

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 23:17:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238629.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_SRR6238629 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238629.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 23:17:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238629.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,473,964
Mapped reads	1,325,703 / 89.94%
Unmapped reads	148,261 / 10.06%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,074 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	293,537 / 19.91%
Duplication rate	17.86%
Clipped reads	901,556 / 61.17%

2.2. ACGT Content

Number/percentage of A's	19,451,875 / 24.25%
Number/percentage of C's	13,774,070 / 17.17%
Number/percentage of T's	27,282,884 / 34.01%
Number/percentage of G's	19,717,014 / 24.58%
Number/percentage of N's	3,858 / 0%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0259

Standard Deviation	0.366
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2.4. Mapping Quality

Mean Mapping Quality	38.63
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2.5. Mismatches and indels

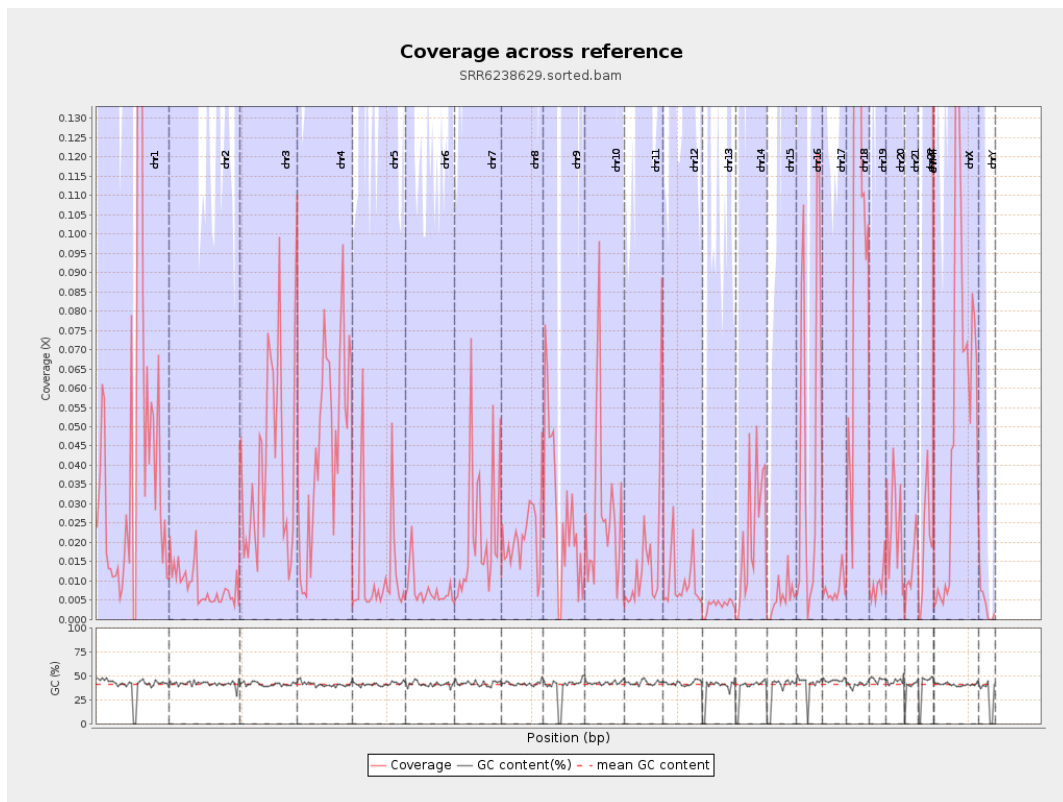
General error rate	0.56%
Mismatches	443,171
Insertions	4,742
Mapped reads with at least one insertion	0.35%
Deletions	22,213
Mapped reads with at least one deletion	1.66%
Homopolymer indels	42.2%

