

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 11:24:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238062.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_SRR6238062 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238062.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 11:24:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238062.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,029,345
Mapped reads	2,780,755 / 91.79%
Unmapped reads	248,590 / 8.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	19,744 / 0.65%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	123,179 / 4.07%
Duplication rate	3.3%
Clipped reads	1,081,175 / 35.69%

2.2. ACGT Content

Number/percentage of A's	51,256,206 / 27.26%
Number/percentage of C's	36,258,763 / 19.28%
Number/percentage of T's	58,011,701 / 30.85%
Number/percentage of G's	42,488,531 / 22.6%
Number/percentage of N's	27,212 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0608

Standard Deviation	0.589
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2.4. Mapping Quality

Mean Mapping Quality	44.64
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2.5. Mismatches and indels

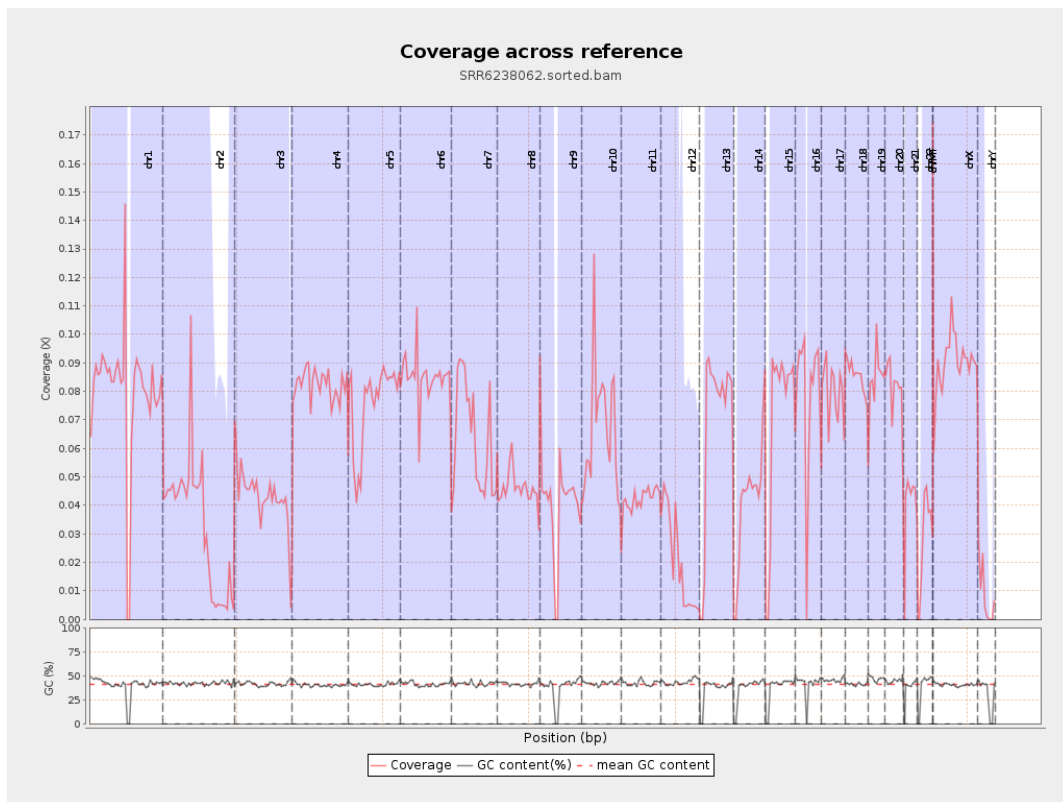
General error rate	0.73%
Mismatches	1,348,908
Insertions	12,520
Mapped reads with at least one insertion	0.45%
Deletions	44,072
Mapped reads with at least one deletion	1.57%
Homopolymer indels	47.27%

