

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:58:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238292.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_SRR6238292 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238292.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:58:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238292.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,216,616
Mapped reads	181,304 / 5.64%
Unmapped reads	3,035,312 / 94.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,570 / 0.05%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	7,373 / 0.23%
Duplication rate	1.35%
Clipped reads	100,734 / 3.13%

2.2. ACGT Content

Number/percentage of A's	3,181,914 / 27.53%
Number/percentage of C's	2,318,406 / 20.06%
Number/percentage of T's	3,389,207 / 29.33%
Number/percentage of G's	2,664,529 / 23.06%
Number/percentage of N's	2,916 / 0.03%
GC Percentage	43.12%

2.3. Coverage

Mean	0.0037

Standard Deviation	0.1952
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2.4. Mapping Quality

Mean Mapping Quality	42.06
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2.5. Mismatches and indels

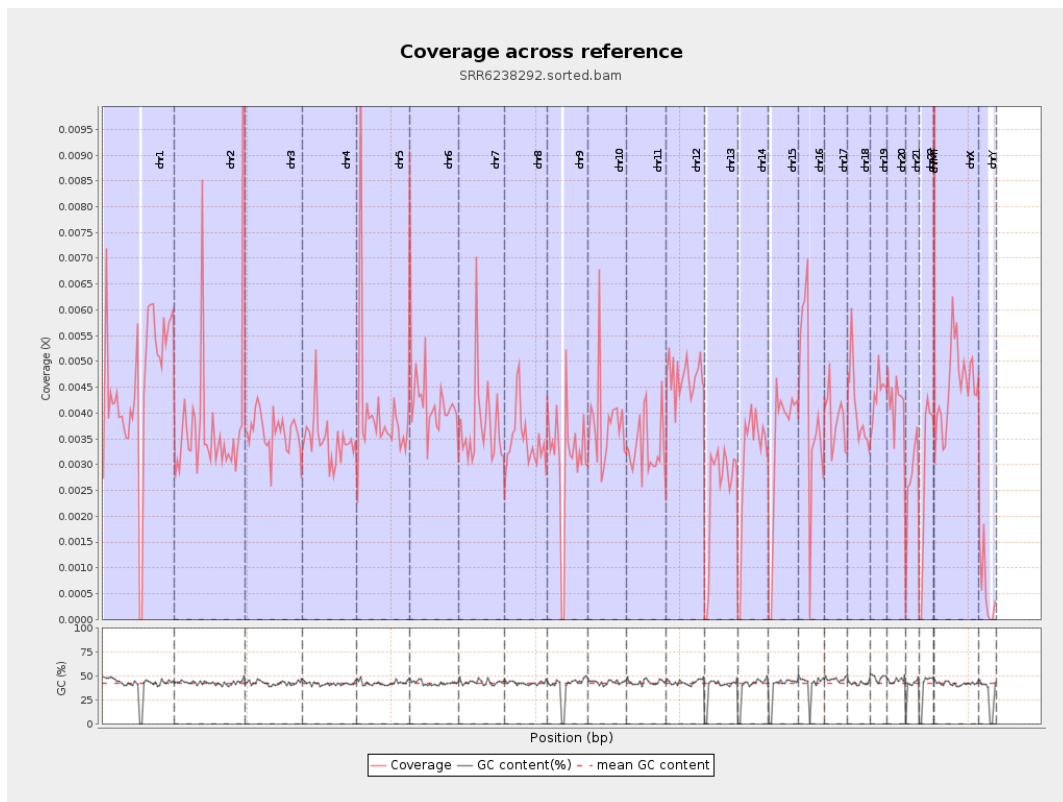
General error rate	1%
Mismatches	109,615
Insertions	2,187
Mapped reads with at least one insertion	1.08%
Deletions	4,547
Mapped reads with at least one deletion	2.28%
Homopolymer indels	44.51%

