

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:07:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238275.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_SRR6238275 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238275.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:07:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238275.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,023,153
Mapped reads	1,655,317 / 81.82%
Unmapped reads	367,836 / 18.18%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,672 / 0.87%
Read min/max/mean length	30 / 76 / 76.31
Duplicated reads (estimated)	155,852 / 7.7%
Duplication rate	7.61%
Clipped reads	893,021 / 44.14%

2.2. ACGT Content

Number/percentage of A's	29,383,024 / 27.43%
Number/percentage of C's	20,301,646 / 18.95%
Number/percentage of T's	33,236,441 / 31.03%
Number/percentage of G's	24,170,099 / 22.56%
Number/percentage of N's	26,004 / 0.02%
GC Percentage	41.52%

2.3. Coverage

Mean	0.0346

Standard Deviation	0.3408
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2.4. Mapping Quality

Mean Mapping Quality	45.41
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2.5. Mismatches and indels

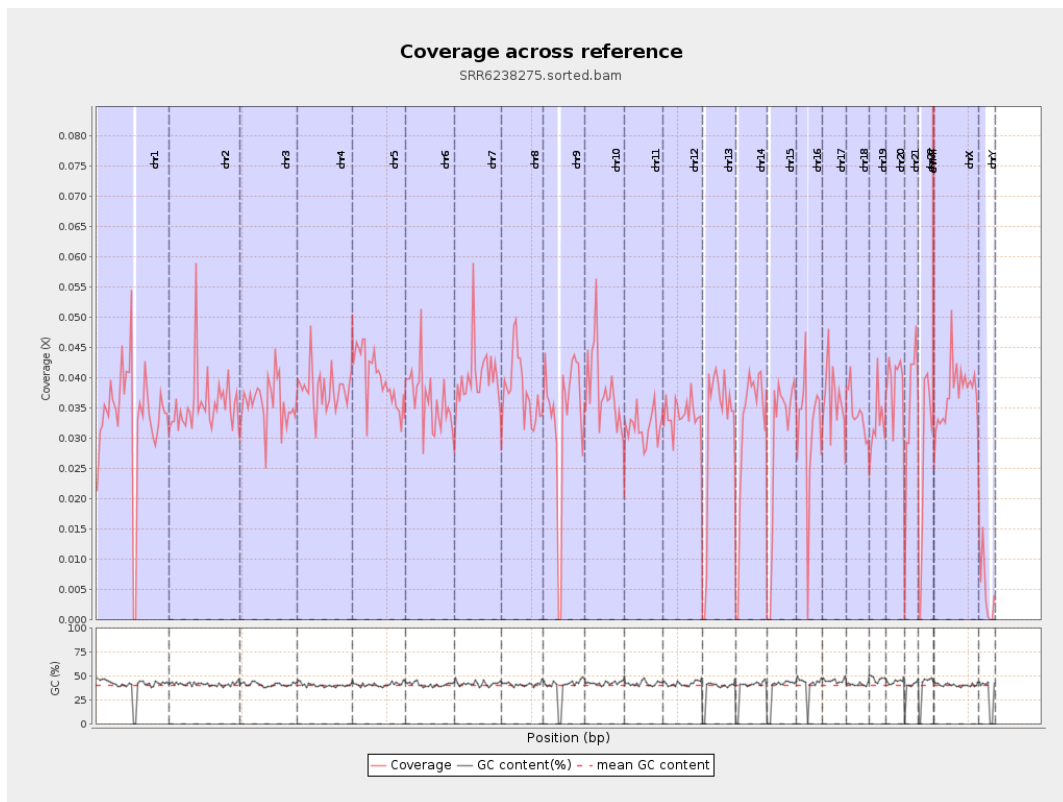
General error rate	1.01%
Mismatches	1,062,457
Insertions	8,989
Mapped reads with at least one insertion	0.54%
Deletions	39,377
Mapped reads with at least one deletion	2.35%
Homopolymer indels	47.07%

