

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 05:51:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008662.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_SRR6008662 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008662.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 05:51:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008662.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,915,433
Mapped reads	1,589,806 / 83%
Unmapped reads	325,627 / 17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,104 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	84,492 / 4.41%
Duplication rate	4.38%
Clipped reads	812,287 / 42.41%

2.2. ACGT Content

Number/percentage of A's	27,543,985 / 26.64%
Number/percentage of C's	19,107,265 / 18.48%
Number/percentage of T's	32,611,446 / 31.54%
Number/percentage of G's	24,089,997 / 23.3%
Number/percentage of N's	38,188 / 0.04%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0334

Standard Deviation	0.3101
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2.4. Mapping Quality

Mean Mapping Quality	45.49
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2.5. Mismatches and indels

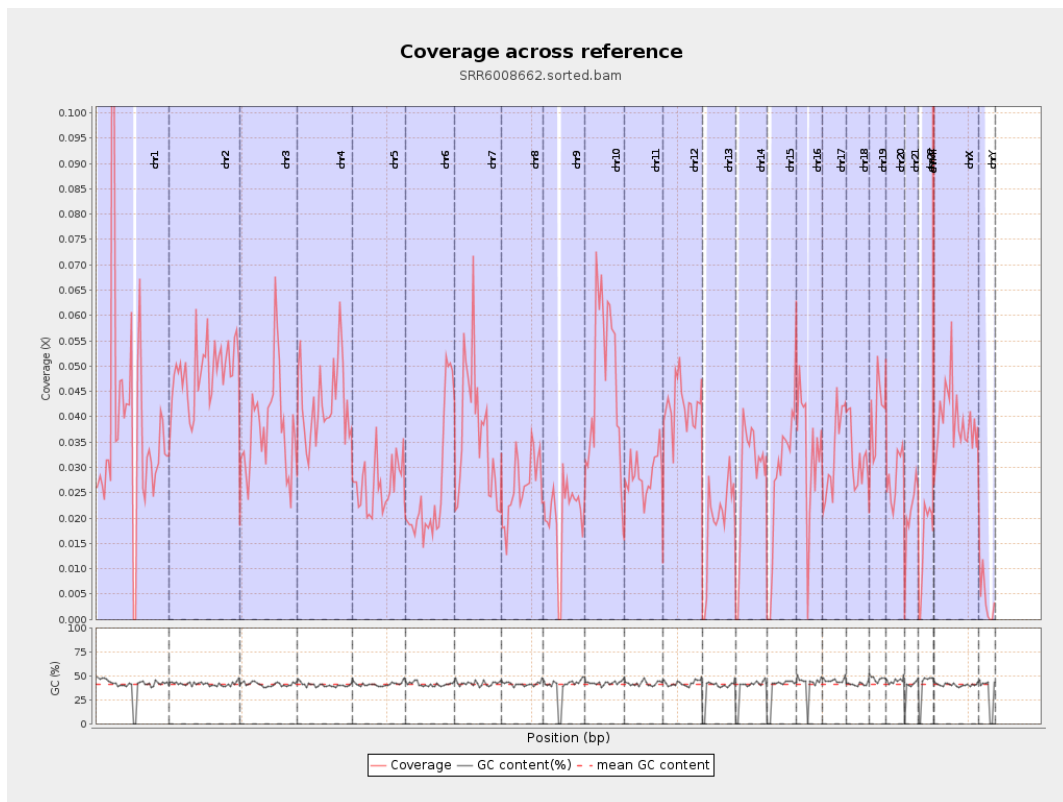
General error rate	0.83%
Mismatches	846,439
Insertions	7,145
Mapped reads with at least one insertion	0.45%
Deletions	25,585
Mapped reads with at least one deletion	1.59%
Homopolymer indels	47.2%

