

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 13:42:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238267.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_SRR6238267 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238267.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 13:42:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238267.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,233,997
Mapped reads	2,914,058 / 90.11%
Unmapped reads	319,939 / 9.89%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,725 / 1.1%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	144,379 / 4.46%
Duplication rate	3.64%
Clipped reads	1,509,937 / 46.69%

2.2. ACGT Content

Number/percentage of A's	53,159,345 / 27.87%
Number/percentage of C's	36,744,990 / 19.26%
Number/percentage of T's	58,407,935 / 30.62%
Number/percentage of G's	42,380,007 / 22.22%
Number/percentage of N's	62,856 / 0.03%
GC Percentage	41.48%

2.3. Coverage

Mean	0.0617

Standard Deviation	0.5757
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2.4. Mapping Quality

Mean Mapping Quality	44.48
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2.5. Mismatches and indels

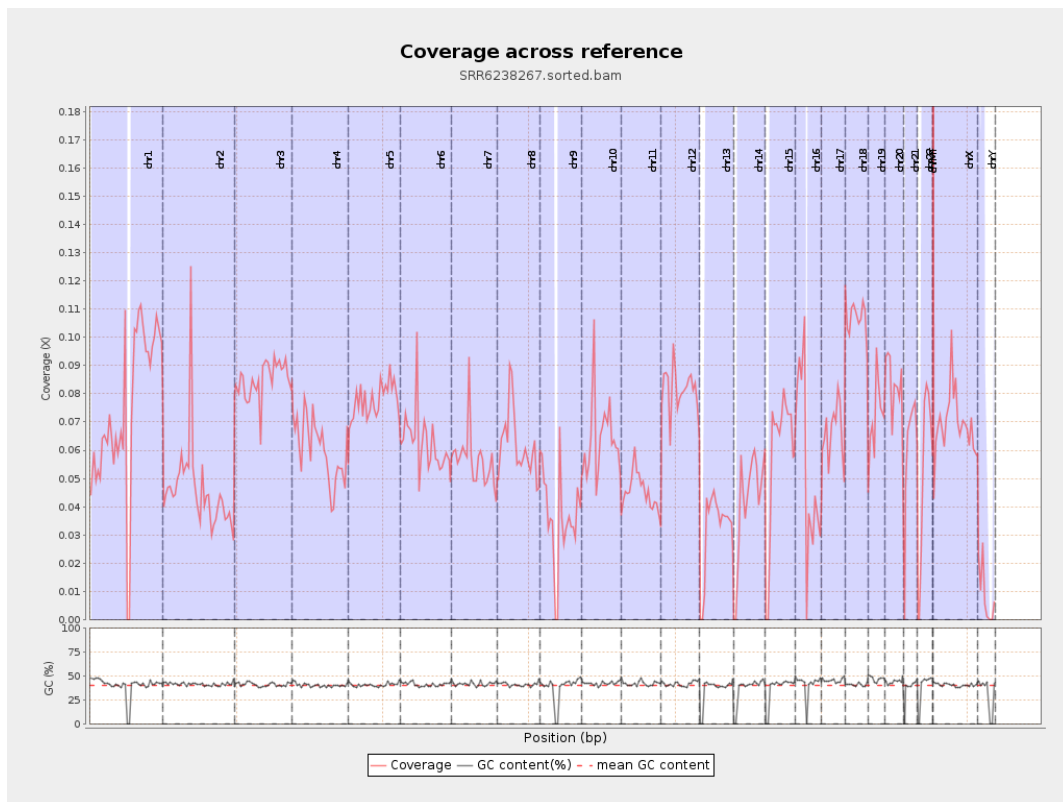
General error rate	0.95%
Mismatches	1,776,905
Insertions	15,435
Mapped reads with at least one insertion	0.53%
Deletions	73,133
Mapped reads with at least one deletion	2.48%
Homopolymer indels	44.25%

