

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 09:22:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008741.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_SRR6008741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 09:22:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,327,378
Mapped reads	1,622,238 / 69.7%
Unmapped reads	705,140 / 30.3%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,245 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	80,858 / 3.47%
Duplication rate	3.65%
Clipped reads	1,170,838 / 50.31%

2.2. ACGT Content

Number/percentage of A's	26,819,437 / 27.85%
Number/percentage of C's	16,050,663 / 16.66%
Number/percentage of T's	29,494,668 / 30.62%
Number/percentage of G's	23,936,124 / 24.85%
Number/percentage of N's	12,847 / 0.01%
GC Percentage	41.52%

2.3. Coverage

Mean	0.0311

Standard Deviation	0.2642
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2.4. Mapping Quality

Mean Mapping Quality	43.54
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2.5. Mismatches and indels

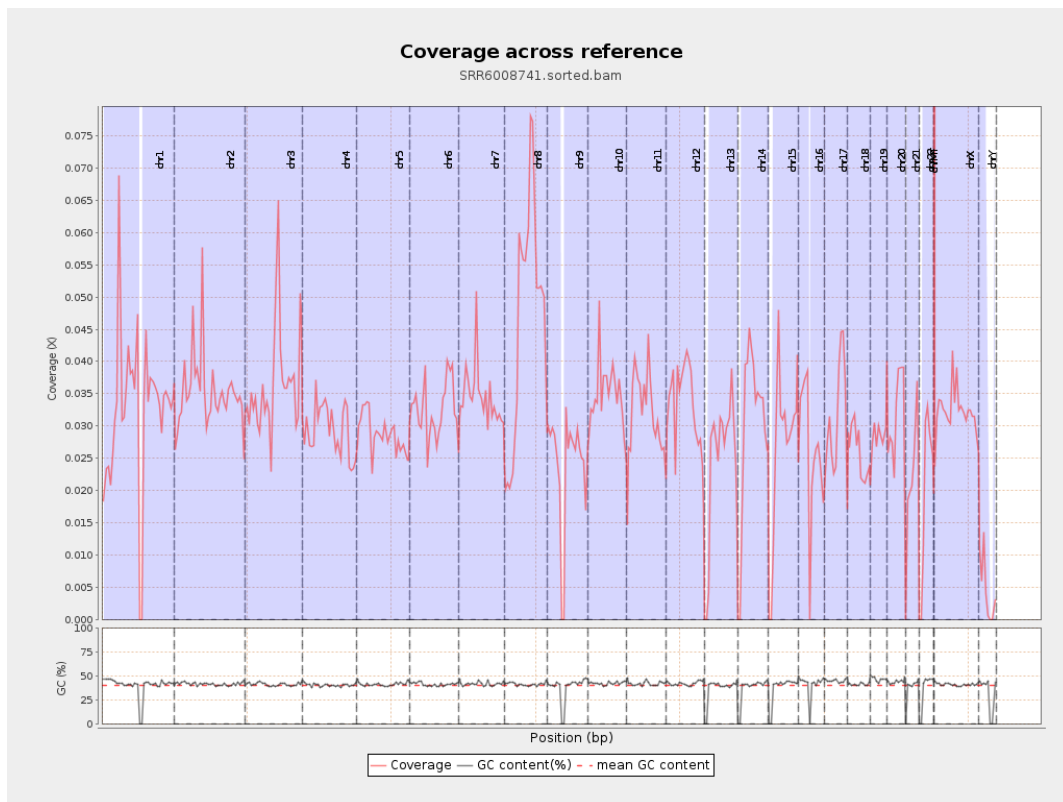
General error rate	1.14%
Mismatches	1,088,712
Insertions	8,375
Mapped reads with at least one insertion	0.51%
Deletions	36,635
Mapped reads with at least one deletion	2.23%
Homopolymer indels	47.42%