2.6. Chromosome stats

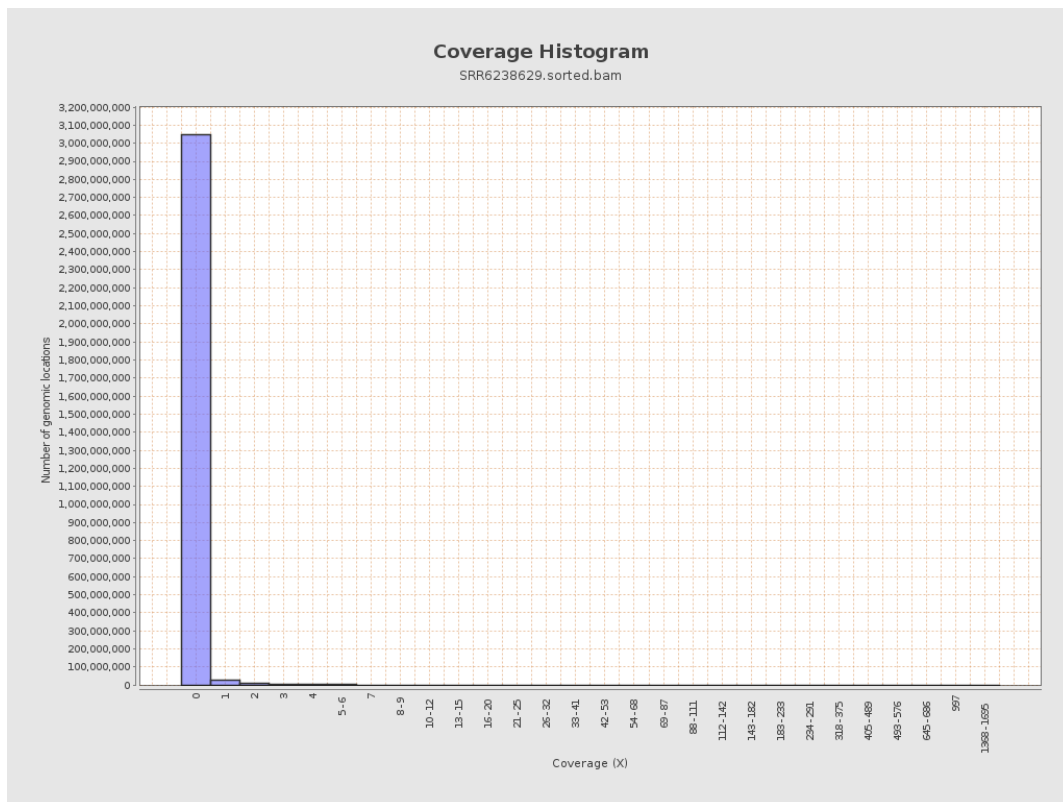
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	10867957	0.0436	0.4072
chr2	243199373	2138906	0.0088	0.7449
chr3	198022430	7952051	0.0402	0.3186
chr4	191154276	8593730	0.045	0.3347
chr5	180915260	2311967	0.0128	0.1797
chr6	171115067	1287692	0.0075	0.2747
chr7	159138663	3506429	0.022	0.2848

chr8	146364022	3168491	0.0216	0.2588
chr9	141213431	3938886	0.0279	0.3049
chr10	135534747	3608492	0.0266	0.2737
chr11	135006516	2287156	0.0169	0.2073
chr12	133851895	1336443	0.01	0.1696
chr13	115169878	409714	0.0036	0.1735
chr14	107349540	2405965	0.0224	0.2667
chr15	102531392	590220	0.0058	0.1816
chr16	90354753	4456845	0.0493	0.3855
chr17	81195210	624588	0.0077	0.1295
chr18	78077248	8452685	0.1083	0.8631
chr19	59128983	547086	0.0093	0.196
chr20	63025520	1523070	0.0242	0.2504
chr21	48129895	648297	0.0135	0.1922
chr22	51304566	966738	0.0188	0.217
chrMT	16571	41509	2.5049	3.0039
chrX	155270560	8372079	0.0539	0.377
chrY	59373566	230463	0.0039	0.1383