2.6. Chromosome stats

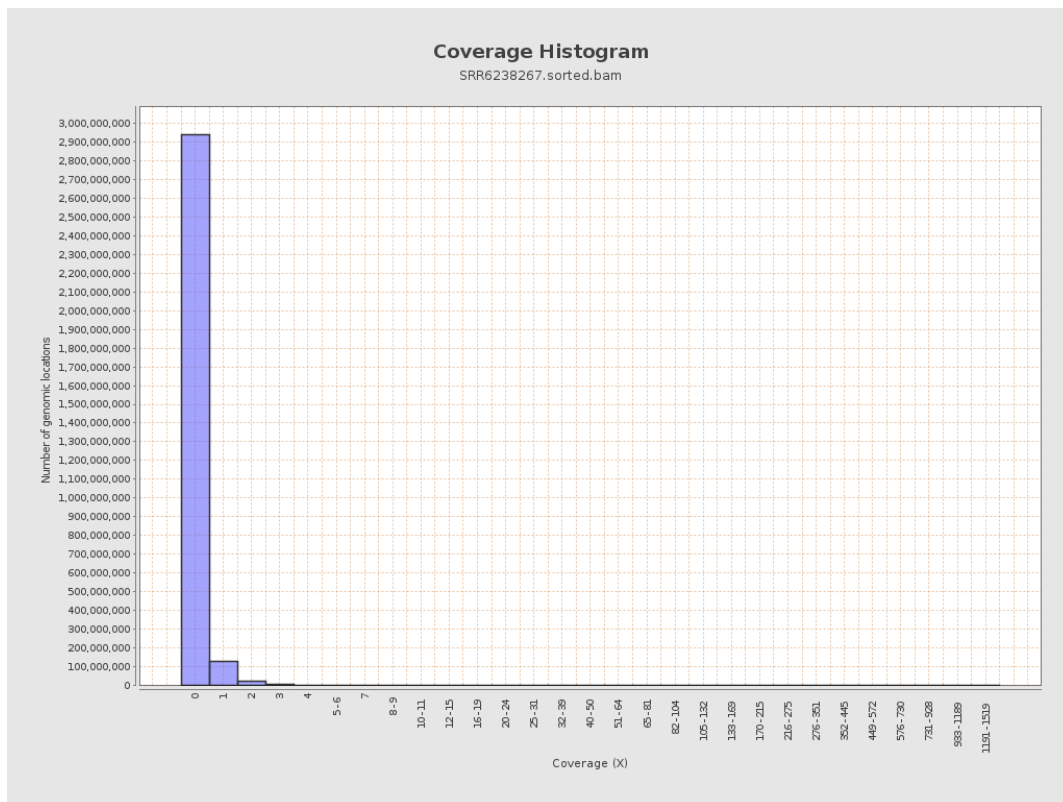
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	18595480	0.0746	1.2086
chr2	243199373	11235997	0.0462	0.7089
chr3	198022430	16809298	0.0849	0.3442
chr4	191154276	11553548	0.0604	0.3053
chr5	180915260	13993881	0.0774	0.3337
chr6	171115067	10670989	0.0624	0.4599
chr7	159138663	9020648	0.0567	0.6

chr8	146364022	8990740	0.0614	0.8201
chr9	141213431	5045557	0.0357	0.4675
chr10	135534747	8618406	0.0636	0.5472
chr11	135006516	6118616	0.0453	0.3705
chr12	133851895	10945307	0.0818	0.3472
chr13	115169878	3700041	0.0321	0.2129
chr14	107349540	4494137	0.0419	0.2659
chr15	102531392	5913139	0.0577	0.2897
chr16	90354753	4789917	0.053	0.313
chr17	81195210	5463591	0.0673	0.3645
chr18	78077248	8378971	0.1073	0.8558
chr19	59128983	4310541	0.0729	0.8377
chr20	63025520	5252053	0.0833	0.3496
chr21	48129895	2928115	0.0608	0.308
chr22	51304566	2734334	0.0533	0.2723
chrMT	16571	10881	0.6566	0.941
chrX	155270560	10793132	0.0695	0.3706
chrY	59373566	508931	0.0086	0.1948

