

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:49:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238289.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_SRR6238289 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238289.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:49:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238289.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,988,214
Mapped reads	2,678,255 / 89.63%
Unmapped reads	309,959 / 10.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	27,409 / 0.92%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	110,932 / 3.71%
Duplication rate	3.01%
Clipped reads	1,272,696 / 42.59%

2.2. ACGT Content

Number/percentage of A's	48,541,716 / 27.37%
Number/percentage of C's	34,342,935 / 19.36%
Number/percentage of T's	54,008,759 / 30.45%
Number/percentage of G's	40,411,928 / 22.79%
Number/percentage of N's	44,959 / 0.03%
GC Percentage	42.15%

2.3. Coverage

Mean	0.0573

Standard Deviation	0.4924
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2.4. Mapping Quality

Mean Mapping Quality	44.35
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2.5. Mismatches and indels

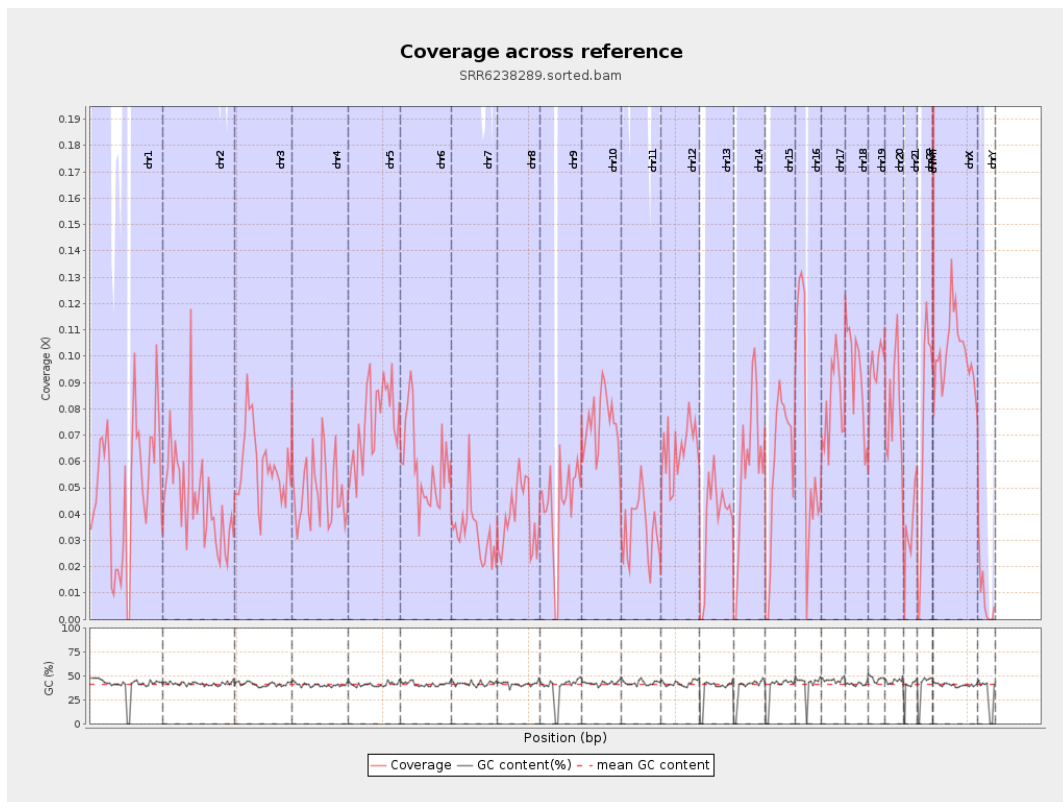
General error rate	0.83%
Mismatches	1,443,568
Insertions	13,886
Mapped reads with at least one insertion	0.51%
Deletions	46,903
Mapped reads with at least one deletion	1.73%
Homopolymer indels	46.43%