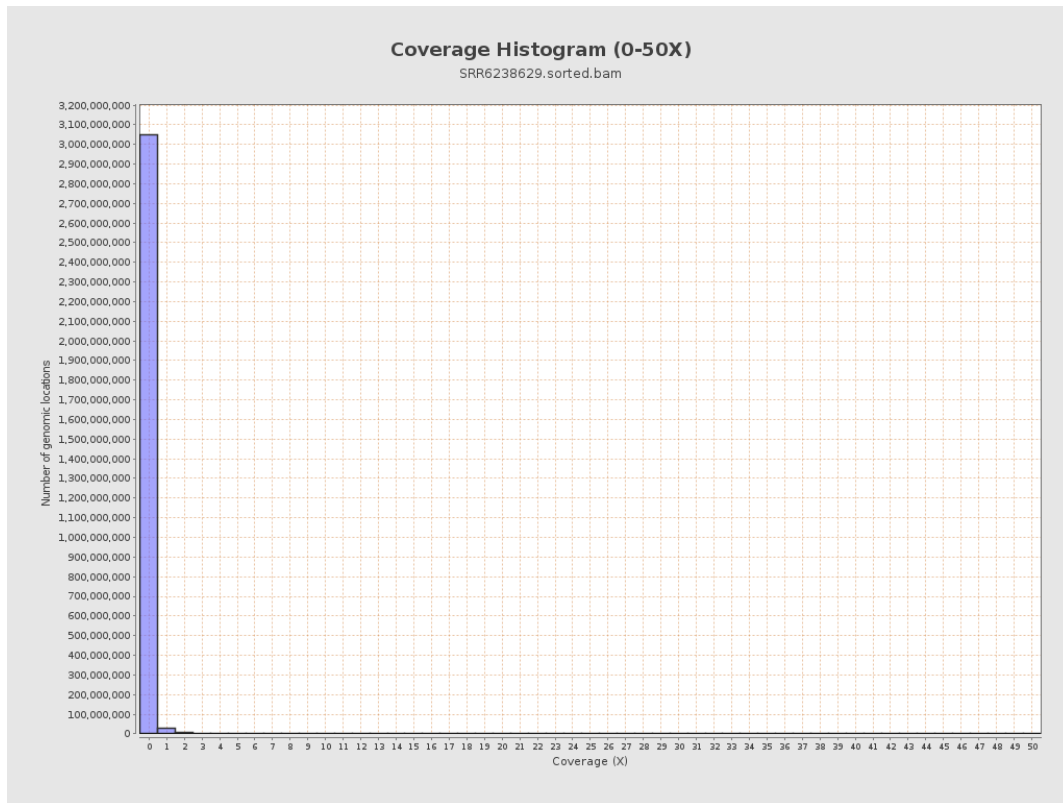
3. Results : Coverage across reference



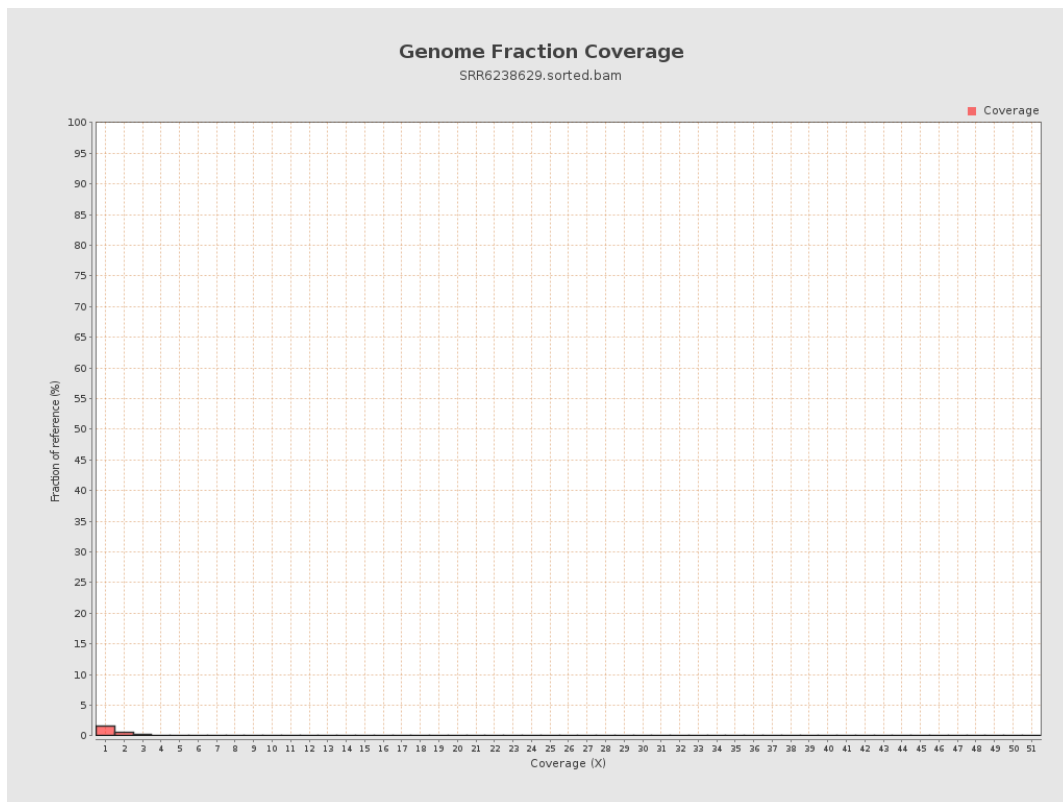
