

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 15:13:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238297.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_SRR6238297 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238297.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 15:13:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238297.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,316,405
Mapped reads	1,949,423 / 84.16%
Unmapped reads	366,982 / 15.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,750 / 1.15%
Read min/max/mean length	30 / 76 / 76.4
Duplicated reads (estimated)	137,388 / 5.93%
Duplication rate	5.65%
Clipped reads	1,158,179 / 50%

2.2. ACGT Content

Number/percentage of A's	33,756,627 / 27.22%
Number/percentage of C's	23,539,951 / 18.98%
Number/percentage of T's	38,420,724 / 30.99%
Number/percentage of G's	28,244,332 / 22.78%
Number/percentage of N's	31,187 / 0.03%
GC Percentage	41.76%

2.3. Coverage

Mean	0.0401

Standard Deviation	0.3758
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2.4. Mapping Quality

Mean Mapping Quality	44.92
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2.5. Mismatches and indels

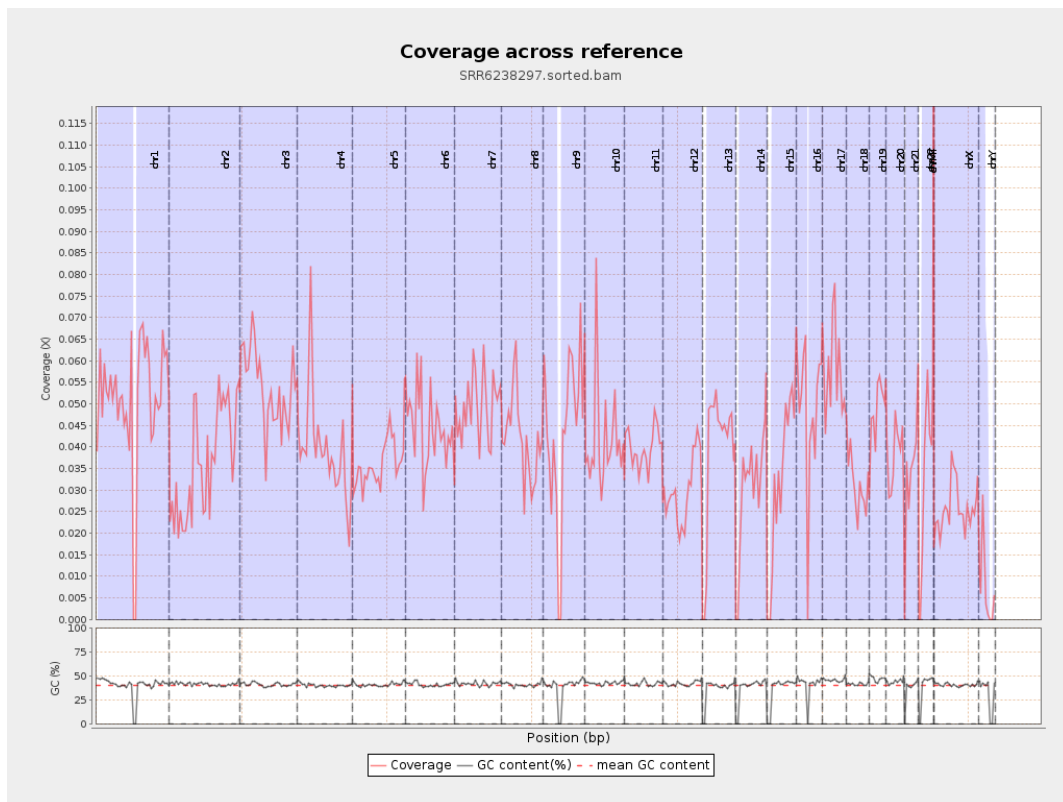
General error rate	0.95%
Mismatches	1,155,607
Insertions	10,123
Mapped reads with at least one insertion	0.52%
Deletions	47,236
Mapped reads with at least one deletion	2.39%
Homopolymer indels	43.28%

