

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 14:50:33

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068175.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_SRR6068175 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068175.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 14:50:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068175.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,463,765
Mapped reads	2,988,394 / 86.28%
Unmapped reads	475,371 / 13.72%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,551 / 0.59%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	1,090,717 / 31.49%
Duplication rate	19.22%
Clipped reads	1,828,818 / 52.8%

2.2. ACGT Content

Number/percentage of A's	46,618,354 / 25.01%
Number/percentage of C's	33,031,925 / 17.72%
Number/percentage of T's	61,375,127 / 32.93%
Number/percentage of G's	45,353,871 / 24.33%
Number/percentage of N's	19,542 / 0.01%
GC Percentage	42.05%

2.3. Coverage

Mean	0.0602

Standard Deviation	0.8025
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2.4. Mapping Quality

Mean Mapping Quality	45.39
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2.5. Mismatches and indels

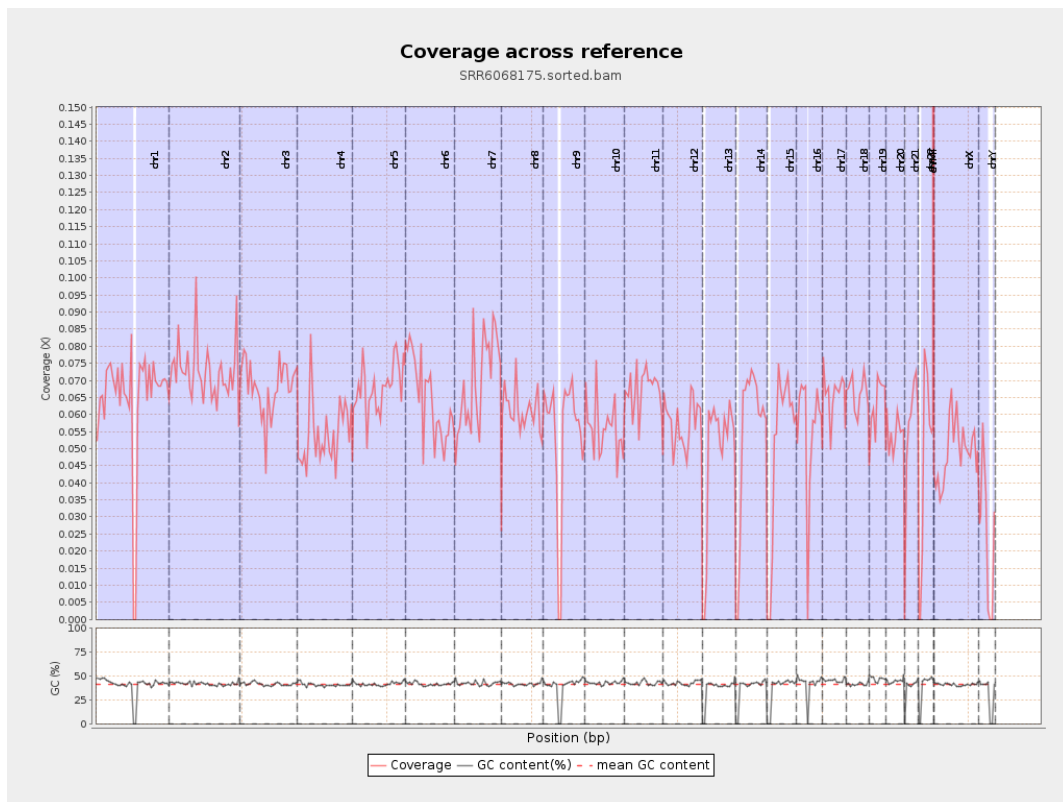
General error rate	0.66%
Mismatches	1,212,990
Insertions	12,115
Mapped reads with at least one insertion	0.4%
Deletions	51,454
Mapped reads with at least one deletion	1.7%
Homopolymer indels	46.07%