2.6. Chromosome stats

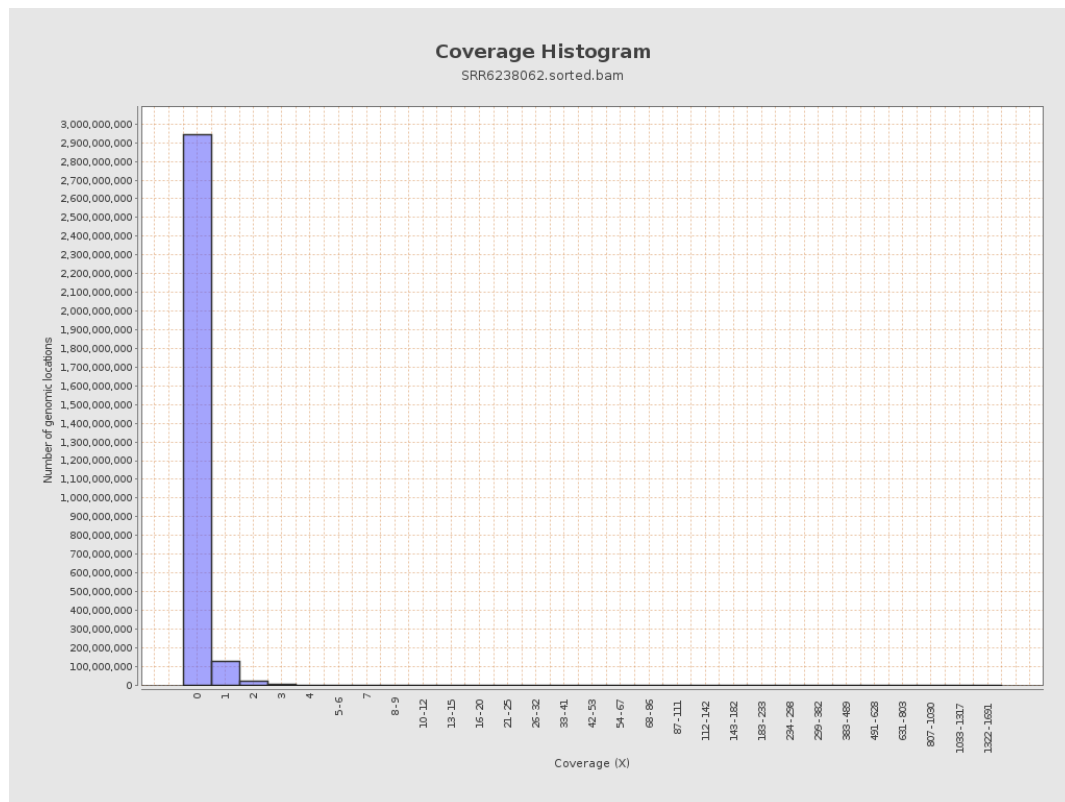
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19928760	0.08	1.4847
chr2	243199373	8017103	0.033	0.5515
chr3	198022430	8569666	0.0433	0.2594
chr4	191154276	15751427	0.0824	0.3522
chr5	180915260	13763704	0.0761	0.3274
chr6	171115067	14540872	0.085	0.4564
chr7	159138663	9960738	0.0626	0.5219

chr8	146364022	6715621	0.0459	0.4812
chr9	141213431	5602047	0.0397	0.3985
chr10	135534747	9026384	0.0666	0.6177
chr11	135006516	5698383	0.0422	0.2936
chr12	133851895	2753495	0.0206	0.1781
chr13	115169878	8027356	0.0697	0.3115
chr14	107349540	4367054	0.0407	0.2561
chr15	102531392	7124014	0.0695	0.3155
chr16	90354753	6968865	0.0771	0.3615
chr17	81195210	6515894	0.0802	0.3887
chr18	78077248	6689519	0.0857	0.7674
chr19	59128983	5035447	0.0852	0.936
chr20	63025520	5157434	0.0818	0.3558
chr21	48129895	1941955	0.0403	0.2576
chr22	51304566	1465968	0.0286	0.1974
chrMT	16571	2893	0.1746	0.4585
chrX	155270560	13999539	0.0902	0.3972
chrY	59373566	496957	0.0084	0.1651