2.6. Chromosome stats

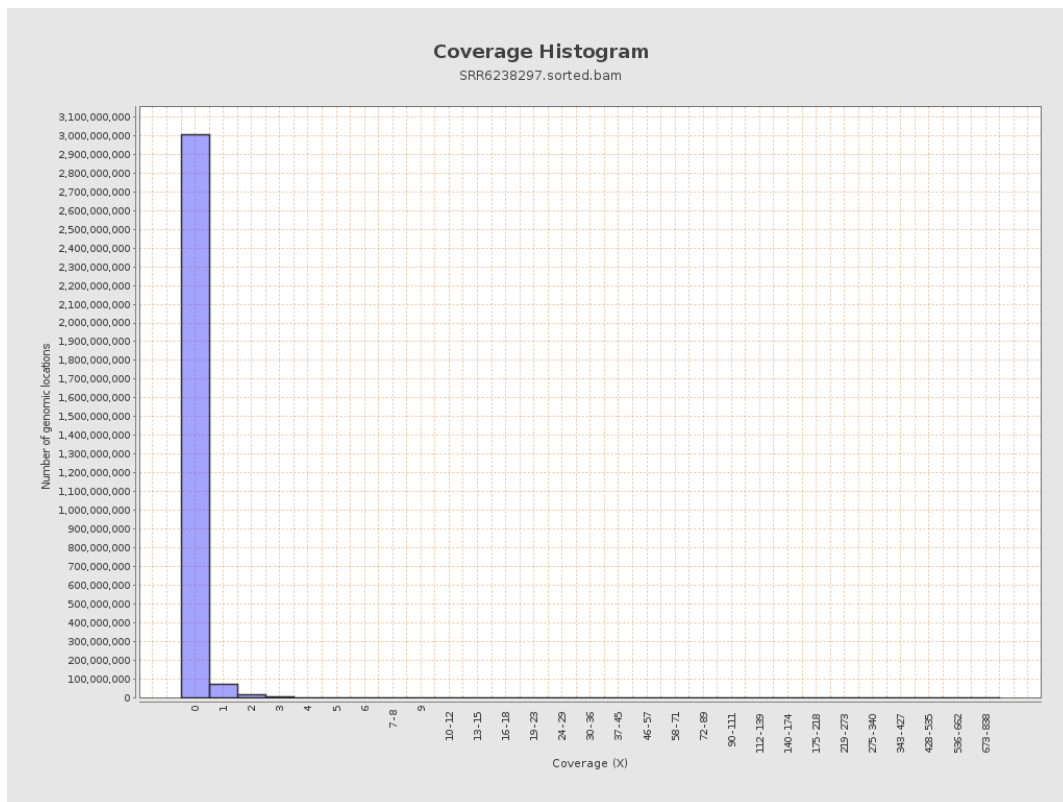
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	12663230	0.0508	0.6416
chr2	243199373	8802330	0.0362	0.4559
chr3	198022430	10626052	0.0537	0.2996
chr4	191154276	7456260	0.039	0.3151
chr5	180915260	6537323	0.0361	0.2435
chr6	171115067	7634946	0.0446	0.3266
chr7	159138663	7852998	0.0493	0.397

chr8	146364022	6095973	0.0416	0.5651
chr9	141213431	6007162	0.0425	0.3142
chr10	135534747	5544910	0.0409	0.4463
chr11	135006516	5335284	0.0395	0.2902
chr12	133851895	3996972	0.0299	0.2237
chr13	115169878	4448036	0.0386	0.2541
chr14	107349540	3234323	0.0301	0.2415
chr15	102531392	3368754	0.0329	0.2484
chr16	90354753	4386488	0.0485	0.2998
chr17	81195210	4689700	0.0578	0.3208
chr18	78077248	2463281	0.0315	0.4371
chr19	59128983	2888918	0.0489	0.4797
chr20	63025520	2391748	0.0379	0.261
chr21	48129895	1650920	0.0343	0.2838
chr22	51304566	1631964	0.0318	0.2268
chrMT	16571	2830	0.1708	0.526
chrX	155270560	3961821	0.0255	0.2164
chrY	59373566	400550	0.0067	0.2611