2.6. Chromosome stats

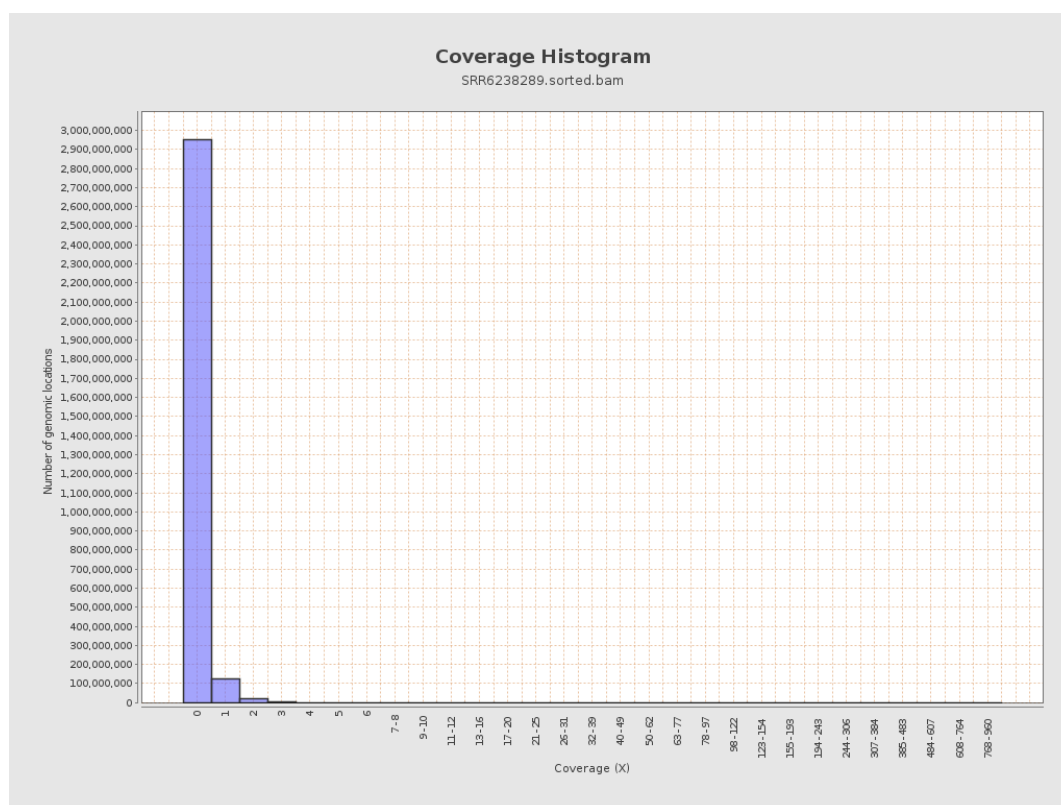
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12192673	0.0489	0.8676
chr2	243199373	11133458	0.0458	0.6403
chr3	198022430	11564188	0.0584	0.2795
chr4	191154276	9282361	0.0486	0.2717
chr5	180915260	13536160	0.0748	0.3238
chr6	171115067	9889959	0.0578	0.3257
chr7	159138663	5218368	0.0328	0.5795

chr8	146364022	5688766	0.0389	0.5757
chr9	141213431	6208957	0.044	0.507
chr10	135534747	10086901	0.0744	0.44
chr11	135006516	4644867	0.0344	0.3521
chr12	133851895	8711175	0.0651	0.3115
chr13	115169878	4406240	0.0383	0.2252
chr14	107349540	6263594	0.0583	0.326
chr15	102531392	5841406	0.057	0.2814
chr16	90354753	6341676	0.0702	0.355
chr17	81195210	6730430	0.0829	0.3794
chr18	78077248	7292115	0.0934	1.0277
chr19	59128983	5691695	0.0963	0.6222
chr20	63025520	5003249	0.0794	0.337
chr21	48129895	1717164	0.0357	0.2611
chr22	51304566	3766037	0.0734	0.3196
chrMT	16571	47114	2.8432	2.4393
chrX	155270560	15688996	0.101	0.4396
chrY	59373566	480432	0.0081	0.1505

