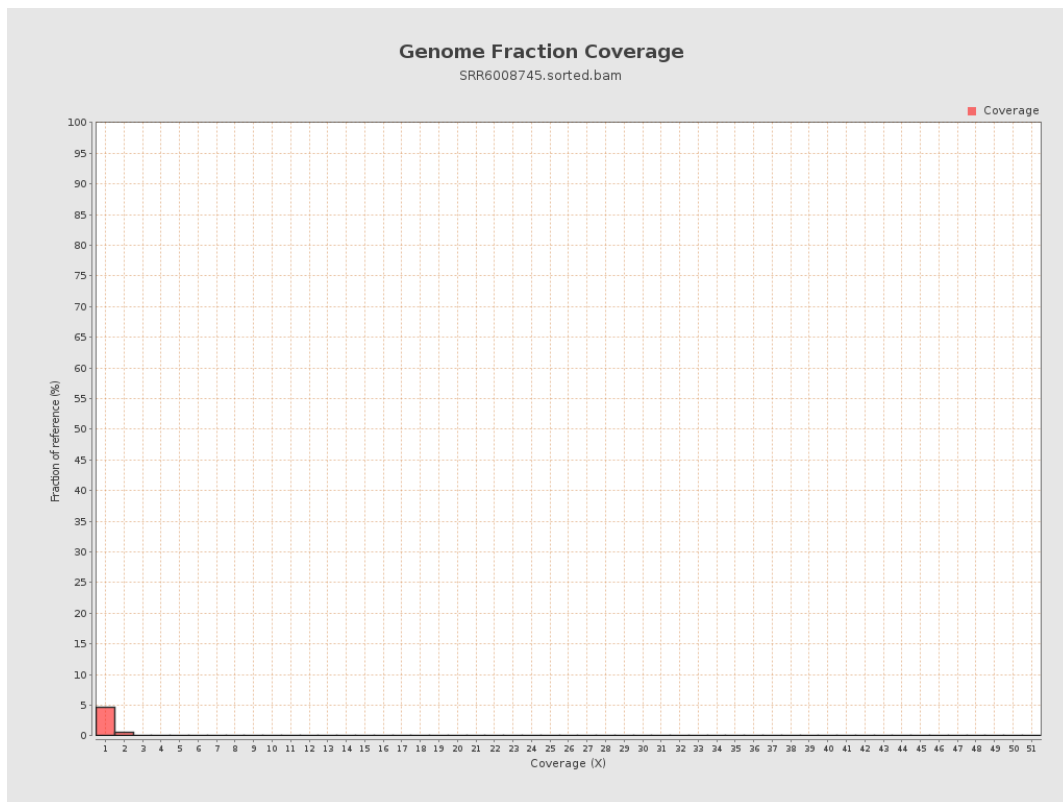
4. Results : Coverage Histogram



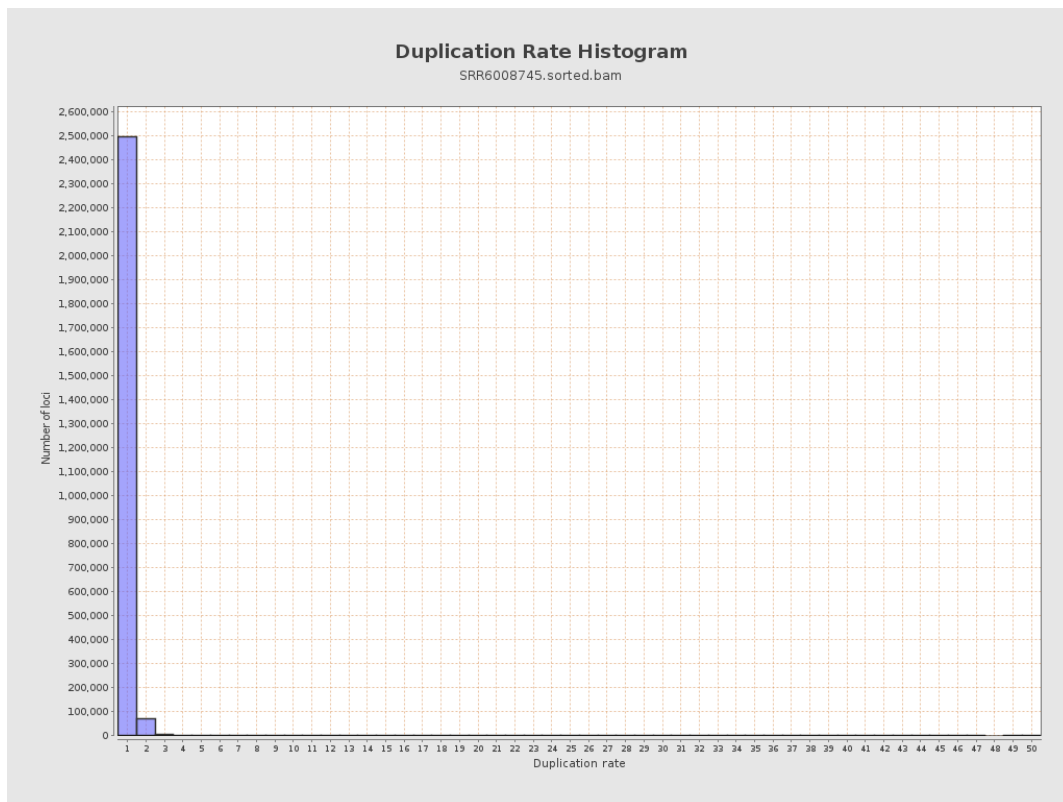