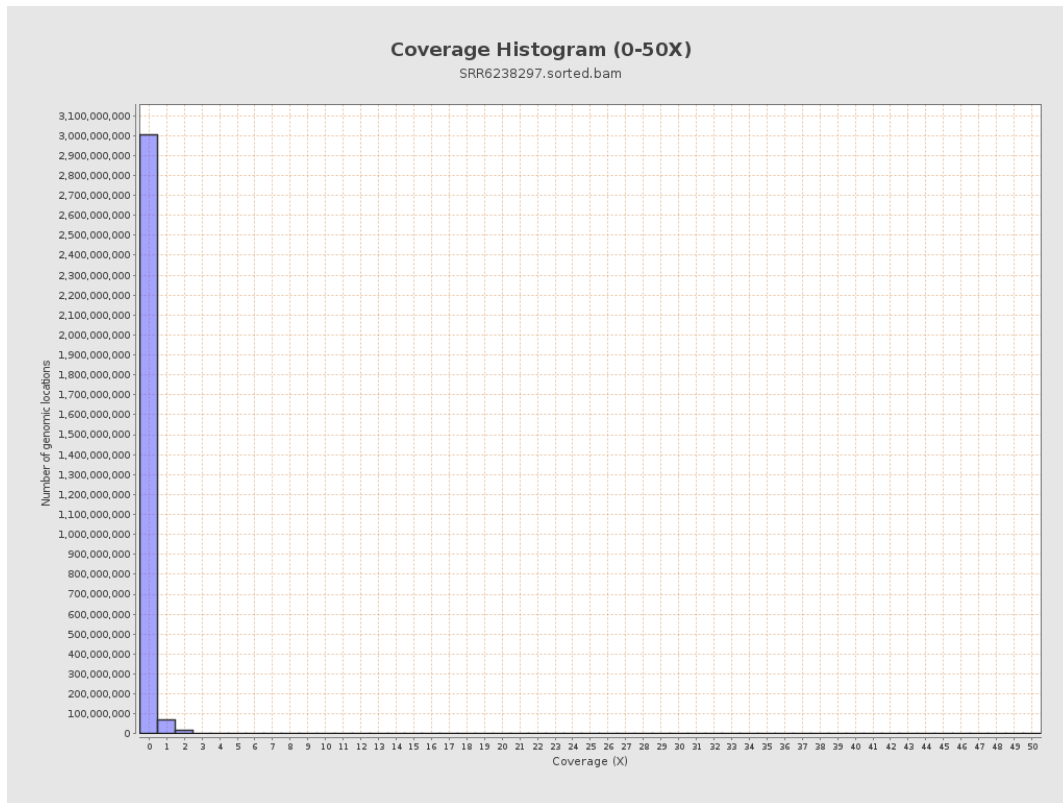
3. Results : Coverage across reference



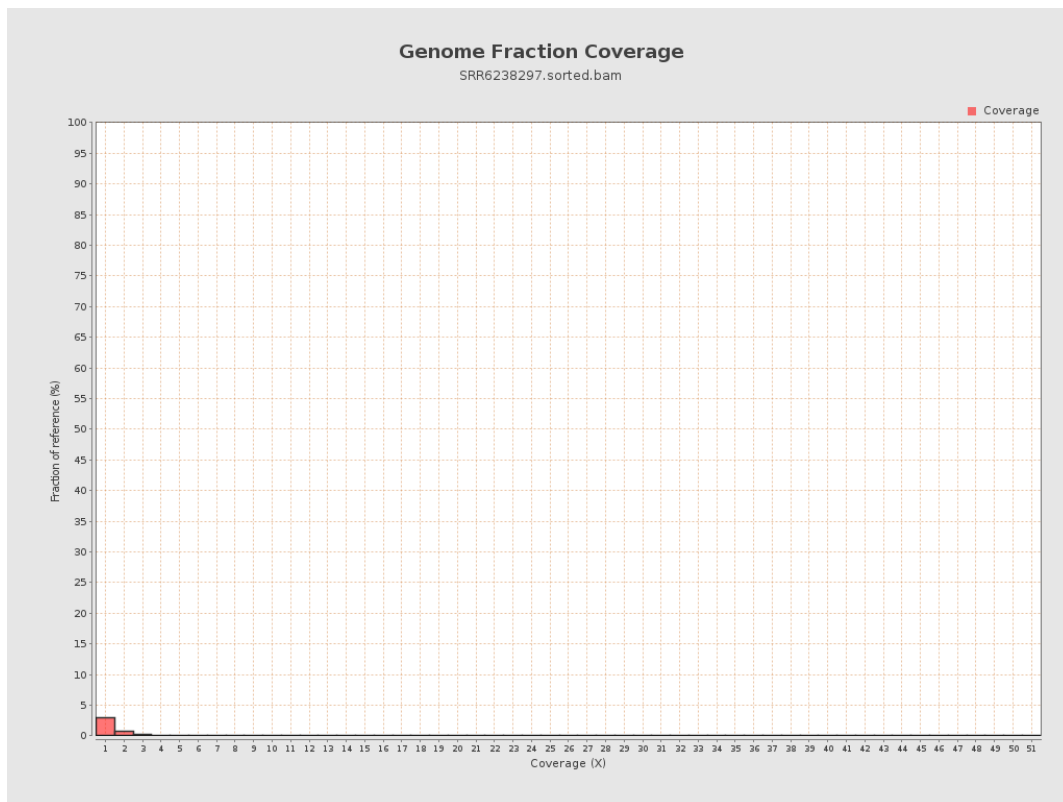