2.6. Chromosome stats

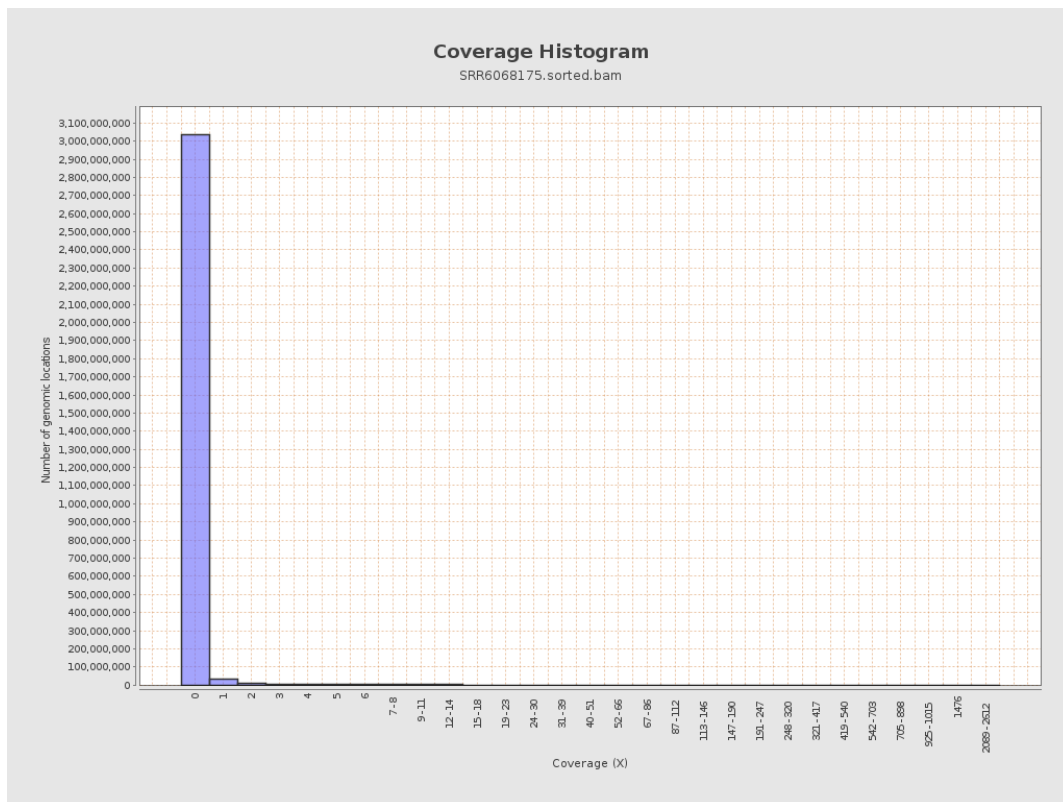
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16126373	0.0647	0.9698
chr2	243199373	17698203	0.0728	1.3824
chr3	198022430	13431694	0.0678	0.7147
chr4	191154276	10297880	0.0539	0.6299
chr5	180915260	12290008	0.0679	0.7173
chr6	171115067	11014307	0.0644	0.7687
chr7	159138663	11105750	0.0698	0.8386

chr8	146364022	8975108	0.0613	0.7782
chr9	141213431	7614367	0.0539	0.6772
chr10	135534747	7565906	0.0558	0.6714
chr11	135006516	9088576	0.0673	0.7635
chr12	133851895	7675373	0.0573	0.6376
chr13	115169878	5538177	0.0481	0.6072
chr14	107349540	5859683	0.0546	0.6473
chr15	102531392	5251743	0.0512	0.6295
chr16	90354753	5026156	0.0556	0.6479
chr17	81195210	5357812	0.066	0.6987
chr18	78077248	5215078	0.0668	1.0689
chr19	59128983	3717070	0.0629	0.8175
chr20	63025520	3419412	0.0543	0.643
chr21	48129895	2668670	0.0554	0.6319
chr22	51304566	2307257	0.045	0.5923
chrMT	16571	201308	12.1482	11.933
chrX	155270560	7666583	0.0494	0.5743
chrY	59373566	1378130	0.0232	0.4119