2.6. Chromosome stats

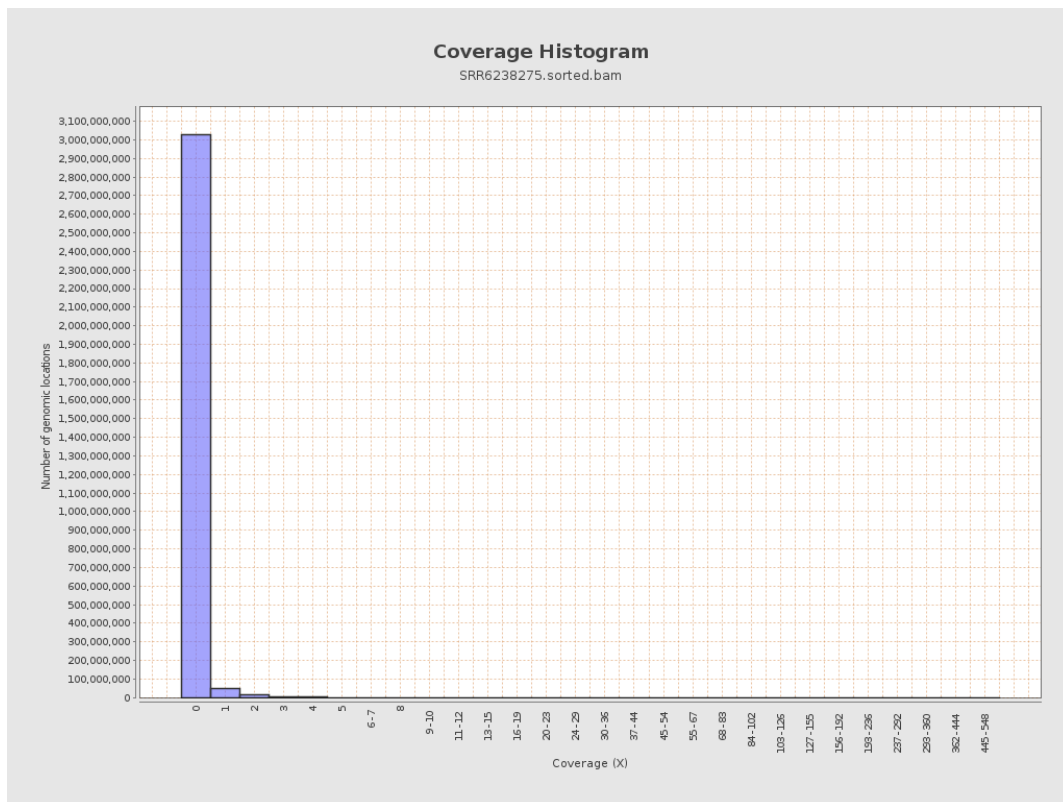
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8320598	0.0334	0.5039
chr2	243199373	8656766	0.0356	0.4009
chr3	198022430	7075002	0.0357	0.2684
chr4	191154276	7273411	0.038	0.2888
chr5	180915260	7200322	0.0398	0.2839
chr6	171115067	6195644	0.0362	0.3126
chr7	159138663	6400450	0.0402	0.4449

chr8	146364022	5523490	0.0377	0.4075
chr9	141213431	4701950	0.0333	0.3159
chr10	135534747	5130263	0.0379	0.3407
chr11	135006516	4274943	0.0317	0.2989
chr12	133851895	4519284	0.0338	0.2626
chr13	115169878	3588050	0.0312	0.252
chr14	107349540	3365252	0.0313	0.2739
chr15	102531392	3015008	0.0294	0.2698
chr16	90354753	2840816	0.0314	0.262
chr17	81195210	2941371	0.0362	0.2928
chr18	78077248	2677171	0.0343	0.4851
chr19	59128983	1931612	0.0327	0.3835
chr20	63025520	2473940	0.0393	0.2884
chr21	48129895	1659413	0.0345	0.2714
chr22	51304566	1340511	0.0261	0.2278
chrMT	16571	13696	0.8265	1.4694
chrX	155270560	5777537	0.0372	0.2896
chrY	59373566	285405	0.0048	0.1273