4. Results : Coverage Histogram



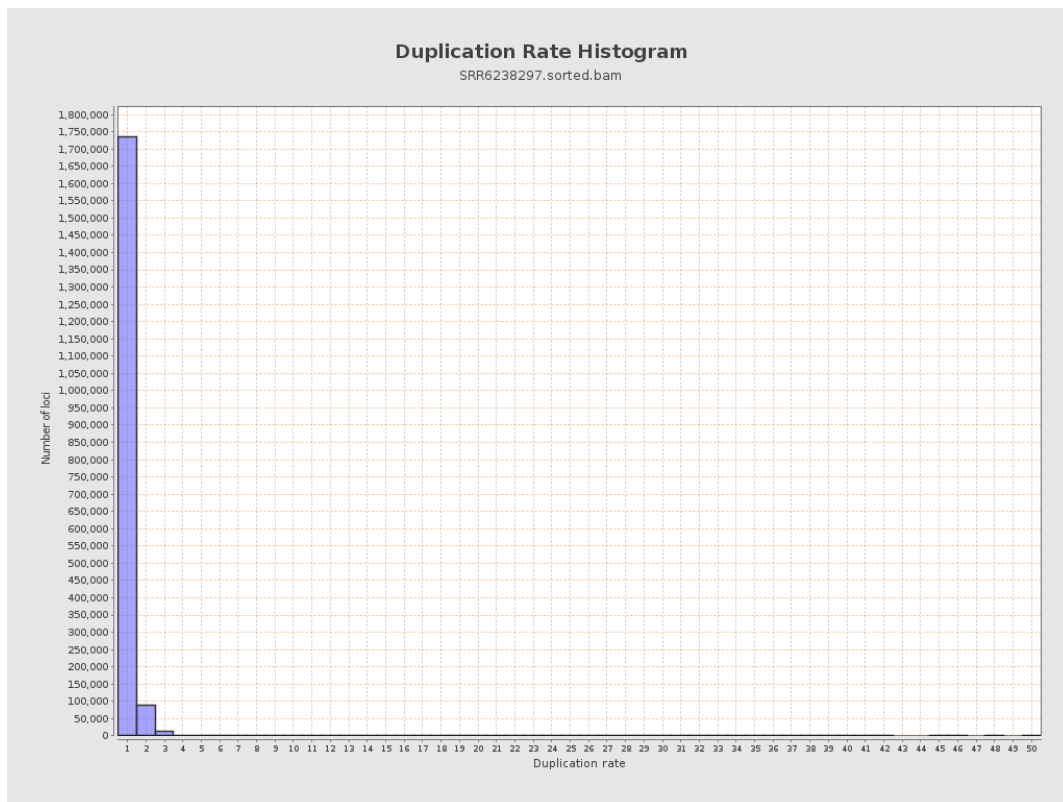
5. Results : Coverage Histogram (0-50X)