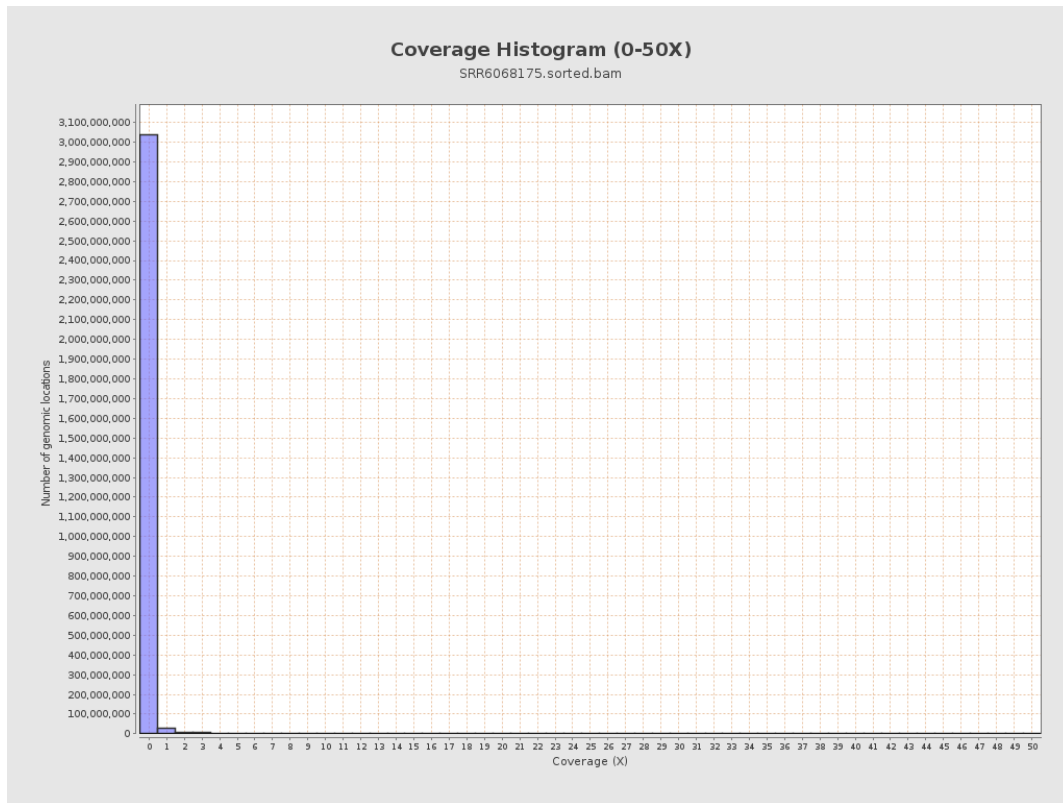
3. Results : Coverage across reference



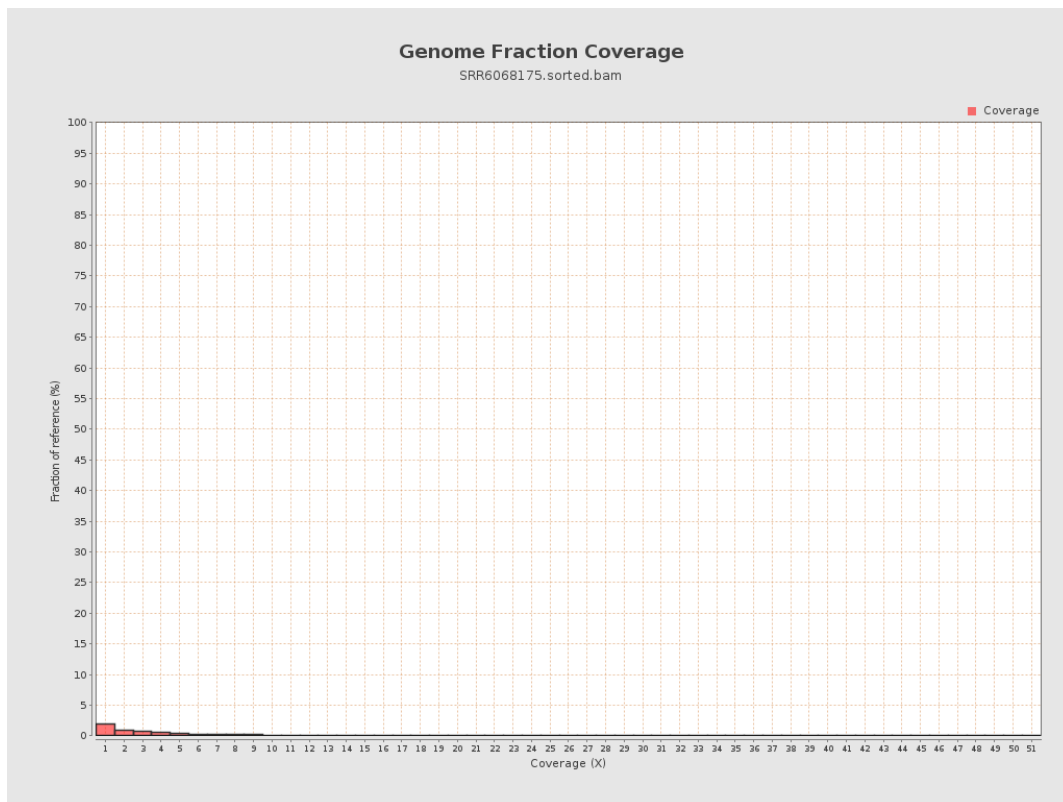