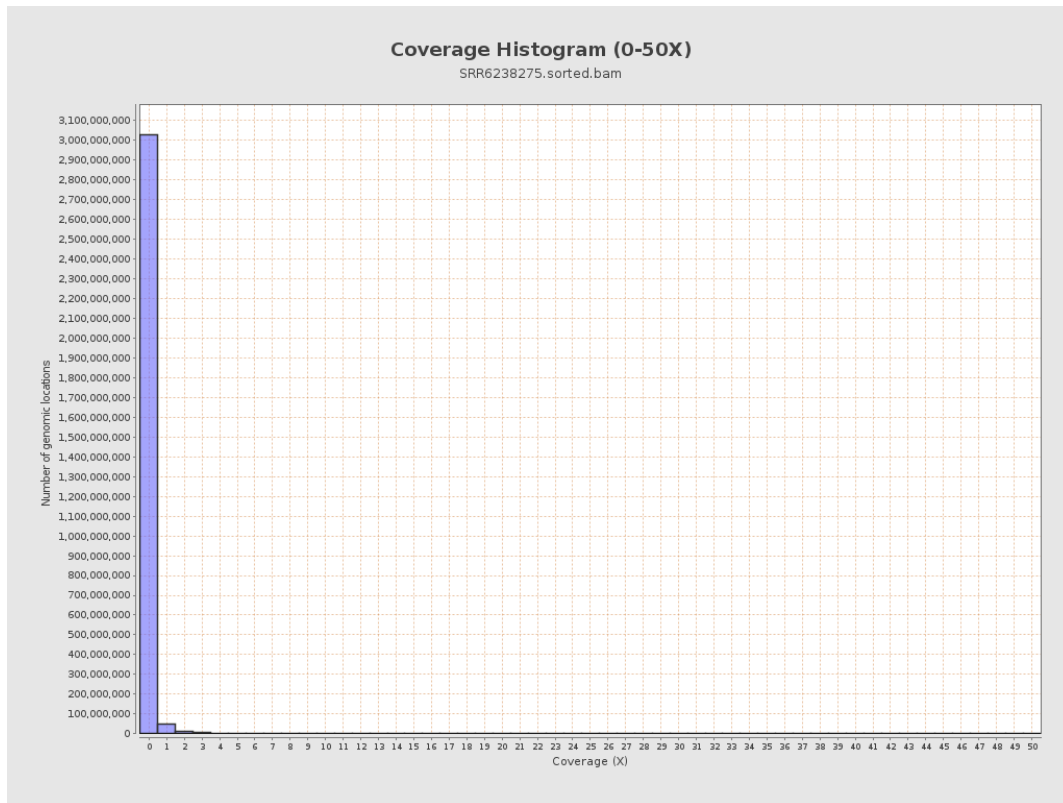
3. Results : Coverage across reference



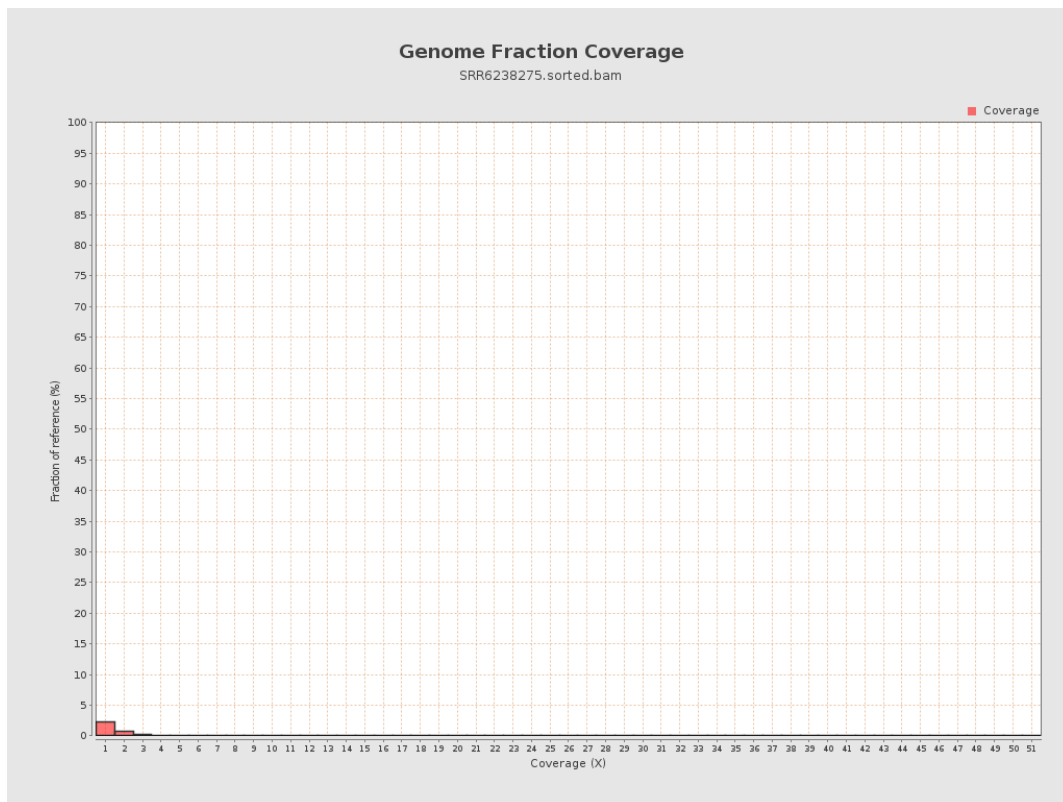