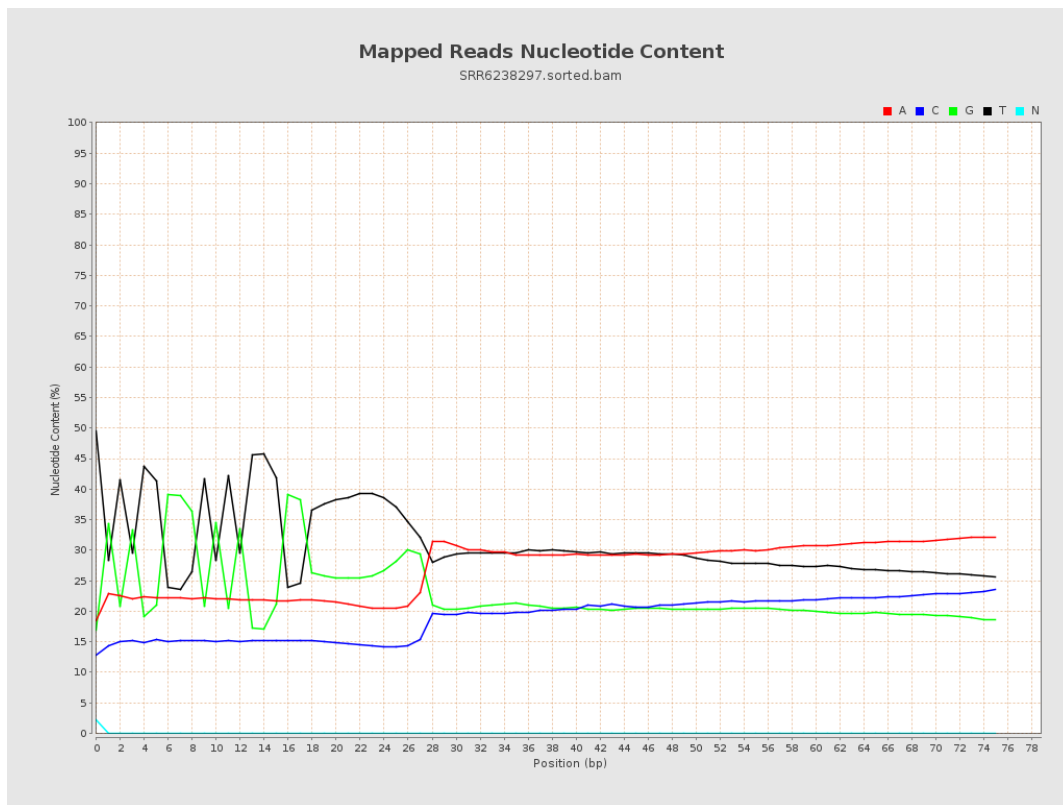
6. Results : Genome Fraction Coverage



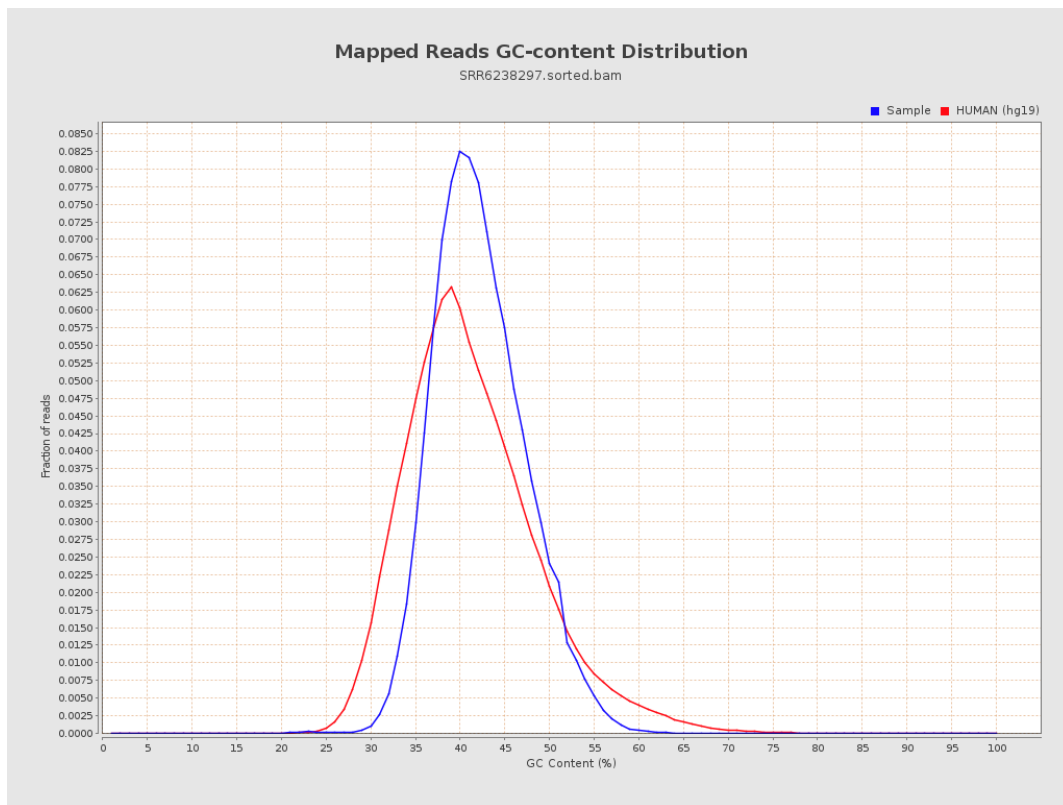