2.6. Chromosome stats

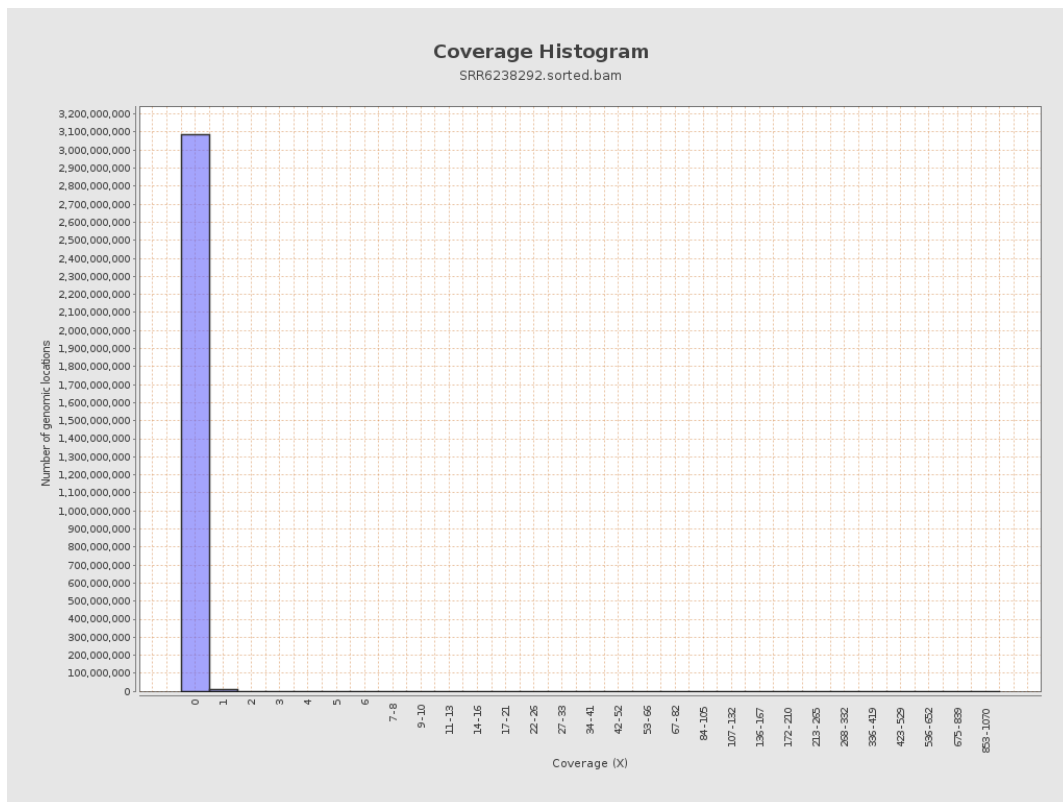
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1126457	0.0045	0.1946
chr2	243199373	941125	0.0039	0.4287
chr3	198022430	720213	0.0036	0.0613
chr4	191154276	663081	0.0035	0.061
chr5	180915260	731054	0.004	0.4335
chr6	171115067	731858	0.0043	0.3227
chr7	159138663	597795	0.0038	0.0759

chr8	146364022	507611	0.0035	0.0728
chr9	141213431	438024	0.0031	0.0634
chr10	135534747	514547	0.0038	0.0713
chr11	135006516	452731	0.0034	0.1369
chr12	133851895	629570	0.0047	0.0699
chr13	115169878	286687	0.0025	0.0507
chr14	107349540	333470	0.0031	0.0592
chr15	102531392	348668	0.0034	0.0594
chr16	90354753	370885	0.0041	0.0672
chr17	81195210	314279	0.0039	0.0744
chr18	78077248	317374	0.0041	0.0971
chr19	59128983	258825	0.0044	0.0804
chr20	63025520	264788	0.0042	0.0669
chr21	48129895	129966	0.0027	0.0563
chr22	51304566	145670	0.0028	0.0543
chrMT	16571	972	0.0587	0.2418
chrX	155270560	706503	0.0046	0.0708
chrY	59373566	33280	0.0006	0.0272