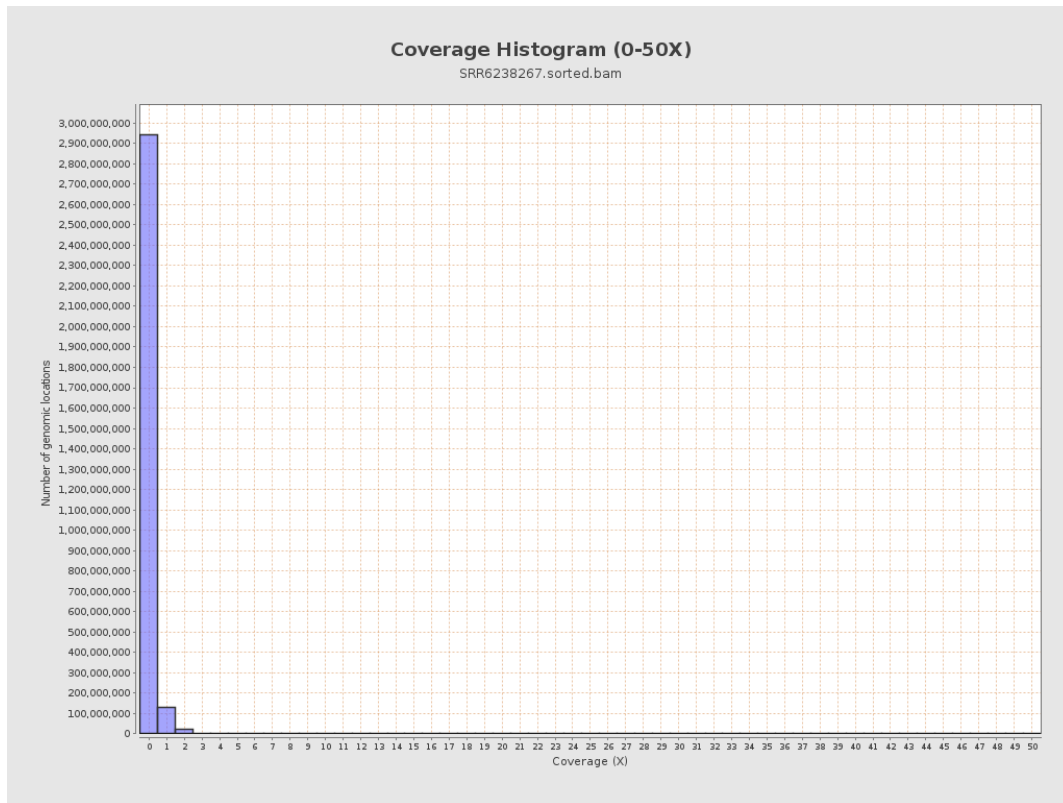
3. Results : Coverage across reference



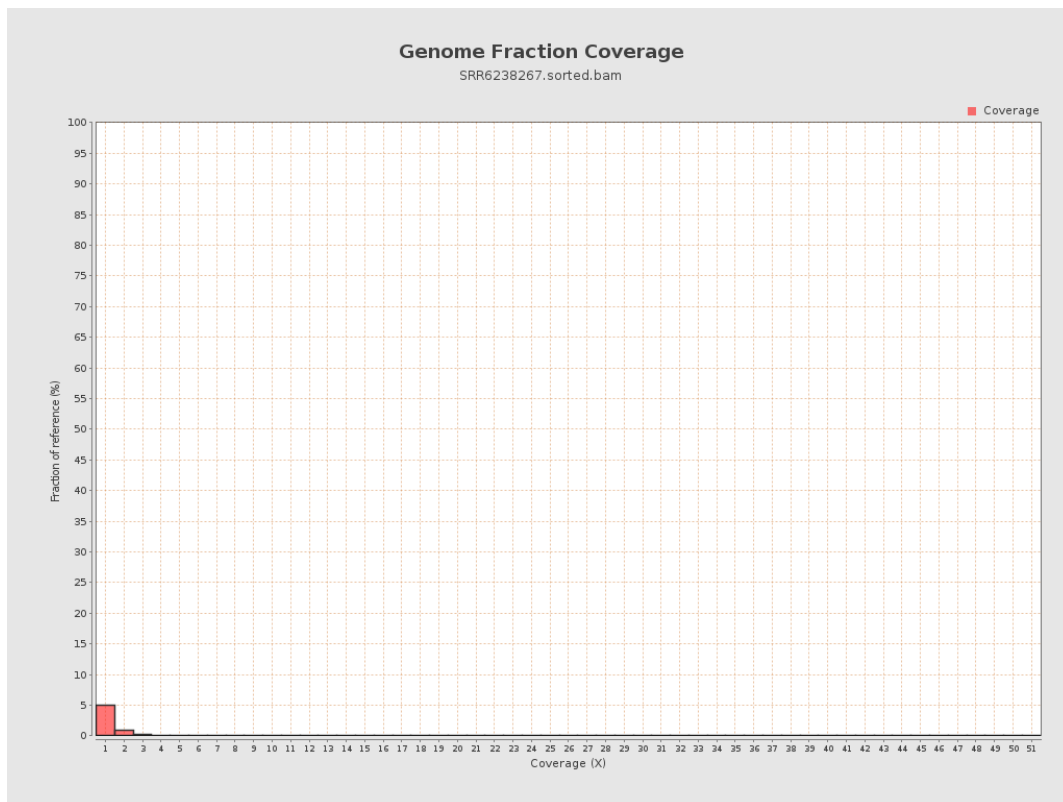