4. Results : Coverage Histogram



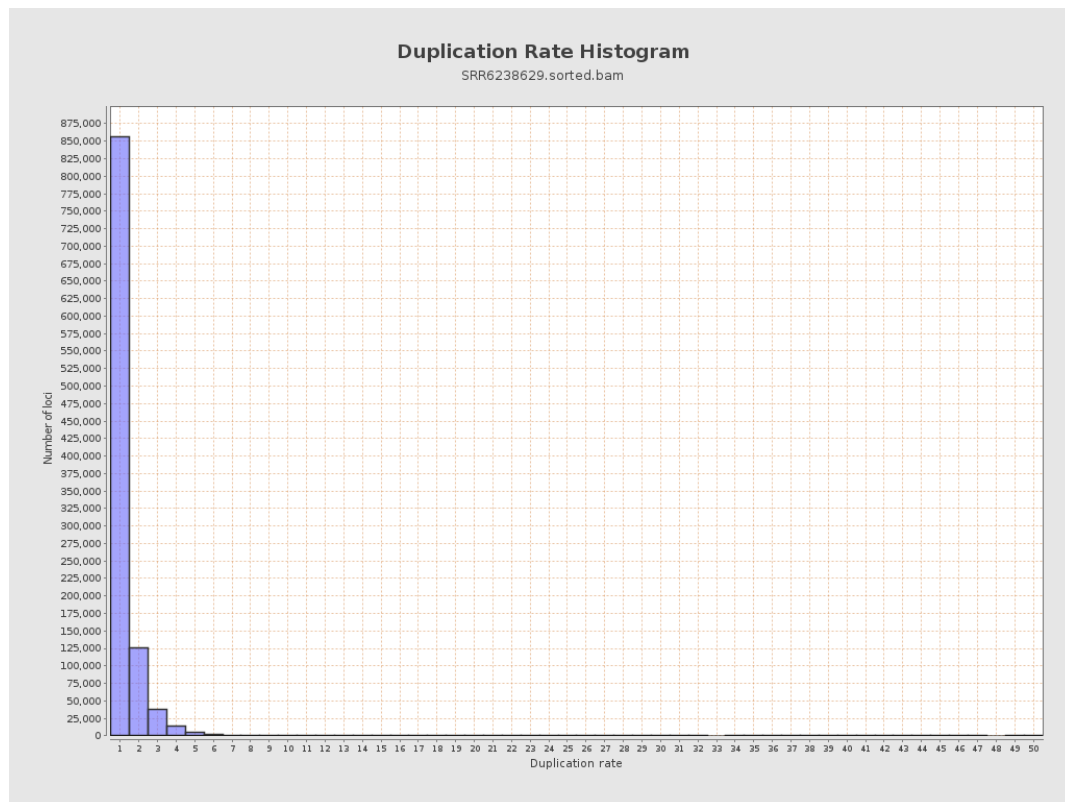
5. Results : Coverage Histogram (0-50X)