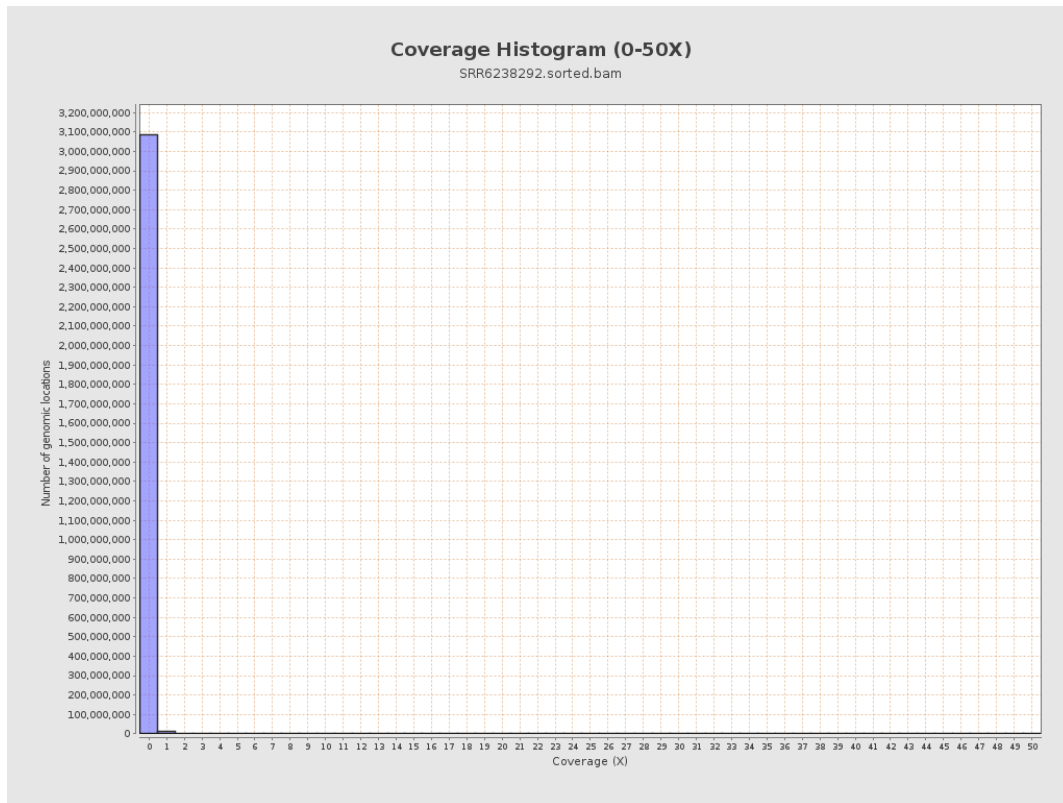
3. Results : Coverage across reference



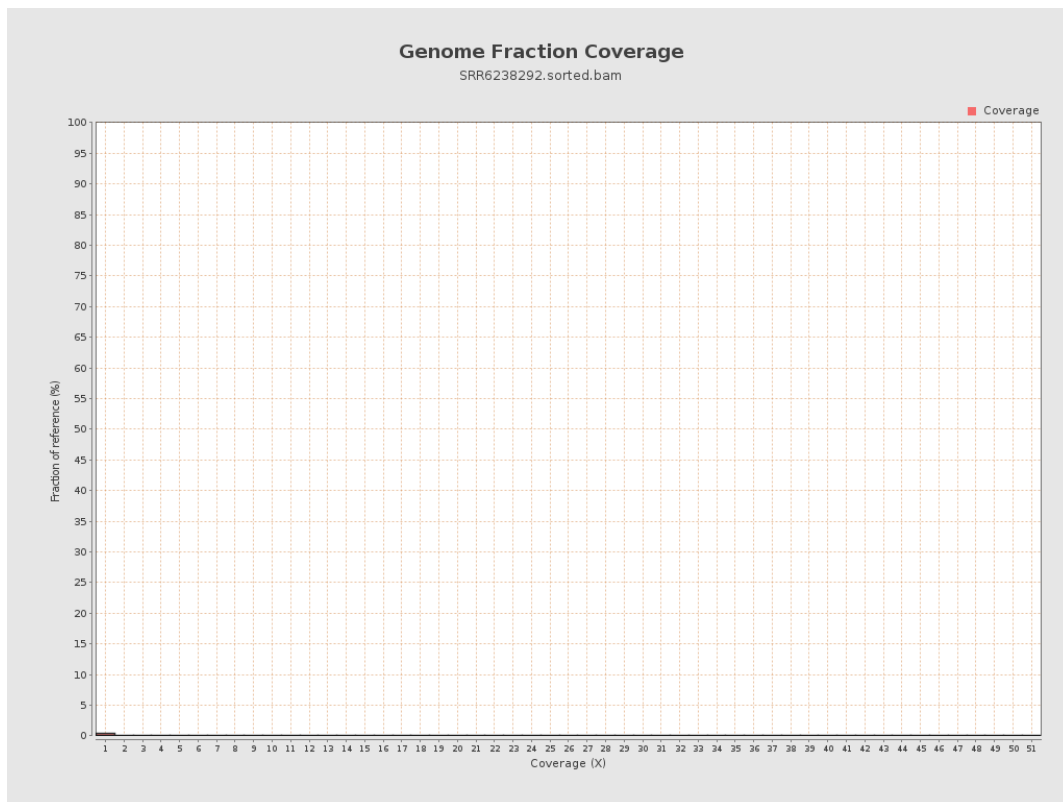