4. Results : Coverage Histogram



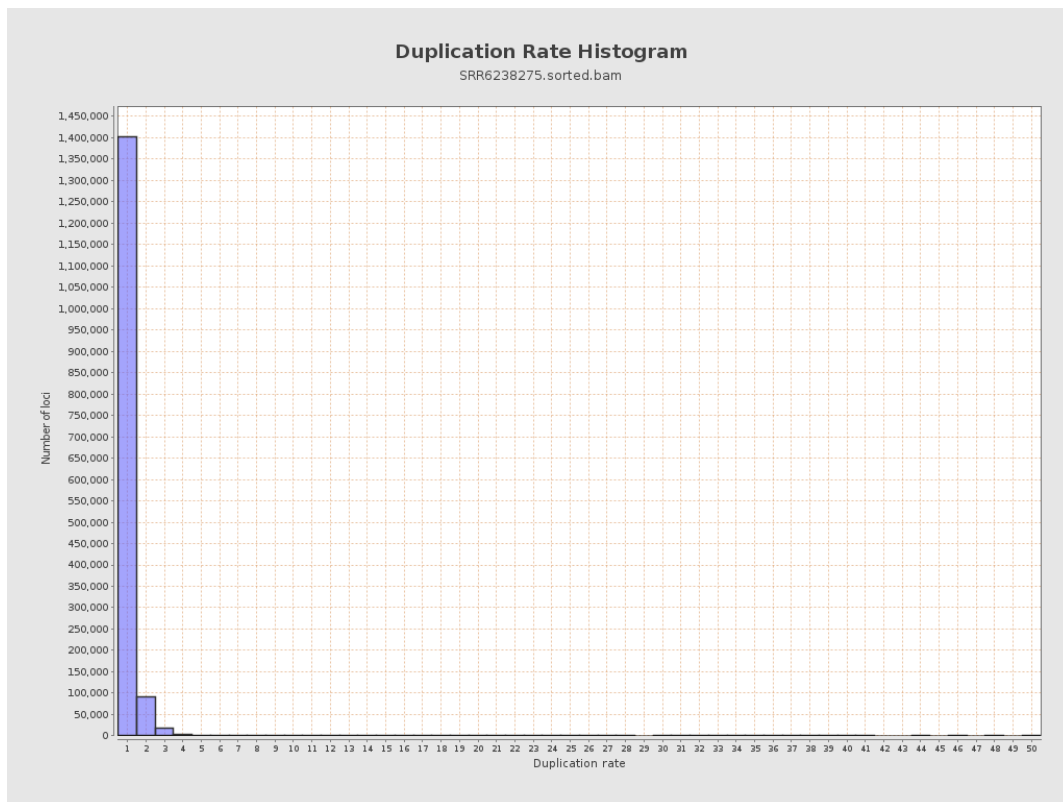
5. Results : Coverage Histogram (0-50X)