5. Results : Coverage Histogram (0-50X)



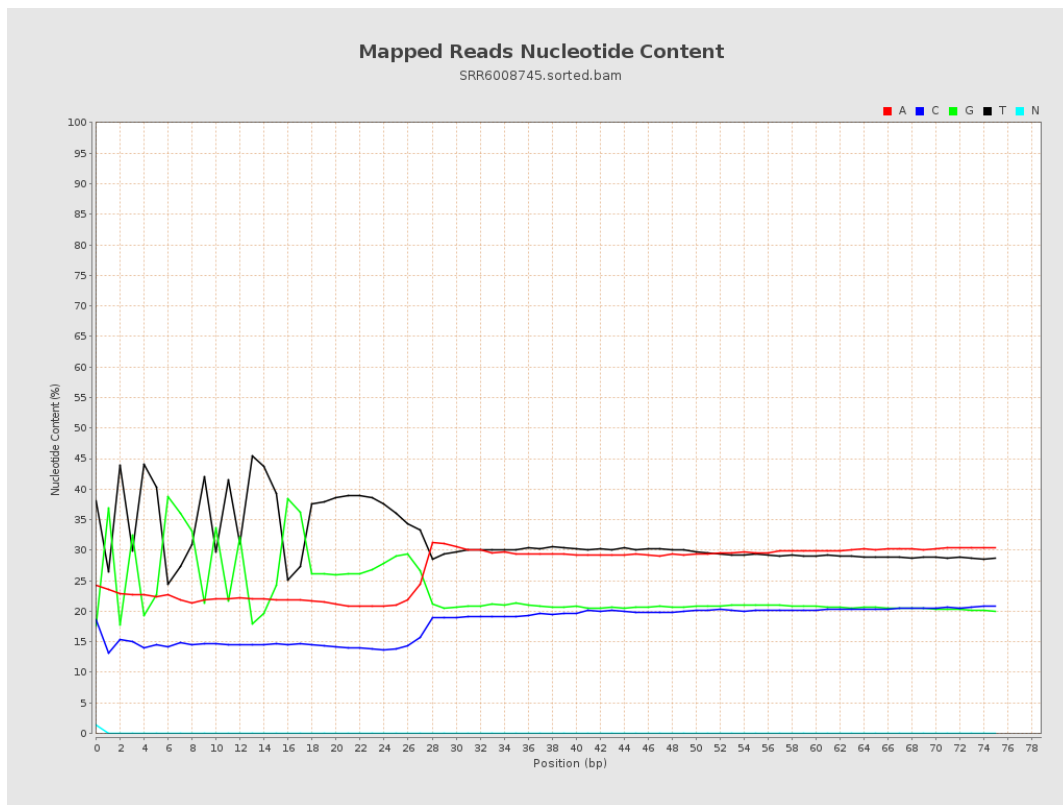
6. Results : Genome Fraction Coverage