4. Results : Coverage Histogram



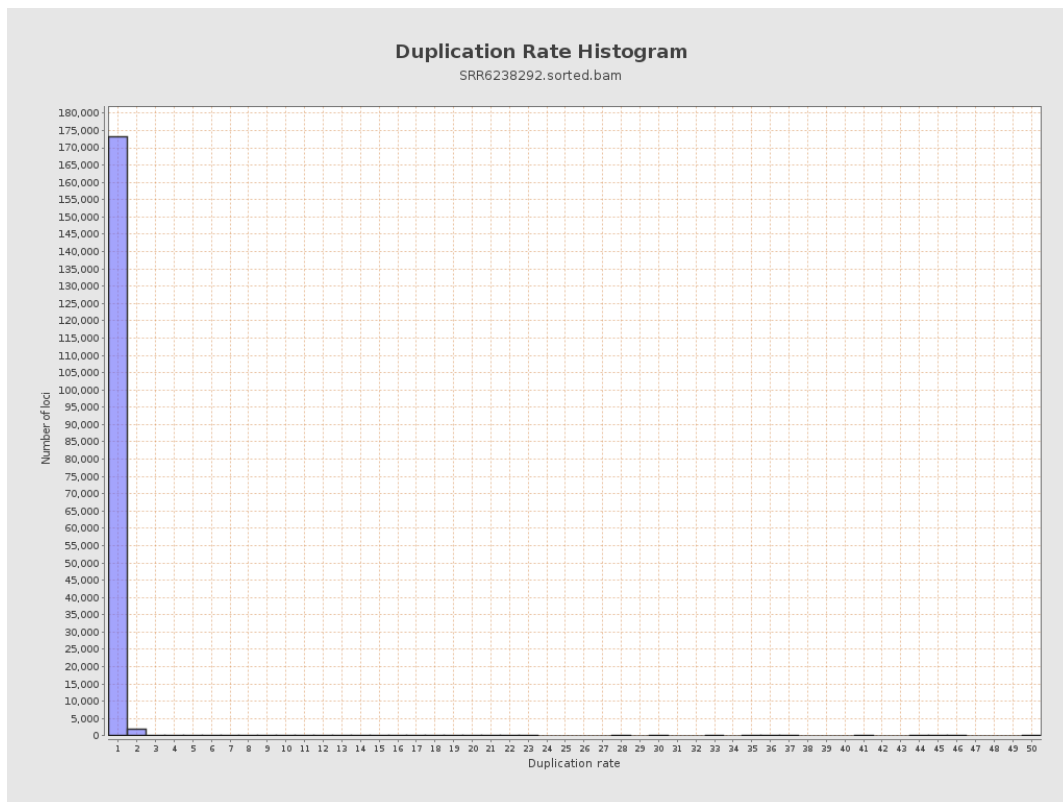
5. Results : Coverage Histogram (0-50X)