2.6. Chromosome stats

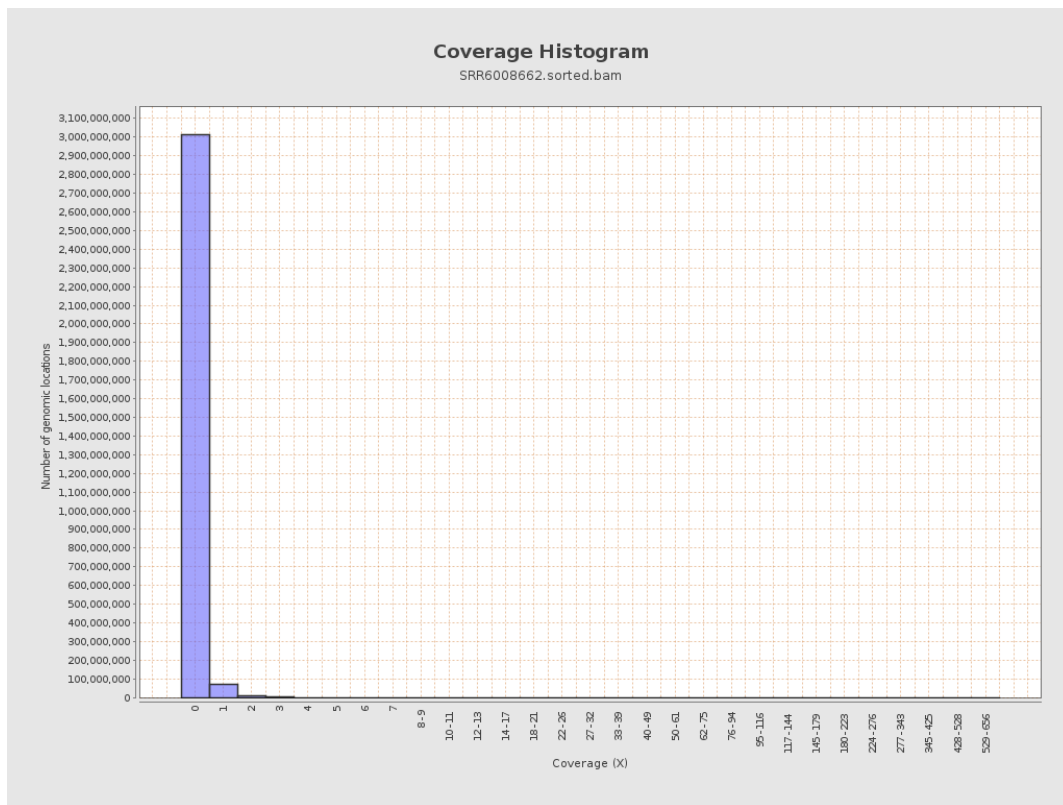
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	9406949	0.0377	0.5582
chr2	243199373	11872772	0.0488	0.3803
chr3	198022430	7477097	0.0378	0.228
chr4	191154276	8123217	0.0425	0.2476
chr5	180915260	4858682	0.0269	0.1926
chr6	171115067	4499664	0.0263	0.2098
chr7	159138663	5828309	0.0366	0.4953

chr8	146364022	3853351	0.0263	0.2859
chr9	141213431	2867376	0.0203	0.2322
chr10	135534747	6384561	0.0471	0.3404
chr11	135006516	3841396	0.0285	0.2443
chr12	133851895	5646851	0.0422	0.2458
chr13	115169878	2251556	0.0195	0.1633
chr14	107349540	3056451	0.0285	0.2042
chr15	102531392	2853950	0.0278	0.2011
chr16	90354753	3025250	0.0335	0.2209
chr17	81195210	2697149	0.0332	0.2341
chr18	78077248	2524498	0.0323	0.3947
chr19	59128983	2407364	0.0407	0.3934
chr20	63025520	1772084	0.0281	0.2028
chr21	48129895	1005883	0.0209	0.1758
chr22	51304566	775405	0.0151	0.1415
chrMT	16571	87367	5.2723	3.7365
chrX	155270560	6074280	0.0391	0.2501
chrY	59373566	242270	0.0041	0.095