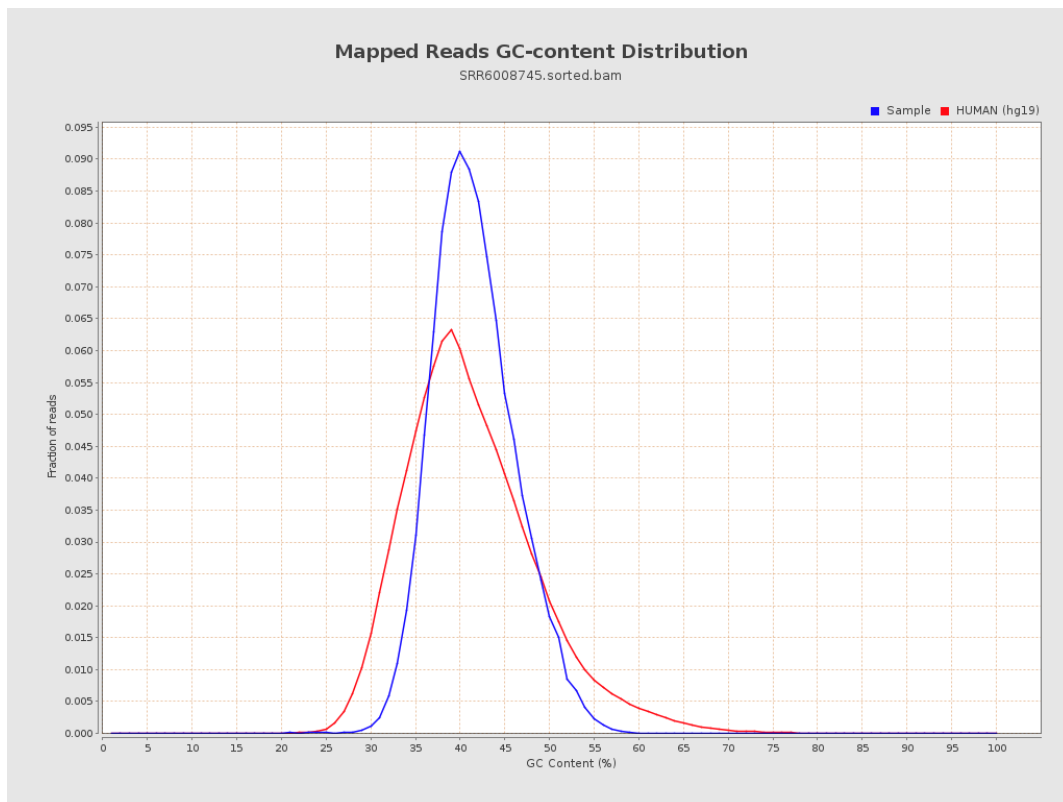
7. Results : Duplication Rate Histogram



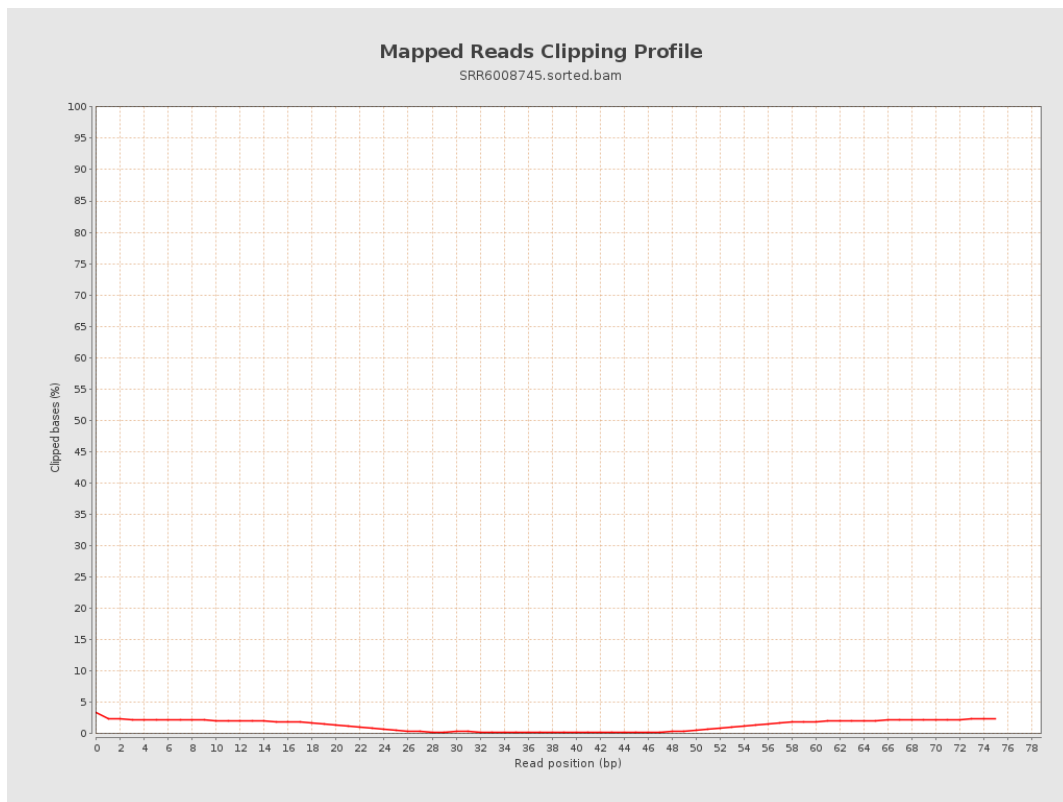