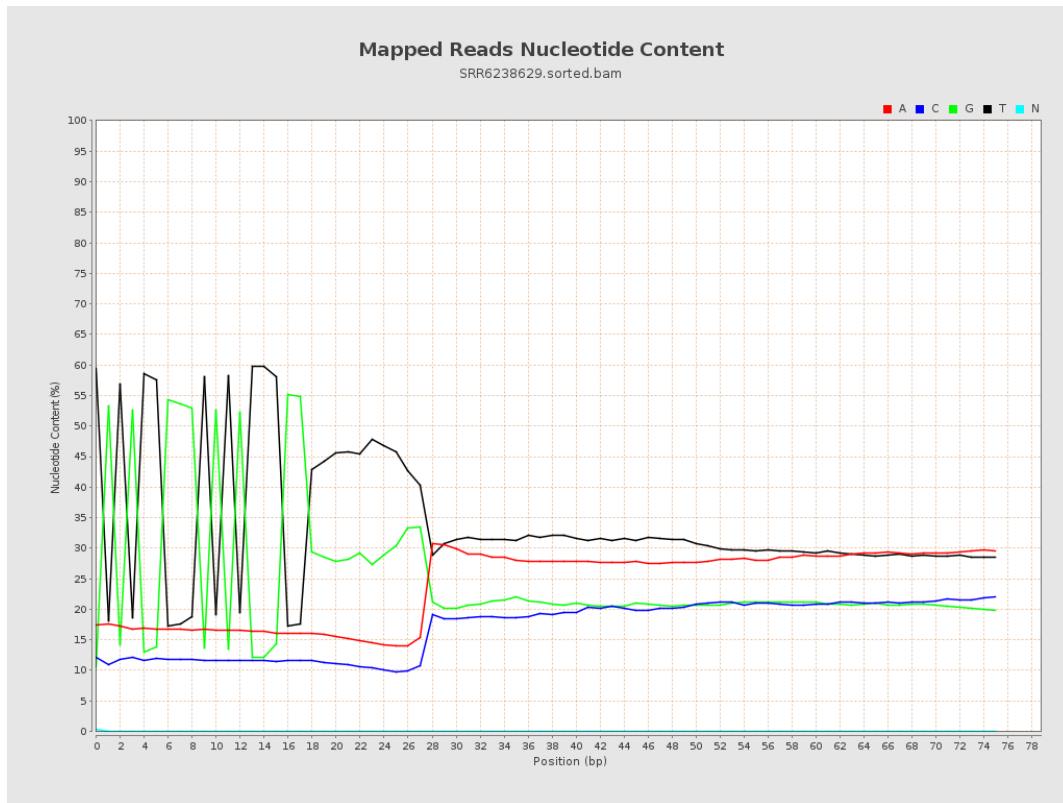
6. Results : Genome Fraction Coverage



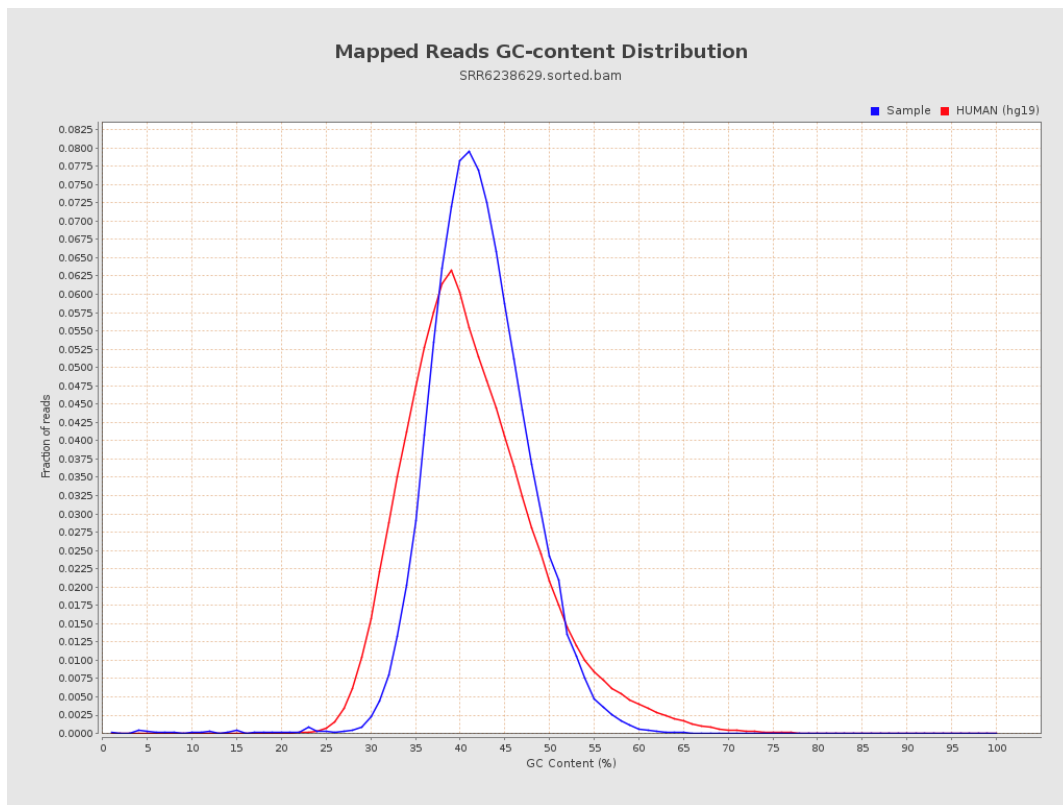