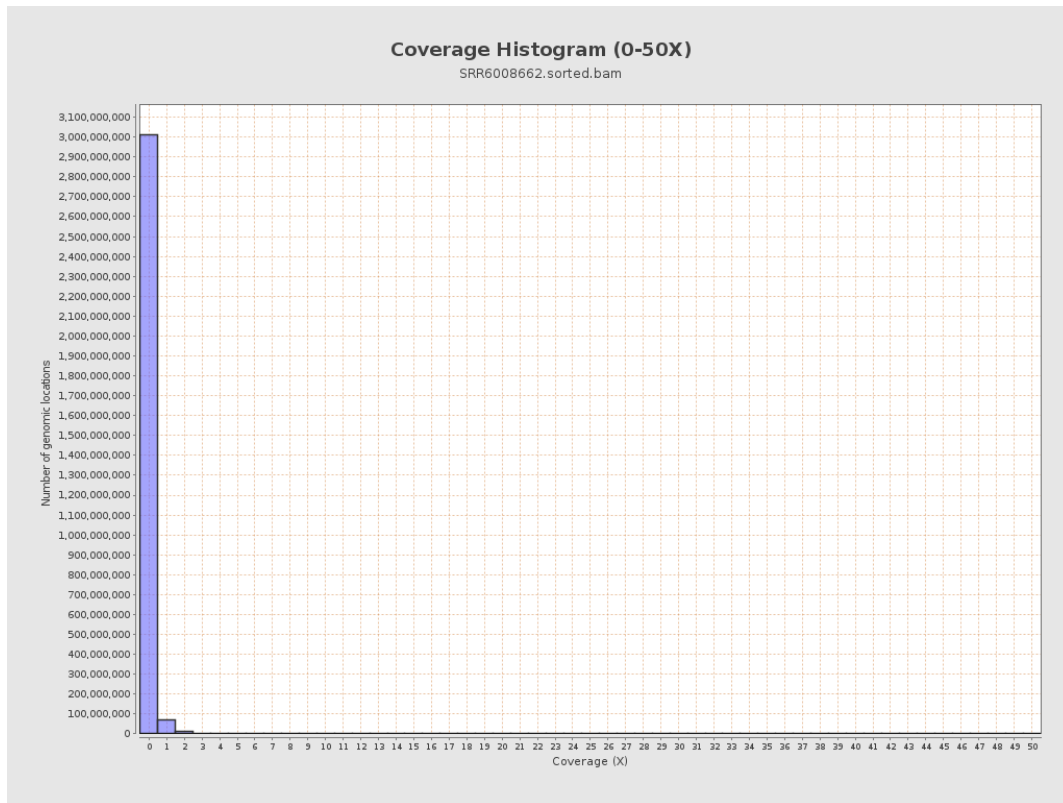
3. Results : Coverage across reference



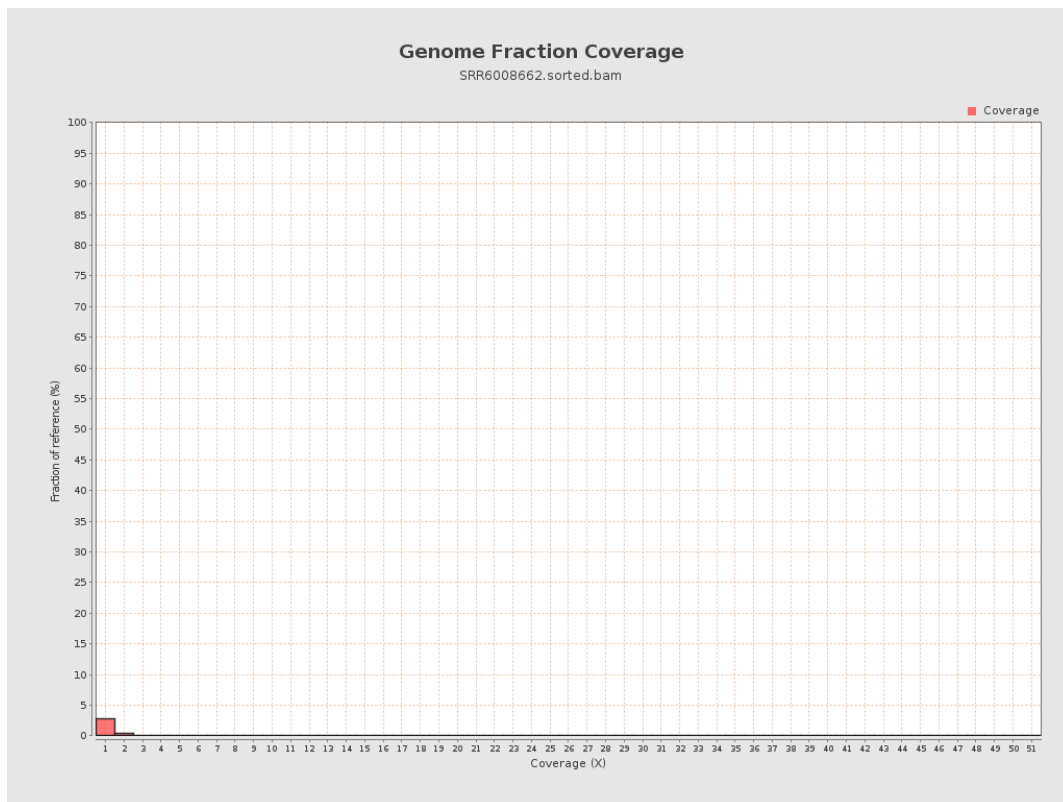