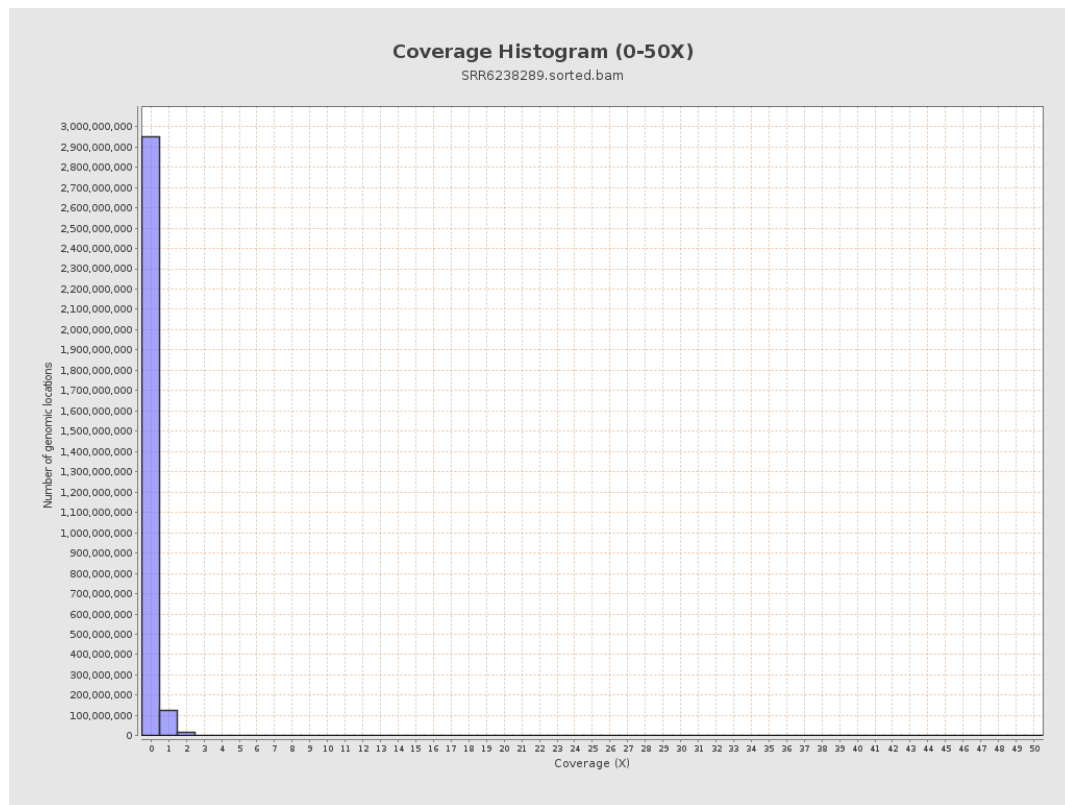
3. Results : Coverage across reference



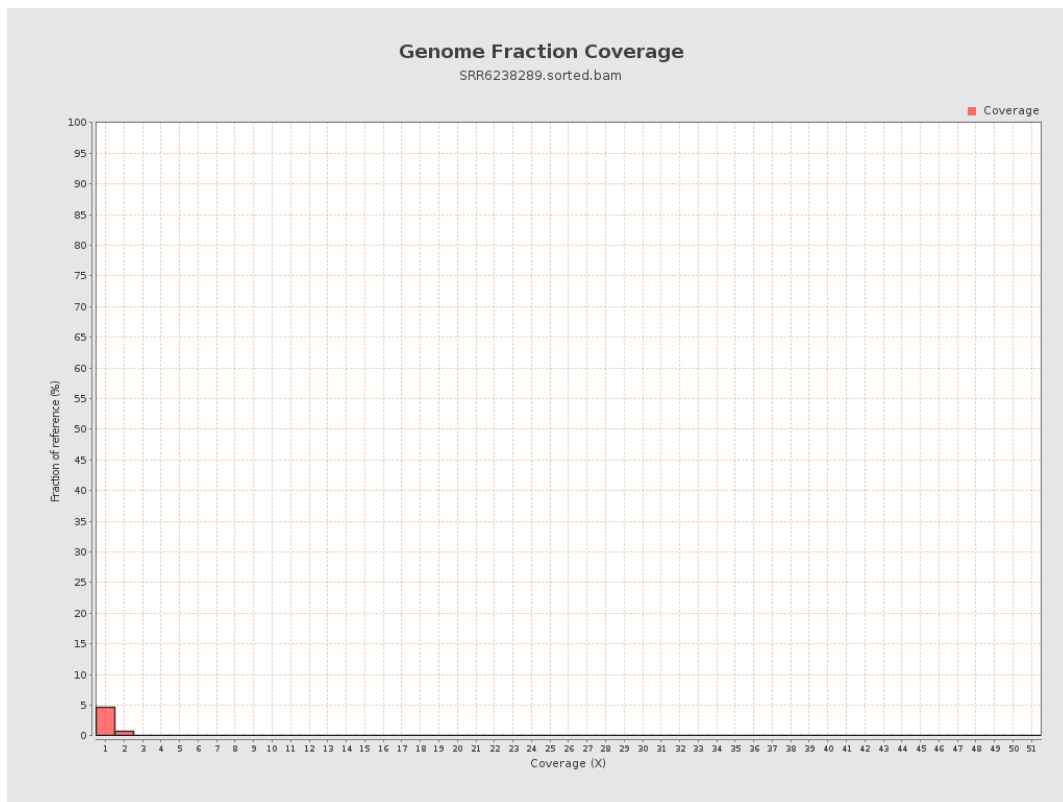