2.6. Chromosome stats

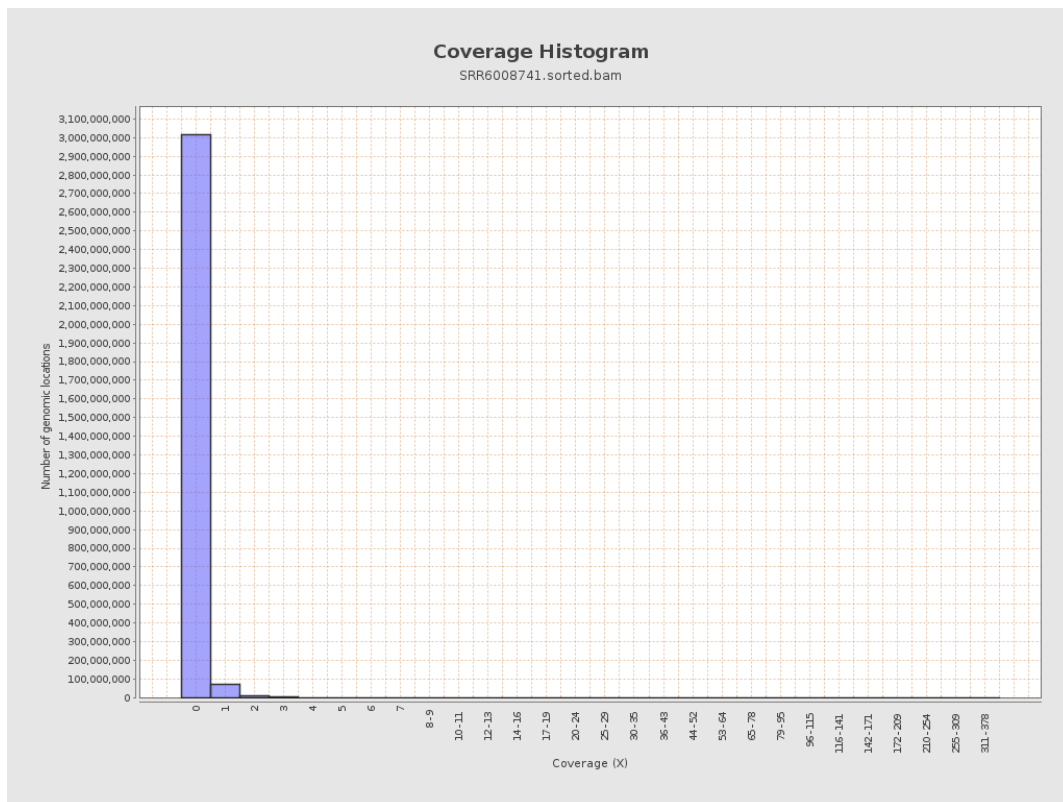
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8087529	0.0324	0.3463
chr2	243199373	8554626	0.0352	0.3357
chr3	198022430	7191891	0.0363	0.2304
chr4	191154276	5618267	0.0294	0.2089
chr5	180915260	5202862	0.0288	0.2006
chr6	171115067	5561514	0.0325	0.2375
chr7	159138663	5493515	0.0345	0.3646

chr8	146364022	6907720	0.0472	0.3411
chr9	141213431	3372867	0.0239	0.2487
chr10	135534747	4714837	0.0348	0.2634
chr11	135006516	4359063	0.0323	0.2704
chr12	133851895	4496257	0.0336	0.2204
chr13	115169878	2812123	0.0244	0.1918
chr14	107349540	3246895	0.0302	0.2111
chr15	102531392	2719847	0.0265	0.1984
chr16	90354753	2348392	0.026	0.2025
chr17	81195210	2536899	0.0312	0.225
chr18	78077248	2015315	0.0258	0.3661
chr19	59128983	1694758	0.0287	0.2565
chr20	63025520	1978790	0.0314	0.2161
chr21	48129895	1074676	0.0223	0.1841
chr22	51304566	1042969	0.0203	0.1641
chrMT	16571	38761	2.3391	2.3128
chrX	155270560	5032927	0.0324	0.23
chrY	59373566	267888	0.0045	0.0988