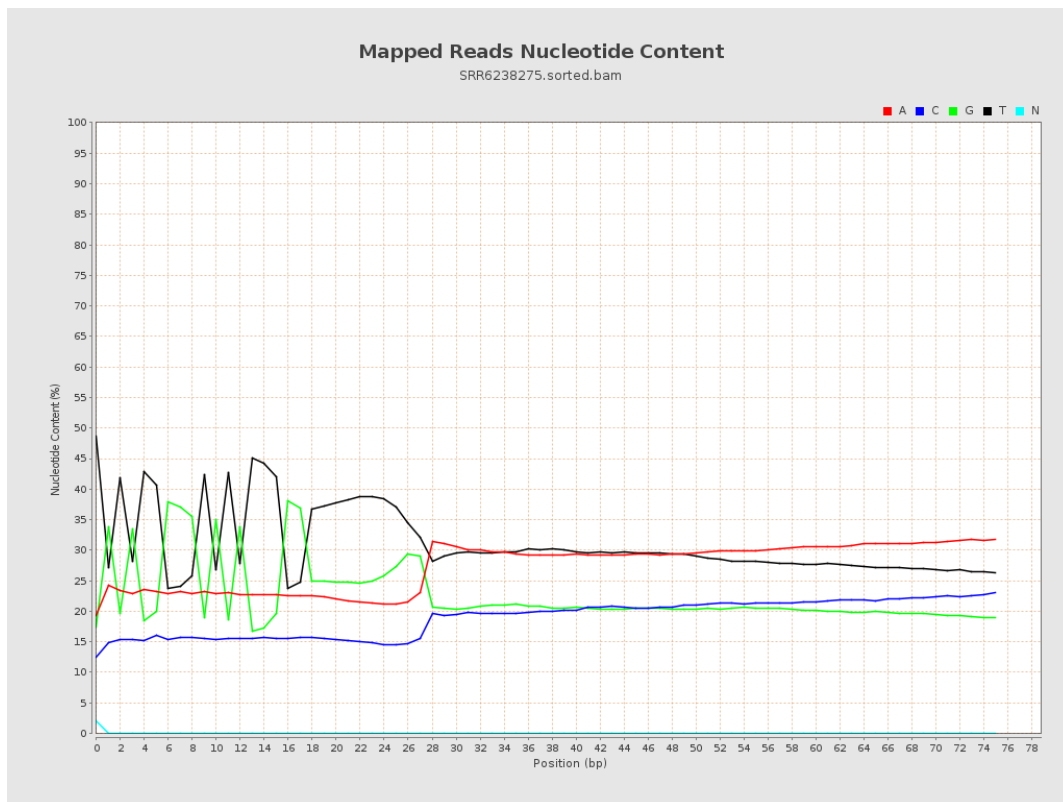
6. Results : Genome Fraction Coverage



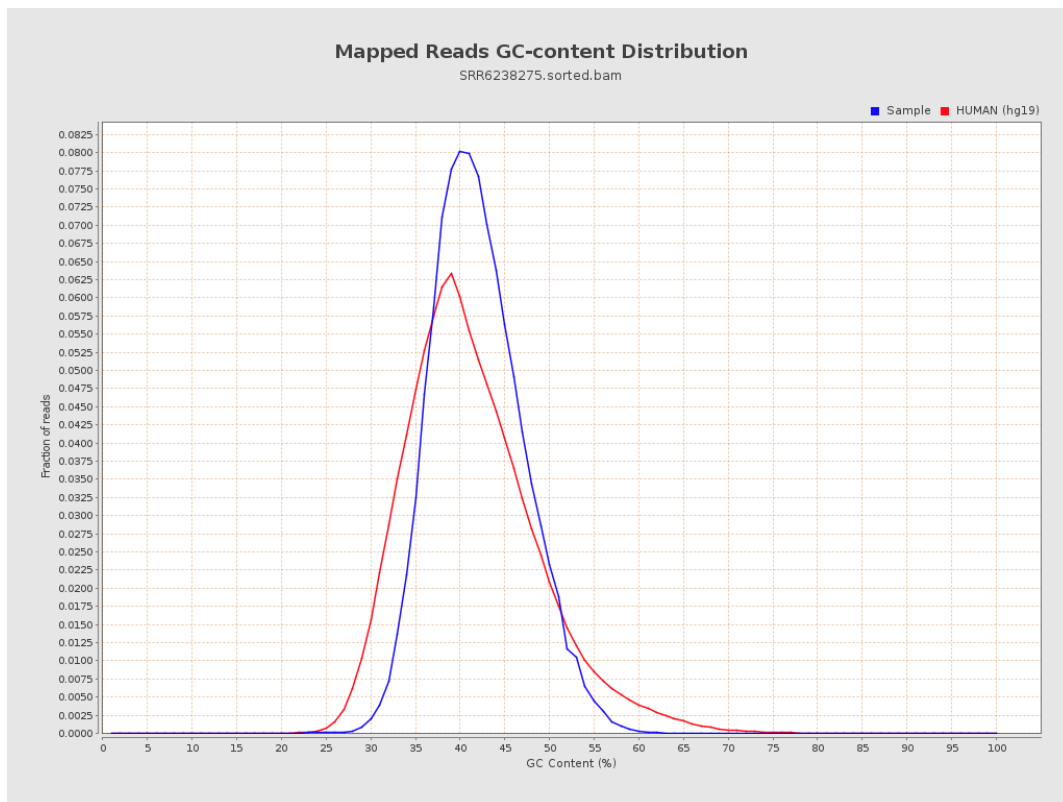