7. Results : Duplication Rate Histogram



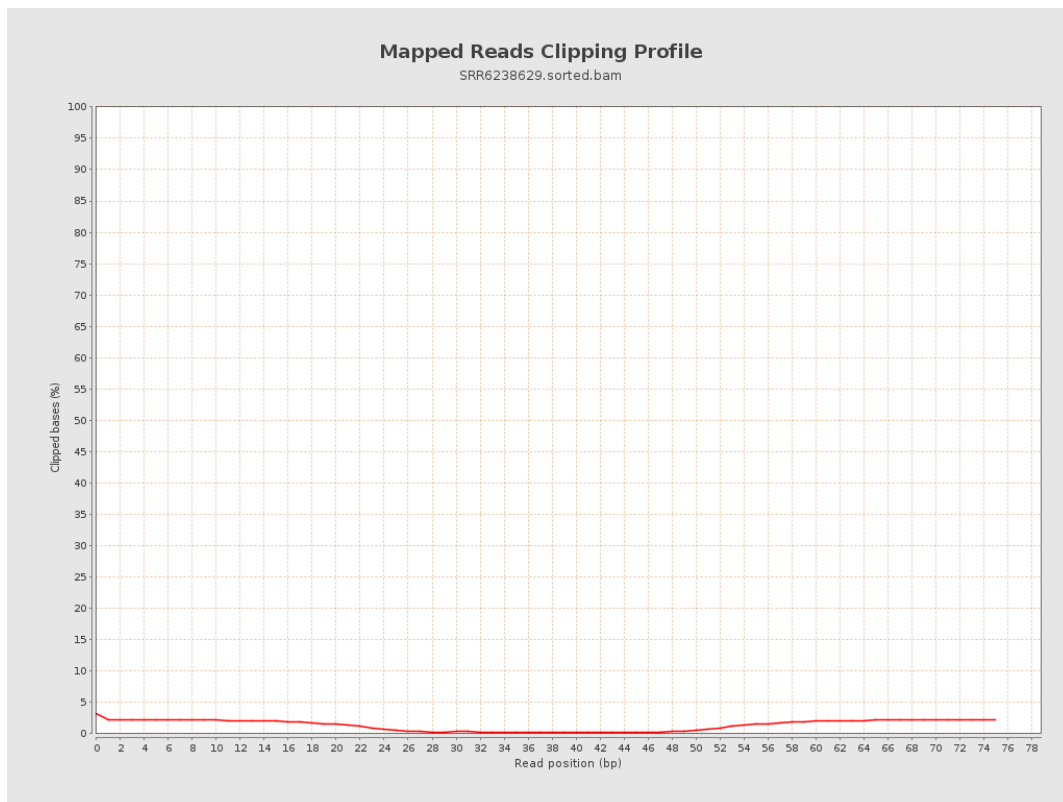
8. Results : Mapped Reads Nucleotide Content