4. Results : Coverage Histogram



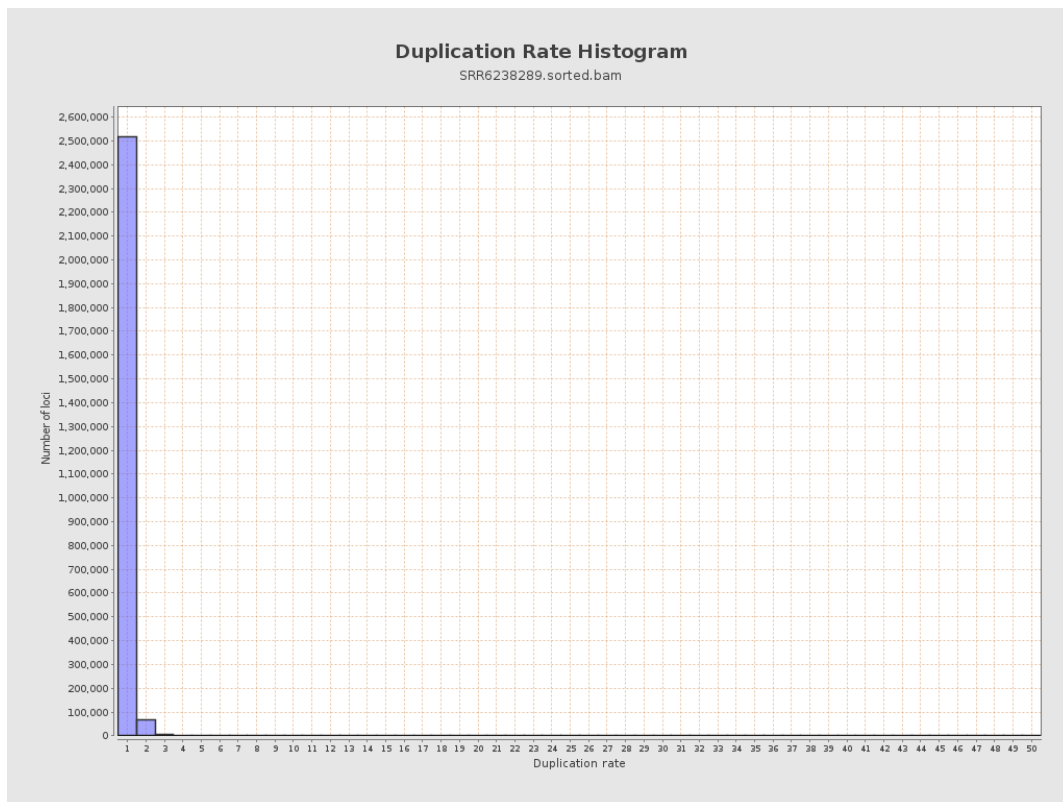
5. Results : Coverage Histogram (0-50X)