4. Results : Coverage Histogram



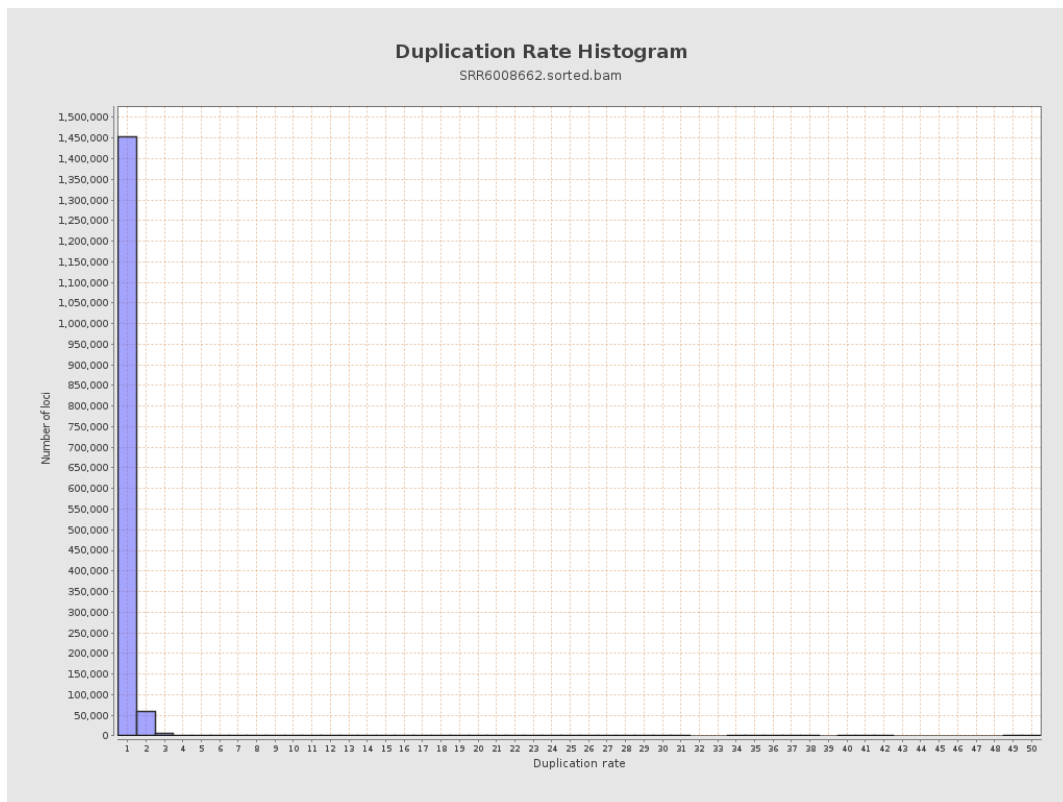
5. Results : Coverage Histogram (0-50X)