4. Results : Coverage Histogram



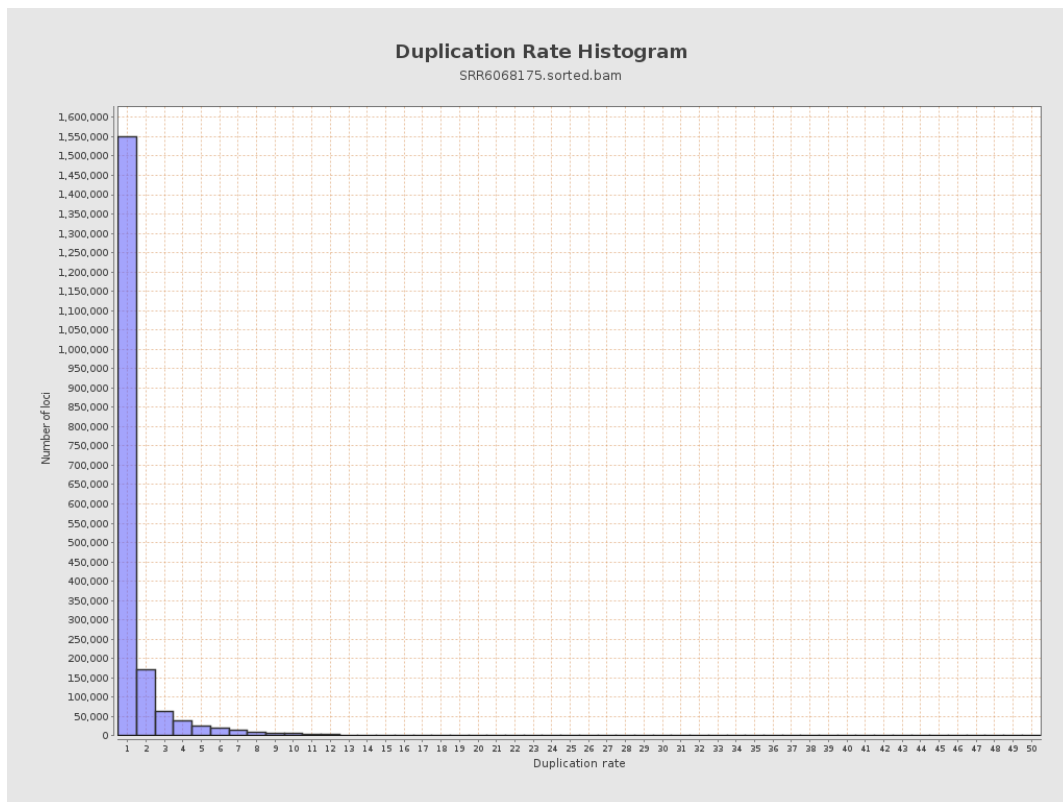
5. Results : Coverage Histogram (0-50X)