4. Results : Coverage Histogram



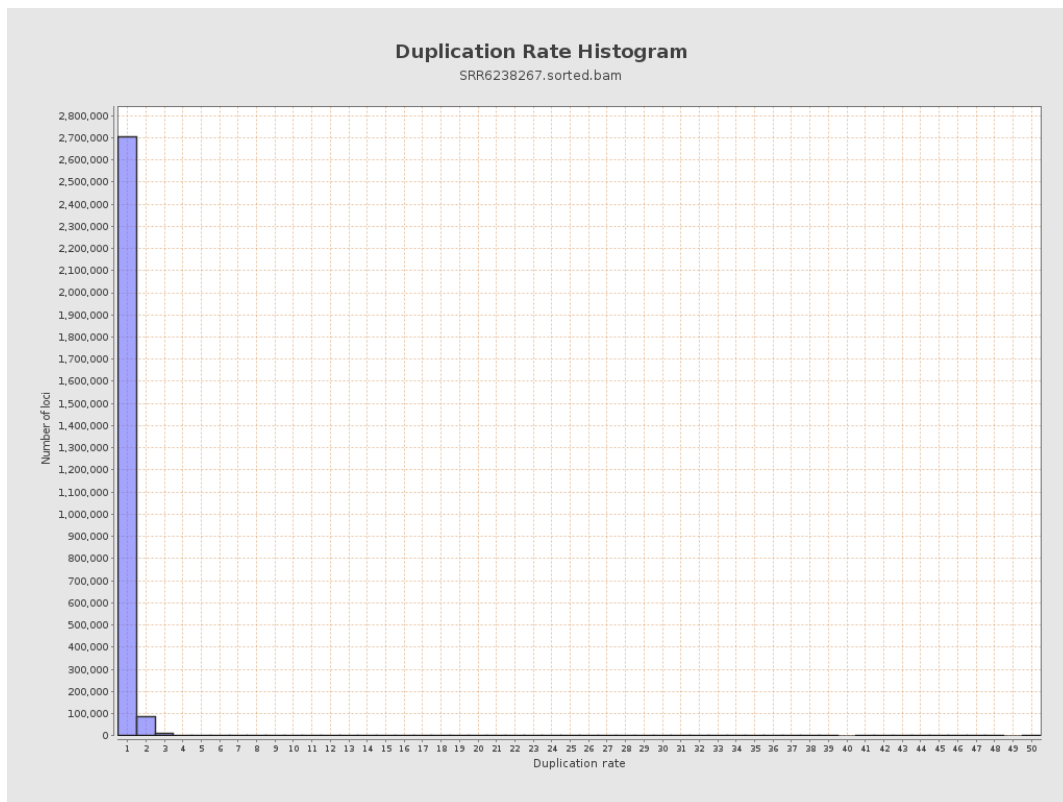
5. Results : Coverage Histogram (0-50X)