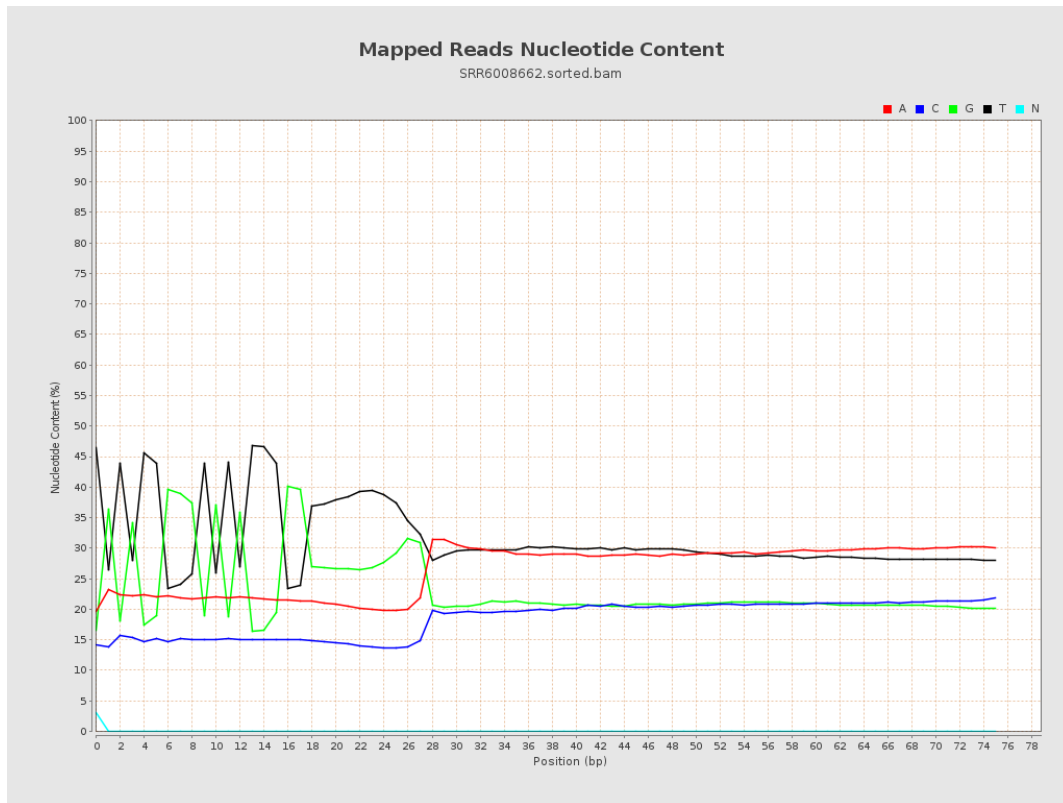
6. Results : Genome Fraction Coverage



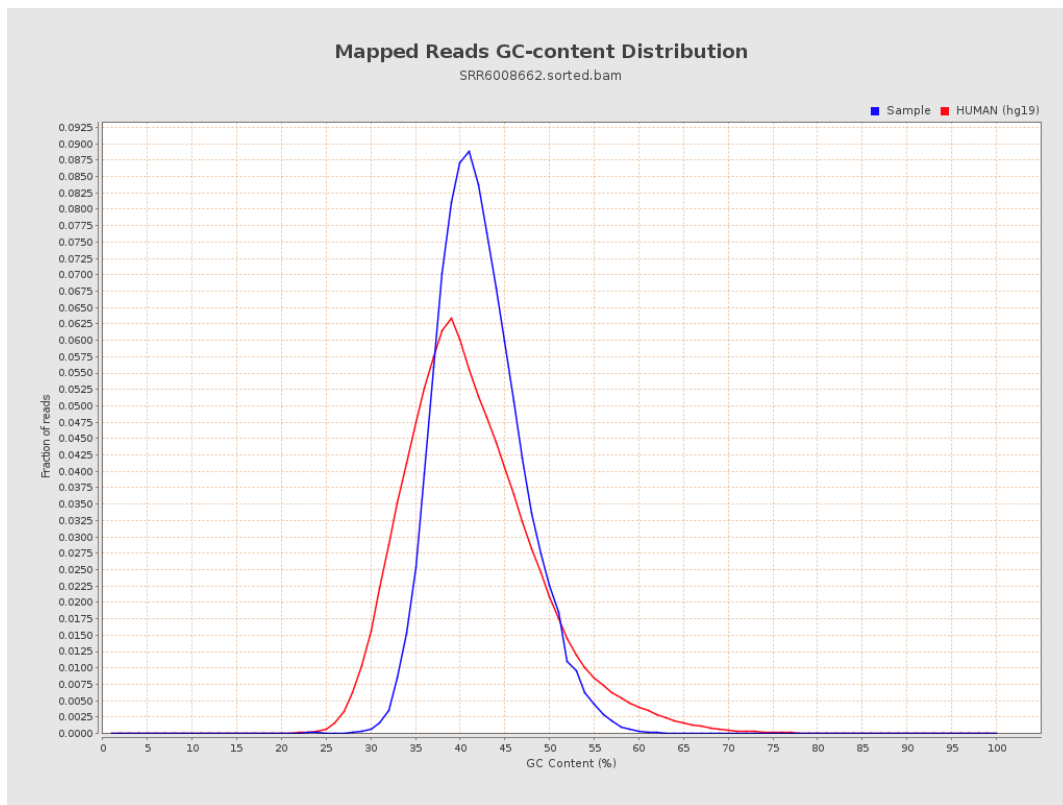