7. Results : Duplication Rate Histogram



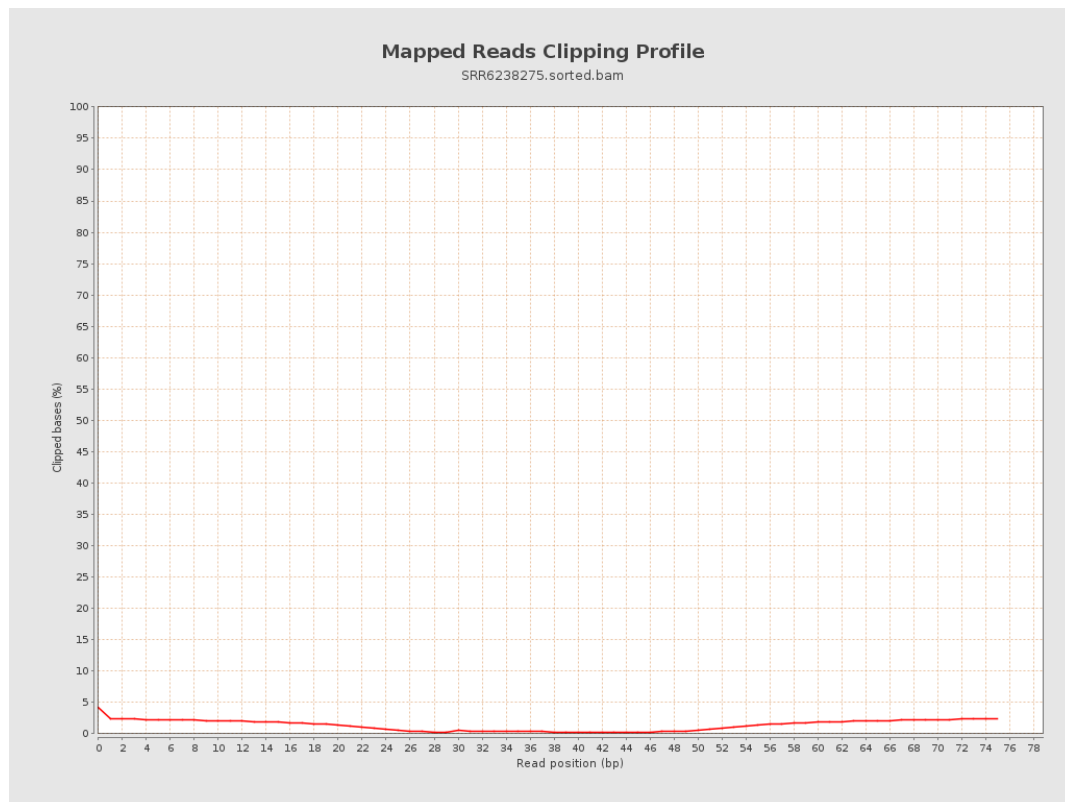
8. Results : Mapped Reads Nucleotide Content