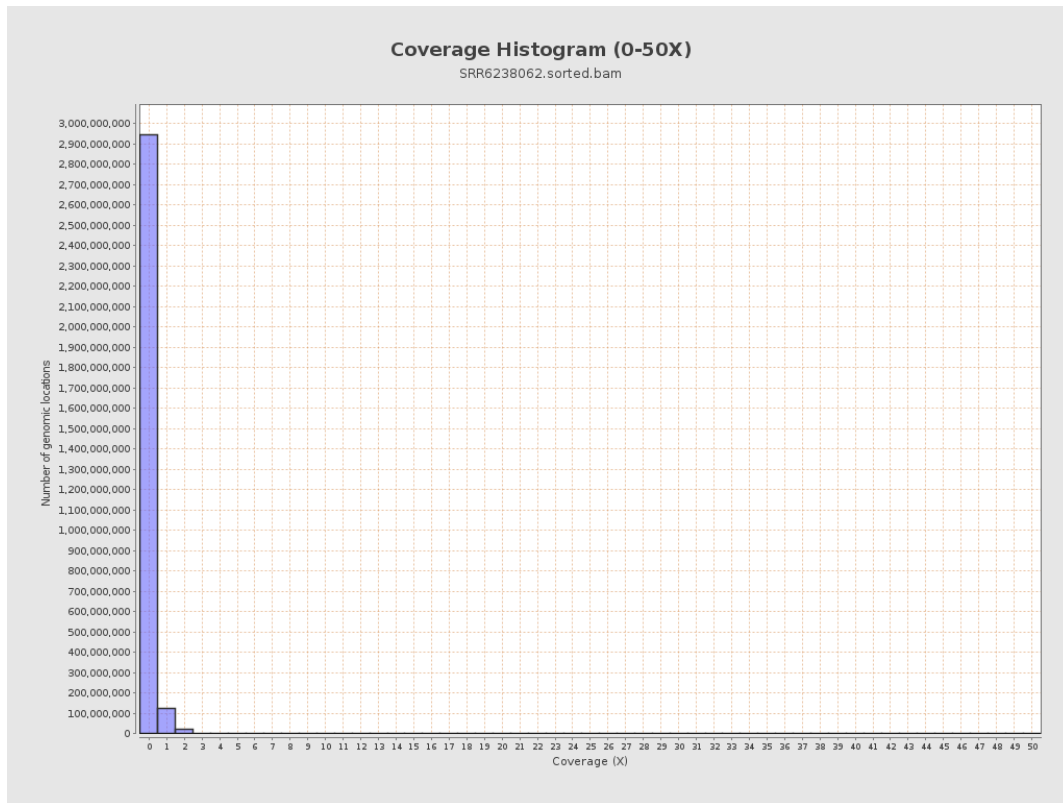
3. Results : Coverage across reference



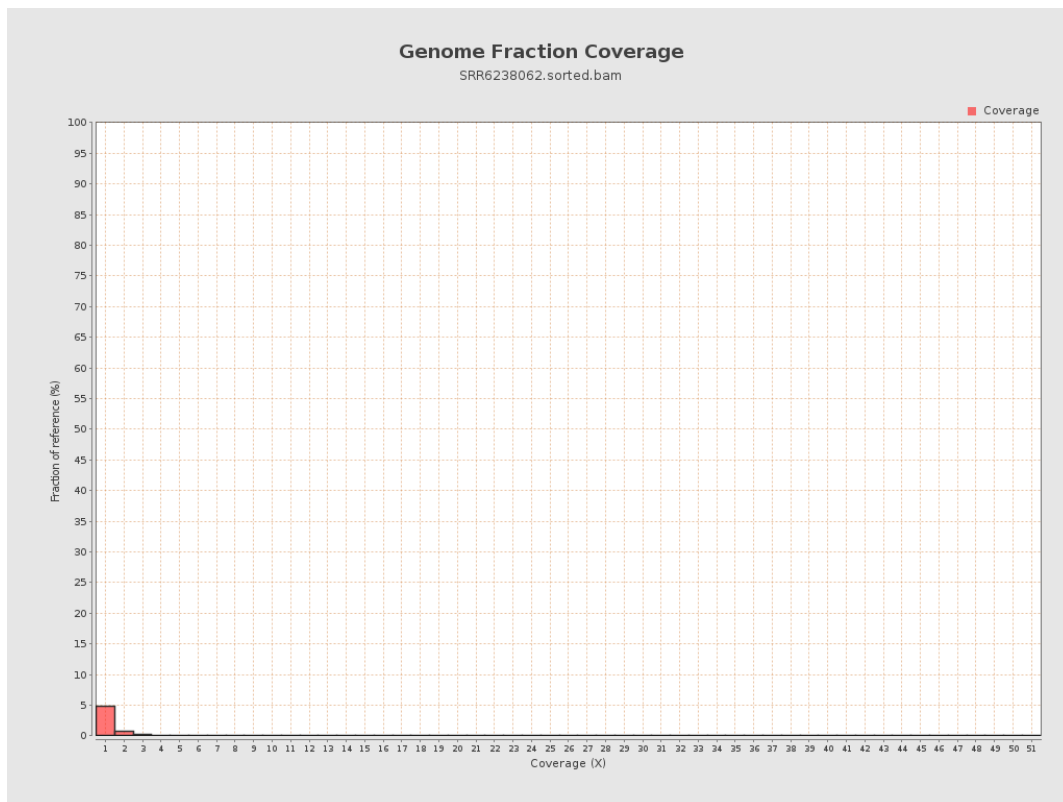