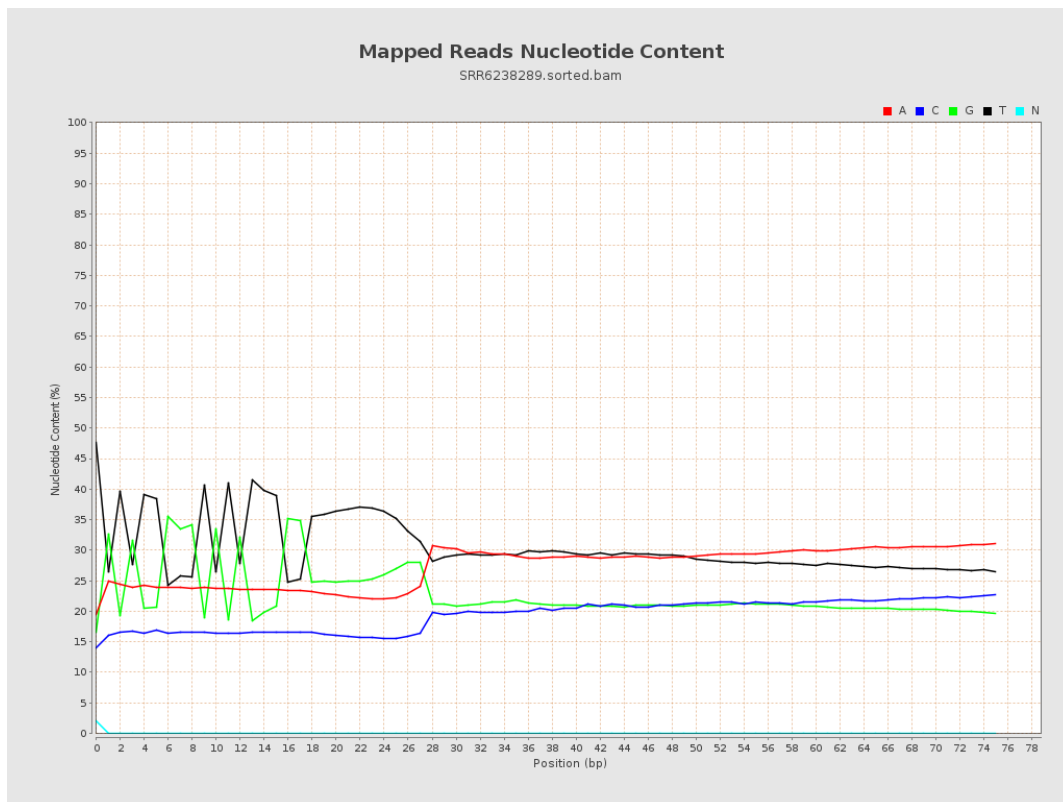
6. Results : Genome Fraction Coverage



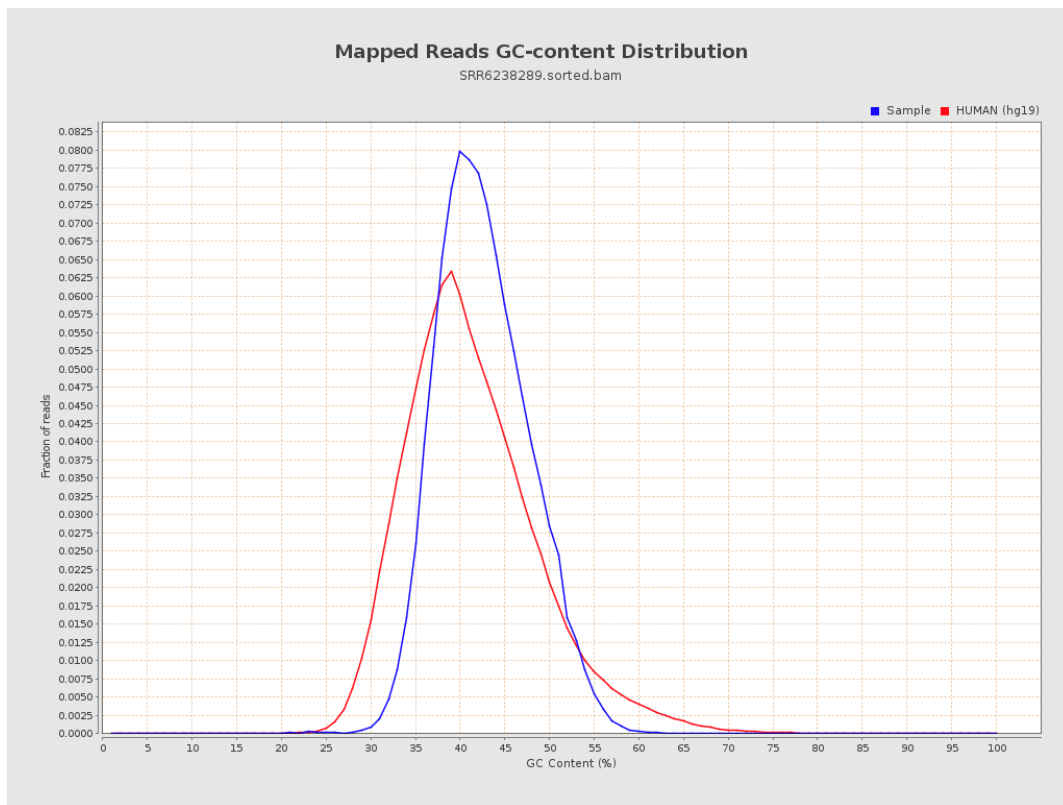