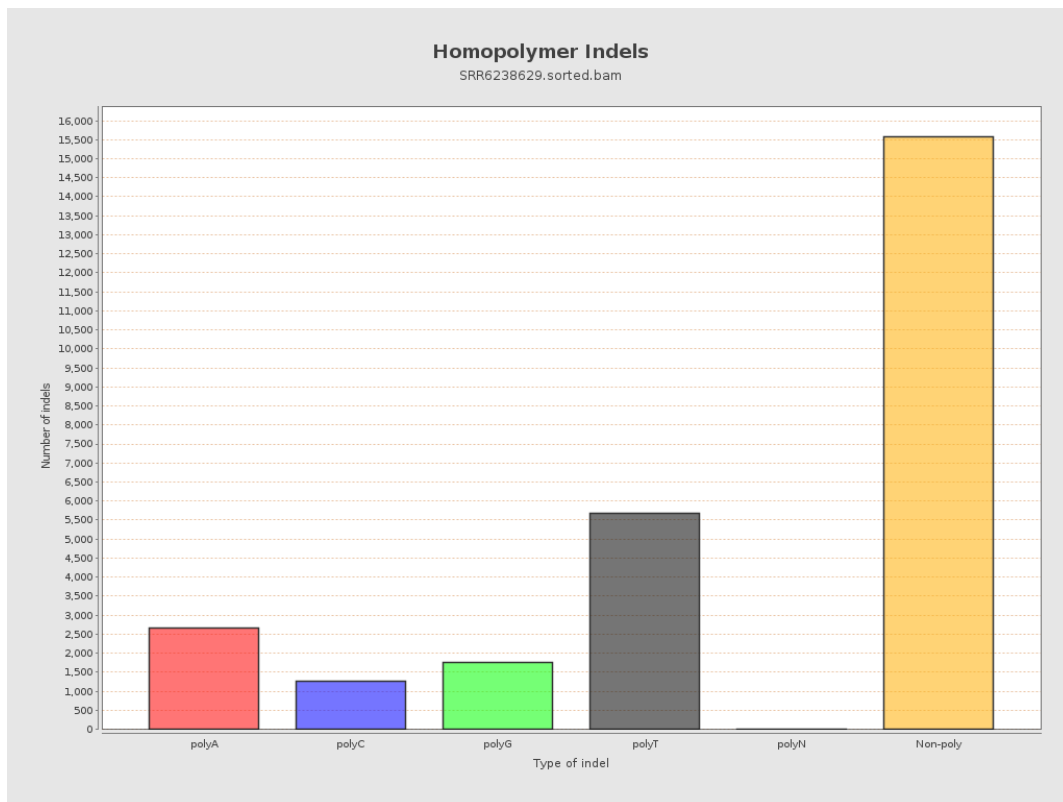
9. Results : Mapped Reads GC-content Distribution



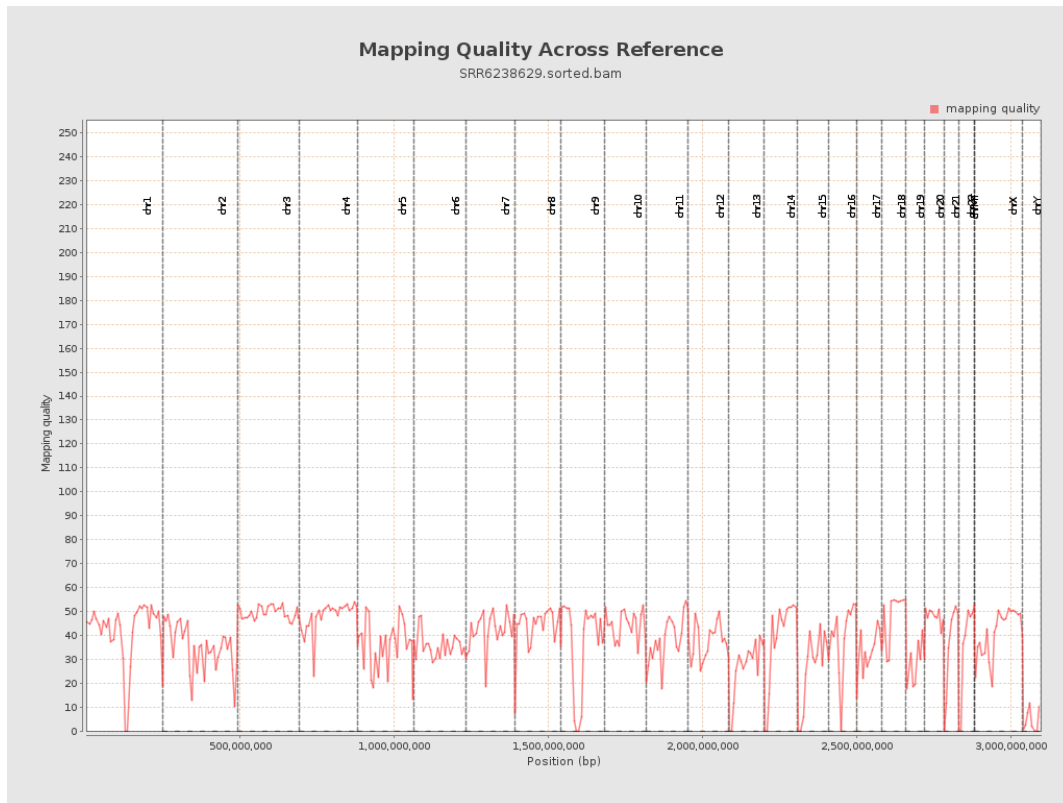
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