8. Results : Mapped Reads Nucleotide Content



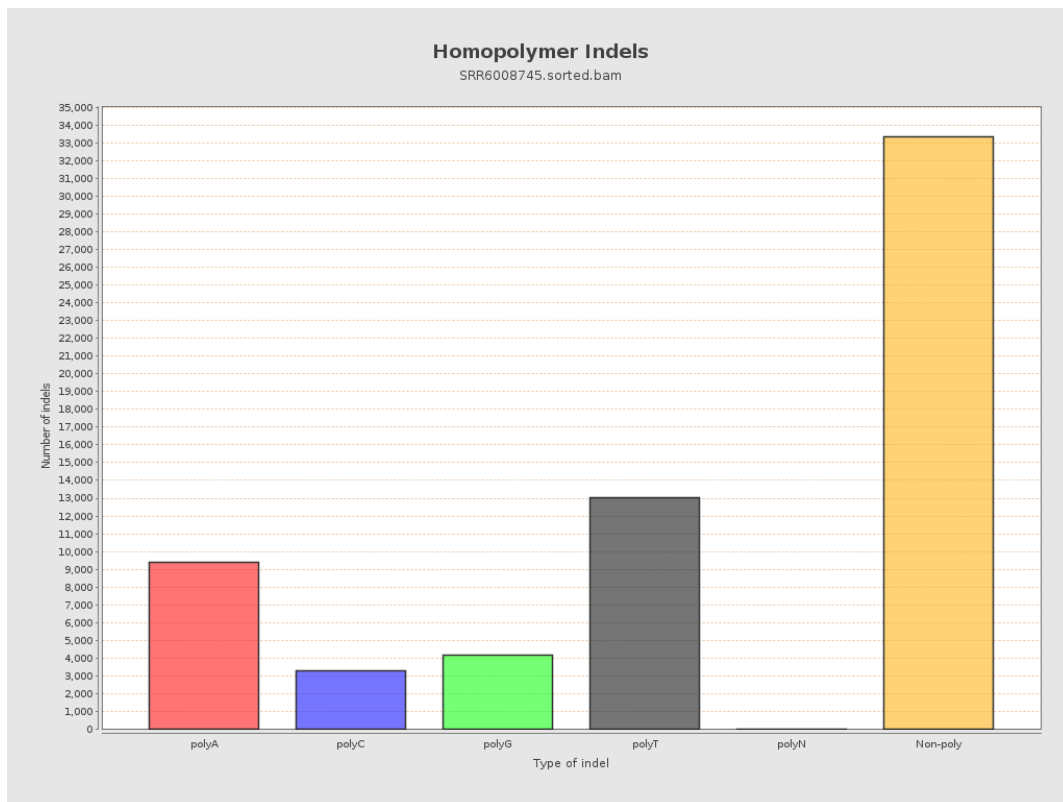
9. Results : Mapped Reads