7. Results : Duplication Rate Histogram



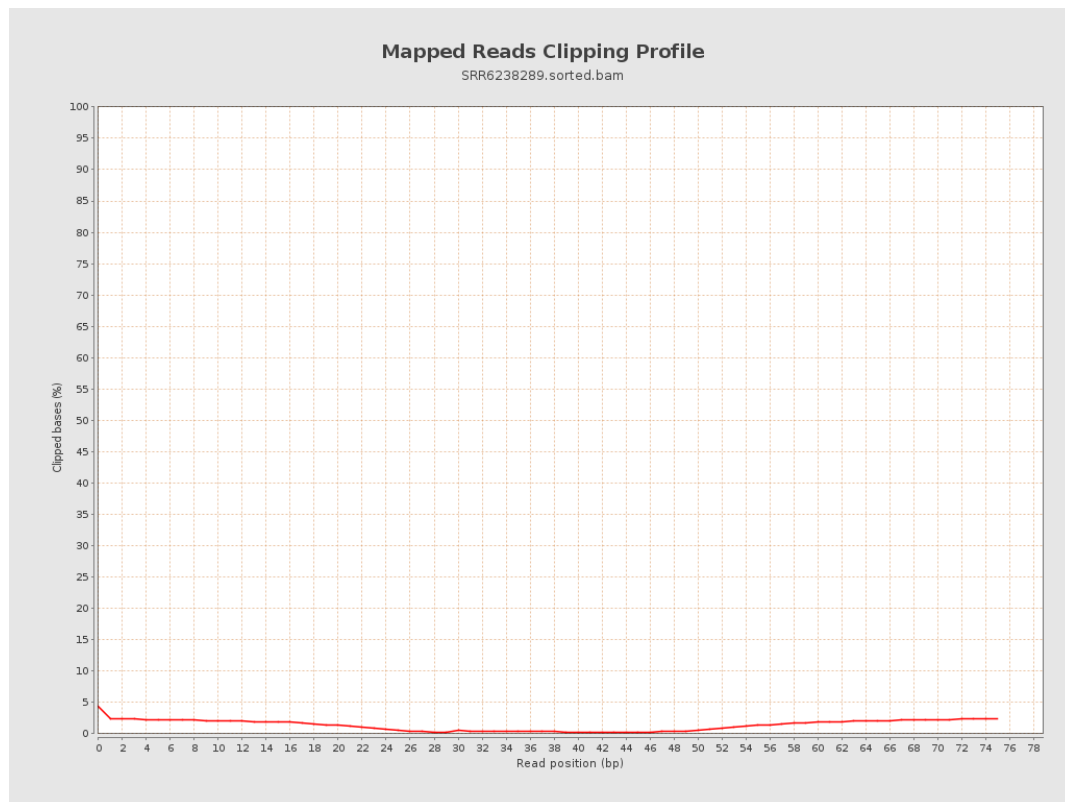
8. Results : Mapped Reads Nucleotide Content