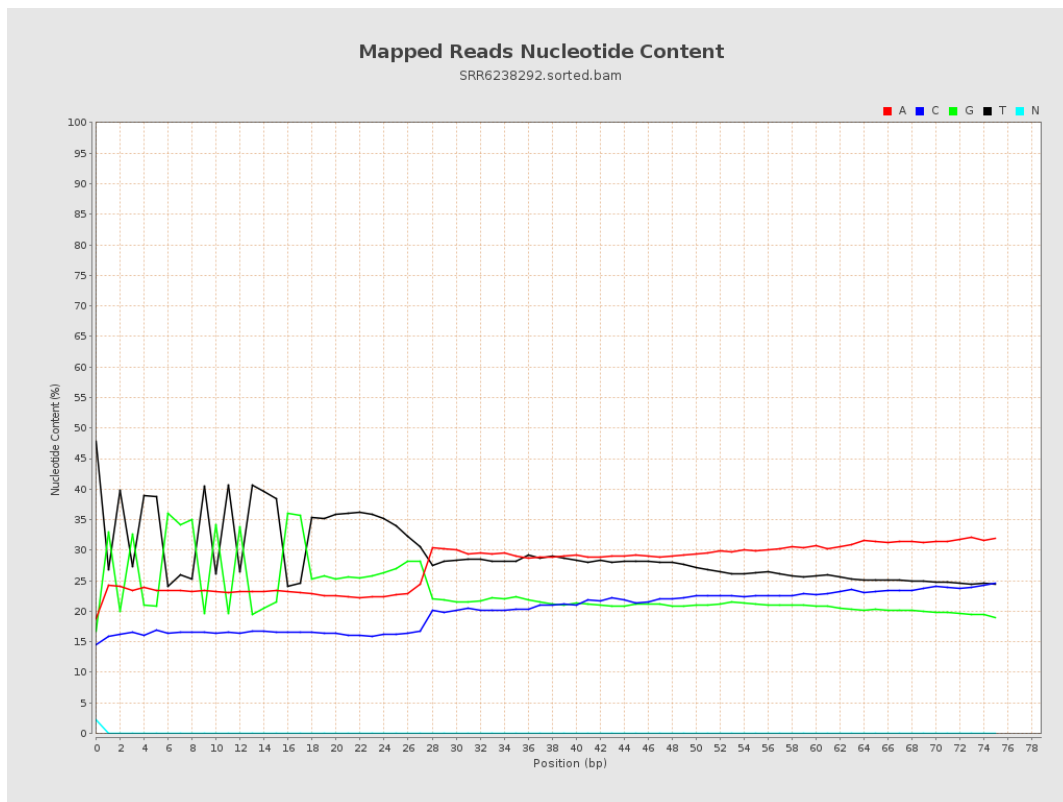
6. Results : Genome Fraction Coverage



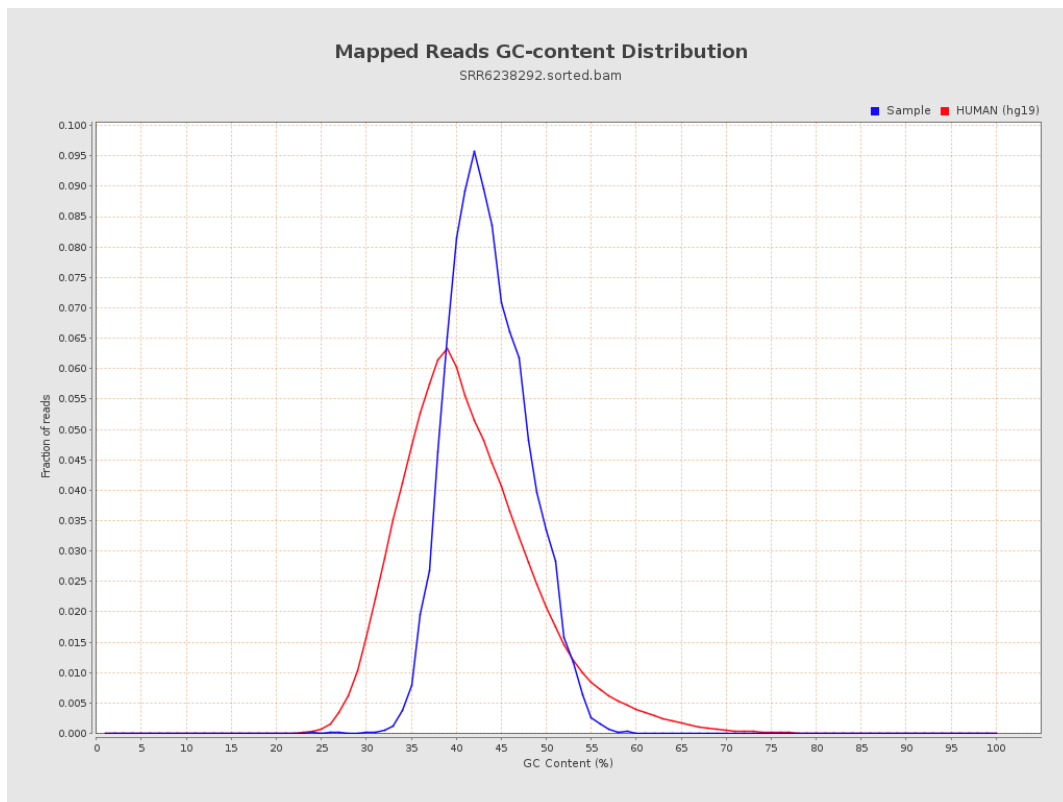