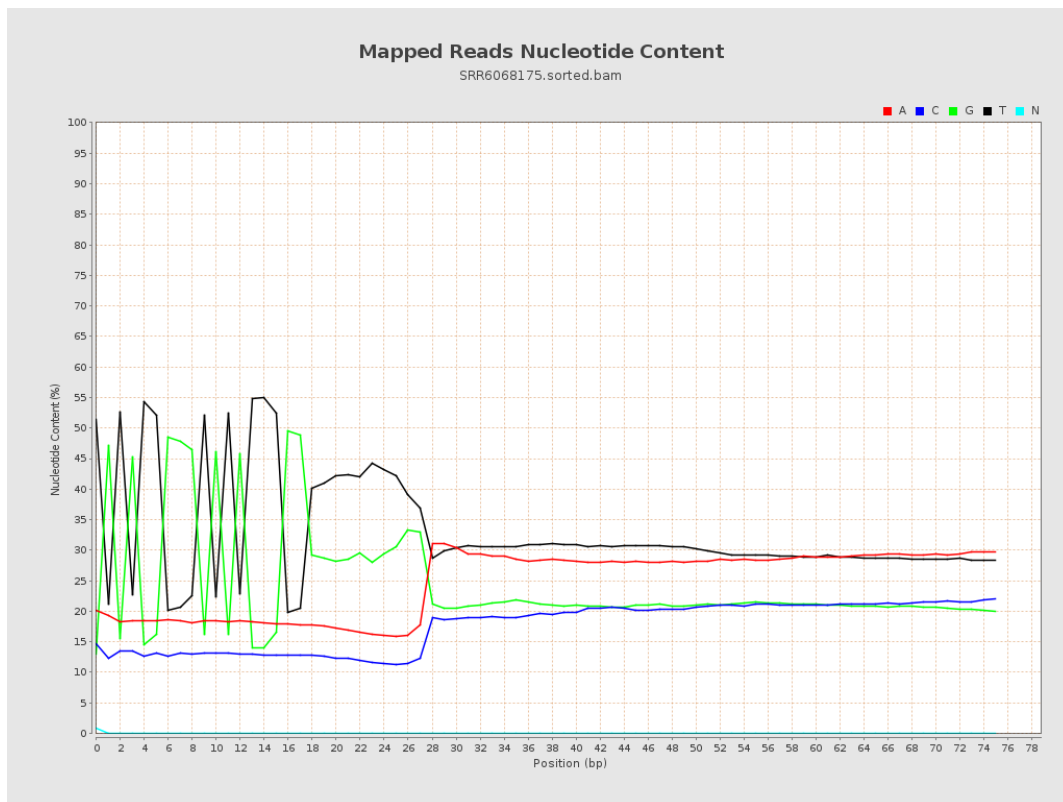
6. Results : Genome Fraction Coverage



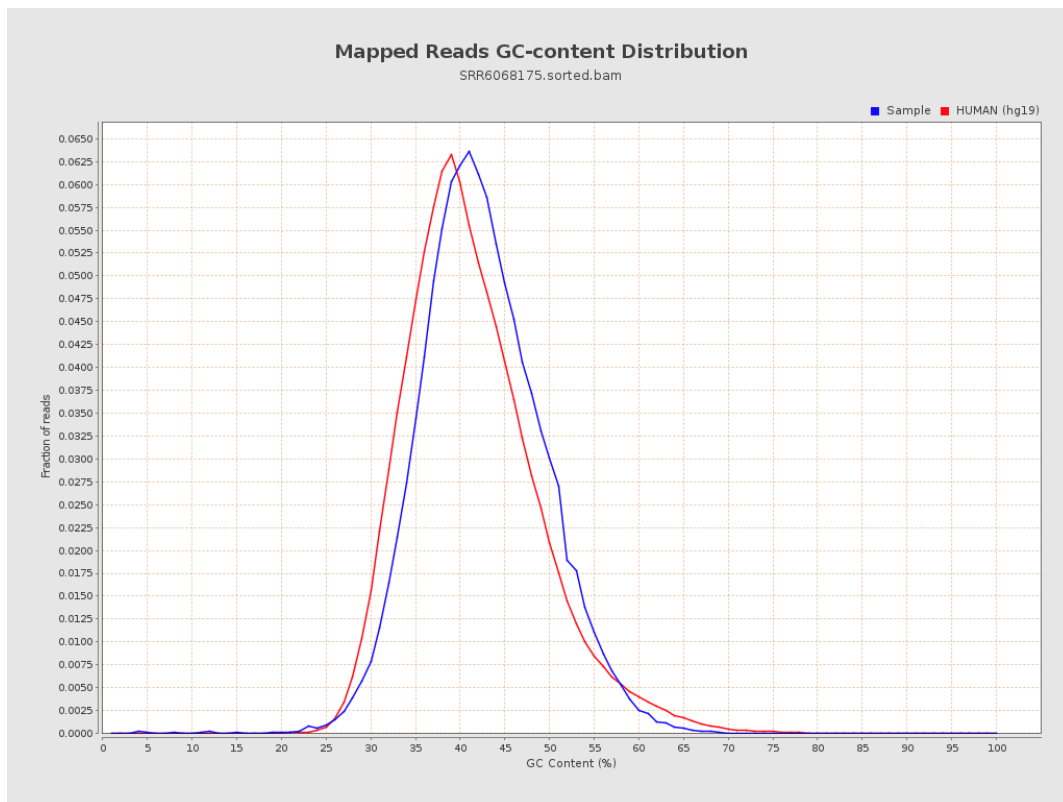