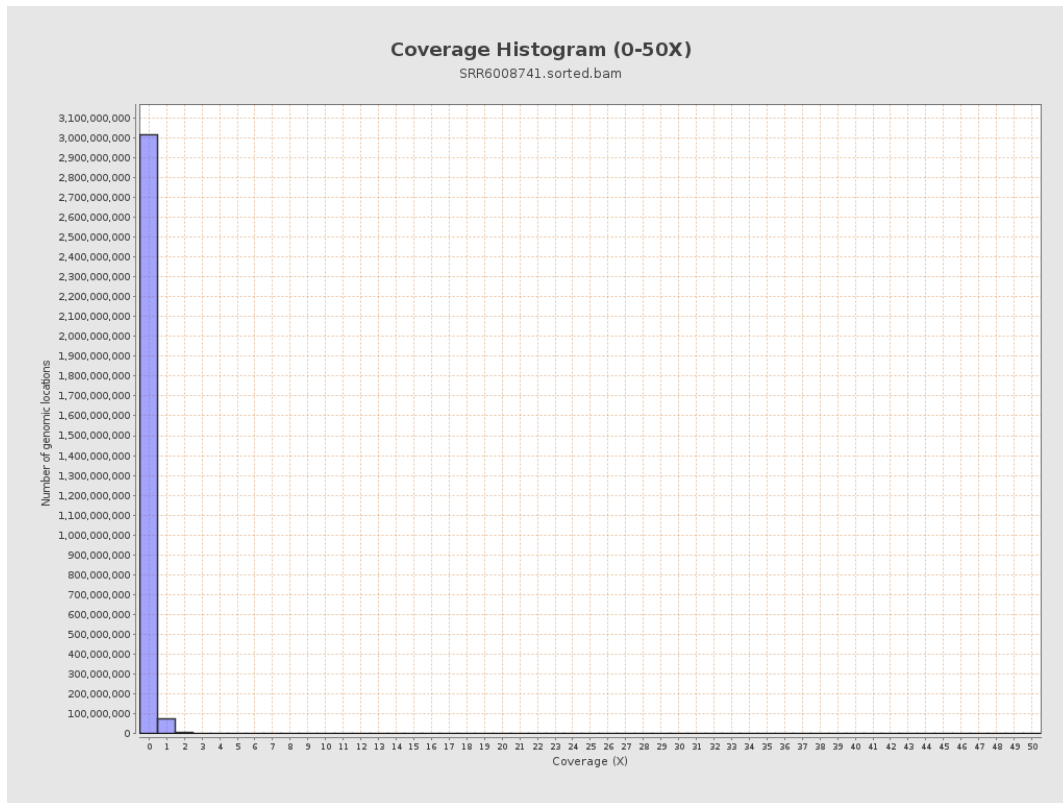
3. Results : Coverage across reference



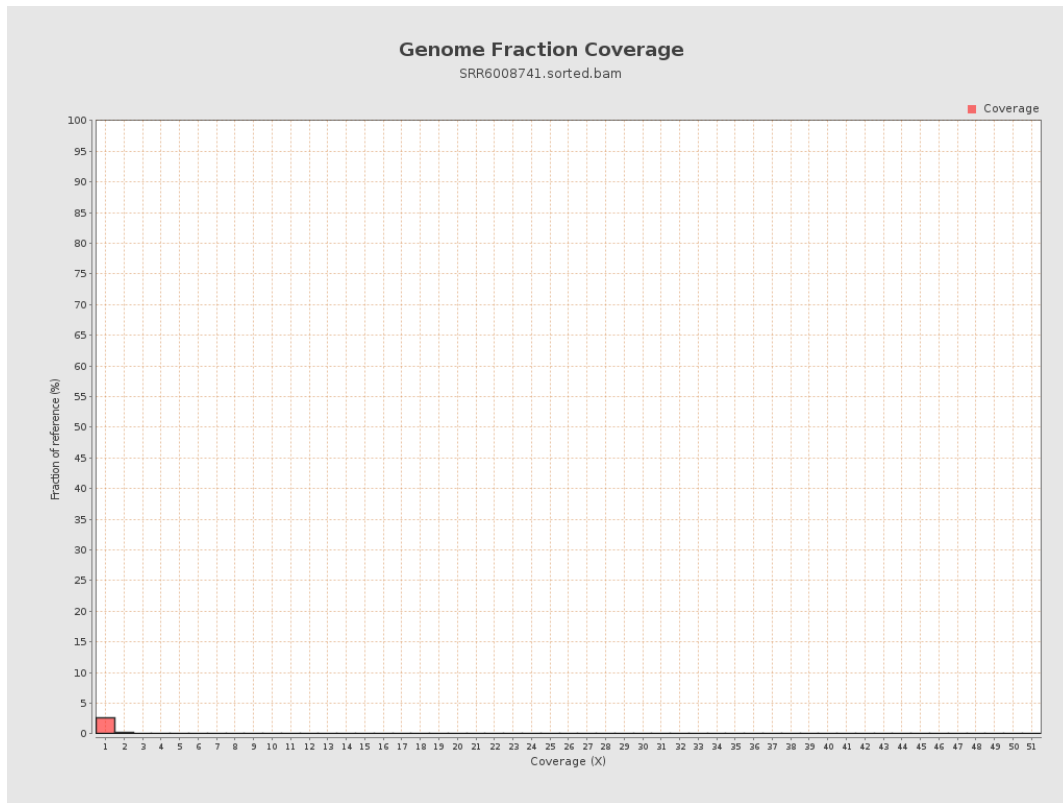