7. Results : Duplication Rate Histogram



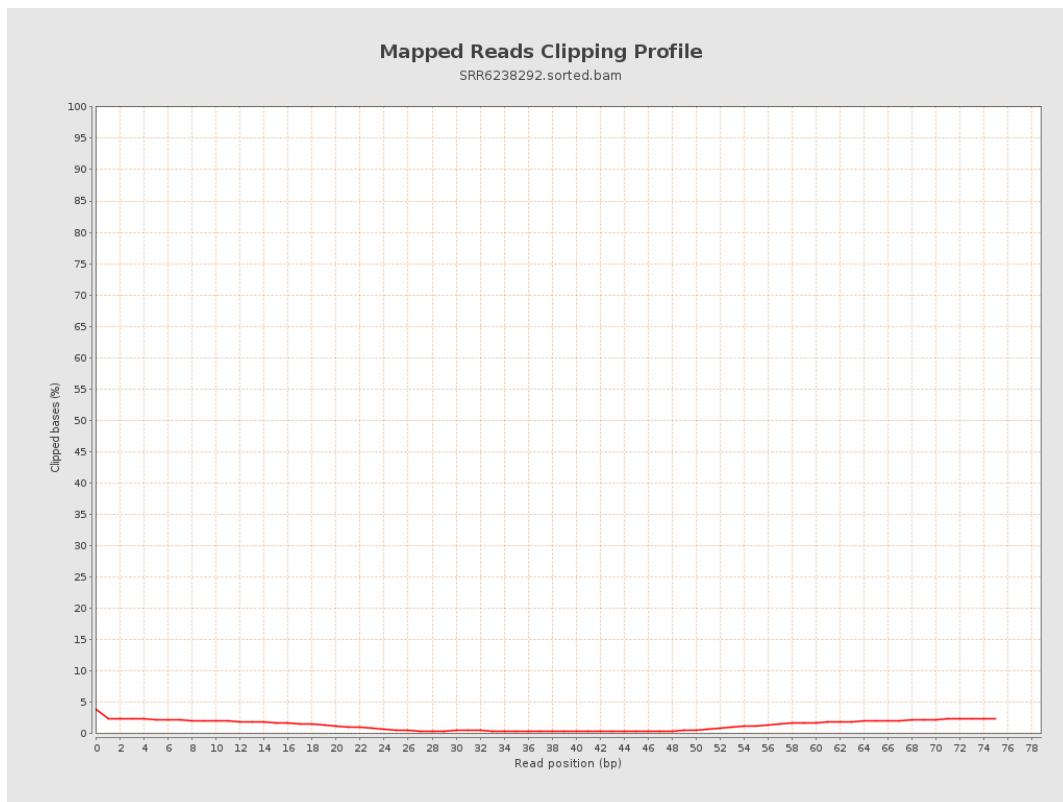
8. Results : Mapped Reads Nucleotide Content