7. Results : Duplication Rate Histogram



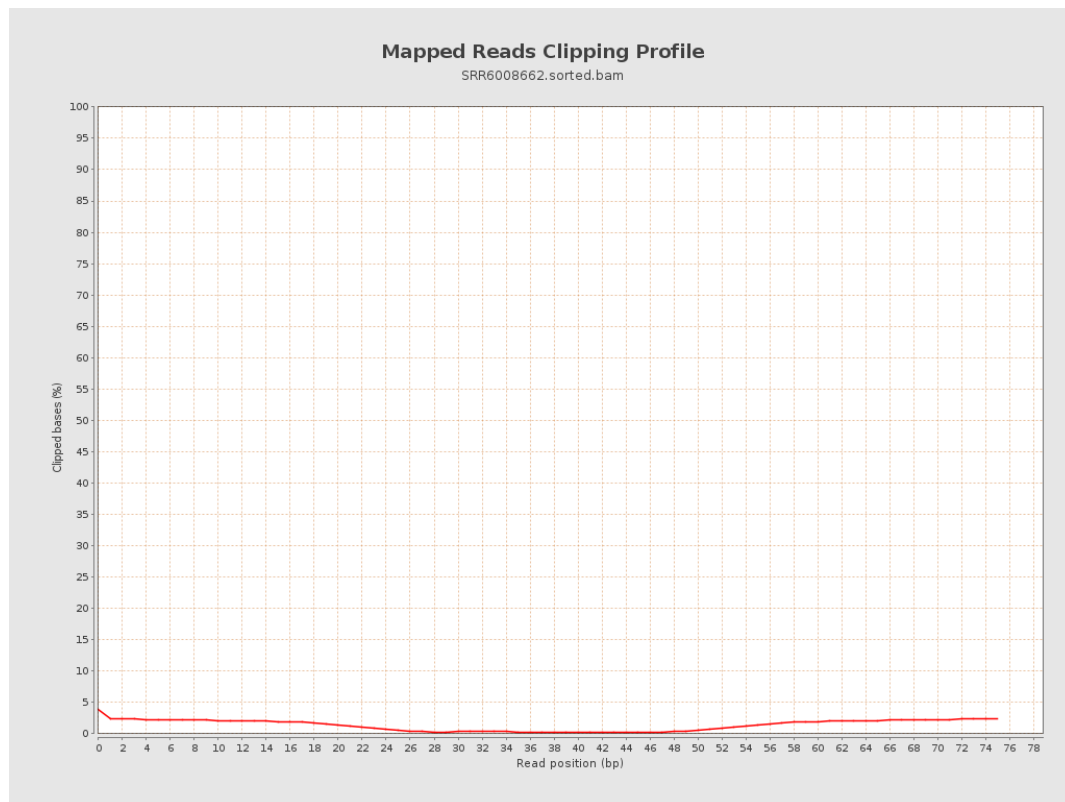
8. Results : Mapped Reads Nucleotide Content