4. Results : Coverage Histogram



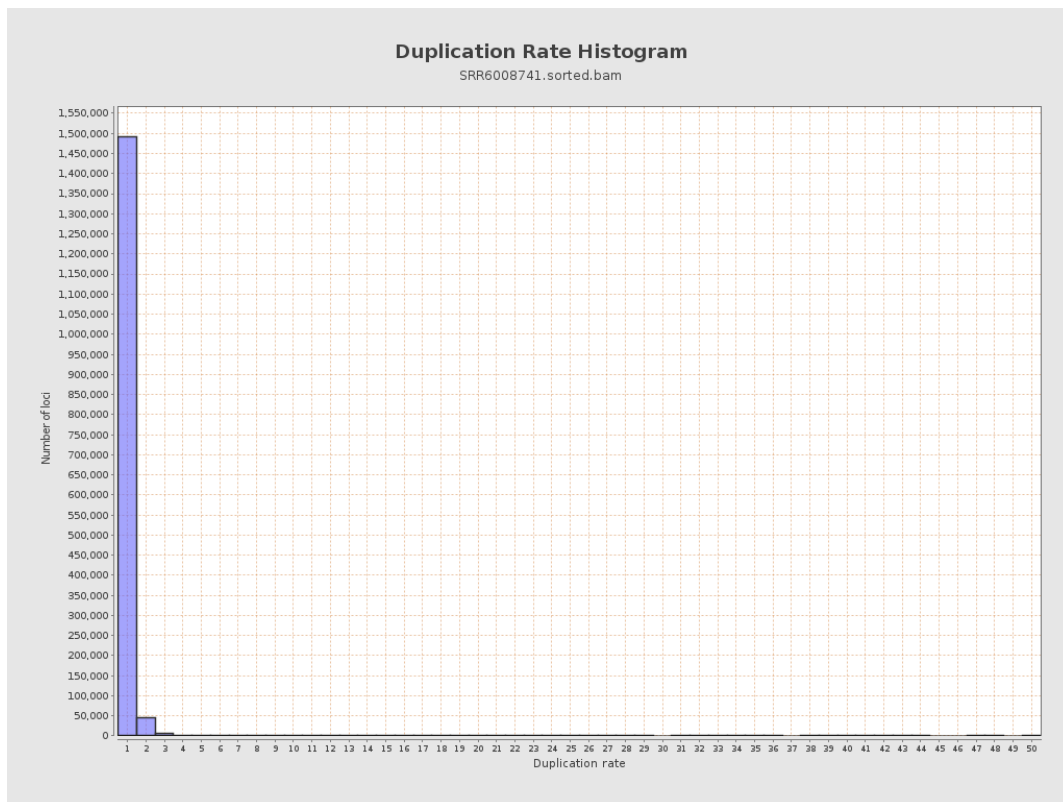
5. Results : Coverage Histogram (0-50X)