GC-content Distribution



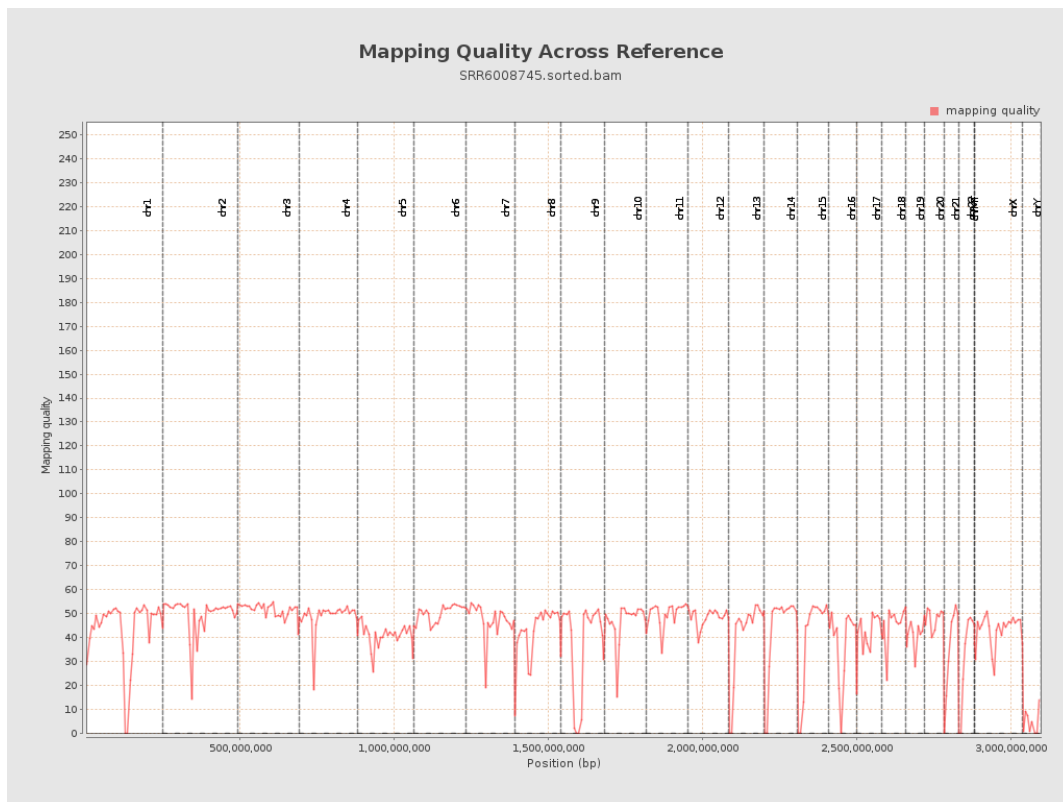
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