4. Results : Coverage Histogram



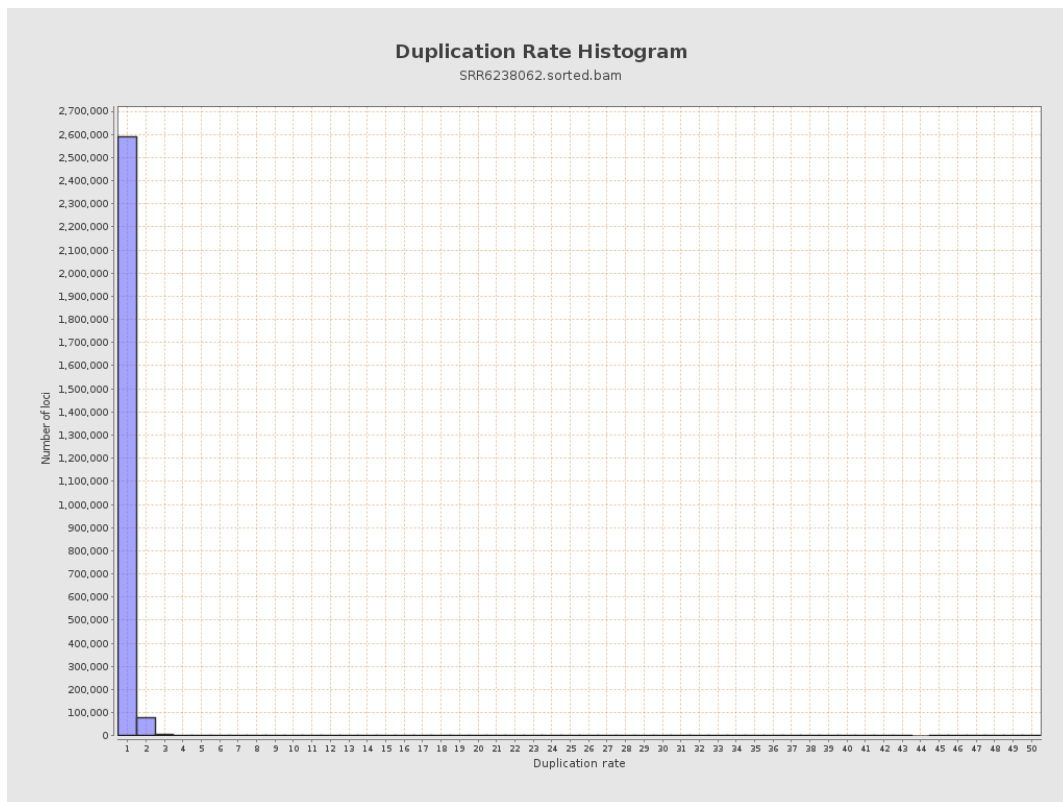
5. Results : Coverage Histogram (0-50X)