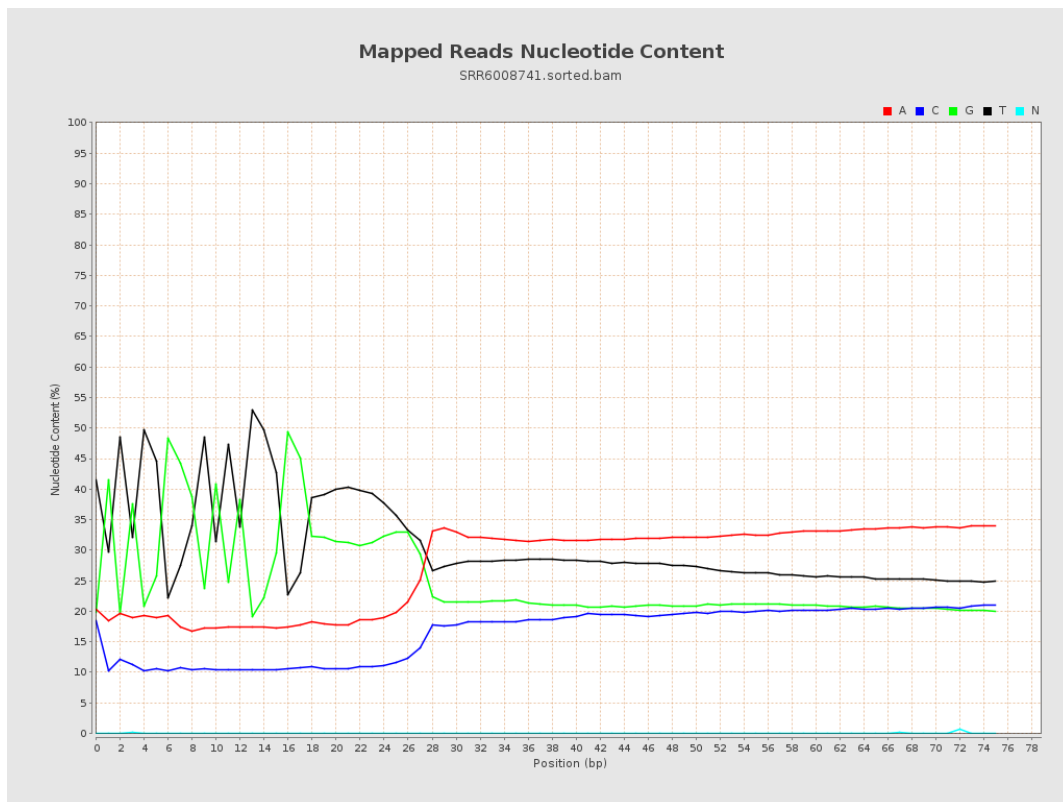
6. Results : Genome Fraction Coverage



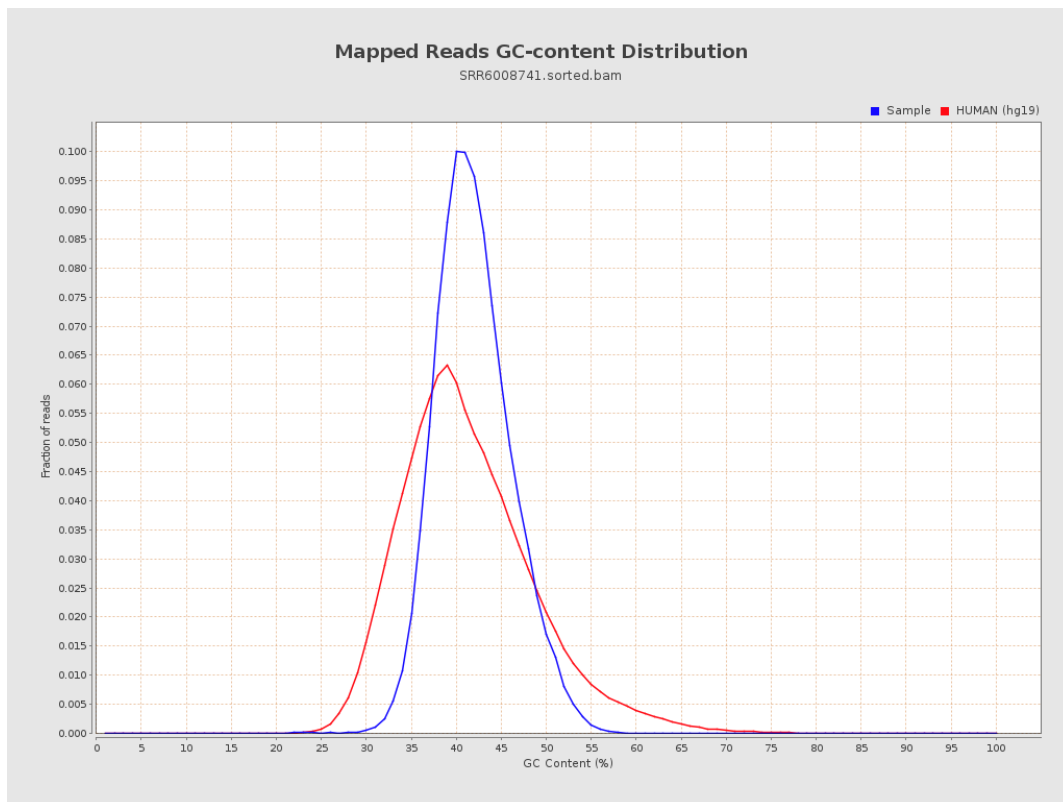