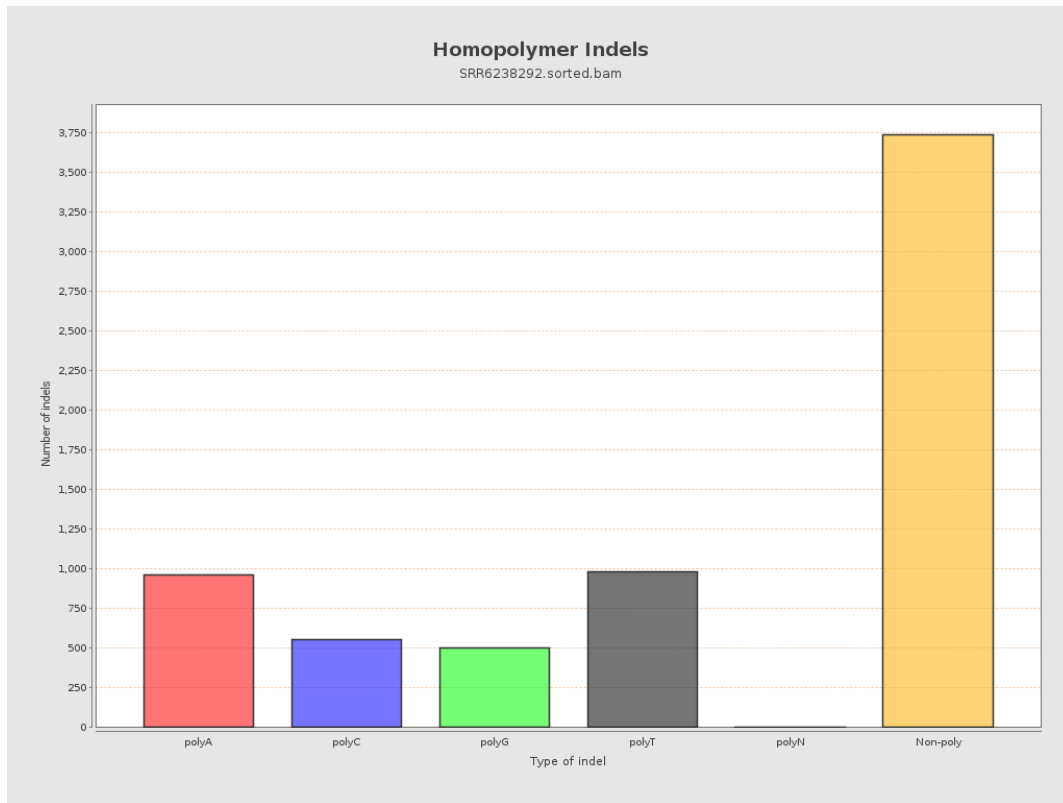
9. Results : Mapped Reads GC-content Distribution



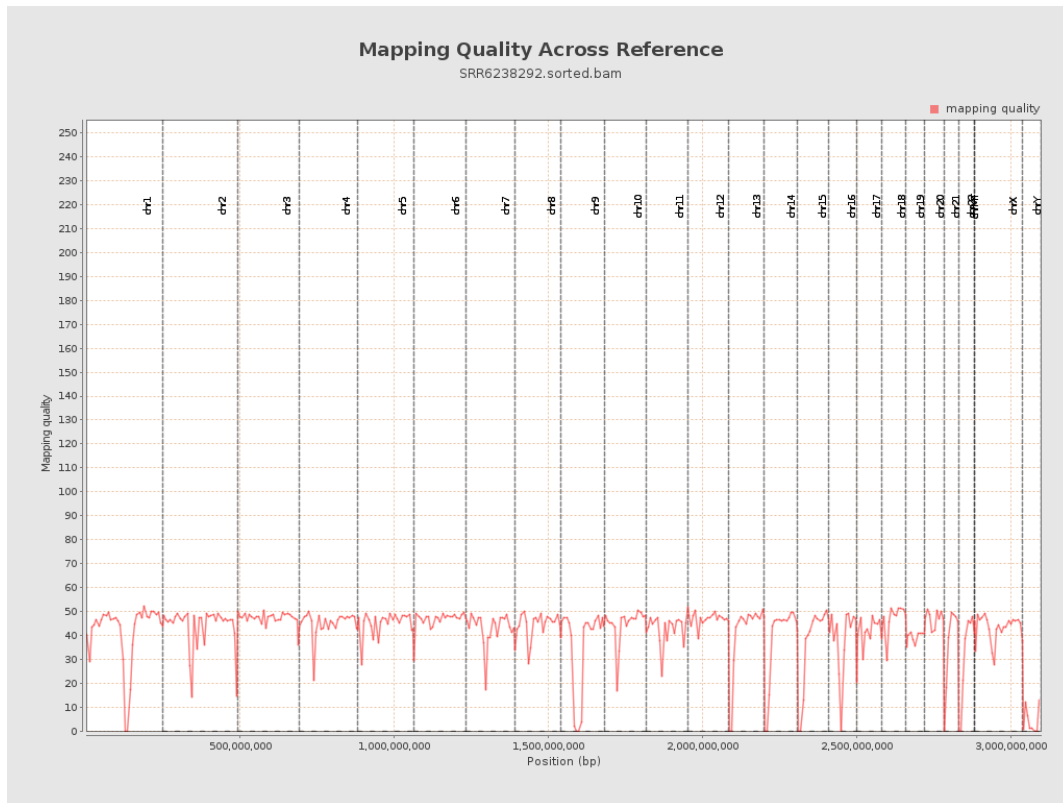
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