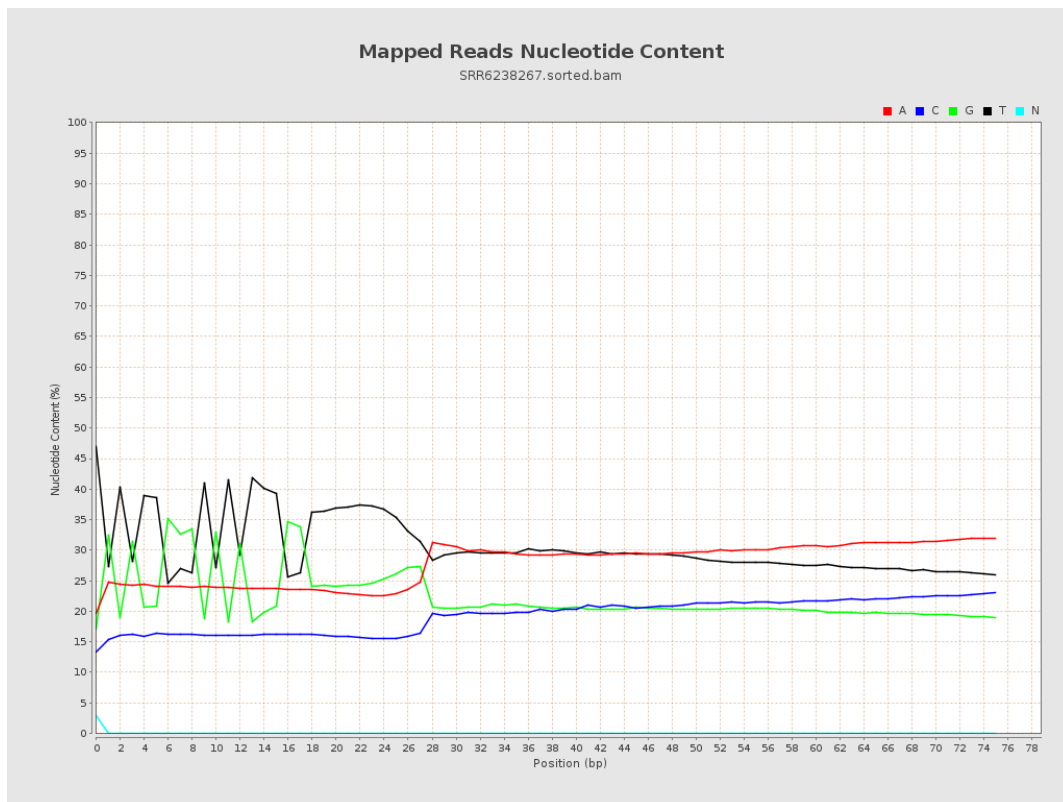
6. Results : Genome Fraction Coverage



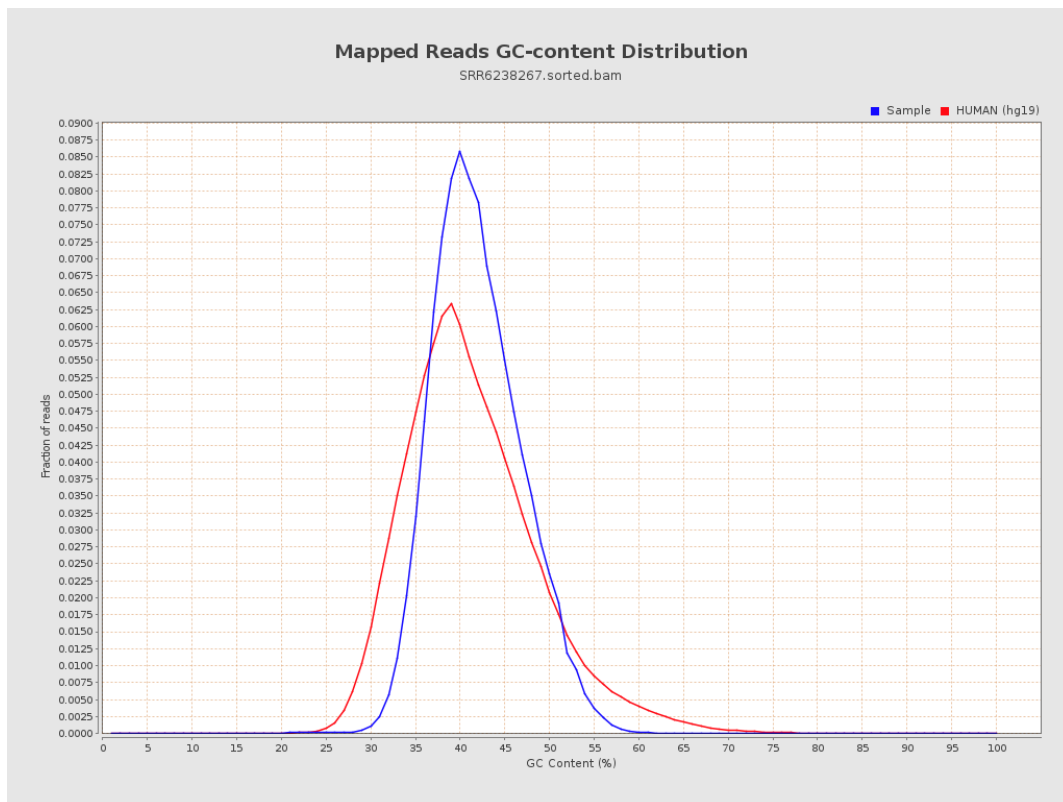