7. Results : Duplication Rate Histogram



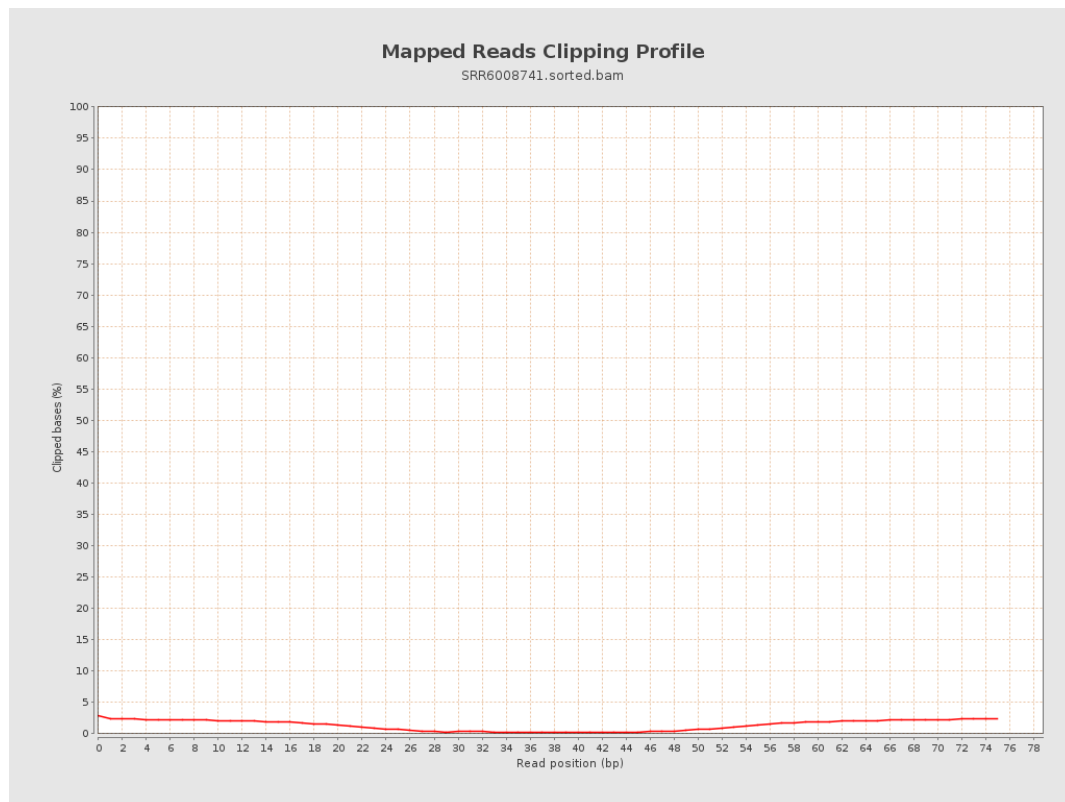
8. Results : Mapped Reads Nucleotide Content