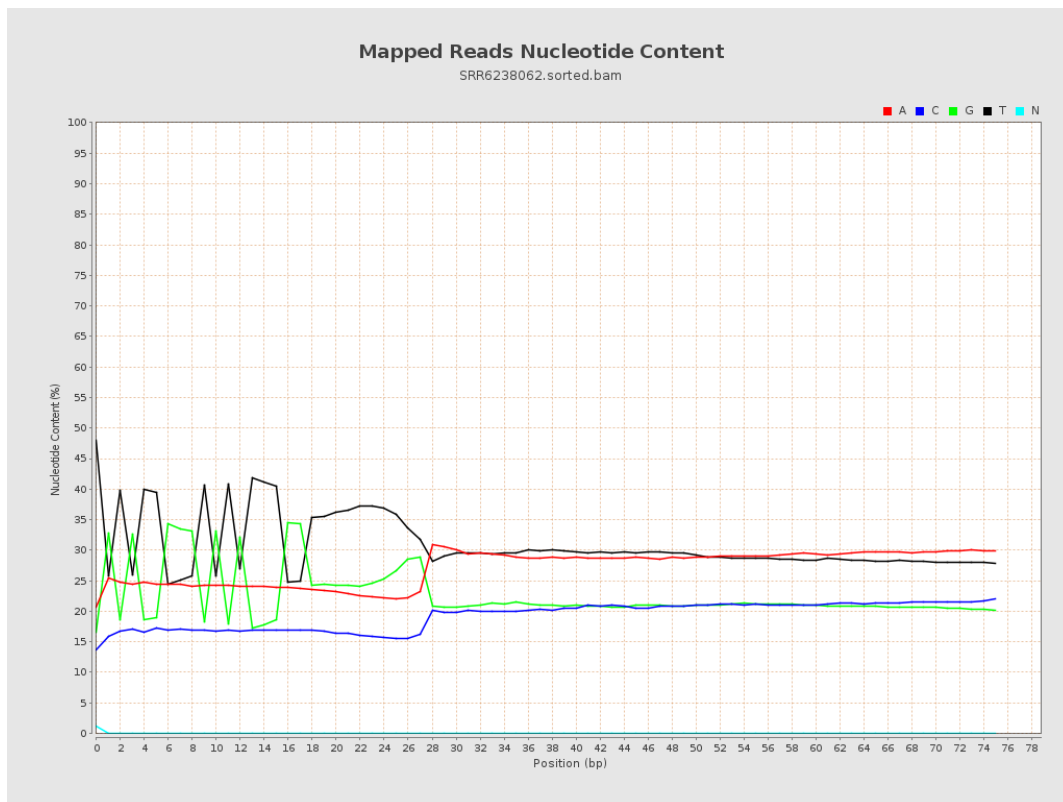
6. Results : Genome Fraction Coverage



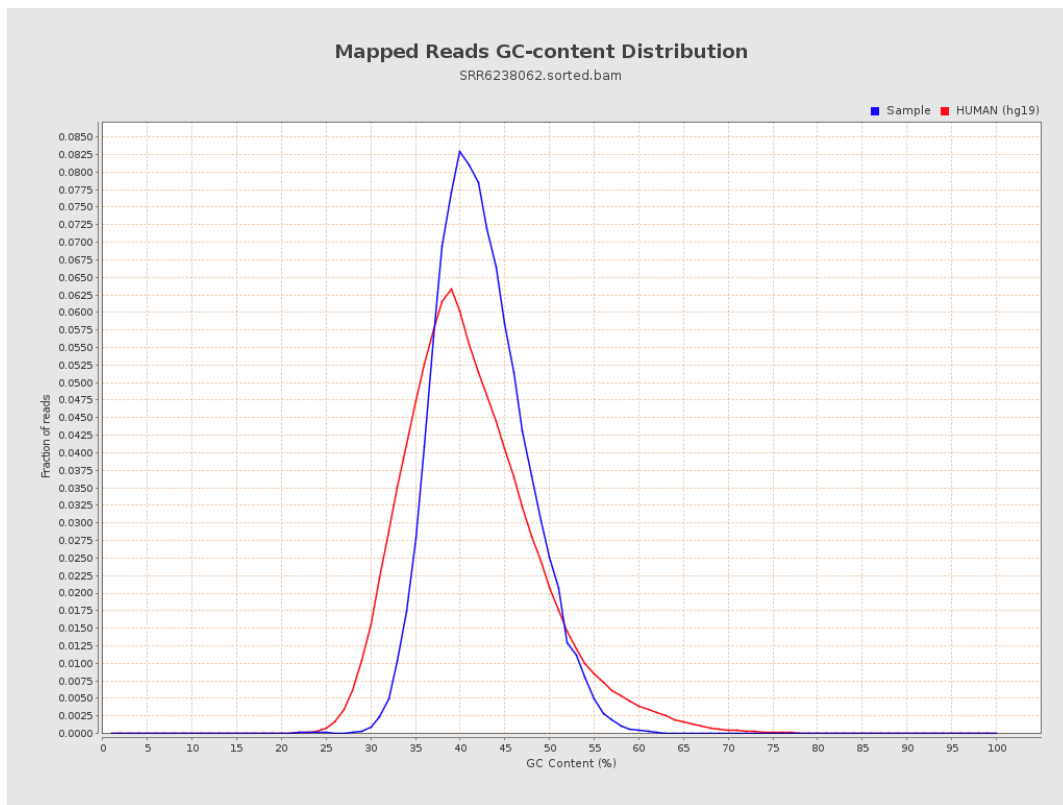