7. Results : Duplication Rate Histogram



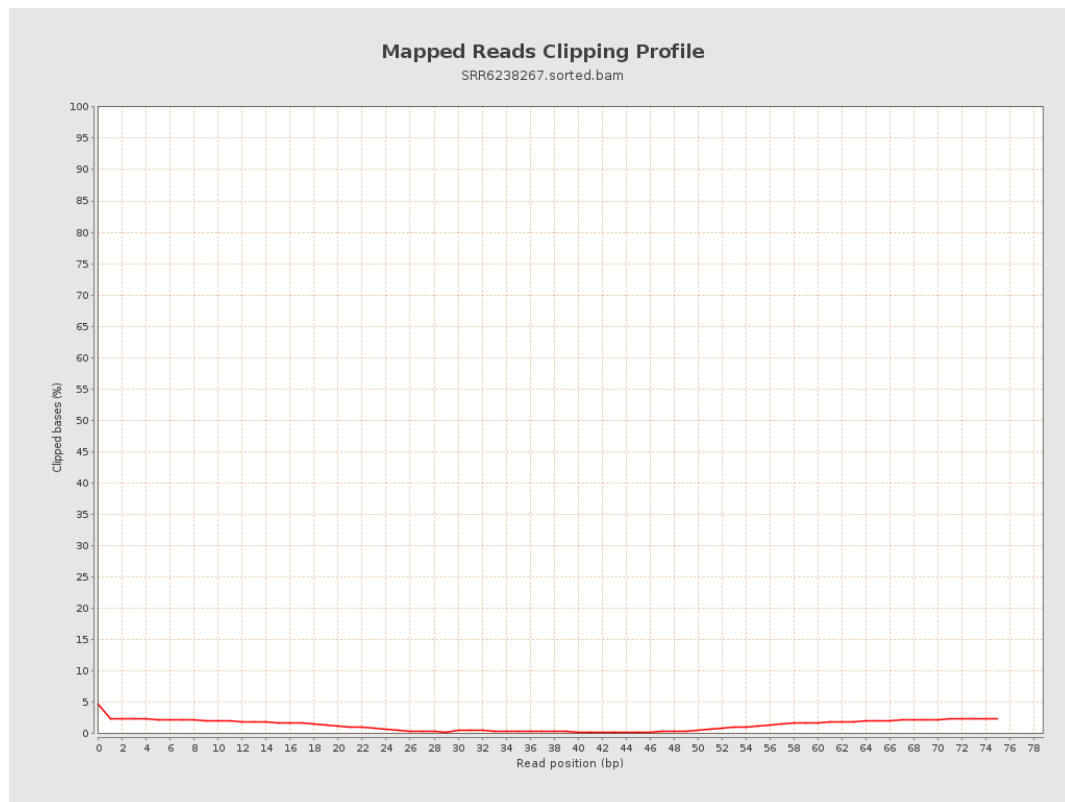
8. Results : Mapped Reads Nucleotide Content