7. Results : Duplication Rate Histogram



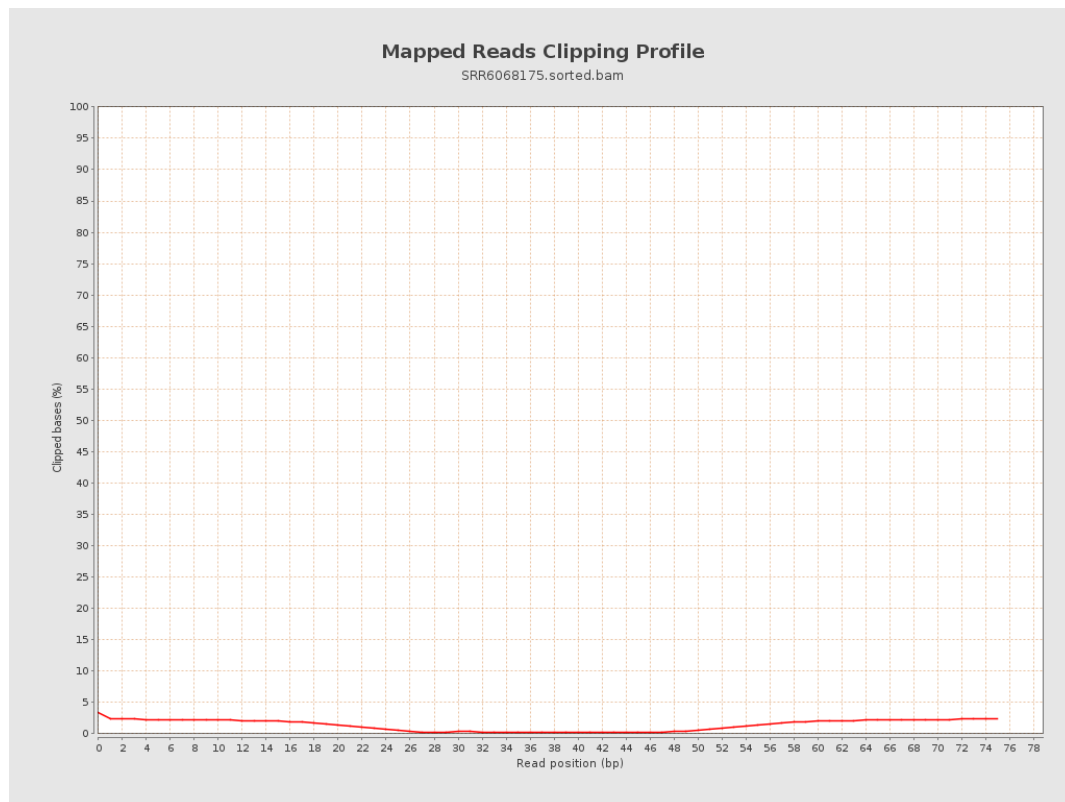
8. Results : Mapped Reads Nucleotide Content