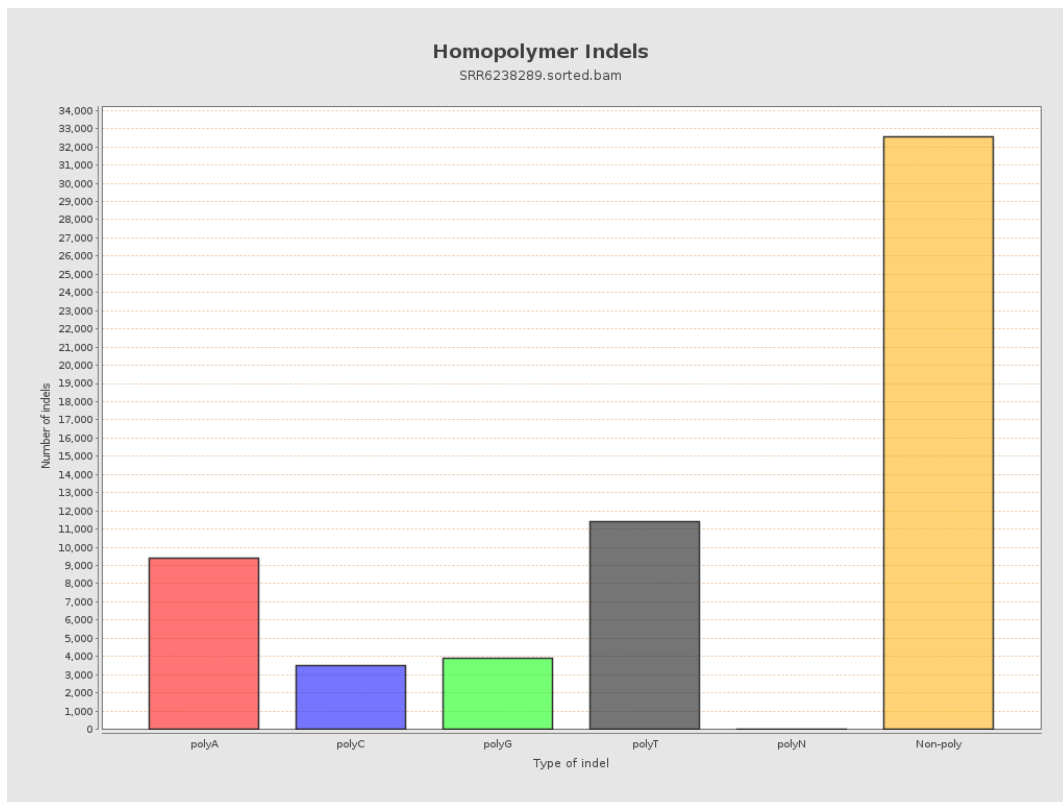
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