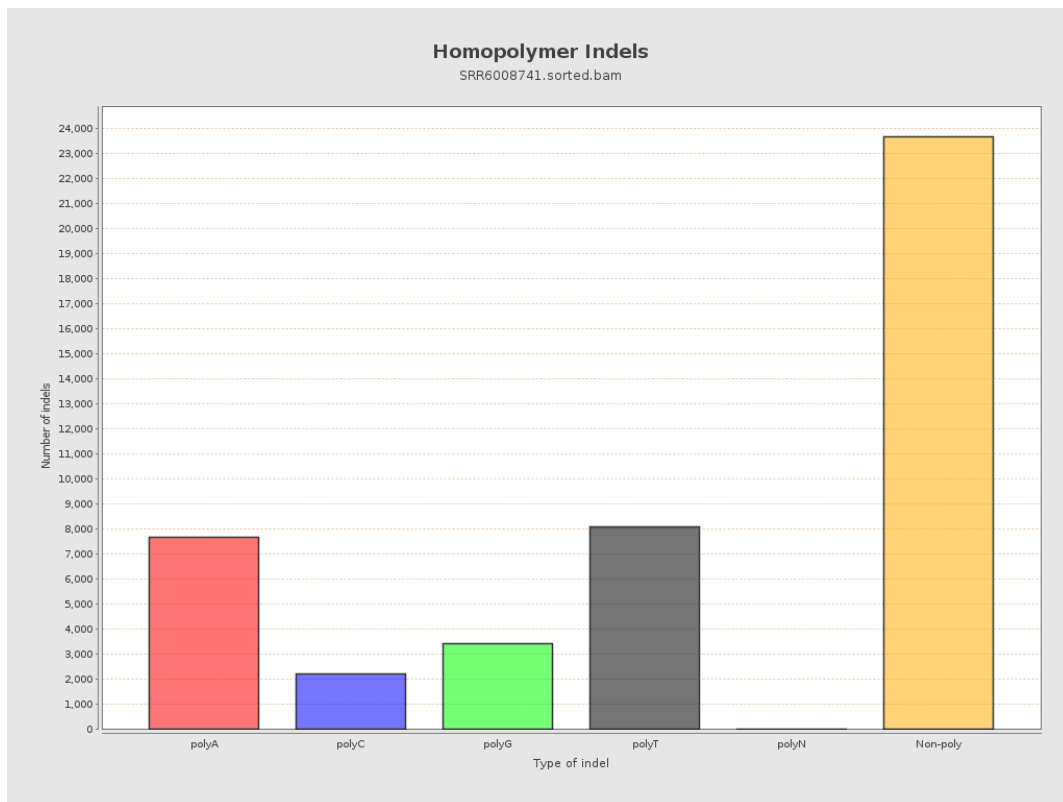
9. Results : Mapped Reads GC-content Distribution



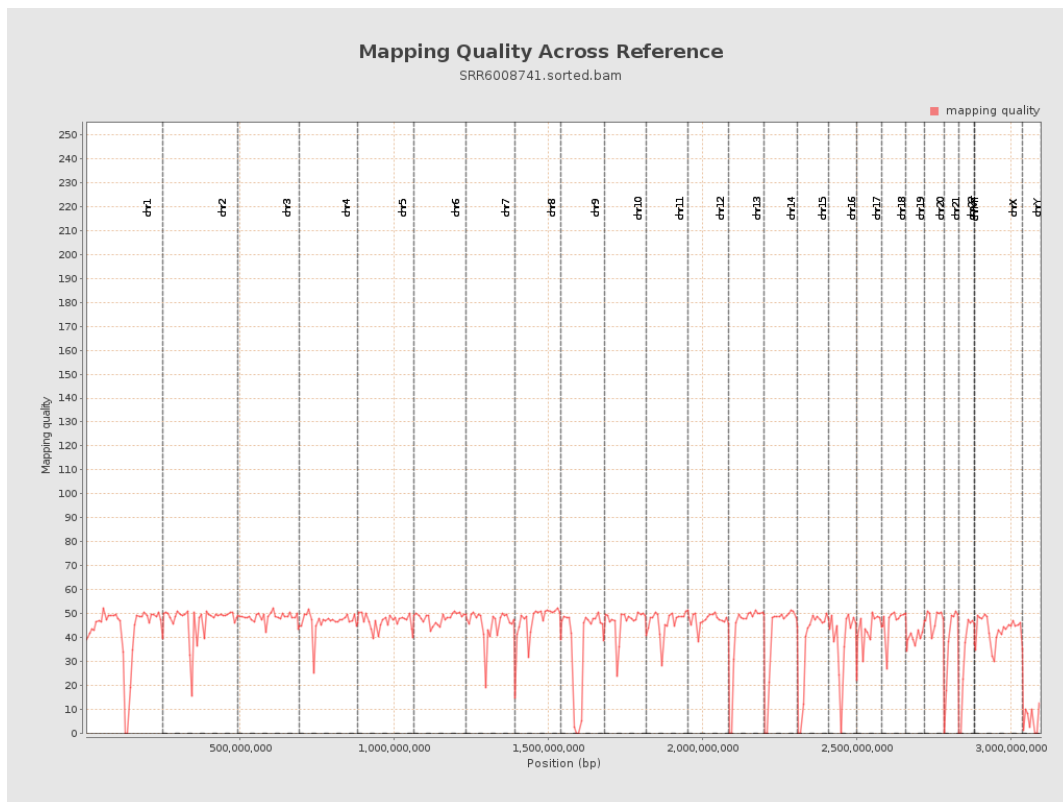
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