7. Results : Duplication Rate Histogram



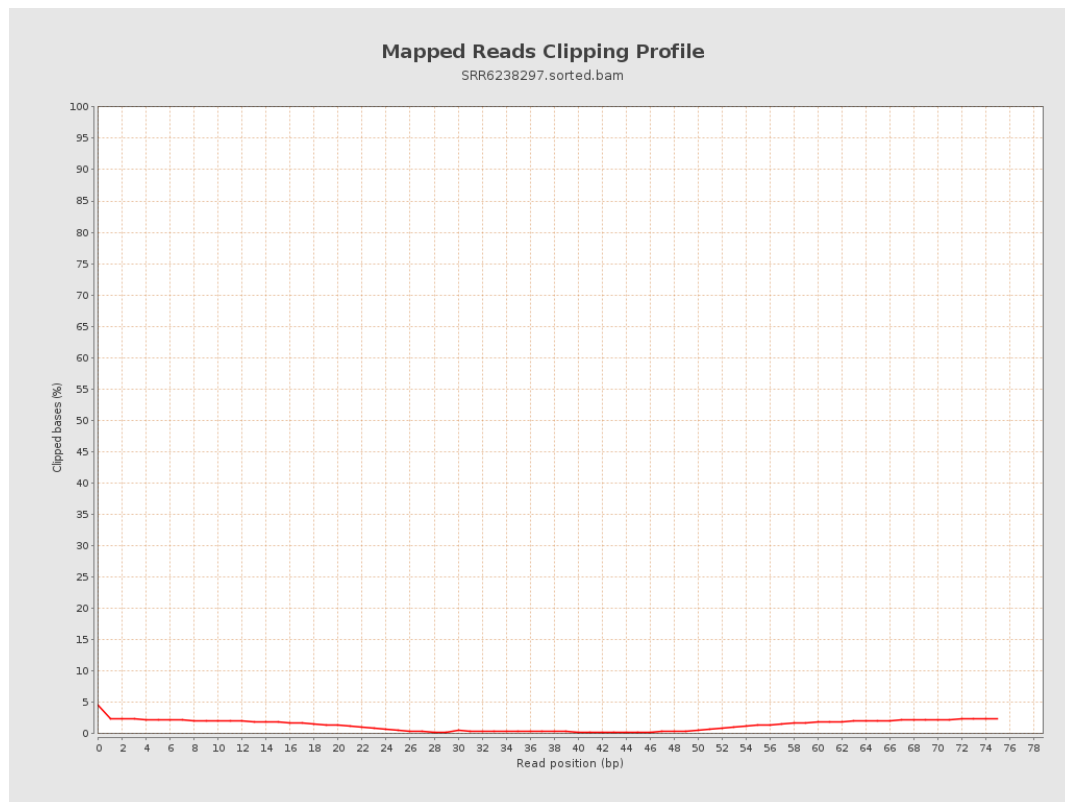
8. Results : Mapped Reads Nucleotide Content