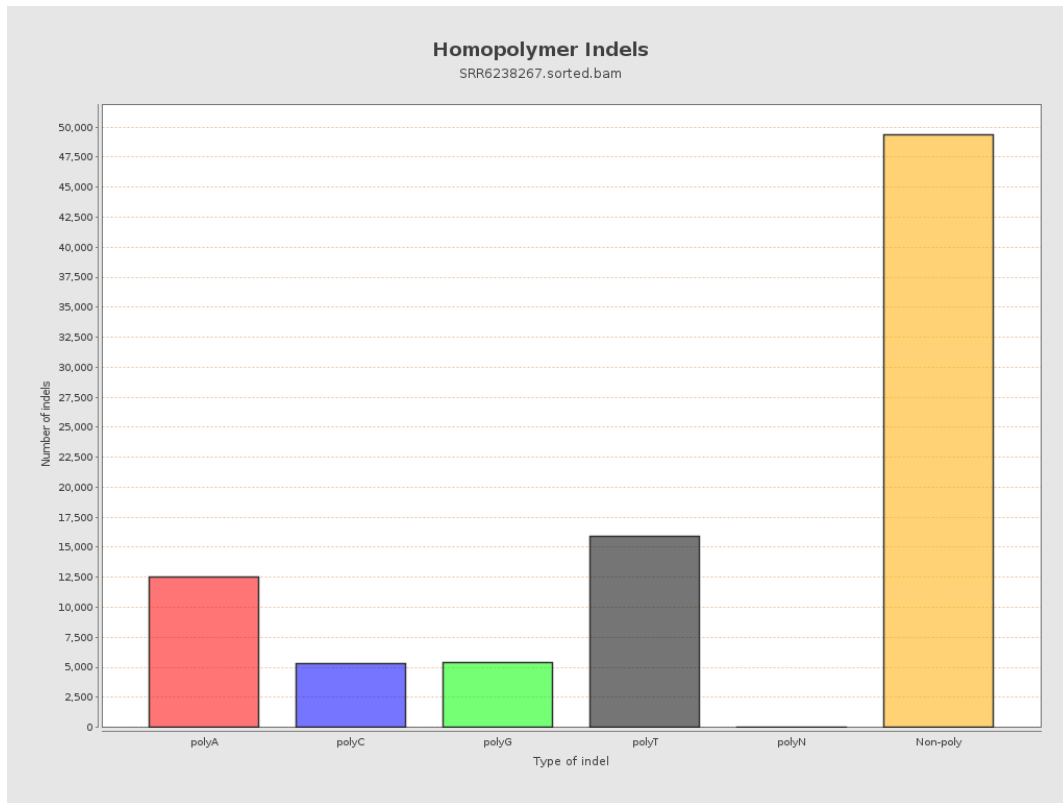
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