7. Results : Duplication Rate Histogram



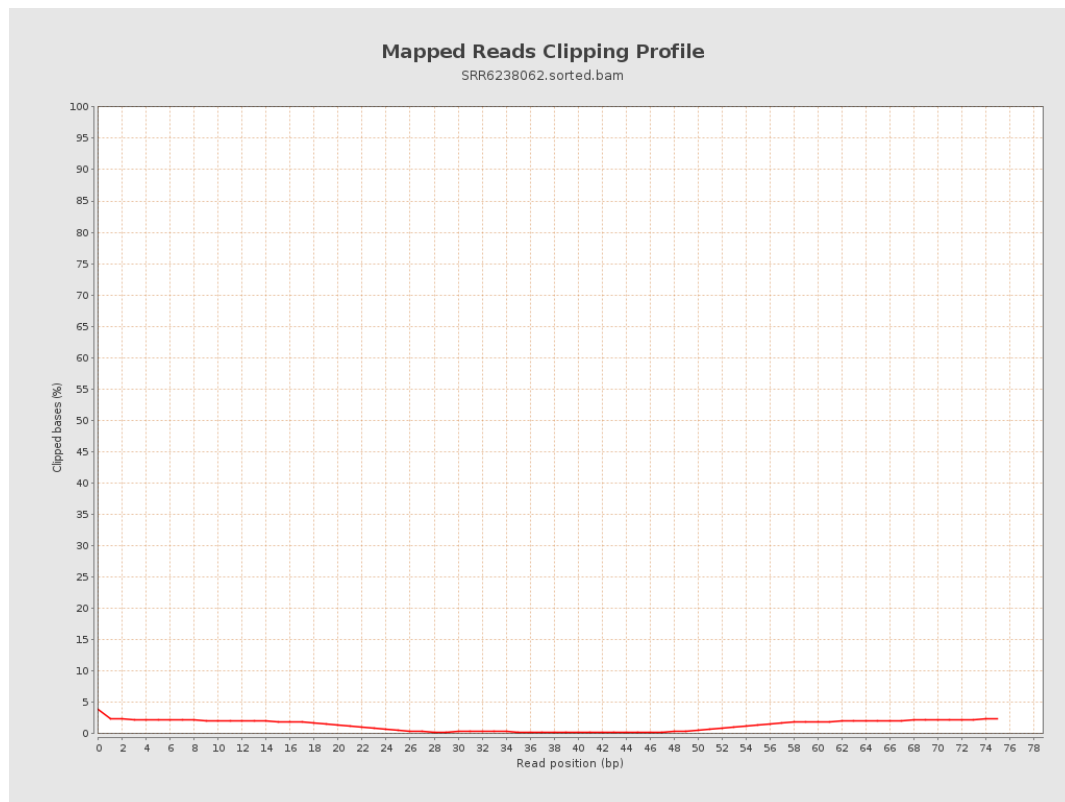
8. Results : Mapped Reads Nucleotide Content