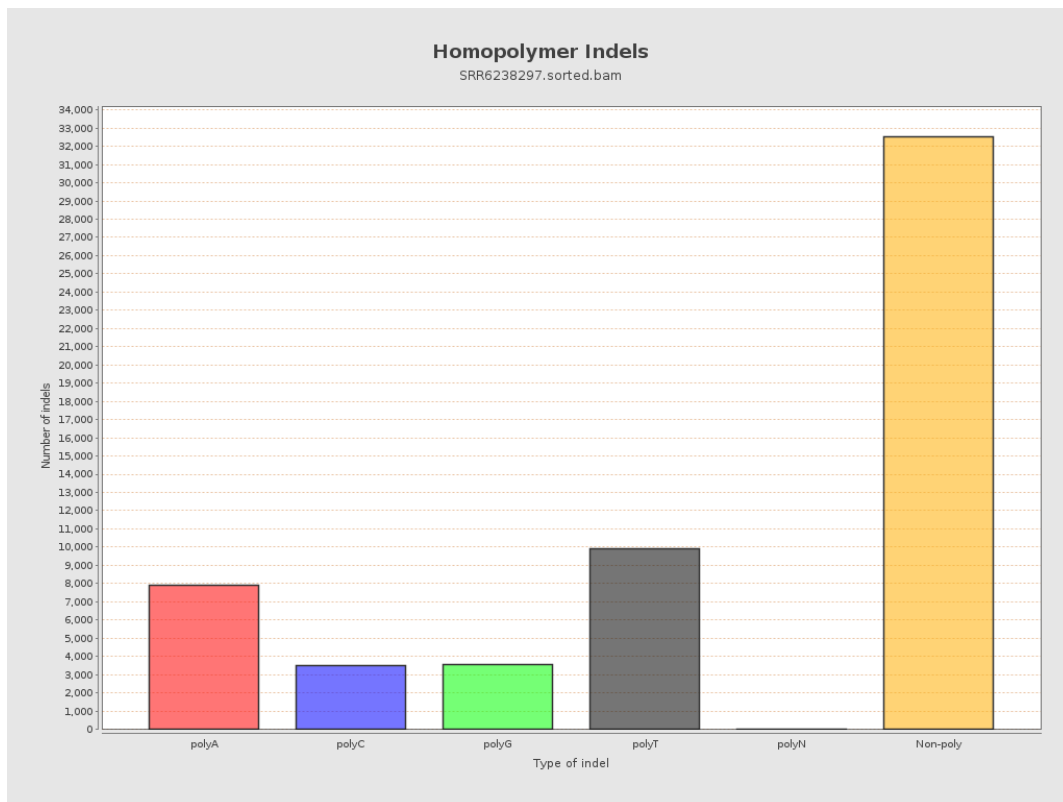
9. Results : Mapped Reads GC-content Distribution



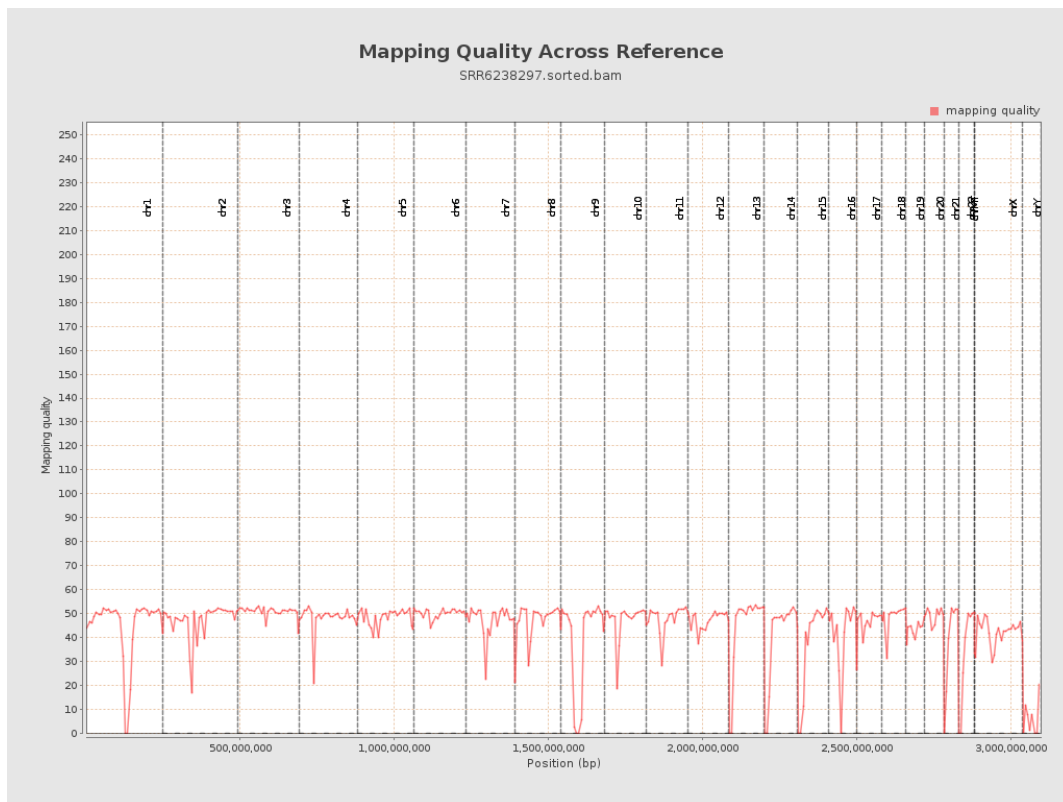
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