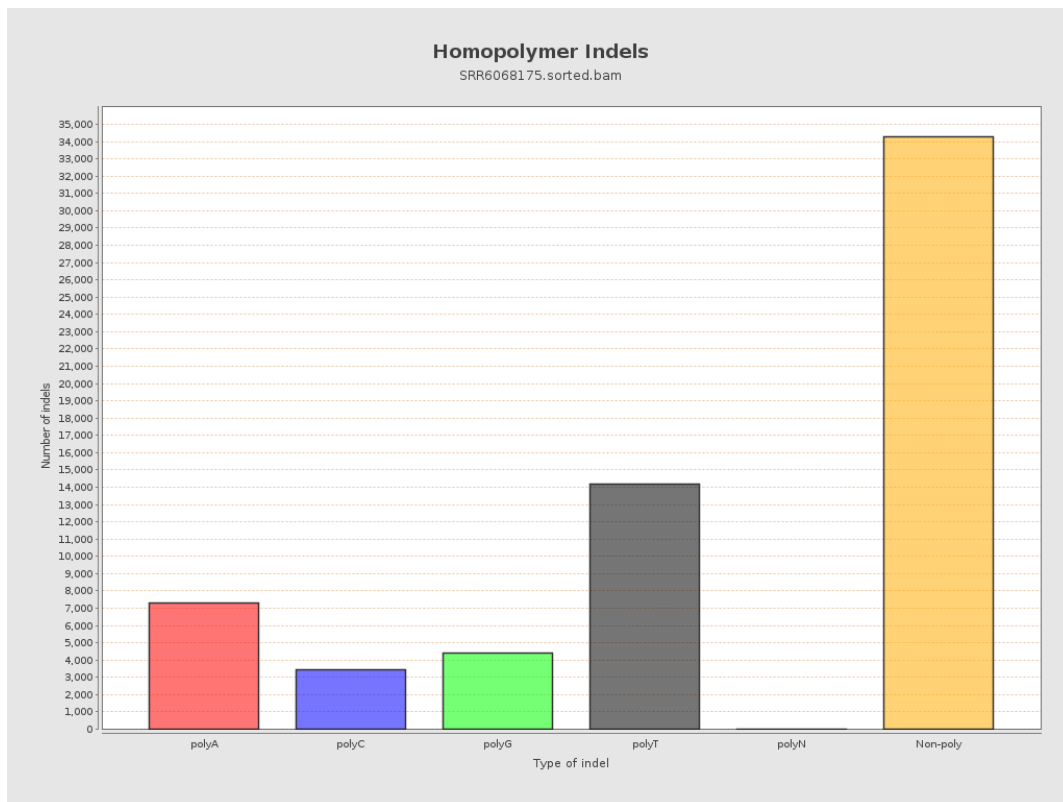
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