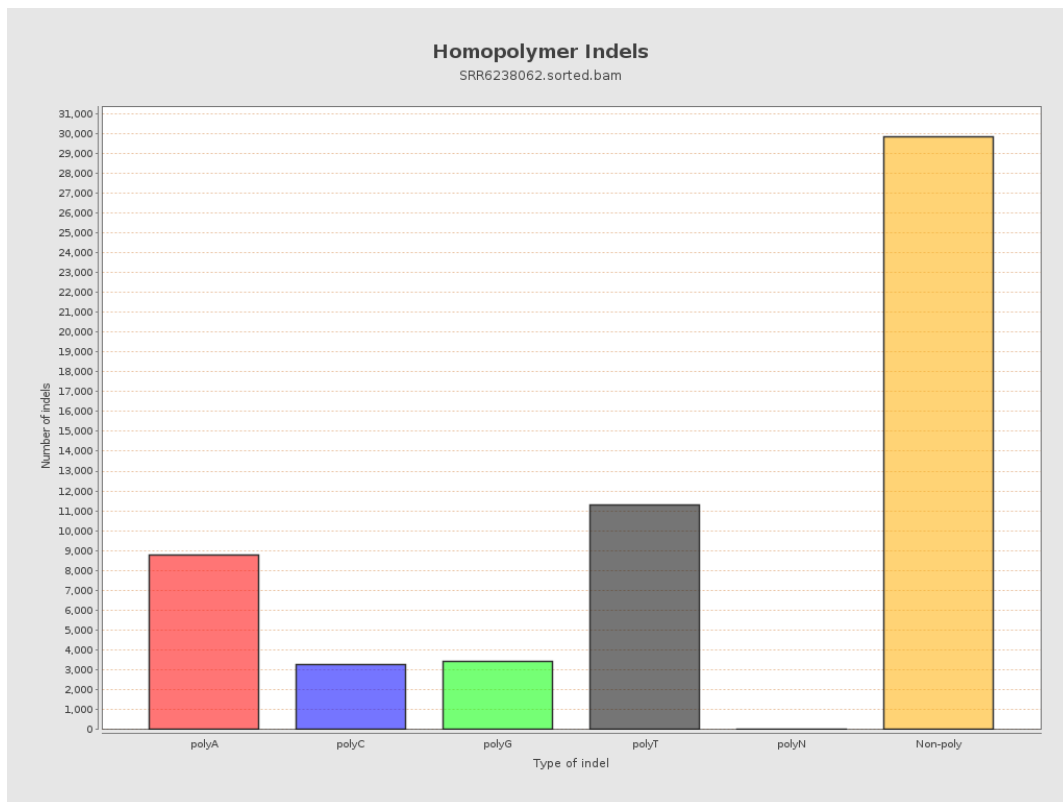
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