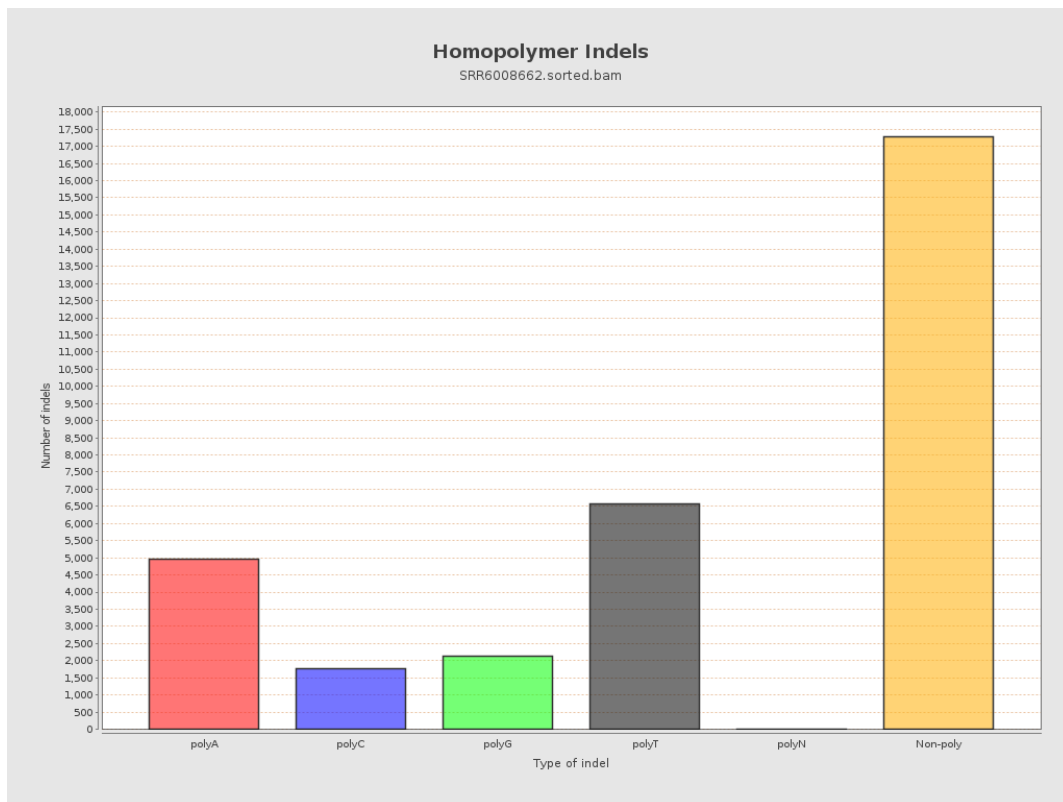
9. Results : Mapped Reads GC-content Distribution



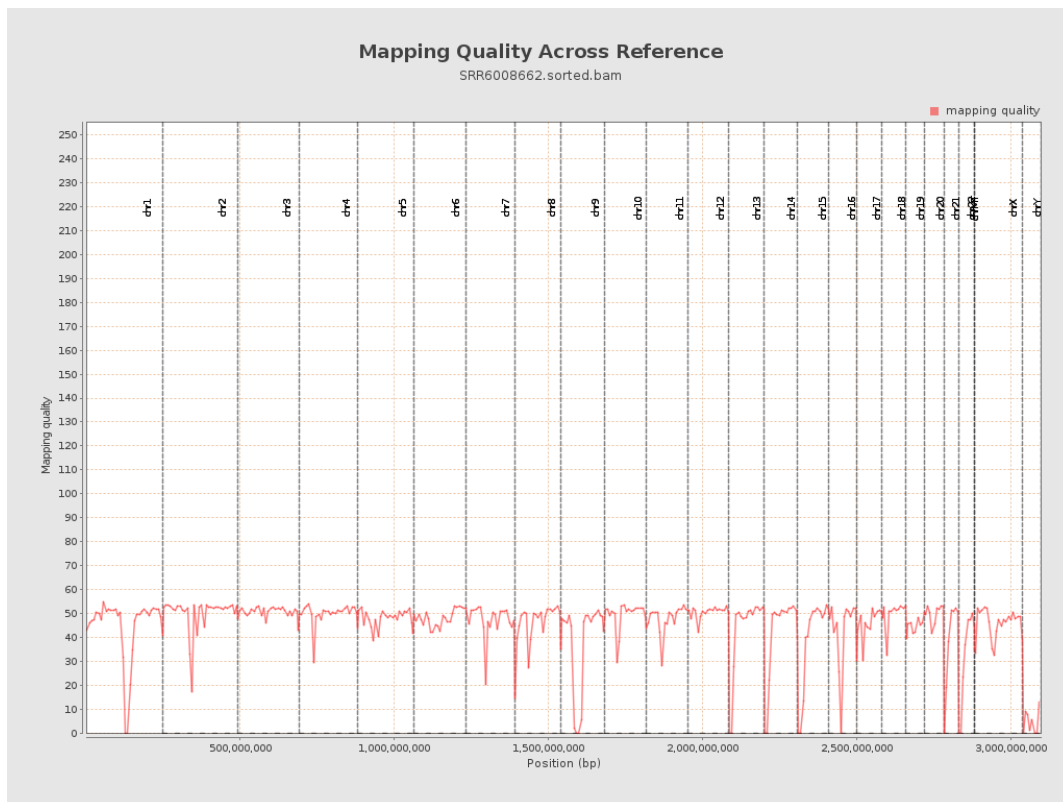
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