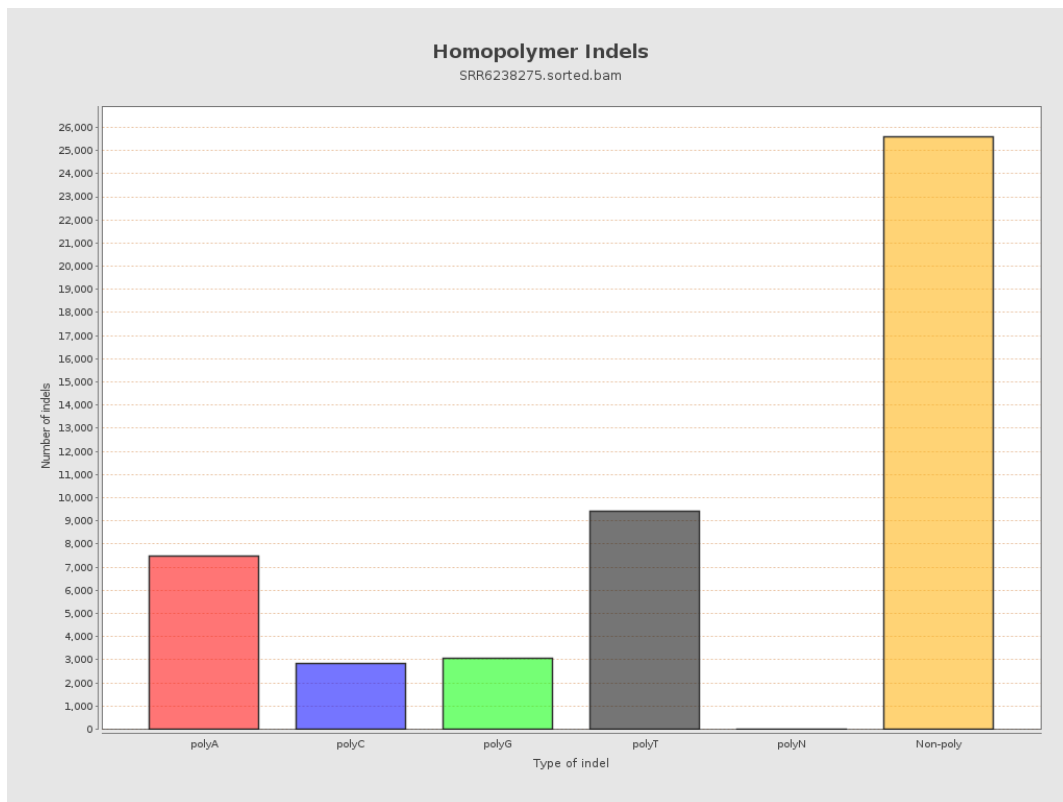
9. Results : Mapped Reads GC-content Distribution



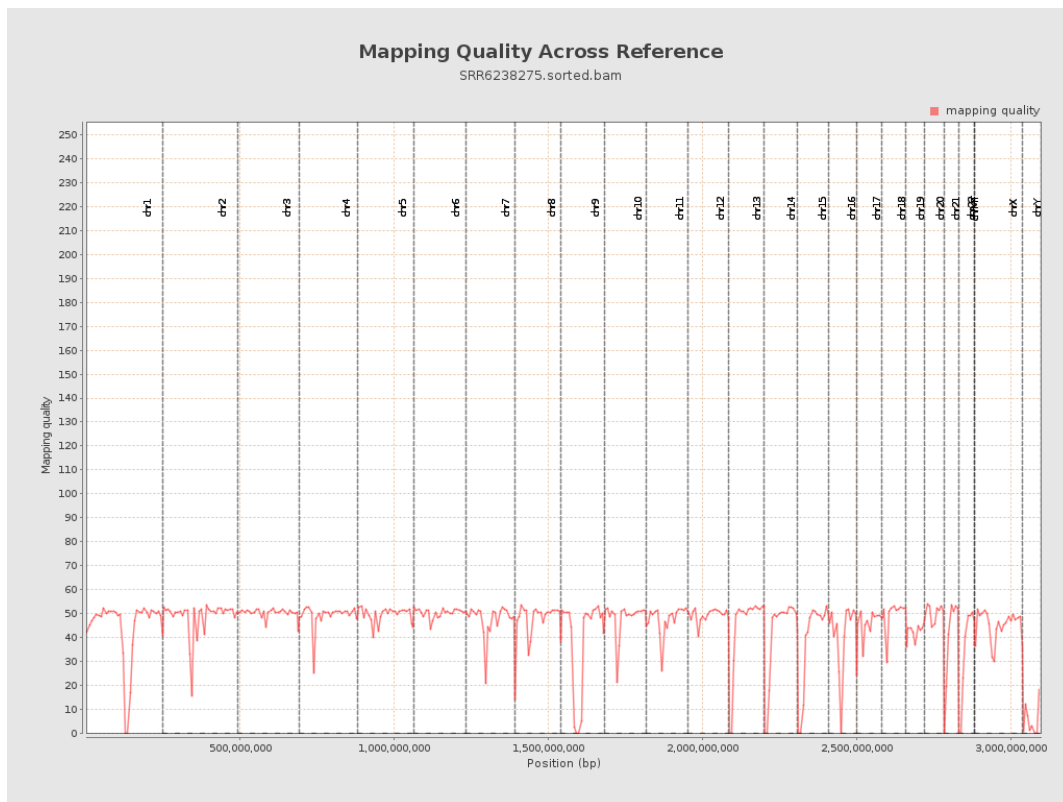
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

